Table 3 (expanded). **Bioti**
Expression systems were (
Shown below are the numb

Expression System	Protein
P35 mouse brain	41
Primary neurons	41
TauKO mouse HC	41
P35 mouse brain	AAK1
Primary neurons	AAK1
TauKO mouse HC	AAK1
TauKO mouse HC	ABI2
TauKO mouse HC	ACAP2
TauKO mouse HC	ACTA
TauKO mouse HC	ACTB
Primary neurons	ACTC
TauKO mouse HC	ACTC
P35 mouse brain	AFF2
TauKO mouse HC	AGFG1
TauKO mouse HC	AHI1
TauKO mouse HC	AINX
Primary neurons	ALBU
P35 mouse brain	ALDOA
Primary neurons	ALDOA
TauKO mouse HC	ALDOA
P35 mouse brain	AMPH
P35 mouse brain	ANK2
Primary neurons	ANK2
TauKO mouse HC	ANK2
P35 mouse brain	AP180
Primary neurons	AP180
TauKO mouse HC	AP180
TauKO mouse HC	APC
P35 mouse brain	ARBK1
Primary neurons	ARBK1
TauKO mouse HC	ARBK1
TauKO mouse HC	ARP3
TauKO mouse HC	ARP3B
TauKO mouse HC	ARP5L
Primary neurons	ARPC2
P35 mouse brain	ASAP1
TauKO mouse HC	ASAP1
TauKO mouse HC	ASAP2
P35 mouse brain	AT1B3
Primary neurons	ATX2L
P35 mouse brain	AUXI

TauKO mouse HC	AUXI
TauKO mouse HC	BAIP2
P35 mouse brain	BASP1
TauKO mouse HC	BASP1
P35 mouse brain	BIN1
Primary neurons	BIN1
TauKO mouse HC	BIN1
P35 mouse brain	BSN
TauKO mouse HC	BSN
P35 mouse brain	CA123
Primary neurons	CA123
TauKO mouse HC	CALB2
TauKO mouse HC	CALM
TauKO mouse HC	CAMKV
P35 mouse brain	CAMP3
Primary neurons	CAMP3
TauKO mouse HC	CAMP3
Primary neurons	CAPS1
TauKO mouse HC	CAPS1
TauKO mouse HC	CAPS2
P35 mouse brain	CC124
TauKO mouse HC	CC171
TauKO mouse HC	CDV3
Primary neurons	CE170
TauKO mouse HC	CE170
P35 mouse brain	CEND
TauKO mouse HC	CEND
TauKO mouse HC	CETN2
TauKO mouse HC	CHM4B
TauKO mouse HC	CKAP5
Primary neurons	CLAP2
TauKO mouse HC	CLAP2
TauKO mouse HC	CLH1
TauKO mouse HC	CLIP2
TauKO mouse HC	CNKR2
P35 mouse brain	CPLX1
Primary neurons	CPLX1
TauKO mouse HC	CPLX1
P35 mouse brain	CPLX2
TauKO mouse HC	CPLX2
Primary neurons	CRKL
TauKO mouse HC	CRKL
TauKO mouse HC	CRTC1
TauKO mouse HC	CSDE1
P35 mouse brain	CSKI1
TauKO mouse HC	CYFP2
TauKO mouse HC	CYH1
TauKO mouse HC	CYH2

TauKO mouse HC	CYH3
TauKO mouse HC	CZIB
TauKO mouse HC	DBNL
P35 mouse brain	DC1L1
TauKO mouse HC	DCE2
P35 mouse brain	DCLK1
TauKO mouse HC	DCLK1
TauKO mouse HC	DCLK2
P35 mouse brain	DCTN2
Primary neurons	DCTN2
TauKO mouse HC	DCTN2
TauKO mouse HC	DEMA
P35 mouse brain	DLGP3
TauKO mouse HC	DLGP3
P35 mouse brain	DNJB1
Primary neurons	DNJB1
TauKO mouse HC	DNJB1
TauKO mouse HC	DNM1L
P35 mouse brain	DPYL2
Primary neurons	DPYL2
TauKO mouse HC	DPYL2
TauKO mouse HC	DPYL4
TauKO mouse HC	DRG2
P35 mouse brain	DYN1
TauKO mouse HC	DYN1
P35 mouse brain	E41L1
Primary neurons	E41L1
TauKO mouse HC	E41L1
Primary neurons	E41L2
TauKO mouse HC	E41L2
P35 mouse brain	E41L3
TauKO mouse HC	E41L3
Primary neurons	EF1A1
TauKO mouse HC	EF1A2
TauKO mouse HC	EF2
Primary neurons	ELOB
TauKO mouse HC	ELOB
TauKO mouse HC	ENSA
TauKO mouse HC	F110B
Primary neurons	G3BP1
P35 mouse brain	G3P
Primary neurons	G3P
TauKO mouse HC	G3P
TauKO mouse HC	GBRA1
P35 mouse brain	GDIR1
Primary neurons	GDIR1
TauKO mouse HC	GDIR1
P35 mouse brain	GLNA

Primary neurons	GLSK
P35 mouse brain	GP158
Primary neurons	GP158
TauKO mouse HC	GP158
P35 mouse brain	GRIN1
TauKO mouse HC	GRIN1
TauKO mouse HC	GSDME
TauKO mouse HC	GSK3A
TauKO mouse HC	GSK3B
Primary neurons	H2A1D
Primary neurons	H2B1B
Primary neurons	H2B1C
Primary neurons	H2B1L
P35 mouse brain	HAP28
TauKO mouse HC	HAP28
Primary neurons	HINT1
P35 mouse brain	HS71A
Primary neurons	HS90A
TauKO mouse HC	HS90A
Primary neurons	HS90B
TauKO mouse HC	HS90B
Primary neurons	HSP7C
Primary neurons	HXK1
P35 mouse brain	IF4B
TauKO mouse HC	IF4B
TauKO mouse HC	IF4G1
P35 mouse brain	IF4G3
Primary neurons	IF4G3
TauKO mouse HC	IF4G3
Primary neurons	IF4H
TauKO mouse HC	IQEC3
TauKO mouse HC	JUPI1
TauKO mouse HC	K1107
Primary neurons	KAP2
TauKO mouse HC	KAP2
TauKO mouse HC	KAPCA
TauKO mouse HC	KC1E
P35 mouse brain	KCC2A
TauKO mouse HC	KCC2A
TauKO mouse HC	KCC2B
P35 mouse brain	KCC2D
Primary neurons	KCC2D
TauKO mouse HC	KCC2D
P35 mouse brain	KI21A
TauKO mouse HC	KI21A
Primary neurons	KIF5C
TauKO mouse HC	KIF5C
P35 mouse brain	KPCB

TauKO mouse HC	KPCB
TauKO mouse HC	KPCG
P35 mouse brain	KT3K
TauKO mouse HC	KT3K
P35 mouse brain	LASP1
Primary neurons	LASP1
TauKO mouse HC	LASP1
TauKO mouse HC	LNEBL
TauKO mouse HC	LUZP1
Primary neurons	M3K10
TauKO mouse HC	M4K4
TauKO mouse HC	MA7D2
P35 mouse brain	MAP1A
Primary neurons	MAP1A
TauKO mouse HC	MAP1A
P35 mouse brain	MAP1B
Primary neurons	MAP1B
TauKO mouse HC	MAP1B
P35 mouse brain	MAP4
Primary neurons	MAP4
TauKO mouse HC	MAP4
P35 mouse brain	MAP6
Primary neurons	MAP6
TauKO mouse HC	MAP6
P35 mouse brain	MARE1
Primary neurons	MARE1
TauKO mouse HC	MARE1
P35 mouse brain	MARE2
P35 mouse brain	MARE3
TauKO mouse HC	MARE3
P35 mouse brain	MCCA
Primary neurons	MCCA
TauKO mouse HC	MCCA
Primary neurons	MDHM
TauKO mouse HC	MINK1
P35 mouse brain	MK12
P35 mouse brain	MTAP2
Primary neurons	MTAP2
TauKO mouse HC	MTAP2
TauKO mouse HC	MYO5A
Primary neurons	NACA
Primary neurons	NACAM
TauKO mouse HC	NACAM
P35 mouse brain	NCAM1
TauKO mouse HC	NECP1
P35 mouse brain	NEUG
TauKO mouse HC	NEUG
Primary neurons	NFAT5

P35 mouse brain	NFM
TauKO mouse HC	NFM
P35 mouse brain	NKTR
Primary neurons	NKTR
TauKO mouse HC	NKTR
Primary neurons	NMT1
P35 mouse brain	NP1L4
Primary neurons	NP1L4
TauKO mouse HC	NP1L4
P35 mouse brain	NSF
Primary neurons	NSF
TauKO mouse HC	NSF
TauKO mouse HC	NSF1C
TauKO mouse HC	OGA
TauKO mouse HC	OXR1
TauKO mouse HC	P33MX
P35 mouse brain	PACS1
TauKO mouse HC	PACS1
P35 mouse brain	PAK2
Primary neurons	PAK2
TauKO mouse HC	PAK2
TauKO mouse HC	PCBP1
P35 mouse brain	PCCA
Primary neurons	PCCA
TauKO mouse HC	PCCA
P35 mouse brain	PCLO
TauKO mouse HC	PCLO
Primary neurons	PEBP1
P35 mouse brain	PFD2
TauKO mouse HC	PFD2
TauKO mouse HC	PGAM1
P35 mouse brain	PI42A
Primary neurons	PI42A
TauKO mouse HC	PI42A
TauKO mouse HC	PI42B
TauKO mouse HC	PI42C
TauKO mouse HC	PLCL2
TauKO mouse HC	PLCX3
P35 mouse brain	PLEC
Primary neurons	PLEC
TauKO mouse HC	PLEC
TauKO mouse HC	PLPR4
TauKO mouse HC	PP1RB
TauKO mouse HC	PRAF3
TauKO mouse HC	PURA2
TauKO mouse HC	PURB
P35 mouse brain	PYC
Primary neurons	PYC

TauKO mouse HC	PYC
TauKO mouse HC	RANG
TauKO mouse HC	RASL1
P35 mouse brain	RBNS5
Primary neurons	RBNS5
TauKO mouse HC	RBNS5
TauKO mouse HC	RGRF1
TauKO mouse HC	RIMKA
TauKO mouse HC	RL24
TauKO mouse HC	RL29
TauKO mouse HC	RN214
TauKO mouse HC	RS20
TauKO mouse HC	RTN1
P35 mouse brain	RTN3
TauKO mouse HC	RTN3
P35 mouse brain	RTN4
Primary neurons	RTN4
TauKO mouse HC	RTN4
TauKO mouse HC	RUFY3
P35 mouse brain	RUVB2
Primary neurons	RUVB2
TauKO mouse HC	S10A6
P35 mouse brain	Sep-05
Primary neurons	Sep-05
TauKO mouse HC	Sep-05
P35 mouse brain	Sep-07
TauKO mouse HC	Sep-07
TauKO mouse HC	Sep-09
P35 mouse brain	SH3G1
P35 mouse brain	SH3G2
Primary neurons	SH3G2
TauKO mouse HC	SH3G2
P35 mouse brain	SHAN2
Primary neurons	SHAN2
TauKO mouse HC	SHAN2
TauKO mouse HC	SHRM2
TauKO mouse HC	SKT
TauKO mouse HC	SMAP1
Primary neurons	SNAG
TauKO mouse HC	SNAG
P35 mouse brain	SNP25
P35 mouse brain	SPAST
TauKO mouse HC	SPAST
TauKO mouse HC	SPTB2
P35 mouse brain	SPTN1
TauKO mouse HC	SPTN1
TauKO mouse HC	SRBS1
P35 mouse brain	SRC8

Primary neurons	SRC8
TauKO mouse HC	SRC8
P35 mouse brain	SRCN1
Primary neurons	SRCN1
TauKO mouse HC	SRCN1
TauKO mouse HC	STAM1
TauKO mouse HC	STAR5
TauKO mouse HC	STAT1
P35 mouse brain	STMN1
Primary neurons	STMN1
TauKO mouse HC	STMN1
P35 mouse brain	SV2A
P35 mouse brain	SYN1
TauKO mouse HC	SYN1
TauKO mouse HC	SYN2
TauKO mouse HC	SYNC
TauKO mouse HC	SYNJ1
TauKO mouse HC	SYNPO
P35 mouse brain	SYUA
Primary neurons	SYUA
TauKO mouse HC	SYUA
P35 mouse brain	SYUB
Primary neurons	SYUB
TauKO mouse HC	SYUB
P35 mouse brain	SYUG
P35 mouse brain	TAGL2
P35 mouse brain	TAGL3
Primary neurons	TAGL3
TauKO mouse HC	TAGL3
TauKO mouse HC	TANC1
TauKO mouse HC	TANC2
BioID2-hTau	**TAU_HUMAN**
P35 mouse brain	TAU
Primary neurons	TAU
TauKO mouse HC	TB10B
TauKO mouse HC	TB182
Primary neurons	TBA1A
TauKO mouse HC	TBA1A
Primary neurons	TBA1B
Primary neurons	TBB2A
Primary neurons	TBB2B
P35 mouse brain	TBB4A
Primary neurons	TBB4B
Primary neurons	TBB6
TauKO mouse HC	TBC21
P35 mouse brain	TBCB
Primary neurons	TBCB
TauKO mouse HC	TBCB

Primary neurons	TCPE
TauKO mouse HC	TM1L2
TauKO mouse HC	TMOD2
P35 mouse brain	TPPP
Primary neurons	TPPP
TauKO mouse HC	TPPP
P35 mouse brain	VAMP1
Primary neurons	VAMP1
P35 mouse brain	VAMP2
Primary neurons	VAMP2
TauKO mouse HC	VAMP2
TauKO mouse HC	VATF
P35 mouse brain	VCIP1
Primary neurons	VCIP1
TauKO mouse HC	VCIP1
TauKO mouse HC	VIAAT
TauKO mouse HC	VIGLN
TauKO mouse HC	VMA5A
TauKO mouse HC	VP13C
TauKO mouse HC	VPS25
TauKO mouse HC	VPS36
TauKO mouse HC	WASC5
P35 mouse brain	WIPF2
Primary neurons	WIPF2
TauKO mouse HC	WIPF2
P35 mouse brain	WIPF3
TauKO mouse HC	WIPF3
P35 mouse brain	ZC21A

nylated tau interactor proteins. 260 unique biotinylated protei
(1) primary cortical mouse neurons (*blue font*), (2) P35 mouse cort
ber of proteins that appeared in more than one system.

Protein Description	Peptide Score
Protein 4.1, Gene: Epb41	52.83
Protein 4.1, Gene: Epb41	45.14
Protein 4.1, Gene: Epb41	49.8
AP2-associated protein kinase 1, Gene: Aak1	54.15
AP2-associated protein kinase 1, Gene: Aak1	82.11
AP2-associated protein kinase 1, Gene: Aak1	96.92
Abl interactor 2, Gene: ABI2	47.59
Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2,	50.63
Actin, aortic smooth muscle, Gene: ACTA1	70.69
Actin, cytoplasmic 1, Gene: ACTB	70.69
Actin, alpha cardiac muscle 1, Gene: Actc1	43.95
Actin, alpha cardiac muscle 1, Gene: ACTC1	70.69
AF4/FMR2 family member 2, Gene: AFF2	43.99
Arf-GAP domain and FG repeat-containing protein 1, Gene: AGFG1	75.44
Jouberin, Gene: Ahi1	49.62
Alpha-internexin, Gene: Ina	90.16
Serum albumin OS=Bos taurus Gene: ALB	74.52
Fructose-bisphosphate aldolase A, Gene: Aldoa	67.13
Fructose-bisphosphate aldolase A, Gene: Aldoa	98.84
Fructose-bisphosphate aldolase A, Gene: Aldoa	42.48
Amphiphysin, Gene: Amph	48.16
Ankyrin-2, Gene: Ank2	50.31
Ankyrin-2, Gene: Ank2	46.38
Ankyrin-2, Gene: Ank2	54.2
Clathrin coat assembly protein AP180, Gene: Snap91	79.7
Clathrin coat assembly protein AP180, Gene: Snap91	42.2
Clathrin coat assembly protein AP180, Gene: Snap91	57.49
Adenomatous polyposis coli protein, Gene: APC	50.61
Beta-adrenergic receptor kinase 1, Gene: Grk2	52.22
Beta-adrenergic receptor kinase 1, Gene: GRK2	67.66
Beta-adrenergic receptor kinase 1, Gene: GRK2	41.2
Actin-related protein 3, Gene: ACTR3	44.96
Actin-related protein 3B, Gene: ACTR3B	46.47
Actin-related protein 2/3 complex subunit 5-like protein, Gene: Arpc5l	51.66
Actin-related protein 2/3 complex subunit 2, Gene: Arpc2	44.21
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein	94.35
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein	56.59
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein	52.75
Sodium/potassium-transporting ATPase subunit beta-3, Gene: Atp1b3	46.22
Ataxin-2-like protein, Gene: Atxn2l	73.01
Putative tyrosine-protein phosphatase auxilin, Gene: Dnajc6	58.15

Putative tyrosine-protein phosphatase auxilin, Gene: Dnajc6	48.95
Brain-specific angiogenesis inhibitor 1-associated protein 2, Gene: BAIAF	40.04
Brain acid soluble protein 1, Gene: Basp1	65.88
Brain acid soluble protein 1, Gene: Basp1	62.31
Myc box-dependent-interacting protein 1, Gene: Bin1	64.31
Myc box-dependent-interacting protein 1, Gene: Bin1	48.17
Myc box-dependent-interacting protein 1, Gene: Bin1	38.99
Protein bassoon, Gene: Bsn	50.91
Protein bassoon, Gene: Bsn	68.74
UPF0587 protein C1orf123 homolog,	68.16
UPF0587 protein C1orf123 homolog	66.31
Calretinin, Gene: Calb2	38.52
Calmodulin, Gene: Calm	100.7
CaM kinase-like vesicle-associated protein, Gene: Camkv	42.21
Calmodulin-regulated spectrin-associated protein 3, Gene: Camsap3	78.77
Calmodulin-regulated spectrin-associated protein 3, Gene: Camsap3	80.41
Calmodulin-regulated spectrin-associated protein 3, Gene: Camsap3	75.66
Calcium-dependent secretion activator 1, Gene: Cadps	69.57
Calcium-dependent secretion activator 1, Gene: Cadps	61.35
Calcium-dependent secretion activator 2, Gene: Cadps2	55.6
Coiled-coil domain-containing protein 124, Gene: Ccdc124	39.63
Coiled-coil domain-containing protein 171, Gene: Ccdc171	38.37
Protein CDV3, Gene: Cdv3	52.4
Centrosomal protein of 170 kDa, Gene: Cep170	40.26
Centrosomal protein of 170 kDa, Gene: Cep170	58.33
Cell cycle exit and neuronal differentiation protein 1, Gene: Cend1	42.76
Cell cycle exit and neuronal differentiation protein 1, Gene: Cend1	39.32
Centrin-2, Gene: CETN2	40.36
Charged multivesicular body protein 4b, Gene: CHMP4B	68.25
Cytoskeleton-associated protein 5, Gene: Ckap5	55.83
CLIP-associating protein 2, Gene: Clasp2	44.95
CLIP-associating protein 2, Gene: Clasp2	88.71
Clathrin heavy chain 1, Gene: CLTC	29.8
CAP-Gly domain-containing linker protein 2, Gene: Clip2	48.09
Connector enhancer of kinase suppressor of ras 2, Gene: CNKSR2	40.7
Complexin-1, Gene: Cplx1	60.28
Complexin-1, Gene: Cplx1	73.92
Complexin-1, Gene: Cplx1	83.33
Complexin-2, Gene: Cplx2	54.72
Complexin-2, Gene: Cplx2	83.33
Crk-like protein, Gene: Crkl	47.65
Crk-like protein, Gene: CRKL	51.03
CREB-regulated transcription coactivator 1, Gene: CRTC1	44.18
Cold shock domain-containing protein E1, Gene: CSDE1	47.7
Caskin-1, Gene: Caskin1	64.63
Cytoplasmic FMR1-interacting protein 2, Gene: Cyfip2	42.32
Cytohesin-2, Gene: CYTH2	49.97
Cytohesin-2, Gene: CYTH2	49.97

Cytohesin-3, Gene: CYTH3	49.97
CXXC motif containing zinc binding protein, Gene: CZIB	67.32
Drebrin-like protein, Gene: Dbnl	54.12
Cytoplasmic dynein 1 light intermediate chain 1, Gene: Dync1li1	55.98
Glutamate decarboxylase 2, Gene: Gad2	58.17
Serine/threonine-protein kinase DCLK1, Gene: Dclk1	55.89
Serine/threonine-protein kinase DCLK1, Gene: Dclk1	75.87
Serine/threonine-protein kinase DCLK2, Gene: Dclk2	73.61
Dynactin subunit 2, Gene: Dctn2	40.88
Dynactin subunit 2, Gene: Dctn2	52.37
Dynactin subunit 2, Gene: DCTN2	47.65
Dematin, Gene: DMTN	43.9
Disks large-associated protein 3, Gene: Dlgap3	47.39
Disks large-associated protein 3, Gene: DLGAP3	62.57
DnaJ homolog subfamily B member 1, Gene: Dnajb1	50
DnaJ homolog subfamily B member 1, Gene: Dnajb1	50.45
DnaJ homolog subfamily B member 1, Gene: DNAJB1	49.14
Dynamin-1-like protein, Gene: Dnm1l	53.25
Dihydropyrimidinase-related protein 2, Gene: Dpysl2	75.21
Dihydropyrimidinase-related protein 2, Gene: Dpysl2	79.41
Dihydropyrimidinase-related protein 2, Gene: Dpysl2	64.69
Dihydropyrimidinase-related protein 4, Gene: Dpysl4	41.51
Developmentally-regulated GTP-binding protein 2, Gene: DRG2	57.73
Dynamin-1, Gene: Dnm1	67.68
Dynamin-1, Gene: Dnm1	105.87
Band 4.1-like protein 1, Gene: Epb41l1	45.52
Band 4.1-like protein 1, Gene: Epb41l1	150.52
Band 4.1-like protein 1, Gene: Epb41l1	62.83
Band 4.1-like protein 2, Gene: EPB41L2	60.22
Band 4.1-like protein 2, Gene: Epb41l2	69.4
Band 4.1-like protein 3, Gene: Epb41l3	69.54
Band 4.1-like protein 3, Gene: Epb41l3	69.4
Elongation factor 1-alpha 1, Gene: EEF1A1	41.44
Elongation factor 1-alpha 2, Gene: EEF1A2	51.58
Elongation factor 2, Gene: Eef2	69
Elongin-B, Gene: Elob	56.89
Elongin-B, Gene: ELOB	56.44
Alpha-endosulfine, Gene: ENSA	46.39
Protein FAM110B, Gene: FAM110B	43.31
Ras GTPase-activating protein-binding protein 1, Gene: G3bp1	58.24
Glyceraldehyde-3-phosphate dehydrogenase, Gene: Gapdh	57.4
Glyceraldehyde-3-phosphate dehydrogenase, Gene: Gapdh	82.31
Glyceraldehyde-3-phosphate dehydrogenase, Gene: Gapdh	55.2
Gamma-aminobutyric acid receptor subunit alpha-1, Gene: GABRA1	47.62
Rho GDP-dissociation inhibitor 1, Gene: Arhgdia	50.74
Rho GDP-dissociation inhibitor 1, Gene: Arhgdia	46.67
Rho GDP-dissociation inhibitor 1, Gene: Arhgdia	43.09
Glutamine synthetase, Gene: Glul	66.7

Glutaminase kidney isoform, mitochondrial, Gene: Gls	56.24
Probable G-protein coupled receptor 158, Gene: Gpr158	47.57
Probable G-protein coupled receptor 158, Gene: Gpr158	39.84
Probable G-protein coupled receptor 158, Gene: Gpr158	50.38
G protein-regulated inducer of neurite outgrowth 1, Gene: Gprin1	41.61
G protein-regulated inducer of neurite outgrowth 1, Gene: Gprin1	81.51
Gasdermin-E, Gene: Gsdme	70.61
Glycogen synthase kinase-3 alpha, Gene: Gsk3a	71.97
Glycogen synthase kinase-3 beta, Gene: GSK3B	77.94
Histone H2A type 1-D, Gene: HIST1H2AD	71.15
Histone H2B type 1-B, Gene: Hist1h2bb	74.21
Histone H2B type 1-C/E/G, Gene: Hist1h2bc	74.21
Histone H2B type 1-L, Gene: HIST1H2BL	60.63
28 kDa heat- and acid-stable phosphoprotein, Gene: Pdap1	75.28
28 kDa heat- and acid-stable phosphoprotein, Gene: PDAP1	49.72
Histidine triad nucleotide-binding protein 1, Gene: Hint1	57.79
Heat shock 70 kDa protein 1A, Gene: Hspa1a	62.05
Heat shock protein HSP 90-alpha, Gene: Hsp90aa1	44.64
Heat shock protein HSP 90-alpha, Gene: Hsp90aa1	44.13
Heat shock protein HSP 90-beta, Gene: HSP90AB1	44.64
Heat shock protein HSP 90-beta Gene: HSP90AB1	44.13
Heat shock cognate 71 kDa protein, Gene: Hspa8	48.49
Hexokinase-1, Gene: Hk1	91.04
Eukaryotic translation initiation factor 4B, Gene: Eif4b	71.51
Eukaryotic translation initiation factor 4B, Gene: Eif4b	49.57
Eukaryotic translation initiation factor 4 gamma 1, Gene: Eif4g1	44.66
Eukaryotic translation initiation factor 4 gamma 3, Gene: Eif4g3	61.85
Eukaryotic translation initiation factor 4 gamma 3, Gene: Eif4g3	58.25
Eukaryotic translation initiation factor 4 gamma 3, Gene: EIF4G3	61.23
Eukaryotic translation initiation factor 4H, Gene: Eif4h	43.04
IQ motif and SEC7 domain-containing protein 3, Gene: Iqsec3	113.73
Jupiter microtubule associated homolog 1, Gene: Jpt1	45.82
AP2-interacting clathrin-endocytosis protein, Gene: Kiaa1107	43.57
cAMP-dependent protein kinase type II-alpha regulatory subunit, Gene: F	52.83
cAMP-dependent protein kinase type II-alpha regulatory subunit, Gene: F	45.33
cAMP-dependent protein kinase catalytic subunit alpha, Gene: PRKACA	46.55
Casein kinase I isoform epsilon, Gene: Csnk1e	41.54
Calcium/calmodulin-dependent protein kinase type II subunit alpha, Gene	51.23
Calcium/calmodulin-dependent protein kinase type II subunit alpha, Gene	41.17
Calcium/calmodulin-dependent protein kinase type II subunit beta, Gene:	45.39
Calcium/calmodulin-dependent protein kinase type II subunit delta, Gene:	56.31
Calcium/calmodulin-dependent protein kinase type II subunit delta, Gene:	59.89
Calcium/calmodulin-dependent protein kinase type II subunit delta, Gene:	60.21
Kinesin-like protein KIF21A, Gene: Kif21a	42.48
Kinesin-like protein KIF21A, Gene: Kif21a	45.39
Kinesin heavy chain isoform 5C, Gene: Kif5c	43.37
Kinesin heavy chain isoform 5C, Gene: Kif5c	44.14
Protein kinase C beta type, Gene: Prkcb	46.75

Protein kinase C beta type, Gene: Prkcb	63.29
Protein kinase C gamma type, Gene: Prkcg	47.39
Ketosamine-3-kinase, Gene: Fn3krp	64.25
Ketosamine-3-kinase, Gene: Fn3krp	56.48
LIM and SH3 domain protein 1, Gene: Lasp1	99.21
LIM and SH3 domain protein 1, Gene: Lasp1	56.02
LIM and SH3 domain protein 1, Gene: Lasp1	66.34
LIM zinc-binding domain-containing Nebulette, Gene: Nebl	70.91
Leucine zipper protein 1, Gene: Luzp1	68.16
Mitogen-activated protein kinase kinase kinase 10, Gene: Map3k10	66.32
Mitogen-activated protein kinase kinase kinase kinase 4, Gene: MAP4K4	54.55
MAP7 domain-containing protein 2, Gene: Map7d2	70.31
Microtubule-associated protein 1A, Gene: Map1a	54.88
Microtubule-associated protein 1A, Gene: Map1a	83.65
Microtubule-associated protein 1A, Gene: Map1a	52.52
Microtubule-associated protein 1B, Gene: Map1b	54.28
Microtubule-associated protein 1B, Gene: Map1b	74.03
Microtubule-associated protein 1B, Gene: Map1b	62.59
Microtubule-associated protein 4, Gene: Map4	54.39
Microtubule-associated protein 4, Gene: Map4	82.82
Microtubule-associated protein 4, Gene: Map4	94.93
Microtubule-associated protein 6, Gene: Map6	77.78
Microtubule-associated protein 6, Gene: Map6	107.18
Microtubule-associated protein 6, Gene: Map6	67.44
Microtubule-associated protein RP/EB family member 1, Gene: Mapre1	66.31
Microtubule-associated protein RP/EB family member 1, Gene: Mapre1	80.36
Microtubule-associated protein RP/EB family member 1, Gene: Mapre1	55.44
Microtubule-associated protein RP/EB family member 2, Gene: Mapre2	44.96
Microtubule-associated protein RP/EB family member 3, Gene: Mapre3	47.04
Microtubule-associated protein RP/EB family member 3, Gene: MAPRE3	57.07
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial, Gene: M(	50.47
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial, Gene: M(	62.27
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial, Gene: M(	42.95
Malate dehydrogenase, mitochondrial, Gene: Mdh2	42.93
Misshapen-like kinase 1, Gene: MINK1	91.27
Mitogen-activated protein kinase 12, Gene: Mapk12	74.9
Microtubule-associated protein 2, Gene: Map2	57.87
Microtubule-associated protein 2, Gene: Map2	102.56
Microtubule-associated protein 2, Gene: Map2	41.66
Unconventional myosin-Va, Gene: Myo5a	37.72
Nascent polypeptide-associated complex subunit alpha,	83.64
Nascent polypeptide-associated complex subunit alpha, muscle-specific	86.13
Nascent polypeptide-associated complex subunit alpha, muscle-specific	78.41
Neural cell adhesion molecule 1, Gene: Ncam1	49.67
Adaptin ear-binding coat-associated protein 1, Gene: NECAP1	56.31
Neurogranin, Gene: Nrgn	95.35
Neurogranin, Gene: NRGN	92.1
Nuclear factor of activated T-cells 5, Gene: NFAT5	79.6

Neurofilament medium polypeptide, Gene: Nefm	46.68
Neurofilament medium polypeptide, Gene: Nefm	61.44
NK-tumor recognition protein, Gene: NKTR	47.16
NK-tumor recognition protein, Gene: NKTR	40.28
NK-tumor recognition protein, Gene: NKTR	38.95
Glycylpeptide N-tetradecanoyltransferase 1, Gene: Nmt1	43.79
Nucleosome assembly protein 1-like 4, Gene: Nap1l4	43.57
Nucleosome assembly protein 1-like 4, Gene: Nap1l4	53.51
Nucleosome assembly protein 1-like 4, Gene: Nap1l4	41.48
Vesicle-fusing ATPase, Gene: Nsf	58.1
Vesicle-fusing ATPase, Gene: Nsf	42.12
Vesicle-fusing ATPase, Gene: Nsf	70.47
NSFL1 cofactor p47, Gene: NSFL1C	41.35
Protein O-GlcNAcase, Gene: OGA	40.85
Oxidation resistance protein 1, Gene: Oxr1	48.2
Putative monooxygenase p33MONOX, Gene: P33MONOX	44.29
Phosphofurin acidic cluster sorting protein 1, Gene: Pacs1	54.03
Phosphofurin acidic cluster sorting protein 1, Gene: Pacs1	83.61
Serine/threonine-protein kinase PAK 2, Gene: Pak2	47.32
Serine/threonine-protein kinase PAK 2, Gene: Pak2	47.47
Serine/threonine-protein kinase PAK 2, Gene: Pak2	81.52
Poly(rC)-binding protein 1, Gene: PCBP1	55.16
Propionyl-CoA carboxylase alpha chain, mitochondrial, Gene: Pcca	88.61
Propionyl-CoA carboxylase alpha chain, mitochondrial, Gene: Pcca	85.52
Propionyl-CoA carboxylase alpha chain, mitochondrial, Gene: PCCA	63.48
Protein piccolo, Gene: Pclo	42.89
Protein piccolo, Gene: Pclo	44.51
Phosphatidylethanolamine-binding protein 1, Gene: Pebp1	127.62
Prefoldin subunit 2, Gene: Pfdn2	58.03
Prefoldin subunit 2, Gene: Pfdn2	55.56
Phosphoglycerate mutase 1, Gene: PGAM1	59.39
Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha, Gene: Pip4k2a	69.13
Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha, Gene: Pip4k2a	56.57
Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha, Gene: PIP4K2A	67.74
Phosphatidylinositol 5-phosphate 4-kinase type-2 beta, Gene: PIP4K2B	67.93
Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma, Gene: PIP4K2	68.39
Inactive phospholipase C-like protein 2, Gene: Plcl2	45.38
PI-PLC X domain-containing protein 3, Gene: Plcxd3	50.08
Plectin (Fragment), Gene: PLEC	71.12
Plectin (Fragment), Gene: PLEC	66.47
Plectin, Gene: Plec	74.39
Phospholipid phosphatase-related protein type 4, Gene: PLPPR4	46.62
E3 ubiquitin-protein ligase PPP1R11, Gene: PPP1R11	42.78
PRA1 family protein 3, Gene: Arl6ip5	46.32
Adenylosuccinate synthetase isozyme 2, Gene: ADSS	53.78
Transcriptional activator protein Pur-beta, Gene: Purb	38.97
Pyruvate carboxylase, mitochondrial, Gene: Pc	117.3
Pyruvate carboxylase, mitochondrial, Gene: Pc	66.52

Pyruvate carboxylase, mitochondrial, Gene: Pc	61.86
Ran-specific GTPase-activating protein, Gene: Ranbp1	55.2
RasGAP-activating-like protein 1, Gene: Rasal1	64.59
Rabenosyn-5, Gene: Rbsn	68.81
Rabenosyn-5, Gene: Rbsn	57.78
Rabenosyn-5, Gene: RBSN	44.49
Ras-specific guanine nucleotide-releasing factor 1, Gene: Rasgrf1	52.44
N-acetylaspartylglutamate synthase A, Gene: Rimkla	63.49
60S ribosomal protein L24, Gene: RPL24	42.92
60S ribosomal protein L29, Gene: Rpl29	49.3
RING finger protein 214, Gene: Rnf214	68.19
40S ribosomal protein S20, Gene: RPS20	47.43
Reticulon-1, Gene: Rtn1	50.6
Reticulon-3, Gene: Rtn3	38.46
Reticulon-3, Gene: Rtn3	43.2
Reticulon-4, Gene: Rtn4	46.81
Reticulon-4, Gene: Rtn4	89.44
Reticulon-4, Gene: Rtn4	51.79
Protein RUFY3, Gene: RUFY3	43.88
RuvB-like 2, Gene: Ruvbl2	42.76
RuvB-like 2, Gene: Ruvbl2	60.26
Protein S100-A6, Gene: S100A6	66
Septin-5 OS=Macaca fascicularis Gene: Sept5	59.12
Septin-5, Gene: Sept5	44.1
Septin-5, Gene: SEPTIN5	62.76
Septin-7, Gene: Sept7	62.34
Septin-7, Gene: SEPTIN7	72.57
Septin-9, Gene: Septin9	60.22
Endophilin-A2, Gene: Sh3gl1	52.91
Endophilin-A1, Gene: Sh3gl2	57.74
Endophilin-A1, Gene: Sh3gl2	57.74
Endophilin-A1, Gene: SH3GL2	60.6
SH3 and multiple ankyrin repeat domains protein 2, Gene: Shank2	53.5
SH3 and multiple ankyrin repeat domains protein 2, Gene: Shank2	42.48
SH3 and multiple ankyrin repeat domains protein 2, Gene: Shank2	47.42
Protein Shroom2, Gene: Shroom2	44.42
Sickle tail protein, Gene: Skt	42.3
Stromal membrane-associated protein 1, Gene: Smap1	41.78
Gamma-soluble NSF attachment protein, Gene: Napg	84.73
Gamma-soluble NSF attachment protein, Gene: NAPG	89.21
Synaptosomal-associated protein 25, Gene: Snap25	46.61
Spastin, Gene: Spast	44
Spastin, Gene: Spast	42.51
Spectrin beta chain, non-erythrocytic 1, Gene: Sptbn1	38.82
Spectrin alpha chain, non-erythrocytic 1, Gene: Sptan1	65.59
Spectrin alpha chain, non-erythrocytic 1, Gene: Sptan1	45.48
Sorbin and SH3 domain-containing protein 1, Gene: SORBS1	47.28
Src substrate cortactin, Gene: Cttn	53.09

Src substrate cortactin, Gene: Cttn	85.07
Src substrate cortactin, Gene: Cttn	42.73
SRC kinase signaling inhibitor 1, Gene: Srcin1	85.38
SRC kinase signaling inhibitor 1, Gene: Srcin1	57.25
SRC kinase signaling inhibitor 1, Gene: Srcin1	43.24
Signal transducing adapter molecule 1, Gene: Stam	50.8
StAR-related lipid transfer protein 5, Gene: STARD5	41.92
Signal transducer and activator of transcription 1-alpha/beta, Gene: STAT	71.15
Stathmin, Gene: Stmn1	63.4
Stathmin, Gene: Stmn1	72.45
Stathmin, Gene: Stmn1	42.5
Synaptic vesicle glycoprotein 2A, Gene: Sv2a	40.2
Synapsin-1, Gene: Syn1	50.7
Synapsin-1, Gene: Syn1	55.86
Synapsin-2, Gene: Syn2	39.71
Asparagine--tRNA ligase, cytoplasmic, Gene: NARS	42.13
Synaptojanin-1, Gene: Synj1	72.69
Synaptopodin, Gene: Synpo	44.41
Alpha-synuclein, Gene: Snca	54.36
Alpha-synuclein, Gene: Snca	75.82
Alpha-synuclein, Gene: Snca	50.76
Beta-synuclein, Gene: Sncb	54.36
Beta-synuclein, Gene: Sncb	152.93
Beta-synuclein, Gene: Sncb	68.29
Gamma-synuclein OS=Macaca fascicularis Gene: SNCG	46.63
Transgelin-2, Gene: Tagln2	61.21
Transgelin-3, Gene: Tagln3	109.71
Transgelin-3, Gene: Tagln3	135.65
Transgelin-3, Gene: TAGLN3	111.12
Protein TANC1, Gene: TANC1	49.82
Protein TANC2, Gene: TANC2	67.47
Microtubule-associated protein tau, Gene: MAPT	**71.17**
Microtubule-associated protein tau, Gene: Mapt	140.24
Microtubule-associated protein tau, Gene: Mapt	71.23
TBC1 domain family member 10B, Gene: Tbc1d10b	36.33
182 kDa tankyrase-1-binding protein, Gene: Tnks1bp1	79.99
Tubulin alpha-1A chain, Gene: TUBA1A	83.95
Tubulin alpha-1A chain, Gene: TUBA1A	62.27
Tubulin alpha-1B chain, Gene: TUBA1B	83.95
Tubulin beta-2A chain, Gene: Tubb2a	60.01
Tubulin beta-2B chain, Gene: Tubb2b	60.01
Tubulin beta-4A chain, Gene: TUBB4A	47.1
Tubulin beta-4B chain, Gene: Tubb4b	60.01
Tubulin beta-6 chain, Gene: TUBB6	60.01
TBC1 domain family member 21, Gene: TBC1D21	40.24
Tubulin-folding cofactor B, Gene: Tbcb	61.61
Tubulin-folding cofactor B, Gene: Tbcb	51.24
Tubulin-folding cofactor B, Gene: Tbcb	60.33

T-complex protein 1 subunit epsilon, Gene: Cct5	50.62
TOM1-like protein 2, Gene: TOM1L2	48.06
Tropomodulin-2, Gene: Tmod2	40.15
Tubulin polymerization-promoting protein, Gene: Tppp	44.79
Tubulin polymerization-promoting protein, Gene: Tppp	41.54
Tubulin polymerization-promoting protein, Gene: Tppp	65.33
Vesicle-associated membrane protein 1, Gene: Vamp1	64.33
Vesicle-associated membrane protein 1, Gene: Vamp1	55.83
Vesicle-associated membrane protein 2, Gene: Vamp2	61.05
Vesicle-associated membrane protein 2, Gene: Vamp2	47.24
Vesicle-associated membrane protein 2, Gene: VAMP2	61.37
V-type proton ATPase subunit F, Gene: Atp6v1f	45.52
Deubiquitinating protein VCIP135, Gene: Vcpip1	65.84
Deubiquitinating protein VCIP135, Gene: Vcpip1	76.41
Deubiquitinating protein VCIP135, Gene: Vcpip1	51.11
Vesicular inhibitory amino acid transporter, Gene: Slc32a1	88.69
Vigilin, Gene: Hdlbp	47.53
von Willebrand factor A domain-containing protein 5A, Gene: Vwa5a	40.5
Vacuolar protein sorting-associated protein 13C, Gene: VPS13C	63.15
Vacuolar protein-sorting-associated protein 25, Gene: VPS25	43.95
Vacuolar protein-sorting-associated protein 36, Gene: Vps36	64.22
WASH complex subunit 5, Gene: WASHC5	57.11
WAS/WASL-interacting protein family member 2, Gene: Wipf2	50.91
WAS/WASL-interacting protein family member 2, Gene: Wipf2	58.58
WAS/WASL-interacting protein family member 2, Gene: Wipf2	65.76
WAS/WASL-interacting protein family member 3, Gene: Wipf3	44.42
WAS/WASL-interacting protein family member 3, Gene: Wipf3	92.6
Zinc finger C2HC domain-containing protein 1A, Gene: Zc2hc1a	66.37

ns were identified across 3 biological expression systems
ex and hippocampus (*black font*), and (3) 6 m.o. Tau(-/-) mouse h

xample biotinylated peptide mass spectrometry read-out
Peptide Sequence (bold K indicates biotinylated lysine)
TV**K**GGISETR
TV**K**GGISETR
TV**K**GGISETR
VAEDEFDPIPVLIT**K**NTQGGHSR
VAEDEFDPIPVLIT**K**NTQGGHSR
VAEDEFDPIPVLIT**K**NTQGGHSR
VSTQNM**K**MGGLPR
IIS**K**SCEDQR
HQGVMVGMGQ**K**DSYVGDEAQSK
HQGVMVGMGQ**K**DSYVGDEAQSK
EITALAPSTMKI**K**
HQGVMVGMGQ**K**DSYVGDEAQSK
QITST**K**PKR
VSTN**K**AGLQTADK
KGQEGFFPANHVASETLYR
TG**K**SATEESTSSSQK
SHCIAEVEKDAIPENLPPLTADFAED**K**DVCK
IVAPG**K**GILAADESTGSIAK
IVAPG**K**GILAADESTGSIAK
IVAPG**K**GILAADESTGSIAK
LGDQHAD**K**
SSESN**K**GK
SSESN**K**GK
THPAVSPSS**K**SSTSSK
KGDLQWNAGEK
KGDLQWNAGEK
KGDLQWNAGEK
TPFSSSSSS**K**HSSPSGTVAAR
SPVVELS**K**VPLIQR
SPVVELS**K**VPLIQR
SPVVELS**K**VPLIQR
ESA**K**VGDQAQR
ESA**K**VVDQAQR
NSPINT**K**NQAVK
TITG**K**TFSSR
TAN**K**FEGLSQQASTSSAK
TAN**K**FEGLSQQASTSSAK
KPASGTDKPTPLTN**K**GQPR
IPSPGLMVFP**K**PQTALEYTFSMSEPQTYKK
FGAQF**K**LQPSSSPETGLDPFPSR
G**K**GSTNLEGK

G**K**GSTNLEGK
SQGS**K**NPQK
APAPAAPAAAEPQAEAPAAAASSEQSVAV**K**E
ETPAASEAPSSAA**K**APAPAAPAAAEPQAEAPAAAASSEQSVAVKE
AAPQWCQG**K**LQAHLVAQTNLLR
IA**K**PVSLLEK
IA**K**PVSLLEK
ASPQAT**K**ASPQATK
TGGTASP**K**HGR
LMDSVAL**K**GGR
LMDSVAL**K**GGR
GSGMMS**K**SDNFGEK
VFD**K**DGNGYISAAELR
ATPATEESTVPATQSSALPAA**K**AAATPEPAVAQPDSTALEGATGQAPPSSK
LG**K**SAFLQVQPR
LG**K**SAFLQVQPR
LG**K**SAFLQVQPR
LNA**K**GGNVPQLDAPISQFYADR
LNA**K**GGNVPQLDAPISQFSGLK
MTVP**K**NSQDSDLK
VAPA**K**VTR
KIETHI**K**
SGDGGSAGPAG**K**AITK
EQAQWTPTKFPS**K**NALGHIDK
EQAQWTPTKFPS**K**NALGHIDK
ATPAADG**K**APLTKPVK
ATPAADG**K**APLTKPVKK
AF**K**LFDDDETGK
AG**K**GGPTPQEAIQR
QDDRPPLTSLLS**K**PAIPPVASSTDMLHSK
AGGDAADGSQPALDN**K**ASLLHSMPLHSSPR
VSVGGS**K**ANPLPGSLQR
V**K**QLPLVKPYLR
EGSPLH**K**QASGPSSSGAATTVSEKPGPK
GHMVG**K**PVHK
QALGGAT**K**DMGK
QALGGAT**K**DMGK
QALGGAT**K**DMGK
QALGGAT**K**DMGK
QALGGAT**K**DMGK
SSPHG**K**HGNR
SSPHG**K**HGNR
RPLSVD**K**HGR
VPS**K**NQNDPLPGR
LRGPA**K**GEASAEGPPLAR
GEKDP**K**GGFDIK
AC**K**TEADGR
AC**K**TEADGR

AC**K**TEADGR
LMDSVAL**K**GGR
AMSTTSVTSSQPG**K**LR
SGQ**K**PVLSDVHAELDR
AATG**K**VACTCDQKPCNCPK
AVSSLATA**K**GGPSEVR
AVSSLATA**K**GGPSEVR
ST**K**SSSSSPTSPGSFR
VGT**K**GLDFSDR
VGT**K**GLDFSDR
VGT**K**GLDFSDR
IYPYEMLVVTN**K**GR
DGYPGAGPG**K**GLLGPETK
DGYPGAGPG**K**GLLGPETK
LNPDG**K**SIR
LNPDG**K**SIR
LNPDG**K**SIR
TS**K**AEELLAEEK
TSPA**K**QQAPPVR
TVTPASSA**K**TSPAK
TSPA**K**QQAPPVR
GLYDGPVHEVMLPA**K**PGSGTQAR
SASS**K**GEGFDVMK
KGWLTINNIGIM**K**GGSK
GWLTINNIGIM**K**GGSK
LQHPDMLVT**K**AVVYR
SLSPIIG**K**DVLTSTYGATAETLSTSTTTHVTK
TV**K**GGFSETR
TV**K**GGISETR
TV**K**GGISETR
TV**K**GGISETR
TV**K**GGISETR
AAGAG**K**VTK
SGGAG**K**VTK
FAA**K**GEGQLSAAER
H**K**TTIFTDAK
H**K**TTIFTDAK
GQ**K**YFDSGDYNMAK
ILN**K**GPDYFR
INSGG**K**LPNFGFVVFDDSEPVQK
TVDGPSG**K**LWR
VIPELNG**K**LTGMAFR
TVDGPSG**K**LWR
GDPGLATIA**K**SATIEPK
Y**K**EALLGR
Y**K**EALLGR
KY**K**EALLGR
YMSLPQGE**K**VQAMYIWVDGTGEGLR

FKKCVQSNIVLLTQAFR
LISKTPVLPGR
LISKTPVLPGR
LISKTPVLPGR
ASLPASEKTDPLASSKAGSASQGK
TVPTSSGKTALVSPGK
LNVGGKGVVESHSSFGTLR
SSKTPPEAIALCSSLLEYTPSSR
TTSFAESCKPVQQPSAFGSMKVSR
KVTIAQGGVLPNIQAVLLPK
VLKQVHPDTGISSK
VLKQVHPDTGISSK
AVTKYTSSK
KGVEGLIDIENPNR
KVTQLDLDGPK
EIPAKIIFEDDR
KTAIGIDLGTTYSCVGVFQHGKVEIIANDQGNR
IMKAQALR
IMKAQALR
IMKAQALR
IMKAQALR
ITITNDKGR
GKFTTSDVAAIETDKEGVQNAK
AASIFGGAKPVDTAAR
AASIFGGAKPVDTAAR
LSWGKGSSGGSGAKPSDTASEATRPATLNR
VLDPSKFLK
VLDPSKFLK
VLDPSKFLK
KGGPDDR
ERPSSCCAAAGALLQHASPAALGKGVLSR
SAGSKSSGGREDSESPGTQR
CATVTSAVSSKCLLGQPSEK
SNKNGGNQEVEIAHCHKG
SNKNGGNQEVEIAHCHK
KGSEQESVK
LAASQTSVPFDHLGK
NFSGGKSGGNK
NFSGGKSGGNK
LKGAILTTMLATR
INNKANVVTSPK
INNKANVVTSPK
INNKANVVTSPK
DKELLAPSGLPSKIGSISR
GIINPFPACKGVR
GGGGGSSNSTHYQK
GGGGGSSNSTHYQK
IGQGTKAPEEK

IGQGT**K**APEEK
MGPSSSPIPSPSPSPTDS**K**R
EAGTVG**K**GGEQAER
EAGTVG**K**GGEQAER
G**K**GFSVVADTPELQR
G**K**GFSVVADTPELQR
KTQDQISNIK
STQVVSDAAY**K**GVQPHVVEMDR
APILS**K**YPYSSR
LDPW**K**LVSFGR
KGSVVNVNPTNTR
TA**K**PTYLGSPVK
DFQEPLPQ**K**GLEVER
SPWASDFKDFQEPLPQ**K**GLEVER
AAP**K**TAMS**K**LAK
AT**K**TTTTPEVK
IT**K**TPQASTYSYETSDR
NAANASAS**K**SAK
CGS**K**DNIK
TTPTVS**K**ATSPSTLVSTGPSSR
MTA**K**SASADLSR
AQSPLLPEPLKNQSPVVPAST**K**DQSFPTPAPR
DQGAVLLGPV**K**DLGPVAPAPIK
YL**K**GHDSVFVAPV**K**NQGPVIPEPVK
TTAAP**K**AGPGMVR
TTAAP**K**AGPGMVR
TTAAP**K**AGPGMVR
SSPAS**K**PGSTPSRPSSAK
KLIGTAVPQR
KLIGTAVPQR
AGDSLMVMIAM**K**MEHTIK
AGDSLMVMIAM**K**MEHTIK
KMEHTIK
VNVPVIGGHAG**K**TIIPLISQCTPK
KGSVVNVNPTNTR
QEVT**K**TAWEVR
AG**K**SGTSTPTTPGSTAITPGTPPSYSSR
TLG**K**VTSEPEAVSER
IDSQ**K**LNFR
VPVKPT**K**GRPGQTAK
IEDLSQQAQLAAAEKF**K**
IEDLSQQAQLAAAEKF**K**
IEDLSQQAQLAAAEKF**K**
APPAS**K**ASPAPTPTPAGAASPLAAVAAPATDAPQAK
KGGAS**K**PR
KGPGPGGPGGAGGAR
KGPGPGGPGGAGGAR
QQQQQQQQQQQQSILFSNQNTMATMASP**K**

AVEEVITISKSV**K**
YIT**K**SVTVTQK
INLIDK**K**
INLIDK**K**
INLIDK**K**
IQEIQ**K**AIELFSVGQGPAK
N**K**VVIAEK
N**K**VVIAEK
N**K**VVIAEK
DIEAMDPSILKGEPASGKR
DIEAMDPSIL**K**GEPASGKR
DIEAMDPSIL**K**GEPASGK
GA**K**EHGAVAVER
ANSSVVSVNC**K**GK
QAPQASKPPAP**K**TPIIEEEQNNSANTQK
DAGYTPH**K**GLTTEETK
SS**K**ADLQGSASPSK
SS**K**ADLQGSASPSK
N**K**IISIFSGTEK
N**K**IISIFSGTEK
N**K**IISIFSGTEK
LVVPATQCGSLIG**K**GGCK
KMQNSMTAGK
KMQNSMTAGK
KMQNSMTAGK
AQGLP**K**GSVPAAAAESPSMHR
MS**K**FSPIQESR
YVWLVYEQEQPLSCDEPILSN**K**SGDNR
VG**K**SGGSGAGK
VG**K**SGGSGAGK
AETAA**K**HGEAQVK
TV**K**HGAGAEISTVNPEQYSK
TV**K**HGAGAEISTVNPEQYSK
TV**K**HGAGAEISTVNPEQYSK
TV**K**HGAGAEISTVNPEQYSK
TV**K**HGAGAEISTVHPEQYAK
GAAGGALPTSPSPALGA**K**GALK
ASTVV**K**GVASGLR
LLASG**K**VAQR
LLASG**K**VAQR
LLASG**K**VAQR
IMQVIAMS**K**QQGVLQSSPK
SS**K**CCCIYEKPR
FADYIS**K**AR
QEQAG**K**NLGTTK
AWG**K**FGGAFCR
GQPLCVLSAM**K**METVVTSPMEGTIR
KMETVVTSPMEGTIR

KMETVVTSPMEGTIR
VAE**K**LEALSVR
ISF**K**GTPTEEQVR
IDHYVVEVN**K**LIIR
IDHYVVEVN**K**LIIR
IDHYVVEVN**K**LIIR
TTLDTG**K**LCMASSLPK
QTG**K**MAILPGLASPR
TAMAAA**K**APTK
GAQAP**K**GAQAPVK
NLSPPSVSSQMIT**K**ESNR
DT**G**KTPVEPEVAIHR
APNQPAPVEG**K**LIKDHLFEESTFAPYIDELSDEQHR
G**K**DPLVLLDK
SETLGSQFVLA**K**GK
LSTEPSPEFSNYSEIA**K**FEK
SSVS**K**VPLLLPNVSALESQIEMGNIVKPK
TPELV**K**DGSR
LQSSDLGV**K**QK
KGTEVQVDDIKR
KGTEVQVDDIKR
ELTIGS**K**LQDAEIAR
ELKESAPFAVIGSNTVVEA**K**GQR
S**K**LATPEDKQDIDK
S**K**LATPEDKQDIDK
K *TVQVEQSK*
KTVQVEQSK
RVETPAS**K**IPEGSAVPATDAAPK
QG**K**IPDEELR
QG**K**IPDEELR
LSMINTMS**K**IR
QG**K**IPDEELR
SVKPGEGLELPVGA**K**SANLAPR
SVKPGEGLELPVGA**K**SANLAPR
IAS**K**AVYVPAKPAR
LTD**K**PPLLIHEDNSAR
DVKPDEDMSS**K**NLVMFR
EKEPEKPA**K**PLTTEKLPK
TGFL**K**WKPDYDSAASEYGK
TGFL**K**WKPDYDSAASEYGK
ADSN**K**TR
TN**K**PSTPTTAVR
TN**K**PSTPTTAVR
A**K**SALPAQSAATLPAR
TASPW**K**SAR
TASPW**K**SAR
SIYEYQPG**K**SSVLTNEK
DYSSGFGG**K**YGVQADRVDK

TGFGG**K**FGVQSER
GFGG**K**FGVQSER
AALTQYSA**K**DINR
TGEVVVTSK**K**
TGEVVVTSK**K**
ASPALVA**K**DPGTVATK
TSTPSAAM**K**LISPR
TGYI**K**TELISVSEVHPSR
EAQMAA**K**LER
S**K**ESVPDFPLSPPK
MEAN**K**ENR
GA**K**DIAK
QASISGPAPT**K**ASGAPPGGQQR
QGPPQ**K**PPGPAGPTR
TPPQRPPPQGGPGQPQGMQPPG**K**VLPPR
WDVIS**K**SQMK
VCAGRPTPDSQS**K**PSETLKGPAVLPEPLKPQAAFPQQPSLPTPAQK
SSILLID**K**VSAPPSAASTFSR
A**K**EGVVAAAEK
TKEGVLYVGS**K**TK
T**K**QGVAEAAGK
A**K**EGVVAAAEK
EGVLYVGS**K**TSGVVQGVASVAEK
QGVTEAAE**K**TK
T**K**QGVTEAAEK
EG**K**NVIGLQMGTNRGASQAGMTGYGMPR
QGQNVIGLQMGSN**K**GASQAGMTGYGMPR
QGQNVIGLQMGSN**K**GASQAGMTGYGMPR
QGQNVIGLQMGSN**K**GASQAGMTGYGMPR
LGVQ**K**GVLHDR
TTPFMGIID**K**TAR
K**LDLSNVQSK**
TDHGAEIVY**K**SPVVSGDTSPR
VQS**K**IGSLDNITHVPGGGNK
MAPGALTA**K**PPLAPKPGTTVASGVTAR
ATAQQNQEFG**K**SAWFQDYSSGGGGSR
TIGGGDDSFNTFFSETGAG**K**HVPR
TIGGGDDSFNTFFSETGAG**K**HVPR
TIGGGDDSFNTFFSETGAG**K**HVPR
KMSATFIGNSTAIQELFKR
KMSATFIGNSTAIQELFKR
YTEGAELVDAVLDVVR**K**EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK
KMSATFIGNSTAIQELFKR
KMASTFIGNSTAIQELFKR
GNVLIDK**K**
S**K**LGPYNEELR
S**K**LGPYNEELR
S**K**LGPYNEELR

T**K**HKLDVMSVEDYK
IISP**K**NNPPTIVQDK
VFIP**K**EKPVETR
AAN**K**TPPK
VDLVDESGYVPGY**K**HAGTYDQK
LTDTS**K**FTGSHK
VNVD**K**VLER
VNVD**K**VLER
VNVD**K**VLER
VNVD**K**VLER
VNVD**K**VLER
A**K**GMFTAEDLR
VGDVQGQELESQLPT**K**IILTGQK
VGDVQGQELESQLPT**K**IILTGQK
VGDVQGQELESQLPT**K**IILTGQK
S**K**LTNVATSVSNK
AACLESAQEPAGAWSN**K**IRPIK
FYSSFSGGF**K**GPQPR
GIG**K**GLVGAVAR
GNLEWLDKN**K**
WETVPVSQSLQTN**K**GPQPGR
LQYN**K**NLGMVCR
ANAPPTPLPLHSN**K**AQAYNR
ANAPPTPLPLHSN**K**AQAYNR
ANAPPTPLPLHSN**K**AQAYNR
DVSGG**K**SGQGPGSR
DVSGG**K**SGQGPGSR
NSVAGVLTN**K**R

ıippocampus (*red font*).

Biotinylated protein overlaps			
50/260 (19.2%)	29/260 (11.2%)	14/260 (5.4%)	6/260 (2.3%)
Tau(-/-) + P35 + Primary	**Tau(-/-) + P35**	**Tau(-/-) + Primary**	**P35 + Primary**
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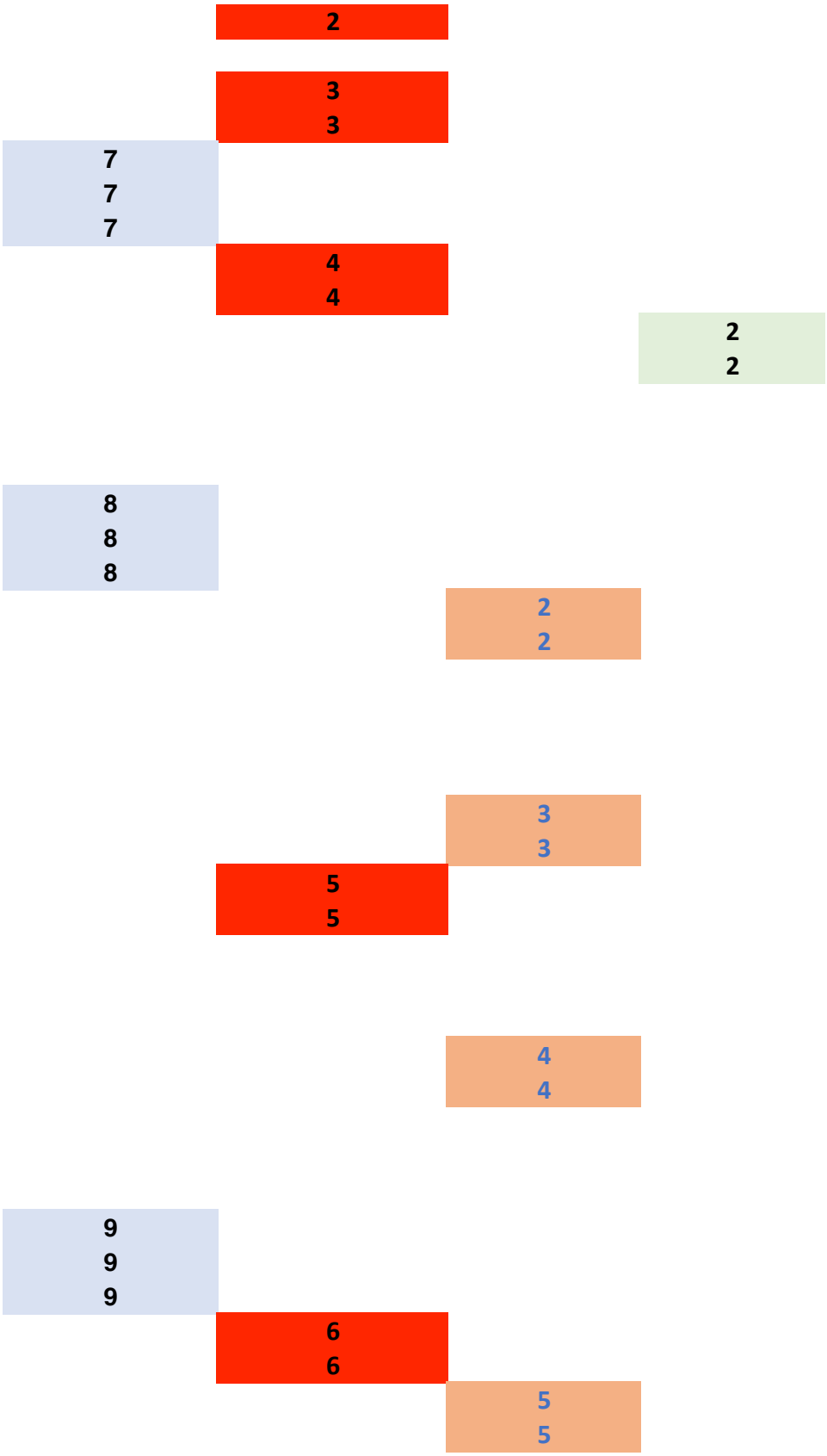
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Table 4. **Protein ontology of network proteins**. STRING-generated protein ontolo

Enriched in primary cortical mouse brain neurons expressing BioID2-hTauFL

Molecular Function

Term ID	Term Description
GO:0008092	cytoskeletal protein binding
GO:0015631	tubulin binding
GO:0008017	microtubule binding
GO:0019901	protein kinase binding
GO:0003779	actin binding

Biological Process

Term ID	Term Description
GO:0006996	organelle organization
GO:0016043	cellular component organization
GO:0031110	regulation of microtubule polymerization or depolymerizat
GO:0031175	neuron projection development
GO:0034622	cellular protein-containing complex assembly

Cell Component

Term ID	Term Description
GO:0005829	cytosol
GO:0043005	neuron projection
GO:0005874	microtubule
GO:0120025	plasma membrane bounded cell projection
GO:0045202	synapse

Reactome Pathway

Term ID	Term Description
MMU-112310	Neurotransmitter release cycle
MMU-109581	Apoptosis
MMU-1266738	Developmental Biology

PFAM Protein Domain

Term ID	Term Description
PF00418	Tau and MAP protein, tubulin-binding repeat
PF00183	Hsp90 protein
PF00307	Calponin homology (CH) domain
PF13589	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
PF00004	ATPase family associated with various cellular activities (A

Enriched in P35 mouse hippocampus and cortex expressing BioID2-hTauFL

Molecular Function

Term ID	Term Description
GO:0008092	cytoskeletal protein binding
GO:0005515	protein binding
GO:0015631	tubulin binding
GO:0005488	binding
GO:0008017	microtubule binding

Biological Process

Term ID	Term Description
GO:0051641	cellular localization

GO:0016043	cellular component organization
GO:0051128	regulation of cellular component organization
GO:0051649	establishment of localization in cell
GO:0031175	neuron projection development

Cell Component

Term ID	Term Description
GO:0044456	synapse part
GO:0097458	neuron part
GO:0043005	neuron projection
GO:0120038	plasma membrane bounded cell projection part
GO:0030424	axon

KEGG Pathway

Term ID	Term Description
mmu04721	Synaptic vesicle cycle
mmu04911	Insulin secretion
mmu04922	Glucagon signaling pathway
mmu05205	Proteoglycans in cancer

Reactome Pathway

Term ID	Term Description
MMU-112316	Neuronal System
MMU-199991	Membrane Trafficking
MMU-8856828	Clathrin-mediated endocytosis
MMU-264870	Caspase-mediated cleavage of cytoskeletal proteins
MMU-112315	Transmission across Chemical Synapses

PFAM Protein Domain

Term ID	Term Description
PF00418	Tau and MAP protein, tubulin-binding repeat
PF03271	EB1-like C-terminal motif
PF00307	Calponin homology (CH) domain
PF14604	Variant SH3 domain
PF00735	Septin

Enriched in Tau(-/-) adult mouse hippocampus expressing BioID2-hTauFL

Molecular Function

Term ID	Term Description
GO:0008092	cytoskeletal protein binding
GO:0008017	microtubule binding
GO:0005515	protein binding
GO:0005488	binding
GO:0043168	anion binding

Biological Process

Term ID	Term Description
GO:0051128	regulation of cellular component organization
GO:0007010	cytoskeleton organization
GO:0033043	regulation of organelle organization
GO:0044087	regulation of cellular component biogenesis
GO:0051656	establishment of organelle localization

Cell Component

Term ID	Term Description
GO:0044463	cell projection part
GO:0097458	neuron part
GO:0005737	cytoplasm
GO:0120038	plasma membrane bounded cell projection part
GO:0044444	cytoplasmic part

KEGG Pathway

Term ID	Term Description
mmu04144	Endocytosis
mmu04728	Dopaminergic synapse
mmu04070	Phosphatidylinositol signaling system
mmu04310	Wnt signaling pathway
mmu04340	Hedgehog signaling pathway

Reactome Pathway

Term ID	Term Description
MMU-2565942	Regulation of PLK1 Activity at G2/M Transition
MMU-380259	Loss of Nlp from mitotic centrosomes
MMU-380270	Recruitment of mitotic centrosome proteins and complexes
MMU-380284	Loss of proteins required for interphase microtubule organ
MMU-380287	Centrosome maturation

PFAM Protein Domain

Term ID	Term Description
PF00418	Tau and MAP protein, tubulin-binding repeat
PF00289	Biotin carboxylase, N-terminal domain
PF07478	D-ala D-ala ligase C-terminus
PF01504	Phosphatidylinositol-4-phosphate 5-Kinase
PF02786	Carbamoyl-phosphate synthase L chain, ATP binding dom
PF00169	PH domain
PF01369	Sec7 domain
PF03271	EB1-like C-terminal motif
PF00069	Protein kinase domain

gy of biotinylated network proteins.

Observed Gene Cou	Background Gene Cour	False Discovery Rate
17	877	5.30E-13
11	336	3.05E-10
9	245	9.95E-09
9	659	1.84E-05
7	397	6.08E-05

Observed Gene Cou	Background Gene Cour	False Discovery Rate
23	2805	2.53E-10
27	4560	2.70E-10
7	83	2.45E-08
12	637	3.08E-08
12	687	6.00E-08

Observed Gene Cou	Background Gene Cour	False Discovery Rate
24	3326	1.58E-10
17	1429	7.64E-10
11	377	7.93E-10
19	2172	2.39E-09
13	968	2.20E-08

Observed Gene Cou	Background Gene Cour	False Discovery Rate
2	44	0.0205
2	93	0.0423
3	340	0.0467

Observed Gene Cou	Background Gene Cour	False Discovery Rate
3	3	3.72E-06
2	4	0.00096
3	67	0.0032
2	14	0.0038
2	56	0.0336

Observed Gene Cou	Background Gene Cour	False Discovery Rate
28	877	3.87E-21
50	6454	1.82E-16
16	336	6.12E-14
57	10884	1.04E-13
14	245	2.75E-13

Observed Gene Cou	Background Gene Cour	False Discovery Rate
28	1792	2.49E-12

39	4560	5.56E-11
29	2337	7.55E-11
22	1260	1.87E-10
17	637	1.91E-10

Observed Gene Cou	Background Gene Cour	False Discovery Rate
35	809	3.91E-32
42	1732	8.21E-31
38	1429	1.33E-28
38	1532	1.31E-27
29	712	1.22E-25

Observed Gene Cou	Background Gene Cour	False Discovery Rate
4	62	0.0018
4	85	0.0029
3	99	0.0431
4	199	0.0431

Observed Gene Cou	Background Gene Cour	False Discovery Rate
8	300	0.00015
10	523	0.00015
6	117	0.00015
3	12	0.00026
6	187	0.00034

Observed Gene Cou	Background Gene Cour	False Discovery Rate
3	3	3.02E-05
3	3	3.02E-05
5	67	3.89E-05
6	150	7.79E-05
3	13	0.00017

Observed Gene Cou	Background Gene Cour	False Discovery Rate
27	877	1.02E-13
16	245	2.36E-12
62	6456	1.24E-11
79	10884	6.86E-11
38	2578	6.86E-11

Observed Gene Cou	Background Gene Cour	False Discovery Rate
41	2337	4.54E-13
24	916	6.53E-10
26	1127	6.53E-10
23	863	6.53E-10
16	324	6.53E-10

Observed Gene Cou	Background Gene Cour	False Discovery Rate
39	1532	9.41E-19
41	1732	9.42E-19
86	9909	9.57E-19
39	1532	9.41E-19
75	7673	1.44E-17

Observed Gene Cou	Background Gene Cour	False Discovery Rate
9	258	0.00027
6	129	0.0017
5	96	0.0022
6	146	0.0022
4	44	0.0022

Observed Gene Cou	Background Gene Cour	False Discovery Rate
6	80	0.00013
6	64	0.00013
6	73	0.00013
6	64	0.00013
6	73	0.00013

Observed Gene Cou	Background Gene Cour	False Discovery Rate
3	3	0.00019
3	5	0.00027
3	6	0.00027
3	8	0.00031
3	8	0.00031
7	189	0.00032
3	15	0.00085
2	3	0.0024
9	492	0.0032

Matching proteins in your network (labels)
Hsp90ab1,Bin1,Mapre1,Stmn1,Map4,Sncb,Map6,Map1b,Plec,Map2,Hsp90aa1,
Mapre1,Stmn1,Map4,Sncb,Map6,Map1b,Map2,Map1a,Mapt,Gapdh,Camsap3
Mapre1,Map4,Map6,Map1b,Map2,Map1a,Mapt,Gapdh,Camsap3
Pak2,Hsp90ab1,Mapre1,Cadps,Map2,Hsp90aa1,Mapt,Actb,Nsf
Bin1,Map1b,Plec,Map2,Map1a,Tagln3,Camsap3

Matching proteins in your network (labels)
G3bp1,Pak2,Hsp90ab1,Bin1,Stmn1,Vamp1,Map4,Atxn2l,Hist1h2be,Cadps,Map
G3bp1,Pak2,Hsp90ab1,Bin1,Napg,Stmn1,Vamp1,Map4,Atxn2l,Sncb,Hist1h2be,
Mapre1,Stmn1,Map1b,Map2,Map1a,Mapt,Camsap3
Pak2,Hsp90ab1,Stmn1,Map4,Map6,Map1b,Map2,Hsp90aa1,Mapt,Actb,Cttn,Ca
G3bp1,Hsp90ab1,Bin1,Vamp1,Atxn2l,Hist1h2be,Cadps,Nap1l4,Hsp90aa1,Map

Matching proteins in your network (labels)
Tbcb,G3bp1,Pak2,Hsp90ab1,Bin1,Stmn1,Map4,Atxn2l,Cplx1,Hist1h2be,Map1b,
Hsp90ab1,Bin1,Stmn1,Vamp1,Map4,Cplx1,Sncb,Map6,Map1b,Nap1l4,Map2,Hs
Tbcb,Bin1,Mapre1,Stmn1,Map4,Map6,Map1b,Map2,Map1a,Mapt,Camsap3
Hsp90ab1,Bin1,Mapre1,Stmn1,Vamp1,Map4,Cplx1,Sncb,Map6,Map1b,Nap1l4,
Bin1,Vamp1,Map4,Cplx1,Sncb,Cadps,Map1b,Map2,Map1a,Mapt,Actb,Nsf,Cttn

Matching proteins in your network (labels)
Cplx1,Gls
Plec,Mapt
Pak2,Hsp90ab1,Actb

Matching proteins in your network (labels)
Map4,Map2,Mapt
Hsp90ab1,Hsp90aa1
Mapre1,Plec,Tagln3
Hsp90ab1,Hsp90aa1
Nsf,Ruvbl2

Matching proteins in your network (labels)
Ank2,Baiap2,Bin1,Camsap3,Dbnl,Dpysl2,Epb4.1l1,Epb4.1l3,Lasp1,Map1a,Map
Aak1,Amph,Ank2,Baiap2,Basp1,Bin1,Bsn,Camk2a,Camk2b,Camsap3,Cplx2,Db
Camsap3,Dpysl2,Map1a,Map1b,Map2,Map4,Map6,Mapre1,Mapre2,Mapre3,Ma
Aak1,Amph,Ank2,Baiap2,Basp1,Bin1,Bsn,Camk2a,Camk2b,Camsap3,Cplx2,Db
Camsap3,Dpysl2,Map1a,Map1b,Map2,Map4,Map6,Mapre1,Mapre2,Mapre3,Ma

Matching proteins in your network (labels)
Amph,Ank2,Bin1,Bsn,Camk2a,Camsap3,Cplx2,Dnajc6,Dpysl2,Epb4.1l3,Gpr158

Ank2,Baiap2,Bin1,Bsn,Camk2a,Camk2b,Camsap3,Dbnl,Dclk1,Dnajc6,Dpysl2,E
Aak1,Baiap2,Bin1,Camk2b,Camsap3,Dnajb1,Dnajc6,Dpysl2,Eif4g3,Epb4.1l3,M
Amph,Bin1,Bsn,Camsap3,Cplx2,Dnajc6,Dpysl2,Map1a,Map1b,Map4,Map6,Map
Baiap2,Camk2a,Camsap3,Dbnl,Dclk1,Dpysl2,Epb4.1l3,Map1b,Map2,Map4,Map

Matching proteins in your network (labels)
Aak1,Amph,Ank2,Baiap2,Bin1,Bsn,Camk2a,Camk2b,Cplx2,Dbnl,Dclk1,Dnajb1,I
Aak1,Amph,Ank2,Baiap2,Basp1,Bin1,Bsn,Camk2a,Camk2b,Cplx2,Dbnl,Dclk1,D
Aak1,Amph,Baiap2,Basp1,Bin1,Bsn,Camk2a,Camk2b,Cplx2,Dbnl,Dnajb1,Dpysl
Aak1,Amph,Baiap2,Basp1,Bin1,Bsn,Camk2a,Camk2b,Cplx2,Dbnl,Dnajb1,Dpysl
Aak1,Amph,Basp1,Bin1,Bsn,Camk2a,Cplx2,Dpysl2,Epb4.1l3,Map1a,Map1b,Ma

Matching proteins in your network (labels)
Cplx2,Nsf,Snap25,Vamp2
Camk2a,Camk2b,Snap25,Vamp2
Camk2a,Camk2b,Pgam1
Ank2,Camk2a,Camk2b,Eif4b

Matching proteins in your network (labels)
Camk2a,Camk2b,Dbnl,Epb4.1l3,Nsf,Snap25,Syn1,Vamp2
Aak1,Amph,Ank2,Bin1,Dnajc6,Napg,Nsf,Sh3gl2,Tubb4a,Vamp2
Aak1,Amph,Bin1,Dnajc6,Sh3gl2,Vamp2
Dbnl,Mapt,Plec
Camk2a,Camk2b,Nsf,Snap25,Syn1,Vamp2

Matching proteins in your network (labels)
Map2,Map4,Mapt
Mapre1,Mapre2,Mapre3
Mapre1,Mapre2,Mapre3,Plec,Tagln3
Amph,Baiap2,Bin1,Dbnl,Lasp1,Sh3gl2
Sept5,Sept7,Sept9

Matching proteins in your network (labels)
Actr3,Actr3b,Ank2,Apc,Camsap3,Cetn2,Clasp2,Clip2,Dctn2,Epb4.1,Gsk3b,Kif5c
Apc,Camsap3,Cetn2,Clasp2,Clip2,Kif5c,Map1b,Map2,Map4,Map6,Mapre1,Map
Abi2,Actr3,Actr3b,Adrbk1,Ahi1,Ank2,Apc,Arhgdia,Asap1,Camk2a,Camsap3,Cetn
Abi2,Actr3,Actr3b,Adrbk1,Adss,Ahi1,Ank2,Apc,Arhgdia,Asap1,Cadps2,Calb2,Ca
Actr3,Actr3b,Adrbk1,Adss,Arhgdia,Asap1,Camk2a,Csnk1e,Cyth2,Cyth3,Dclk2,D

Matching proteins in your network (labels)
Abi2,Actr3,Actr3b,Ahi1,Apc,Arhgdia,Asap1,Camsap3,Clasp2,Crkl,Csnk1e,Cyth2
Abi2,Actr3,Actr3b,Apc,Camsap3,Cetn2,Clasp2,Dclk2,Dctn2,Epb4.1,Gsk3b,Map1
Abi2,Actr3,Actr3b,Apc,Arhgdia,Asap1,Camsap3,Clasp2,Gsk3a,Gsk3b,Map1b,Ma
Abi2,Actr3,Actr3b,Apc,Asap1,Camsap3,Clasp2,Dnajb1,Eif4g1,Gsk3b,Map1b,Ma
Actr3,Ahi1,Cadps2,Clasp2,Cplx1,Dctn2,Kiaa1107,Map1b,Map4,Map6,Mapt,Myo

Matching proteins in your network (labels)
Abi2,Actr3,Adrbk1,Ahi1,Apc,Asap1,Calb2,Camk2a,Cep170,Cetn2,Clasp2,Clip2,
Abi2,Adrbk1,Ahi1,Ank2,Apc,Asap1,Cadps2,Calb2,Camk2a,Cetn2,Clasp2,Clip2,
Abi2,Actr3,Actr3b,Adrbk1,Adss,Ahi1,Ank2,Apc,Arhgdia,Asap1,Cadps2,Calb2,Ca
Abi2,Actr3,Adrbk1,Ahi1,Apc,Asap1,Calb2,Camk2a,Cep170,Cetn2,Clasp2,Clip2,
Abi2,Actr3,Adrbk1,Adss,Ahi1,Ank2,Apc,Arhgdia,Asap1,Cadps2,Calb2,Camk2a,(

Matching proteins in your network (labels)
Adrbk1,Asap1,Cyth1,Cyth2,Cyth3,Kif5c,Smap1,Vps25,Zfyve20
Camk2a,Gsk3a,Gsk3b,Kif5c,Prkaca,Prkcg
Pip4k2a,Pip4k2b,Pip4k2c,Prkcg,Synj1
Apc,Camk2a,Csnk1e,Gsk3b,Prkaca,Prkcg
Adrbk1,Csnk1e,Gsk3b,Prkaca

Matching proteins in your network (labels)
Cetn2,Csnk1e,Dctn2,Mapre1,Prkaca,Tuba1a
Cetn2,Csnk1e,Dctn2,Mapre1,Prkaca,Tuba1a
Cetn2,Csnk1e,Dctn2,Mapre1,Prkaca,Tuba1a
Cetn2,Csnk1e,Dctn2,Mapre1,Prkaca,Tuba1a
Cetn2,Csnk1e,Dctn2,Mapre1,Prkaca,Tuba1a

Matching proteins in your network (labels)
Map2,Map4,Mapt
Mccc1,Pcca,Pcx
Mccc1,Pcca,Pcx
Pip4k2a,Pip4k2b,Pip4k2c
Mccc1,Pcca,Pcx
Adrbk1,Asap1,Cadps2,Cnksr2,Cyth1,Cyth2,Cyth3
Cyth1,Cyth2,Cyth3
Mapre1,Mapre3
Adrbk1,Camk2a,Csnk1e,Dclk2,Gsk3a,Gsk3b,Map4k4,Prkaca,Prkcg

Map1a,Tagln3,Mapt,Actb,Gapdh,Camsap3

6,Map1b,Nap1l4,Plec,Map2,Hsp90aa1,Map1a,Mapt,Actb,Cttn,Ruvbl2,Gapdh,Ca
,Cadps,Map6,Map1b,Nap1l4,Plec,Map2,Hsp90aa1,Map1a,Mapt,Actb,Nsf,Cttn,Ru

msap3
t,Cttn,Ruvbl2

,Plec,Map2,Hsp90aa1,Map1a,Hk1,Mapt,Actb,Nsf,Cttn,Ruvbl2,Gls,Gapdh,Nfat5
sp90aa1,Map1a,Mapt,Actb,Nsf,Cttn

Map2,Hsp90aa1,Map1a,Hk1,Mapt,Actb,Nsf,Cttn

1b,Map2,Map4,Map6,Mapre1,Mapre2,Mapre3,Mapt,Plec,Snap25,Snca,Sncb,Sp
nl,Dnajb1,Dnajc6,Dpysl2,Epb4.1l1,Epb4.1l3,Lasp1,Map1a,Map1b,Map2,Map4,I
pt,Snca,Sncb,Spast,Stmn1,Tppp
nl,Dclk1,Dnajb1,Dnajc6,Dpysl2,Eif4b,Eif4g3,Eif4h,Epb4.1l1,Epb4.1l3,Lasp1,Ma
pt,Snca,Spast,Tppp

,Map1a,Map1b,Map4,Map6,Mapre1,Mapt,Napg,Nefm,Nsf,Pacs1,Sh3gl2,Snap25

if4b,Eif4h,Epb4.1l1,Epb4.1l3,Map1a,Map1b,Map2,Map4,Map6,Mapt,Nap1l4,Na
ap1a,Map1b,Map2,Map4,Map6,Mapre1,Mapt,Nefm,Nsf,Sept7,Sept9,Sh3gl2,Sna
t,Napg,Nefm,Nsf,Sh3gl2,Snap25,Snap91,Snca,Spast,Syn1,Vamp2
6,Mapt,Nefm,Sept7,Sh3gl2,Snap91,Stmn1

Dnajc6,Dpysl2,Epb4.1l1,Epb4.1l3,Map1a,Map1b,Map2,Map4,Mapt,Nefm,Nrgn,N
najb1,Dnajc6,Dpysl2,Eif4b,Epb4.1l1,Epb4.1l3,Map1a,Map1b,Map2,Map4,Map6
l2,Eif4b,Epb4.1l3,Map1a,Map1b,Map2,Map4,Map6,Mapt,Nap1l4,Nefm,Nrgn,Nsf,
l2,Eif4b,Epb4.1l3,Map1a,Map1b,Map2,Map4,Map6,Mapre1,Mapt,Nap1l4,Nrgn,N
p2,Map4,Map6,Mapt,Nefm,Nrgn,Sept5,Sept7,Snap25,Snap91,Snca,Sncb,Spast,

,Lasp1,Map1b,Map2,Map4,Map6,Mapre1,Mapre3,Mapt,Myo5a,S100a6,Shroom2
re3,Mapt,Myo5a,Spast,Tppp
n2,Clasp2,Clip2,Cnksr2,Cplx1,Crkl,Cyth1,Cyth2,Cyth3,Dctn2,Dnajb1,Eef1a2,Eif4
mk2a,Camsap3,Cetn2,Clasp2,Clip2,Cnksr2,Cplx1,Crkl,Csnk1e,Cyth1,Cyth2,Cy
fna5,Drg2,Eef1a2,Eif4g1,Epb4.1,Gsk3a,Gsk3b,Kif5c,Map1b,Map4k4,Mccc1,Myo

,Dnajb1,Eif4g1,Epb4.1,Gsk3a,Gsk3b,Map1b,Map2,Map4,Map4k4,Map6,Mapre1
b,Map2,Map4,Map6,Map7d2,Mapt,Ranbp1,Rufy3,Sept7,Spast,Tmod2,Tppp,Tub
ap2,Map4,Map6,Mapre1,Mapt,Pip4k2a,Pip4k2b,Pip4k2c,Ranbp1,Sept7,Sept9,S
p4,Mapre1,Mapt,Pip4k2a,Pip4k2b,Pip4k2c,Prkaca,Sept7,Sept9,Snap91,Tmod2,
5a,Shroom2,Snap91,Spast,Synj1

,Cplx1,Csnk1e,Cyth2,Dctn2,Dnajb1,Gsk3b,Kiaa1107,Kif5c,Map1b,Map2,Map4,M
Cnksr2,Cplx1,Csnk1e,Cyth2,Dctn2,Dnajb1,Eef1a2,Epb4.1,Gsk3b,Kiaa1107,Kif5
ımk2a,Camsap3,Cdv3,Cep170,Cetn2,Clasp2,Clip2,Cnksr2,Cplx1,Crkl,Csnk1e,C
,Cplx1,Csnk1e,Cyth2,Dctn2,Dnajb1,Gsk3b,Kiaa1107,Kif5c,Map1b,Map2,Map4,M
Cdv3,Cep170,Cetn2,Clasp2,Clip2,Cplx1,Crkl,Csnk1e,Cyth1,Cyth3,Dctn2,Dfna5,I

ımsap3
ɹvbl2,Gls,Gapdh,Camsap3

ast,Stmn1,Syn1,Tagln3,Tppp,Vamp2
Map6,Mapre1,Mapre2,Mapre3,Mapt,Napg,Nefm,Nrgn,Nsf,Pacs1,Pcx,Pgam1,Ple

p1a,Map1b,Map2,Map4,Map6,Mapre1,Mapre2,Mapre3,Mapt,Nap1l4,Napg,Nefm

5,Snap91,Snca,Spast,Syn1,Vamp2

ɔg,Nefm,Nsf,Plec,Sept7,Sept9,Sh3gl2,Snap25,Snap91,Snca,Sncb,Spast,Srcin1,
ıp25,Snap91,Snca,Srcin1,Stmn1,Tppp,Tubb4a

lsf,Sept5,Sept7,Sh3gl2,Snap25,Snap91,Snca,Sncb,Srcin1,Sv2a,Syn1,Vamp2
,Mapt,Nap1l4,Nefm,Nrgn,Nsf,Sept5,Sept7,Sh3gl2,Snap25,Snap91,Snca,Sncb,S
Sept5,Sept7,Sh3gl2,Snap25,Snap91,Snca,Sncb,Spast,Srcin1,Stmn1,Sv2a,Syn1
lsf,Sept5,Sept7,Sept9,Sh3gl2,Snap25,Snap91,Snca,Sncb,Spast,Srcin1,Sv2a,Syı
Srcin1,Sv2a,Syn1,Tubb4a,Vamp2

2,Spast,Tagln3,Tmod2,Tppp

ŀg1,Ensa,Epb4.1,Gsk3a,Gsk3b,Kif5c,Lasp1,Map1b,Map2,Map4,Map6,Mapre1,M
th3,Dclk2,Dctn2,Dfna5,Dnajb1,Drg2,Eef1a2,Eif4g1,Ensa,Epb4.1,Gsk3a,Gsk3b,K
5a,Nars,Nrgn,Pcca,Pcx,Pip4k2a,Pip4k2b,Pip4k2c,Prkaca,Prkcg,Sept7,Sept9,Sna

,Mapt,Mgea5,Pip4k2a,Pip4k2b,Pip4k2c,Prkaca,Prkcg,Ranbp1,Rufy3,Sept7,Sept
ɔa1a
hroom2,Synj1,Tmod2,Zfyve20
Tppp

Map6,Mapre1,Mapt,Myo5a,Nap1l4,Nrgn,Prkaca,Prkcg,Ranbp1,Rufy3,Sept7,Sept9
c,Map1b,Map2,Map4,Map6,Mapt,Myo5a,Nap1l4,Nrgn,Prkaca,Prkcg,Ranbp1,Ruf
Cyth1,Cyth2,Cyth3,Dclk2,Dctn2,Dfna5,Dnajb1,Drg2,Eef1a2,Eif4g1,Ensa,Epb4.1,F
Map6,Mapre1,Mapt,Myo5a,Nap1l4,Nrgn,Prkaca,Prkcg,Ranbp1,Rufy3,Sept7,Sept9
Dnajb1,Drg2,Eef1a2,Eif4g1,Epb4.1,Fam110b,Gsk3a,Gsk3b,Kiaa1107,Kif5c,Lasp

c,Sept5,Sept7,Sh3gl2,Snap25,Snap91,Snca,Sncb,Spast,Srcin1,Stmn1,Sv2a,Syn

ı,Nrgn,Nsf,Pacs1,Pcx,Pgam1,Plec,Sept5,Sept7,Sept9,Sh3gl2,Snap25,Snap91,Sı

Stmn1,Tppp,Tubb4a,Vamp2

past,Srcin1,Stmn1,Sv2a,Syn1,Tubb4a,Vamp2
,Tubb4a,Vamp2
ɲ1,Tubb4a,Vamp2

apre3,Mapt,Myo5a,Naca,Nrgn,Pcca,Pcx,Pdap1,Pgam1,Pip4k2b,Pip4k2c,Ppp1r1
if5c,Lasp1,Map1b,Map2,Map4,Map4k4,Map6,Mapre1,Mapre3,Mapt,Mccc1,Myo5
ap91,Spast,Stard5,Tuba1a

:9,Shroom2,Smap1,Snap91,Synj1,Tmod2,Tppp,Zfyve20

9,Snap91,Spast,Synj1,Tmod2
fy3,Sept7,Shroom2,Snap91,Spast,Synj1,Tmod2
:am110b,Gsk3a,Gsk3b,Hn1,Kiaa1107,Kif5c,Lasp1,Map1b,Map2,Map4,Map4k4,M
9,Snap91,Spast,Synj1,Tmod2
)1,Map1b,Map2,Map4,Map6,Mapre1,Mapre3,Mapt,Mccc1,Mgea5,Myo5a,Naca,N

ı1,Tagln3,Tppp,Vamp2

ıca,Sncb,Spast,Srcin1,Stmn1,Sv2a,Syn1,Tagln3,Tppp,Tubb4a,Vamp2

1,Prkaca,Ranbp1,S100a6,Sept7,Shroom2,Smap1,Snap91,Spast,Synj1,Tagln3,T
ba,Naca,Nap1l4,Nars,Nktr,Nrgn,Pcca,Pcx,Pdap1,Pgam1,Pip4k2a,Pip4k2b,Pip4k

Map6,Mapre1,Mapre3,Mapt,Mccc1,Mgea5,Myo5a,Naca,Nap1l4,Nars,Nktr,Nrgn,P

lars,Nktr,Nrgn,Pcca,Pcx,Pdap1,Pgam1,Pip4k2a,Pip4k2b,Pip4k2c,Ppp1r11,Prkac

Γmod2,Tppp,Tuba1a,Vps25,Zfyve20
2c,Ppp1r11,Prkaca,Prkcg,Ranbp1,Rnf214,S100a6,Sept7,Sept9,Shroom2,Smap´

ᵖcca,Pcx,Pdap1,Pgam1,Pip4k2a,Pip4k2b,Pip4k2c,Plcxd3,Ppp1r11,Prkaca,Prkcg

ːa,Prkcg,Ranbp1,Rtn1,Rufy3,S100a6,Sept7,Sept9,Shroom2,Snap91,Spast,Stard

l,Snap91,Spast,Stard5,Synj1,Tagln3,Tmod2,Tppp,Tuba1a,Vps25,Zfyve20

,Ranbp1,Rtn1,Rufy3,S100a6,Sept7,Sept9,Shroom2,Smap1,Snap91,Spast,Stard

5,Synj1,Tmod2,Tppp,Tuba1a,Vps25,Zfyve20

5,Synj1,Tmod2,Tppp,Tuba1a,Vps25,Zfyve20

Table 5. **Reported tau interactors**. Biotinylated proteins previously identified as tau

Tau interactor (Gene Name)	Experimental Method	Author
ACTA1	Reconstituted Complex	He HJ (2009)
ACTB	Affinity Capture-Western	Brandt R (1995)
Alb	Affinity Capture-MS	Hashimoto S (2019)
Aldoa	Affinity Capture-MS	Hashimoto S (2019)
AMPH	Reconstituted Complex	Chapuis J (2013)
Ank2	Imaging analysis	Higham J (2019)
Snap91	Affinity Capture-MS	Hashimoto S (2019)
Apc	Affinity Capture-MS	Hashimoto S (2019)
Atxn2l	Affinity Capture-MS	Hashimoto S (2019)
Baiap2	Cross link-MS	Sinsky J (2020)
Basp1	Affinity Capture-MS	Tagawa K (2015)
BIN1	Affinity Capture-Western, Reconstitu	Chapuis J (2013)
CALM1	Affinity Capture-MS	Gunawardana CG (2015)
Camsap3	Affinity Capture-MS	Hashimoto S (2019)
CCDC124	Affinity Capture-MS	Gunawardana CG (2015)
CKAP5	Affinity Capture-MS	Hein MY (2015)
Clasp2	Affinity Capture-MS	Hashimoto S (2019)
Clip2	Affinity Capture-MS	Hashimoto S (2019)
Dlgap3	Affinity Capture-MS	Hashimoto S (2019)
Dpysl2	Affinity Capture-MS	Hashimoto S (2019)
G3BP1	Affinity Capture-MS	Gunawardana CG (2015)
Glul	Affinity Capture-MS	Hashimoto S (2019)
GSK3A	Biochemical Activity	Sengupta A (2006)
GSK3B	Biochemical Activity	Sadik G (2009)
HSPA1A	Affinity Capture-Western, Reconstitu	Jinwal UK (2012)
Hsp90aa1	Affinity Capture-MS	Hashimoto S (2019)
HSPA8	Affinity Capture-Western	Elliott E (2007)
Eif4b	Affinity Capture-MS	Hashimoto S (2019)
Eif4g1	Affinity Capture-MS	Hashimoto S (2019)
PRKACA	Biochemical Activity	Cook C (2014)
CAMK2A	Biochemical Activity	Sengupta A (2006)
Camk2b	Affinity Capture-MS	Hashimoto S (2019)
CAMK2D	Protein Kinase Assay	Seward M (2008)
Kif5c	Affinity Capture-MS	Hashimoto S (2019)
PRKCB	Biochemical Activity	Taniguchi T (2001)
PRKCG	Biochemical Activity	Taniguchi T (2001)
Map4	Affinity Capture-MS	Gunawardana CG (2015)
Map6	Imaging analysis	Tortosa E (2017)
MAPRE1	Affinity Capture-Western & Chromat	Sayas C (2019)
Mapre2	Affinity Capture-MS	Maziuk B (2018)
MAPRE3	Affinity Capture-Western & Chromat	Sayas C (2019)
MAPK12	Biochemical Activity	Feijoo C (2005)
MAP2	Reconstituted Complex, Co-fraction	Alonso AD (1997)
Nrgn	Affinity Capture-Western	Stefanoska K (2018)

Nefm	Biochemical Activity	Farias G (2002)
Nktr	Affinity Capture-MS	Hashimoto S (2019)
NMT1	Affinity Capture-MS	Gunawardana CG (2015)
Nsf	Affinity Capture-MS	Hashimoto S (2019)
Sh3gl2	Biochemical Activity	Pérez M (1996)
Snap25	Imaging analysis	Batista A (2017)
Spast	Imaging analysis	Zempel H (2015)
Sptbn2	Affinity Capture-MS	Hashimoto S (2019)
SPTAN1	Affinity Capture-Radiolabelling	Carlier MF (1984)
Sorbs1	Affinity Capture-MS	Hashimoto S (2019)
Stmn1	Affinity Capture-MS	Weingarten J (2014)
Sv2a	Affinity Capture-MS	Hashimoto S (2019)
Syn1	Affinity Capture-Western	Stefanoska K (2018)
SNCA	Affinity Capture-Western	Benussi L (2005)
Sncb	Affinity Capture-MS	Hashimoto S (2019)
TAGLN3	Affinity Capture-MS	Hashimoto S (2019)
Tanc1	Affinity Capture-MS	Hashimoto S (2019)
MAPT	Reconstituted Complex	Alonso Adel C (2006)
Mapt	Affinity Capture-MS	Hashimoto S (2019)
Tnks1bp1	Affinity Capture-MS	Hashimoto S (2019)
TUBA1A	Co-purification	Alim MA (2002)
TUBA1B	Reconstituted Complex	Ding H (2006)
TUBB2A	In vitro Assay	Chau M (1998)
Tubb4a	Affinity Capture-MS	Hashimoto S (2019)
TUBB4B	Co-sedimentation Assay	Kislinger T (2006)
Tbcb	Affinity Capture-MS	Hashimoto S (2019)
Tppp	Affinity Capture-MS	Weingarten J (2014)
VAMP2	FRAP, Affinity Capture-Western	Zhou L (2017)

protein-protein interactors (72).

Publication Source Identifier	Throughput	Search Source
PMID: 19895707	Low Throughput	BioGRID
PMID: 8522593	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 23399914	Low Throughput	BioGRID
PMID: 31244615	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 32357304	High Throughput	Manual search
PMID: 25231903	High Throughput	Manual search
PMID: 23399914	Low Throughput	STRING
PMID: 26269332	High Throughput	BioGRID
PMID: 31263162	High Throughput	Manual search
PMID: 26269332	High Throughput	BioGRID
PMID: 26496610	High Throughput	BioGRID
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 26269332	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 17045592	Low Throughput	Manual search
PMID: 19014373	Low Throughput	STRING
PMID: 23271055	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 17954934	Low Throughput	Manual search
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PMID: 23962722	Low Throughput	Manual search
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PMID: 18588881	Low Throughput	STRING
PMID: 31263162	High Throughput	Manual search
PMID: 11104762	Low Throughput	Manual search
PMID: 11104762	Low Throughput	Manual search
PMID: 26269332	High Throughput	Manual search
PMID: 28521134	Low Throughput	Manual search
PMCID:6342323	Low Throughput	Manual search
PMID: 30068389	High Throughput	BioGRID
PMCID:6342323	Low Throughput	Manual search
PMID: 15632108	Low Throughput	Manual search
PMID: 8990203	Low Throughput	Manual search
PMCID:5846163	Low Throughput	Manual search

PMID: 11948687	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 26269332	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 8752125	Low Throughput	Manual search
PMID: 28954226	Low Throughput	Manual search
PMID: 26691836	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 6743699	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 24534009	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMCID:5846163	Low Throughput	Manual search
PMID: 15904919	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 16735465	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 11698390	Low Throughput	STRING
PMID: 16687396	Low Throughput	Manual search
PMID: 9922135	Low Throughput	Manual search
PMID: 31263162	High Throughput	Manual search
PMID: 16615898	High Throughput	STRING
PMID: 31263162	High Throughput	Manual search
PMID: 24534009	High Throughput	Manual search
PMID: 28492240	Low Throughput	Manual search

Table 6. **Tau interactors in primary neurons.** Expression of BioID2-tau in primary cortical

Protein	Protein description and gene name
41	Protein 4.1, Gene: Epb41
AAK1	AP2-associated protein kinase 1, Gene: Aak1
ACTC	Actin, alpha cardiac muscle 1, Gene: Actc1
ALBU	Serum albumin OS=Bos taurus Gene: ALB
ALDOA	Fructose-bisphosphate aldolase A, Gene: Aldoa
ANK2	Ankyrin-2, Gene: Ank2
AP180	Clathrin coat assembly protein AP180, Gene: Snap91
ARBK1	Beta-adrenergic receptor kinase 1, Gene: GRK2
ARPC2	Actin-related protein 2/3 complex subunit 2, Gene: Arpc2
ATX2L	Ataxin-2-like protein, Gene: Atxn2l
BIN1	Myc box-dependent-interacting protein 1, Gene: Bin1
CA123	UPF0587 protein C1orf123 homolog
CAMP3	Calmodulin-regulated spectrin-associated protein 3, Gene: Camsap3
CAPS1	Calcium-dependent secretion activator 1, Gene: Cadps
CE170	Centrosomal protein of 170 kDa, Gene: Cep170
CLAP2	CLIP-associating protein 2, Gene: Clasp2
CPLX1	Complexin-1, Gene: Cplx1
CRKL	Crk-like protein, Gene: Crkl
DCTN2	Dynactin subunit 2, Gene: Dctn2
DNJB1	DnaJ homolog subfamily B member 1, Gene: Dnajb1
DPYL2	Dihydropyrimidinase-related protein 2, Gene: Dpysl2
E41L1	Band 4.1-like protein 1, Gene: Epb41l1
E41L2	Band 4.1-like protein 2, Gene: EPB41L2
EF1A1	Elongation factor 1-alpha 1, Gene: EEF1A1
ELOB	Elongin-B, Gene: Elob
G3BP1	Ras GTPase-activating protein-binding protein 1, Gene: G3bp1
G3P	Glyceraldehyde-3-phosphate dehydrogenase, Gene: Gapdh
GDIR1	Rho GDP-dissociation inhibitor 1, Gene: Arhgdia
GLSK	Glutaminase kidney isoform, mitochondrial, Gene: Gls
GP158	Probable G-protein coupled receptor 158, Gene: Gpr158
H2A1D	Histone H2A type 1-D, Gene: HIST1H2AD
H2B1B	Histone H2B type 1-B, Gene: Hist1h2bb
H2B1C	Histone H2B type 1-C/E/G, Gene: Hist1h2bc
H2B1L	Histone H2B type 1-L, Gene: HIST1H2BL
HINT1	Histidine triad nucleotide-binding protein 1, Gene: Hint1
HS90A	Heat shock protein HSP 90-alpha, Gene: Hsp90aa1
HS90B	Heat shock protein HSP 90-beta, Gene: HSP90AB1
HSP7C	Heat shock cognate 71 kDa protein, Gene: Hspa8
HXK1	Hexokinase-1, Gene: Hk1
IF4G3	Eukaryotic translation initiation factor 4 gamma 3, Gene: Eif4g3
IF4H	Eukaryotic translation initiation factor 4H, Gene: Eif4h
KAP2	cAMP-dependent protein kinase type II-alpha regulatory subunit, Gene: Prkar2a
KCC2D	Calcium/calmodulin-dependent protein kinase type II subunit delta, Gene: Camk2d
KIF5C	Kinesin heavy chain isoform 5C, Gene: Kif5c
LASP1	LIM and SH3 domain protein 1, Gene: Lasp1

M3K10	Mitogen-activated protein kinase kinase kinase 10, Gene: Map3k10
MAP1A	Microtubule-associated protein 1A, Gene: Map1a
MAP1B	Microtubule-associated protein 1B, Gene: Map1b
MAP4	Microtubule-associated protein 4, Gene: Map4
MAP6	Microtubule-associated protein 6, Gene: Map6
MARE1	Microtubule-associated protein RP/EB family member 1, Gene: Mapre1
MCCA	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial, Gene: Mccc1
MDHM	Malate dehydrogenase, mitochondrial, Gene: Mdh2
MTAP2	Microtubule-associated protein 2, Gene: Map2
NACA	Nascent polypeptide-associated complex subunit alpha,
NACAM	Nascent polypeptide-associated complex subunit alpha, muscle-specific form, Gene: N
NFAT5	Nuclear factor of activated T-cells 5, Gene: NFAT5
NKTR	NK-tumor recognition protein, Gene: NKTR
NMT1	Glycylpeptide N-tetradecanoyltransferase 1, Gene: Nmt1
NP1L4	Nucleosome assembly protein 1-like 4, Gene: Nap1l4
NSF	Vesicle-fusing ATPase, Gene: Nsf
PAK2	Serine/threonine-protein kinase PAK 2, Gene: Pak2
PCCA	Propionyl-CoA carboxylase alpha chain, mitochondrial, Gene: Pcca
PEBP1	Phosphatidylethanolamine-binding protein 1, Gene: Pebp1
PI42A	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha, Gene: Pip4k2a
PLEC	Plectin (Fragment), Gene: PLEC
PYC	Pyruvate carboxylase, mitochondrial, Gene: Pc
RBNS5	Rabenosyn-5, Gene: Rbsn
RTN4	Reticulon-4, Gene: Rtn4
RUVB2	RuvB-like 2, Gene: Ruvbl2
SEP5	Septin-5, Gene: Sept5
SH3G2	Endophilin-A1, Gene: Sh3gl2
SHAN2	SH3 and multiple ankyrin repeat domains protein 2, Gene: Shank2
SNAG	Gamma-soluble NSF attachment protein, Gene: Napg
SRC8	Src substrate cortactin, Gene: Cttn
SRCN1	SRC kinase signaling inhibitor 1, Gene: Srcin1
STMN1	Stathmin, Gene: Stmn1
SYUA	Alpha-synuclein, Gene: Snca
SYUB	Beta-synuclein, Gene: Sncb
TAGL3	Transgelin-3, Gene: Tagln3
TAU	Microtubule-associated protein tau, Gene: Mapt
TBA1A	Tubulin alpha-1A chain, Gene: TUBA1A
TBA1B	Tubulin alpha-1B chain, Gene: TUBA1B
TBB2A	Tubulin beta-2A chain, Gene: Tubb2a
TBB2B	Tubulin beta-2B chain, Gene: Tubb2b
TBB4B	Tubulin beta-4B chain, Gene: Tubb4b
TBB6	Tubulin beta-6 chain, Gene: TUBB6
TBCB	Tubulin-folding cofactor B, Gene: Tbcb
TCPE	T-complex protein 1 subunit epsilon, Gene: Cct5
TPPP	Tubulin polymerization-promoting protein, Gene: Tppp
VAMP1	Vesicle-associated membrane protein 1, Gene: Vamp1
VAMP2	Vesicle-associated membrane protein 2, Gene: Vamp2
VCIP1	Deubiquitinating protein VCIP135, Gene: Vcpip1

WIPF2	WAS/WASL-interacting protein family member 2, Gene: Wipf2

mouse neurons yields 93 unique biotinylated proteins (proteins unique to this exper

Jaca

imental group).

Table 7. **Ta**

Protein
41
AAK1
AFF2
ALDOA
AMPH
ANK2
AP180
ARBK1
ASAP1
AT1B3
AUXI
BASP1
BIN1
BSN
CA123
CAMP3
CC124
CEND
CPLX1
CPLX2
CSKI1
DC1L1
DCLK1
DCTN2
DLGP3
DNJB1
DPYL2
DYN1
E41L1
E41L3
G3P
GDIR1
GLNA
GP158
GRIN1
HAP28
HS71A
IF4B
IF4G3
KCC2A
KCC2D
KI21A
KPCB
KT3K
LASP1

MAP1A
MAP1B
MAP4
MAP6
MARE1
MARE2
MARE3
MCCA
MK12
MTAP2
NCAM1
NEUG
NFM
NKTR
NP1L4
NSF
PACS1
PAK2
PCCA
PCLO
PFD2
PI42A
PLEC
PYC
RBNS5
RTN3
RTN4
RUVB2
SEP5
SEP7
SH3G1
SH3G2
SHAN2
SNP25
SPAST
SPTN1
SRC8
SRCN1
STMN1
SV2A
SYN1
SYUA
SYUB
SYUG
TAGL2
TAGL3
TAU
TBB4A

TBCB
TPPP
VAMP1
VAMP2
VCIP1
WIPF2
WIPF3
ZC21A

ıu interactors in P35 mouse brain. Expression of BioID2-tau in P35 mouse cortex

Protein description and gene name
Protein 4.1, Gene: Epb41
AP2-associated protein kinase 1, Gene: Aak1
AF4/FMR2 family member 2, Gene: AFF2
Fructose-bisphosphate aldolase A, Gene: Aldoa
Amphiphysin, Gene: Amph
Ankyrin-2, Gene: Ank2
Clathrin coat assembly protein AP180, Gene: Snap91
Beta-adrenergic receptor kinase 1, Gene: Grk2
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1, Gene: Asap1
Sodium/potassium-transporting ATPase subunit beta-3, Gene: Atp1b3
Putative tyrosine-protein phosphatase auxilin, Gene: Dnajc6
Brain acid soluble protein 1, Gene: Basp1
Myc box-dependent-interacting protein 1, Gene: Bin1
Protein bassoon, Gene: Bsn
UPF0587 protein C1orf123 homolog,
Calmodulin-regulated spectrin-associated protein 3, Gene: Camsap3
Coiled-coil domain-containing protein 124, Gene: Ccdc124
Cell cycle exit and neuronal differentiation protein 1, Gene: Cend1
Complexin-1, Gene: Cplx1
Complexin-2, Gene: Cplx2
Caskin-1, Gene: Caskin1
Cytoplasmic dynein 1 light intermediate chain 1, Gene: Dync1li1
Serine/threonine-protein kinase DCLK1, Gene: Dclk1
Dynactin subunit 2, Gene: Dctn2
Disks large-associated protein 3, Gene: Dlgap3
DnaJ homolog subfamily B member 1, Gene: Dnajb1
Dihydropyrimidinase-related protein 2, Gene: Dpysl2
Dynamin-1, Gene: Dnm1
Band 4.1-like protein 1, Gene: Epb41l1
Band 4.1-like protein 3, Gene: Epb41l3
Glyceraldehyde-3-phosphate dehydrogenase, Gene: Gapdh
Rho GDP-dissociation inhibitor 1, Gene: Arhgdia
Glutamine synthetase, Gene: Glul
Probable G-protein coupled receptor 158, Gene: Gpr158
G protein-regulated inducer of neurite outgrowth 1, Gene: Gprin1
28 kDa heat- and acid-stable phosphoprotein, Gene: Pdap1
Heat shock 70 kDa protein 1A, Gene: Hspa1a
Eukaryotic translation initiation factor 4B, Gene: Eif4b
Eukaryotic translation initiation factor 4 gamma 3, Gene: Eif4g3
Calcium/calmodulin-dependent protein kinase type II subunit alpha, Gene: Camk2a
Calcium/calmodulin-dependent protein kinase type II subunit delta, Gene: Camk2d
Kinesin-like protein KIF21A, Gene: Kif21a
Protein kinase C beta type, Gene: Prkcb
Ketosamine-3-kinase, Gene: Fn3krp
LIM and SH3 domain protein 1, Gene: Lasp1

Microtubule-associated protein 1A, Gene: Map1a
Microtubule-associated protein 1B, Gene: Map1b
Microtubule-associated protein 4, Gene: Map4
Microtubule-associated protein 6, Gene: Map6
Microtubule-associated protein RP/EB family member 1, Gene: Mapre1
Microtubule-associated protein RP/EB family member 2, Gene: Mapre2
Microtubule-associated protein RP/EB family member 3, Gene: Mapre3
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial, Gene: MCCC1
Mitogen-activated protein kinase 12, Gene: Mapk12
Microtubule-associated protein 2, Gene: Map2
Neural cell adhesion molecule 1, Gene: Ncam1
Neurogranin, Gene: Nrgn
Neurofilament medium polypeptide, Gene: Nefm
NK-tumor recognition protein, Gene: NKTR
Nucleosome assembly protein 1-like 4, Gene: Nap1l4
Vesicle-fusing ATPase, Gene: Nsf
Phosphofurin acidic cluster sorting protein 1, Gene: Pacs1
Serine/threonine-protein kinase PAK 2, Gene: Pak2
Propionyl-CoA carboxylase alpha chain, mitochondrial, Gene: Pcca
Protein piccolo, Gene: Pclo
Prefoldin subunit 2, Gene: Pfdn2
Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha, Gene: Pip4k2a
Plectin (Fragment), Gene: PLEC
Pyruvate carboxylase, mitochondrial, Gene: Pc
Rabenosyn-5, Gene: Rbsn
Reticulon-3, Gene: Rtn3
Reticulon-4, Gene: Rtn4
RuvB-like 2, Gene: Ruvbl2
Septin-5 OS=Macaca fascicularis Gene: Sept5
Septin-7, Gene: Sept7
Endophilin-A2, Gene: Sh3gl1
Endophilin-A1, Gene: Sh3gl2
SH3 and multiple ankyrin repeat domains protein 2, Gene: Shank2
Synaptosomal-associated protein 25, Gene: Snap25
Spastin, Gene: Spast
Spectrin alpha chain, non-erythrocytic 1, Gene: Sptan1
Src substrate cortactin, Gene: Cttn
SRC kinase signaling inhibitor 1, Gene: Srcin1
Stathmin, Gene: Stmn1
Synaptic vesicle glycoprotein 2A, Gene: Sv2a
Synapsin-1, Gene: Syn1
Alpha-synuclein, Gene: Snca
Beta-synuclein, Gene: Sncb
Gamma-synuclein OS=Macaca fascicularis Gene: SNCG
Transgelin-2, Gene: Tagln2
Transgelin-3, Gene: Tagln3
Microtubule-associated protein tau, Gene: Mapt
Tubulin beta-4A chain, Gene: TUBB4A

Tubulin-folding cofactor B, Gene: Tbcb
Tubulin polymerization-promoting protein, Gene: Tppp
Vesicle-associated membrane protein 1, Gene: Vamp1
Vesicle-associated membrane protein 2, Gene: Vamp2
Deubiquitinating protein VCIP135, Gene: Vcpip1
WAS/WASL-interacting protein family member 2, Gene: Wipf2
WAS/WASL-interacting protein family member 3, Gene: Wipf3
Zinc finger C2HC domain-containing protein 1A, Gene: Zc2hc1a

and hippocampus yields 101 unique biotinylated proteins (proteins unique to this experi

imental group).

Table 8. **Tau**

Protein
41
AAK1
ABI2
ACAP2
ACTA
ACTB
ACTC
AGFG1
AHI1
AINX
ALDOA
ANK2
AP180
APC
ARBK1
ARP3
ARP3B
ARP5L
ASAP1
ASAP2
AUXI
BAIP2
BASP1
BIN1
BSN
CALB2
CALM
CAMKV
CAMP3
CAPS1
CAPS2
CC171
CDV3
CE170
CEND
CETN2
CHM4B
CKAP5
CLAP2
CLH1
CLIP2
CNKR2
CPLX1
CPLX2
CRKL

CRTC1
CSDE1
CYFP2
CYH1
CYH2
CYH3
CZIB
DBNL
DCE2
DCLK1
DCLK2
DCTN2
DEMA
DLGP3
DNJB1
DNM1L
DPYL2
DPYL4
DRG2
DYN1
E41L1
E41L2
E41L3
EF1A2
EF2
ELOB
ENSA
F110B
G3P
GBRA1
GDIR1
GP158
GRIN1
GSDME
GSK3A
GSK3B
HAP28
HS90A
HS90B
IF4B
IF4G1
IF4G3
IQEC3
JUPI1
K1107
KAP2
KAPCA
KC1E

KCC2A
KCC2B
KCC2D
KI21A
KIF5C
KPCB
KPCG
KT3K
LASP1
LNEBL
LUZP1
M4K4
MA7D2
MAP1A
MAP1B
MAP4
MAP6
MARE1
MARE3
MCCA
MINK1
MTAP2
MYO5A
NACAM
NECP1
NEUG
NFM
NKTR
NP1L4
NSF
NSF1C
OGA
OXR1
P33MX
PACS1
PAK2
PCBP1
PCCA
PCLO
PFD2
PGAM1
PI42A
PI42B
PI42C
PLCL2
PLCX3
PLEC
PLPR4

PP1RB
PRAF3
PURA2
PURB
PYC
RANG
RASL1
RBNS5
RGRF1
RIMKA
RL24
RL29
RN214
RS20
RTN1
RTN3
RTN4
RUFY3
S10A6
SEP5
SEP7
SEP9
SH3G2
SHAN2
SHRM2
SKT
SMAP1
SNAG
SPAST
SPTB2
SPTN1
SRBS1
SRC8
SRCN1
STAM1
STAR5
STAT1
STMN1
SYN1
SYN2
SYNC
SYNJ1
SYNPO
SYUA
SYUB
TAGL3
TANC1
TANC2

TAU
TB10B
TB182
TBA1A
TBC21
TBCB
TM1L2
TMOD2
TPPP
VAMP2
VATF
VCIP1
VIAAT
VIGLN
VMA5A
VP13C
VPS25
VPS36
WASC5
WIPF2
WIPF3

ı interactors in tau(-/-) mouse (6 mo.) hippocampus. Expression of BioID2-tau in

Protein description and gene name
Protein 4.1, Gene: Epb41
AP2-associated protein kinase 1, Gene: Aak1
Abl interactor 2, Gene: ABI2
Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2, Gene: Acap2
Actin, aortic smooth muscle, Gene: ACTA1
Actin, cytoplasmic 1, Gene: ACTB
Actin, alpha cardiac muscle 1, Gene: ACTC1
Arf-GAP domain and FG repeat-containing protein 1, Gene: AGFG1
Jouberin, Gene: Ahi1
Alpha-internexin, Gene: Ina
Fructose-bisphosphate aldolase A, Gene: Aldoa
Ankyrin-2, Gene: Ank2
Clathrin coat assembly protein AP180, Gene: Snap91
Adenomatous polyposis coli protein, Gene: APC
Beta-adrenergic receptor kinase 1, Gene: GRK2
Actin-related protein 3, Gene: ACTR3
Actin-related protein 3B, Gene: ACTR3B
Actin-related protein 2/3 complex subunit 5-like protein, Gene: Arpc5l
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1, Gene: Asap1
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2, Gene: Asap2
Putative tyrosine-protein phosphatase auxilin, Gene: Dnajc6
Brain-specific angiogenesis inhibitor 1-associated protein 2, Gene: BAIAP2
Brain acid soluble protein 1, Gene: Basp1
Myc box-dependent-interacting protein 1, Gene: Bin1
Protein bassoon, Gene: Bsn
Calretinin, Gene: Calb2
Calmodulin, Gene: Calm
CaM kinase-like vesicle-associated protein, Gene: Camkv
Calmodulin-regulated spectrin-associated protein 3, Gene: Camsap3
Calcium-dependent secretion activator 1, Gene: Cadps
Calcium-dependent secretion activator 2, Gene: Cadps2
Coiled-coil domain-containing protein 171, Gene: Ccdc171
Protein CDV3, Gene: Cdv3
Centrosomal protein of 170 kDa, Gene: Cep170
Cell cycle exit and neuronal differentiation protein 1, Gene: Cend1
Centrin-2, Gene: CETN2
Charged multivesicular body protein 4b, Gene: CHMP4B
Cytoskeleton-associated protein 5, Gene: Ckap5
CLIP-associating protein 2, Gene: Clasp2
Clathrin heavy chain 1, Gene: CLTC
CAP-Gly domain-containing linker protein 2, Gene: Clip2
Connector enhancer of kinase suppressor of ras 2, Gene: CNKSR2
Complexin-1, Gene: Cplx1
Complexin-2, Gene: Cplx2
Crk-like protein, Gene: CRKL

CREB-regulated transcription coactivator 1, Gene: CRTC1
Cold shock domain-containing protein E1, Gene: CSDE1
Cytoplasmic FMR1-interacting protein 2, Gene: Cyfip2
Cytohesin-2, Gene: CYTH2
Cytohesin-2, Gene: CYTH2
Cytohesin-3, Gene: CYTH3
CXXC motif containing zinc binding protein, Gene: CZIB
Drebrin-like protein, Gene: Dbnl
Glutamate decarboxylase 2, Gene: Gad2
Serine/threonine-protein kinase DCLK1, Gene: Dclk1
Serine/threonine-protein kinase DCLK2, Gene: Dclk2
Dynactin subunit 2, Gene: DCTN2
Dematin, Gene: DMTN
Disks large-associated protein 3, Gene: DLGAP3
DnaJ homolog subfamily B member 1, Gene: DNAJB1
Dynamin-1-like protein, Gene: Dnm1l
Dihydropyrimidinase-related protein 2, Gene: Dpysl2
Dihydropyrimidinase-related protein 4, Gene: Dpysl4
Developmentally-regulated GTP-binding protein 2, Gene: DRG2
Dynamin-1, Gene: Dnm1
Band 4.1-like protein 1, Gene: Epb41l1
Band 4.1-like protein 2, Gene: Epb41l2
Band 4.1-like protein 3, Gene: Epb41l3
Elongation factor 1-alpha 2, Gene: EEF1A2
Elongation factor 2, Gene: Eef2
Elongin-B, Gene: ELOB
Alpha-endosulfine, Gene: ENSA
Protein FAM110B, Gene: FAM110B
Glyceraldehyde-3-phosphate dehydrogenase, Gene: Gapdh
Gamma-aminobutyric acid receptor subunit alpha-1, Gene: GABRA1
Rho GDP-dissociation inhibitor 1, Gene: Arhgdia
Probable G-protein coupled receptor 158, Gene: Gpr158
G protein-regulated inducer of neurite outgrowth 1, Gene: Gprin1
Gasdermin-E, Gene: Gsdme
Glycogen synthase kinase-3 alpha, Gene: Gsk3a
Glycogen synthase kinase-3 beta, Gene: GSK3B
28 kDa heat- and acid-stable phosphoprotein, Gene: PDAP1
Heat shock protein HSP 90-alpha, Gene: Hsp90aa1
Heat shock protein HSP 90-beta, Gene: Hsp90ab1
Eukaryotic translation initiation factor 4B, Gene: Eif4b
Eukaryotic translation initiation factor 4 gamma 1, Gene: Eif4g1
Eukaryotic translation initiation factor 4 gamma 3, Gene: EIF4G3
IQ motif and SEC7 domain-containing protein 3, Gene: Iqsec3
Jupiter microtubule associated homolog 1, Gene: Jpt1
AP2-interacting clathrin-endocytosis protein, Gene: Kiaa1107
cAMP-dependent protein kinase type II-alpha regulatory subunit, Gene: Prkar2a
cAMP-dependent protein kinase catalytic subunit alpha, Gene: PRKACA
Casein kinase I isoform epsilon, Gene: Csnk1e

Calcium/calmodulin-dependent protein kinase type II subunit alpha, Gene: Camk2a
Calcium/calmodulin-dependent protein kinase type II subunit beta, Gene: Camk2b
Calcium/calmodulin-dependent protein kinase type II subunit delta, Gene: Camk2d
Kinesin-like protein KIF21A, Gene: Kif21a
Kinesin heavy chain isoform 5C, Gene: Kif5c
Protein kinase C beta type, Gene: Prkcb
Protein kinase C gamma type, Gene: Prkcg
Ketosamine-3-kinase, Gene: Fn3krp
LIM and SH3 domain protein 1, Gene: Lasp1
LIM zinc-binding domain-containing Nebulette, Gene: Nebl
Leucine zipper protein 1, Gene: Luzp1
Mitogen-activated protein kinase kinase kinase kinase 4, Gene: MAP4K4
MAP7 domain-containing protein 2, Gene: Map7d2
Microtubule-associated protein 1A, Gene: Map1a
Microtubule-associated protein 1B, Gene: Map1b
Microtubule-associated protein 4, Gene: Map4
Microtubule-associated protein 6, Gene: Map6
Microtubule-associated protein RP/EB family member 1, Gene: Mapre1
Microtubule-associated protein RP/EB family member 3, Gene: MAPRE3
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial, Gene: Mccc1
Misshapen-like kinase 1, Gene: MINK1
Microtubule-associated protein 2, Gene: Map2
Unconventional myosin-Va, Gene: Myo5a
Nascent polypeptide-associated complex subunit alpha, muscle-specific form, Gene: Naca
Adaptin ear-binding coat-associated protein 1, Gene: NECAP1
Neurogranin, Gene: NRGN
Neurofilament medium polypeptide, Gene: Nefm
NK-tumor recognition protein, Gene: NKTR
Nucleosome assembly protein 1-like 4, Gene: Nap1l4
Vesicle-fusing ATPase, Gene: Nsf
NSFL1 cofactor p47, Gene: NSFL1C
Protein O-GlcNAcase, Gene: OGA
Oxidation resistance protein 1, Gene: Oxr1
Putative monooxygenase p33MONOX, Gene: P33MONOX
Phosphofurin acidic cluster sorting protein 1, Gene: Pacs1
Serine/threonine-protein kinase PAK 2, Gene: Pak2
Poly(rC)-binding protein 1, Gene: PCBP1
Propionyl-CoA carboxylase alpha chain, mitochondrial, Gene: PCCA
Protein piccolo, Gene: Pclo
Prefoldin subunit 2, Gene: Pfdn2
Phosphoglycerate mutase 1, Gene: PGAM1
Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha, Gene: PIP4K2A
Phosphatidylinositol 5-phosphate 4-kinase type-2 beta, Gene: PIP4K2B
Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma, Gene: PIP4K2C
Inactive phospholipase C-like protein 2, Gene: Plcl2
PI-PLC X domain-containing protein 3, Gene: Plcxd3
Plectin, Gene: Plec
Phospholipid phosphatase-related protein type 4, Gene: PLPPR4

E3 ubiquitin-protein ligase PPP1R11, Gene: PPP1R11
PRA1 family protein 3, Gene: Arl6ip5
Adenylosuccinate synthetase isozyme 2, Gene: ADSS
Transcriptional activator protein Pur-beta, Gene: Purb
Pyruvate carboxylase, mitochondrial, Gene: Pc
Ran-specific GTPase-activating protein, Gene: Ranbp1
RasGAP-activating-like protein 1, Gene: Rasal1
Rabenosyn-5, Gene: RBSN
Ras-specific guanine nucleotide-releasing factor 1, Gene: Rasgrf1
N-acetylaspartylglutamate synthase A, Gene: Rimkla
60S ribosomal protein L24, Gene: RPL24
60S ribosomal protein L29, Gene: Rpl29
RING finger protein 214, Gene: Rnf214
40S ribosomal protein S20, Gene: RPS20
Reticulon-1, Gene: Rtn1
Reticulon-3, Gene: Rtn3
Reticulon-4, Gene: Rtn4
Protein RUFY3, Gene: RUFY3
Protein S100-A6, Gene: S100A6
Septin-5, Gene: SEPTIN5
Septin-7, Gene: SEPTIN7
Septin-9, Gene: Septin9
Endophilin-A1, Gene: SH3GL2
SH3 and multiple ankyrin repeat domains protein 2, Gene: Shank2
Protein Shroom2, Gene: Shroom2
Sickle tail protein, Gene: Skt
Stromal membrane-associated protein 1, Gene: Smap1
Gamma-soluble NSF attachment protein, Gene: NAPG
Spastin, Gene: Spast
Spectrin beta chain, non-erythrocytic 1, Gene: Sptbn1
Spectrin alpha chain, non-erythrocytic 1, Gene: Sptan1
Sorbin and SH3 domain-containing protein 1, Gene: SORBS1
Src substrate cortactin, Gene: Cttn
SRC kinase signaling inhibitor 1, Gene: Srcin1
Signal transducing adapter molecule 1, Gene: Stam
StAR-related lipid transfer protein 5, Gene: STARD5
Signal transducer and activator of transcription 1-alpha/beta, Gene: STAT1
Stathmin, Gene: Stmn1
Synapsin-1, Gene: Syn1
Synapsin-2, Gene: Syn2
Asparagine--tRNA ligase, cytoplasmic, Gene: NARS
Synaptojanin-1, Gene: Synj1
Synaptopodin, Gene: Synpo
Alpha-synuclein, Gene: Snca
Beta-synuclein, Gene: Sncb
Transgelin-3, Gene: TAGLN3
Protein TANC1, Gene: TANC1
Protein TANC2, Gene: TANC2

Microtubule-associated protein tau, Gene: Mapt
TBC1 domain family member 10B, Gene: Tbc1d10b
182 kDa tankyrase-1-binding protein, Gene: Tnks1bp1
Tubulin alpha-1A chain, Gene: TUBA1A
TBC1 domain family member 21, Gene: TBC1D21
Tubulin-folding cofactor B, Gene: Tbcb
TOM1-like protein 2, Gene: TOM1L2
Tropomodulin-2, Gene: Tmod2
Tubulin polymerization-promoting protein, Gene: Tppp
Vesicle-associated membrane protein 2, Gene: VAMP2
V-type proton ATPase subunit F, Gene: Atp6v1f
Deubiquitinating protein VCIP135, Gene: Vcpip1
Vesicular inhibitory amino acid transporter, Gene: Slc32a1
Vigilin, Gene: Hdlbp
von Willebrand factor A domain-containing protein 5A, Gene: Vwa5a
Vacuolar protein sorting-associated protein 13C, Gene: VPS13C
Vacuolar protein-sorting-associated protein 25, Gene: VPS25
Vacuolar protein-sorting-associated protein 36, Gene: Vps36
WASH complex subunit 5, Gene: WASHC5
WAS/WASL-interacting protein family member 2, Gene: Wipf2
WAS/WASL-interacting protein family member 3, Gene: Wipf3

ı adult tau knock-out mouse hippocampus yields 210 unique biotinylated proteins (pr

oteins unique to this experimental group)

Table 9. **Biotinylated peptide list from primary**
Samples include neurons expressing BioID2-tau

AAV condition	Sample No.	Protein	Peptide Score
mycBioID2	*2*	41	54.94
mycBioID2	*4*	41	67.39
mycBioID2	*6*	41	66.68
mycBioID2tau	1	41	45.14
mycBioID2tau	3	41	45.04
mycBioID2tau	3	SEP5	44.1
mycBioID2	*2*	AAK1	58.68
mycBioID2	*4*	AAK1	43.48
mycBioID2	*6*	AAK1	85
mycBioID2tau	1	AAK1	82.11
mycBioID2tau	5	AAK1	78.68
mycBioID2tau	3	AAK1	74.88
mycBioID2tau	1	AAK1	72.25
mycBioID2tau	3	AAK1	56.39
mycBioID2tau	5	ACTB	48.74
mycBioID2tau	3	ACTB	43.95
mycBioID2tau	5	ACTB	42.6
mycBioID2tau	3	ACTB	42.05
mycBioID2tau	3	ACTC	43.95
mycBioID2	*2*	ALBU	68.78
mycBioID2	*2*	ALBU	68.78
mycBioID2	*2*	ALBU	48.54
mycBioID2	*4*	ALBU	64.82
mycBioID2	*4*	ALBU	51.65
mycBioID2	*4*	ALBU	43.08
mycBioID2	*4*	ALBU	41.12
mycBioID2	*6*	ALBU	46.09
mycBioID2	*6*	ALBU	45.01
mycBioID2	*6*	ALBU	44.73
mycBioID2	*6*	ALBU	44.21
mycBioID2	*6*	ALBU	44.21
mycBioID2	*6*	ALBU	46.09
mycBioID2tau	1	ALBU	74.52
mycBioID2tau	5	ALBU	65.57
mycBioID2tau	1	ALBU	62.95
mycBioID2tau	3	ALBU	58.57
mycBioID2tau	3	ALBU	56.17
mycBioID2tau	5	ALBU	56.05
mycBioID2tau	1	ALBU	53.14
mycBioID2tau	5	ALBU	50.44
mycBioID2tau	5	ALBU	45.5
mycBioID2tau	1	ALBU	44.8
mycBioID2tau	3	ALBU	44.45
mycBioID2tau	3	ALBU	43.23

mycBioID2tau	1	ALBU	41.31
mycBioID2	2	ALDOA	41.43
mycBioID2	6	ALDOA	97
mycBioID2	6	ALDOA	89.03
mycBioID2tau	1	ALDOA	98.84
mycBioID2tau	1	ALDOA	91.48
mycBioID2tau	1	ALDOA	63.97
mycBioID2tau	5	ALDOA	61.77
mycBioID2tau	1	ALDOA	43.5
mycBioID2tau	5	ALDOA	41.53
mycBioID2tau	3	ANK2	46.38
mycBioID2	4	AP180	41.68
mycBioID2tau	3	AP180	42.2
mycBioID2	6	ARBK1	67.21
mycBioID2	6	ARBK1	52.27
mycBioID2tau	3	ARBK1	67.66
mycBioID2tau	5	ARBK1	52.29
mycBioID2tau	1	ARBK1	46.13
mycBioID2	2	ARPC2	42
mycBioID2	6	ARPC2	49.58
mycBioID2tau	3	ARPC2	44.21
mycBioID2tau	3	ATX2L	73.01
mycBioID2tau	5	ATX2L	68.9
mycBioID2	6	BIN1	44.93
mycBioID2tau	5	BIN1	48.17
mycBioID2tau	3	BIN1	44.3
mycBioID2tau	1	BIN1	43.11
mycBioID2tau	3	BIN1	42.97
mycBioID2	6	CA123	53.68
mycBioID2tau	1	CA123	66.31
mycBioID2tau	3	CA123	50.67
mycBioID2	2	CAMP3	64.5
mycBioID2	4	CAMP3	41.69
mycBioID2tau	1	CAMP3	80.41
mycBioID2tau	3	CAMP3	75.9
mycBioID2tau	1	CAMP3	73.09
mycBioID2tau	5	CAMP3	68.41
mycBioID2tau	5	CAPS1	69.57
mycBioID2tau	1	CAPS1	49.98
mycBioID2tau	3	CE170	40.26
mycBioID2	6	CEND	48.81
mycBioID2tau	3	CLAP2	44.95
mycBioID2tau	1	CPLX1	73.92
mycBioID2tau	3	CPLX1	56.13
mycBioID2tau	3	CPLX1	55.92
mycBioID2	6	CPSF5	59.06
mycBioID2tau	5	CRKL	47.65
mycBioID2tau	1	DCTN2	52.37

mycBioID2	2	DLGP3	70.59
mycBioID2	6	DLGP3	45.54
mycBioID2tau	5	DNJB1	50.45
mycBioID2	2	DPYL2	59.51
mycBioID2	6	DPYL2	74.51
mycBioID2	6	DPYL2	59.01
mycBioID2	6	DPYL2	52.29
mycBioID2tau	1	DPYL2	79.41
mycBioID2tau	3	DPYL2	71.91
mycBioID2tau	1	DPYL2	55.47
mycBioID2tau	5	DPYL2	55.1
mycBioID2	2	E41L1	59.11
mycBioID2	2	E41L1	56.02
mycBioID2	2	E41L1	43.85
mycBioID2	4	E41L1	144.24
mycBioID2	4	E41L1	111.6
mycBioID2	4	E41L1	76.47
mycBioID2	4	E41L1	40.79
mycBioID2	6	E41L1	93.01
mycBioID2	6	E41L1	71.12
mycBioID2	6	E41L1	66.96
mycBioID2	6	E41L1	63.27
mycBioID2	6	E41L1	51.85
mycBioID2tau	5	E41L1	150.52
mycBioID2tau	1	E41L1	129.95
mycBioID2tau	5	E41L1	59.72
mycBioID2tau	5	E41L1	57.61
mycBioID2tau	1	E41L1	56.57
mycBioID2tau	1	E41L1	54.77
mycBioID2tau	3	E41L1	52.41
mycBioID2tau	3	E41L1	47.46
mycBioID2tau	5	E41L1	44.91
mycBioID2tau	5	E41L1	43.37
mycBioID2tau	5	E41L1	40.64
mycBioID2tau	3	E41L2	60.22
mycBioID2	2	E41L3	51.58
mycBioID2tau	1	EF1A1	41.44
mycBioID2	4	ELFN1	84.22
mycBioID2	4	ELFN1	43.2
mycBioID2	2	ELOB	49.11
mycBioID2tau	1	ELOB	56.89
mycBioID2tau	1	ELOB	41.1
mycBioID2	2	F169A	82.36
mycBioID2	6	F169A	86.75
mycBioID2	6	F169A	70.97
mycBioID2	6	F1712	43.96
mycBioID2tau	3	G3BP1	58.24
mycBioID2tau	5	G3BP1	50.78

mycBioID2tau	1	G3BP1	43.56
mycBioID2tau	1	G3P	82.31
mycBioID2tau	3	G3P	45.97
mycBioID2	*6*	GCR	62.42
mycBioID2	*6*	GCR	53.79
mycBioID2tau	5	GDIR1	46.67
mycBioID2tau	3	GLSK	56.24
mycBioID2tau	1	GLSK	45.11
mycBioID2tau	*5*	GP158	39.84
mycBioID2	*6*	GRIN1	61.28
mycBioID2tau	1	H21D	71.15
mycBioID2tau	1	H21D	53.55
mycBioID2	*2*	H2B1B	54.91
mycBioID2	*6*	H2B1B	66.84
mycBioID2	*6*	H2B1B	46.38
mycBioID2tau	1	H2B1B	74.21
mycBioID2tau	1	H2B1B	56.42
mycBioID2tau	1	H2B1B	53.31
mycBioID2tau	*5*	H2B1B	52.97
mycBioID2tau	*5*	H2B1B	51.7
mycBioID2tau	1	H2B1B	45.53
mycBioID2tau	1	H2B1B	44.83
mycBioID2tau	*5*	H2B1B	42.58
mycBioID2tau	1	H2B1B	41.74
mycBioID2	*4*	H2B1C	42.82
mycBioID2	*4*	H2B1C	42.46
mycBioID2	*6*	H2B1C	77.18
mycBioID2	*6*	H2B1C	47.41
mycBioID2tau	1	H2B1C	74.21
mycBioID2tau	3	H2B1C	60.63
mycBioID2tau	3	H2B1C	58.24
mycBioID2tau	1	H2B1C	56.42
mycBioID2tau	5	H2B1C	52.97
mycBioID2tau	*5*	H2B1C	51.7
mycBioID2tau	1	H2B1C	45.53
mycBioID2tau	1	H2B1C	44.83
mycBioID2	*6*	H2B1F	77.18
mycBioID2	*6*	H2B1F	47.41
mycBioID2tau	3	H2B1L	60.63
mycBioID2tau	3	H2B1L	58.24
mycBioID2tau	1	HINT1	57.79
mycBioID2tau	3	HS90A	44.64
mycBioID2tau	5	HS90A	44.35
mycBioID2tau	1	HS90A	40.17
mycBioID2tau	3	HS90B	44.64
mycBioID2tau	5	HS90B	44.35
mycBioID2tau	1	HS90B	40.17
mycBioID2	*2*	HSP7C	53.72

mycBioID2tau	1	HSP7C	48.49
mycBioID2tau	5	HXK1	91.04
mycBioID2tau	1	HXK1	78.47
mycBioID2tau	3	HXK1	54.26
mycBioID2	*2*	IF4G3	56.06
mycBioID2	*4*	IF4G3	50.79
mycBioID2	*4*	IF4G3	41.26
mycBioID2	*6*	IF4G3	47.69
mycBioID2tau	3	IF4G3	58.25
mycBioID2tau	5	IF4G3	50.74
mycBioID2tau	1	IF4G3	47.76
mycBioID2tau	1	IF4H	43.04
mycBioID2	*2*	IL1A	43.82
mycBioID2	*2*	KAP2	42.81
mycBioID2	*4*	KAP2	54.05
mycBioID2tau	5	KAP2	52.83
mycBioID2tau	1	KAP2	43.67
mycBioID2	*2*	KCC2D	46.51
mycBioID2tau	1	KCC2D	59.89
mycBioID2tau	5	KCC2D	57.08
mycBioID2	*6*	KCNB2	71.69
mycBioID2	*6*	KIF5C	46.87
mycBioID2tau	1	KIF5C	43.37
mycBioID2tau	3	LASP1	56.02
mycBioID2tau	5	LASP1	52.71
mycBioID2	*6*	LRRC7	40.57
mycBioID2	*4*	M3K10	57.98
mycBioID2	*6*	M3K10	50.18
mycBioID2tau	1	M3K10	66.32
mycBioID2tau	3	M3K10	54.38
mycBioID2tau	5	M3K10	52.8
mycBioID2	*4*	MAP1A	59.79
mycBioID2	*6*	MAP1A	47.64
mycBioID2tau	1	MAP1A	83.65
mycBioID2tau	3	MAP1A	80.93
mycBioID2tau	1	MAP1A	77.56
mycBioID2tau	3	MAP1A	71.56
mycBioID2tau	5	MAP1A	63.02
mycBioID2tau	1	MAP1A	56.59
mycBioID2tau	3	MAP1A	52.79
mycBioID2tau	3	MAP1B	74.03
mycBioID2tau	3	MAP1B	67.45
mycBioID2tau	3	MAP1B	65.68
mycBioID2tau	5	MAP1B	47.21
mycBioID2tau	5	MAP1B	44.56
mycBioID2tau	1	MAP1B	44.55
mycBioID2tau	1	MAP1B	44.18
mycBioID2tau	5	MAP1B	42.99

mycBioID2tau	1	MAP1B	41.73
mycBioID2	*4*	MAP4	57.58
mycBioID2	*6*	MAP4	54.48
mycBioID2	*6*	MAP4	45.78
mycBioID2tau	3	MAP4	82.82
mycBioID2tau	1	MAP4	72.81
mycBioID2tau	3	MAP4	70.55
mycBioID2tau	5	MAP4	70.45
mycBioID2tau	1	MAP4	56.8
mycBioID2tau	1	MAP4	44.71
mycBioID2tau	1	MAP6	107.18
mycBioID2tau	3	MAP6	96.99
mycBioID2tau	5	MAP6	96.83
mycBioID2tau	1	MAP6	91.55
mycBioID2tau	5	MAP6	85.55
mycBioID2tau	3	MAP6	76.63
mycBioID2tau	3	MAP6	75.2
mycBioID2tau	5	MAP6	68.49
mycBioID2tau	1	MAP6	66.04
mycBioID2tau	3	MAP6	65.68
mycBioID2tau	1	MAP6	65.67
mycBioID2tau	3	MAP6	63.78
mycBioID2tau	3	MAP6	62.07
mycBioID2tau	5	MAP6	61.97
mycBioID2tau	3	MAP6	61.1
mycBioID2tau	5	MAP6	61.1
mycBioID2tau	1	MAP6	60.16
mycBioID2tau	3	MAP6	59.97
mycBioID2tau	1	MAP6	59.7
mycBioID2tau	5	MAP6	59.08
mycBioID2tau	1	MAP6	58.84
mycBioID2tau	3	MAP6	56.13
mycBioID2tau	5	MAP6	55.18
mycBioID2tau	1	MAP6	54.73
mycBioID2tau	1	MAP6	54.16
mycBioID2tau	3	MAP6	53.85
mycBioID2tau	5	MAP6	51.67
mycBioID2tau	5	MAP6	51.39
mycBioID2tau	5	MAP6	51.02
mycBioID2tau	1	MAP6	50.42
mycBioID2tau	3	MAP6	50.23
mycBioID2tau	5	MAP6	48.18
mycBioID2tau	5	MAP6	46.32
mycBioID2tau	3	MAP6	46.23
mycBioID2tau	1	MAP6	45.17
mycBioID2tau	3	MAP6	44.14
mycBioID2tau	1	MAP6	44.07
mycBioID2tau	1	MAP6	43.47

mycBioID2tau	5	MAP6	43.07
mycBioID2tau	1	MAP6	42.9
mycBioID2tau	5	MAP6	42.65
mycBioID2tau	5	MAP6	42.47
mycBioID2tau	1	MAP6	41.15
mycBioID2tau	3	MAP6	40.91
mycBioID2tau	1	MAP6	40.9
mycBioID2tau	3	MAP6	40.39
mycBioID2tau	3	MAP6	39.04
mycBioID2	*6*	MARE1	60.03
mycBioID2tau	3	MARE1	80.36
mycBioID2tau	1	MARE1	72.67
mycBioID2tau	5	MARE1	59.05
mycBioID2	*4*	MCCA	59.3
mycBioID2tau	1	MCCA	62.27
mycBioID2tau	1	MDHM	42.93
mycBioID2	*2*	MTAP2	62.07
mycBioID2	*2*	MTAP2	53.84
mycBioID2	*4*	MTAP2	55.81
mycBioID2	*4*	MTAP2	50.48
mycBioID2	*4*	MTAP2	49.61
mycBioID2	*4*	MTAP2	43.62
mycBioID2	*4*	MTAP2	42.37
mycBioID2	*6*	MTAP2	75.53
mycBioID2	*6*	MTAP2	54.1
mycBioID2	*6*	MTAP2	53.71
mycBioID2	*6*	MTAP2	53.58
mycBioID2	*6*	MTAP2	53.14
mycBioID2	*6*	MTAP2	51.3
mycBioID2	*6*	MTAP2	47.7
mycBioID2	*6*	MTAP2	44.17
mycBioID2	*6*	MTAP2	44.12
mycBioID2	*6*	MTAP2	42.61
mycBioID2	*6*	MTAP2	42.05
mycBioID2	*6*	MTAP2	40.77
mycBioID2	*6*	MTAP2	40.52
mycBioID2	*6*	MTAP2	40.24
mycBioID2tau	5	MTAP2	102.56
mycBioID2tau	3	MTAP2	88.85
mycBioID2tau	1	MTAP2	79.25
mycBioID2tau	5	MTAP2	69.22
mycBioID2tau	3	MTAP2	66.39
mycBioID2tau	3	MTAP2	63.28
mycBioID2tau	5	MTAP2	60.24
mycBioID2tau	3	MTAP2	59.08
mycBioID2tau	3	MTAP2	58.93
mycBioID2tau	1	MTAP2	54.91
mycBioID2tau	5	MTAP2	53.29

mycBioID2tau	1	MTAP2	52.69
mycBioID2tau	5	MTAP2	51.79
mycBioID2tau	3	MTAP2	51.39
mycBioID2tau	3	MTAP2	51.02
mycBioID2tau	1	MTAP2	48.7
mycBioID2tau	5	MTAP2	48.6
mycBioID2tau	5	MTAP2	48.07
mycBioID2tau	5	MTAP2	47.64
mycBioID2tau	3	MTAP2	46.85
mycBioID2tau	3	MTAP2	43.92
mycBioID2tau	5	MTAP2	43.88
mycBioID2tau	5	MTAP2	43.45
mycBioID2tau	5	MTAP2	42.76
mycBioID2tau	5	MTAP2	42.16
mycBioID2tau	1	MTAP2	42.13
mycBioID2tau	1	MTAP2	41.96
mycBioID2tau	3	MTAP2	41.63
mycBioID2tau	5	MTAP2	41.39
mycBioID2tau	5	MTAP2	40.99
mycBioID2tau	3	MTAP2	40.67
mycBioID2tau	1	MTAP2	39.98
mycBioID2tau	1	MTAP2	39.95
mycBioID2	*2*	NACA	88.71
mycBioID2tau	3	NACA	83.64
mycBioID2	*2*	NACAM	91.16
mycBioID2	*4*	NACAM	86.38
mycBioID2	*4*	NACAM	84.88
mycBioID2	*4*	NACAM	73.61
mycBioID2tau	3	NACAM	86.13
mycBioID2tau	5	NACAM	85.51
mycBioID2tau	5	NACAM	77.23
mycBioID2tau	5	NACAM	75.73
mycBioID2tau	1	NACAM	72.94
mycBioID2tau	3	NACAM	69.2
mycBioID2tau	1	NACAM	57.5
mycBioID2	*6*	NFAT5	45.56
mycBioID2tau	5	NFAT5	79.6
mycBioID2tau	5	NFAT5	59.85
mycBioID2tau	1	NFAT5	58.77
mycBioID2tau	1	NKTR	40.28
mycBioID2	*4*	NMDE2	40.49
mycBioID2	*6*	NMDE2	58.67
mycBioID2tau	5	NMT1	43.79
mycBioID2tau	3	NP1L4	53.51
mycBioID2tau	1	NP1L4	45.24
mycBioID2tau	3	NSF	42.12
mycBioID2tau	3	NSF	41.21
mycBioID2	*2*	NSF1C	47.93

mycBioID2	*2*	NSF1C	40.56
mycBioID2	*4*	NSF1C	47.79
mycBioID2tau	5	PAK2	47.47
mycBioID2tau	3	PAK2	40.32
mycBioID2tau	3	PCCA	85.52
mycBioID2	*4*	PEBP1	79.17
mycBioID2tau	1	PEBP1	127.62
mycBioID2tau	5	PI42	56.57
mycBioID2	*2*	PLEC	61.83
mycBioID2	*4*	PLEC	61.12
mycBioID2tau	5	PLEC	66.47
mycBioID2tau	1	PLEC	60.92
mycBioID2tau	1	PLEC	60.92
mycBioID2tau	3	PLEC	58.84
mycBioID2tau	5	PLEC	41.52
mycBioID2	*2*	PYC	51.29
mycBioID2	*4*	PYC	61.3
mycBioID2	*4*	PYC	51.35
mycBioID2	*4*	PYC	47.8
mycBioID2	*4*	PYC	45.98
mycBioID2	*6*	PYC	66.02
mycBioID2	*6*	PYC	53.62
mycBioID2	*6*	PYC	41.27
mycBioID2tau	3	PYC	66.52
mycBioID2tau	1	PYC	61.42
mycBioID2tau	1	PYC	50.93
mycBioID2tau	1	PYC	49.69
mycBioID2tau	1	PYC	48.12
mycBioID2tau	1	PYC	47.67
mycBioID2	*2*	RBNS5	43.41
mycBioID2	*4*	RBNS5	64.67
mycBioID2	*4*	RBNS5	63.76
mycBioID2tau	3	RBNS5	57.78
mycBioID2	*6*	RTN4	63.85
mycBioID2	*6*	RTN4	54.29
mycBioID2tau	1	RTN4	89.44
mycBioID2tau	5	RTN4	80.95
mycBioID2tau	1	RTN4	74.47
mycBioID2	*2*	RUVB2	60.54
mycBioID2tau	5	RUVB2	60.26
mycBioID2tau	1	RUVB2	41.48
mycBioID2tau	1	SH3G2	57.74
mycBioID2tau	3	SH3G2	53.45
mycBioID2tau	1	SH3G2	50.14
mycBioID2tau	5	SH3G2	45.31
mycBioID2tau	3	SH3G2	42.58
mycBioID2	*2*	SHAN2	49.4
mycBioID2	*4*	SHAN2	60.45

mycBioID2	6	SHAN2	82.09
mycBioID2	6	SHAN2	43.57
mycBioID2tau	1	SHAN2	42.48
mycBioID2tau	5	SNAG	84.73
mycBioID2tau	3	SNAG	56.06
mycBioID2tau	3	SNAG	55.71
mycBioID2	2	SPKAP	53.55
mycBioID2	2	SRBS2	69.39
mycBioID2	4	SRBS2	67.45
mycBioID2	6	SRBS2	80.45
mycBioID2	2	SRC8	71.69
mycBioID2	2	SRC8	66.34
mycBioID2	2	SRC8	41.86
mycBioID2	6	SRC8	52.26
mycBioID2tau	5	SRC8	85.07
mycBioID2tau	5	SRC8	78.45
mycBioID2tau	3	SRC8	78.44
mycBioID2tau	1	SRC8	54.66
mycBioID2tau	1	SRC8	53.38
mycBioID2tau	1	SRC8	53.11
mycBioID2tau	5	SRC8	53.08
mycBioID2tau	3	SRC8	53.01
mycBioID2tau	1	SRC8	46.15
mycBioID2	2	SRCN1	39.81
mycBioID2tau	1	SRCN1	57.25
mycBioID2tau	3	SRCN1	48.22
mycBioID2tau	1	STMN1	72.45
mycBioID2tau	5	STMN1	71.77
mycBioID2tau	3	STMN1	59.33
mycBioID2tau	3	STMN1	50.2
mycBioID2tau	5	STMN1	45.36
mycBioID2tau	1	STMN1	39.87
mycBioID2	6	SYN1	44.38
mycBioID2	6	SYNPO	53.93
mycBioID2	2	SYUA	48.67
mycBioID2	2	SYUA	44.52
mycBioID2tau	1	SYUA	75.82
mycBioID2tau	3	SYUA	55.04
mycBioID2tau	1	SYUA	47.94
mycBioID2	2	SYUB	48.93
mycBioID2	4	SYUB	89.39
mycBioID2	4	SYUB	59.83
mycBioID2	6	SYUB	97.38
mycBioID2	6	SYUB	80.4
mycBioID2tau	1	SYUB	152.93
mycBioID2tau	1	SYUB	136.87
mycBioID2tau	5	SYUB	133.55
mycBioID2tau	3	SYUB	105.65

mycBioID2tau	1	SYUB	102.21
mycBioID2tau	5	SYUB	100.84
mycBioID2tau	1	SYUB	98.85
mycBioID2tau	1	SYUB	86.17
mycBioID2tau	3	SYUB	78.67
mycBioID2tau	1	SYUB	75.82
mycBioID2tau	3	SYUB	74.28
mycBioID2tau	5	SYUB	67.54
mycBioID2tau	3	SYUB	60.99
mycBioID2tau	5	SYUB	60.48
mycBioID2tau	1	SYUB	47.94
mycBioID2tau	1	SYUB	40.87
mycBioID2tau	3	TAGL3	135.65
mycBioID2tau	3	TAGL3	103.42
mycBioID2tau	5	TAGL3	83.31
mycBioID2tau	1	TAGL3	78.74
mycBioID2tau	1	TAGL3	48.71
mycBioID2	6	TANC2	64.47
mycBioID2	6	TANC2	45.14
mycBioID2	6	TANC2	42.55
mycBioID2	2	TAU	63.17
mycBioID2	2	TAU	52.37
mycBioID2	2	TAU	49.86
mycBioID2	2	TAU	49.06
mycBioID2	2	TAU	45.76
mycBioID2	2	TAU	45.26
mycBioID2	2	TAU	40.25
mycBioID2	4	TAU	60.04
mycBioID2	4	TAU	50.65
mycBioID2	4	TAU	44.28
mycBioID2	6	TAU	53.44
mycBioID2	6	TAU	50.35
mycBioID2	6	TAU	50.35
mycBioID2	6	TAU	45.94
mycBioID2tau	All samples	AU_HUMA	71.23
mycBioID2tau	All samples	AU_HUMA	71.17
mycBioID2	2	TBA1A	64.52
mycBioID2tau	3	TBA1A	83.95
mycBioID2tau	1	TBA1A	52.2
mycBioID2tau	1	TBA1A	45.06
mycBioID2	2	TBA1B	64.52
mycBioID2tau	3	TBA1B	83.95
mycBioID2tau	1	TBA1B	52.2
mycBioID2tau	3	TBB	60.01
mycBioID2tau	3	TBB2	60.01
mycBioID2tau	3	TBB2B	60.01
mycBioID2tau	3	TBB4B	60.01
mycBioID2tau	3	TBB6	60.01

mycBioID2tau	5	TBCB	51.24
mycBioID2tau	3	TBCB	46.3
mycBioID2tau	5	TBCB	43.15
mycBioID2tau	1	TBCB	42.23
mycBioID2tau	5	TCPE	50.62
mycBioID2tau	3	TPPP	41.54
mycBioID2tau	1	VAMP1	55.83
mycBioID2tau	3	VAMP1	48.04
mycBioID2	*4*	VAMP2	54.82
mycBioID2	*6*	VAMP2	46.53
mycBioID2tau	5	VAMP2	47.24
mycBioID2tau	5	VAMP2	46.47
mycBioID2	*4*	VCIP1	76.53
mycBioID2	*6*	VCIP1	75.67
mycBioID2	*6*	VCIP1	67.77
mycBioID2tau	1	VCIP1	76.41
mycBioID2tau	5	VCIP1	62.54
mycBioID2tau	3	VCIP1	59.83
mycBioID2tau	1	VCIP1	56.42
mycBioID2tau	5	WIPF2	58.58

y cortical mouse neurons.

experimental and BioID2 control.

Biotinylated Peptide Sequence	Biotinylated Lysine (K = '1')
TVKGGISETR	0.0010000000.0
TVKGGISETR	0.0010000000.0
TVKGGISETR	0.0010000000.0
TVKGGISETR	0.0010000000.0
TVKGGISETR	0.0010000000.0
SKLATPEDKQDIDK	0.01000000000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
VAEDEFDPIPVLITKNTQGGHSR	0.00000000000000100000000.0
EITALAPSTMKIK	0.0000000000001.0
EITALAPSTMKIK	0.0000000000001.0
EITALAPSTMKIK	0.0000000000001.0
EITALAPSTMKIK	0.0000000000001.0
EITALAPSTMKIK	0.0000000000001.0
LCVLHEKTPVSEK	0.0200001000000.0
LCVLHEKTPVSEK	0.0200001000000.0
FPKAEFVEVTK	0.00100000000.0
CDQFEKLGEYGFQNALIVR	0.20000100000000000000.0
LCVLHEKTPVSEK	0.0200001000000.0
LSQKFPKAEFVEVTK	0.000000100000000.0
FPKAEFVEVTK	0.00100000000.0
DTHKSEIAHR	0.0001000000.0
DTHKSEIAHR	0.0001000000.0
KVPQVSTPTLVEVSR	0.100000000000000.0
LCVLHEKTPVSEKVTK	0.02000010000000000.0
LCVLHEKTPVSEKVTK	0.02000010000000000.0
DTHKSEIAHR	0.0001000000.0
SHCIAEVEKDAIPENLPPLTADFAEDKDVCK	0.00200000000000000000000000001
FPKAEFVEVTK	0.00100000000.0
LCVLHEKTPVSEK	0.0200001000000.0
LSQKFPKAEFVEVTK	0.000000100000000.0
FPKAEFVEVTK	0.00100000000.0
FPKAEFVEVTK	0.00100000000.0
FPKAEFVEVTK	0.00100000000.0
LSQKFPKAEFVEVTK	0.000000100000000.0
KTVMENFVAFVDK	0.1000000000000.0
RPCFSALTPDETYVPKAFDEK	0.00200000000000000100000.0
FPKAEFVEVTK	0.00100000000.0
KVPQVSTPTLVEVSR	0.100000000000000.0

DTHKSEIAHR	0.0001000000.0
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IVAPGKGILAADESTGSIAKR	0.0000010000000000000000.0
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IVAPGKGILAADESTGSIAK	0.000001000000000000000.0
IVAPGKGILAADESTGSIAK	0.000001000000000000000.0
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KGDLQWNAGEK	0.10000000000.0
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SPVVELSKVPLIQR	0.00000001000000.0
SPVVELSKVPLIQR	0.00000001000000.0
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SPVVELSKVPLIQR	0.00000001000000.0
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TITGKTFSSR	0.0000100000.0
TITGKTFSSR	0.0000100000.0
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FGAQFKLQPSSSPETGLDPFPSR	0.000001000000000000000000.0
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IAKPVSLLEK	0.0010000000.0
IAKPVSLLEK	0.0010000000.0
IAKPVSLLEK	0.0010000000.0
IAKPVSLLEK	0.0010000000.0
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LMDSVALKGGR	0.00000001000.0
LMDSVALKGGR	0.00000001000.0
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LGKSAFLQVQPR	0.001000000000.0
LGKSAFLQVQPR	0.001000000000.0
LGKSAFLQVQPR	0.001000000000.0
LGKSAFLQVQPR	0.001000000000.0
LGKSAFLQVQPR	0.001000000000.0
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LNAKGGNVPQLDAPISQFYADR	0.00010000000000000000000.0
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GKSASSPKPDTKVPQATAEAK	0.010000000000000000000.0
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QALGGATKDMGK	0.000000010000.0
YLPGPLQDMFKK	0.000000000001.0
YLPGPLQDMFKK	0.000000000001.0
GVNQFGNKYIQQTKPLTLER	0.00000001000000000000.0
SSPHGKHGNR	0.0000010000.0
VGTKGLDFSDR	0.00010000000.0

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DGYPGAGPGKGLLGPETK	0.000000000100000000.0
LNPDGKSIR	0.000001000.0
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TSPAKQQAPPVR	0.000010000000.0
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TVTPASSAKTSPAK	0.00000000100000.0
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TVKGGFSETR	0.0010000000.0
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SLSPIIGKDVLTSTYGATAETLSTSTTTHVTK	0.0000000100000000000000000000
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TLKEPNSKLIHR	0.000000010000.0
SLSPIIGKDVLTSTYGATAETLSTSTTTHVTK	0.0000000100000000000000000000
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SGKGAAAMIPGPQTVATEIR	0.00100000000000000000.0
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TVKGGFSETR	0.0010000000.0
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SLSPIIGKDVLTSTYGATAETLSTSTTTHVTK	0.0000000100000000000000000000
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TVKGGFSETR	0.0010000000.0
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SGKGAAAMIPGPQTVATEIR	0.00100000000000000000.0
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TVKGGISETR	0.0010000000.0
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HKTTIFTDAK	0.0100000000.0
HKTTIFTDAK	0.0100000000.0
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TSPTASVNKIEYAAR	0.000000001000000.0
TSPTASVNKIEYAAR	0.000000001000000.0
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INSGGKLPNFGFVVFDDSEPVQK	0.00000100000000000000000.0

INSGGKLPNFGFVVFDDSEPVQK	0.000001000000000000000000.0
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YKEALLGR	0.01000000.0
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FKKCVQSNIVLLTQAFR	0.011000000000000000.0
LISKTPVLPGR	0.00010000000.0
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GKVTIAQGGVLPNIQAVLLPK	0.01000000000000000000.0
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AVTKYTSSK	0.000000001.0
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VLKQVHPDTGISSK	0.00100000000000.0
VLKQVHPDTGISSK	0.00100000000000.0
VLKQVHPDTGISSK	0.00100000000000.0
AVTKYTSSK	0.000000001.0
AVTKYTSSK	0.000000001.0
LLLPGELAKHAVSEGTK	0.000000001000000000.0
VLKQVHPDTGISSK	0.00100000000000.0
AVTKYTSSK	0.000000001.0
AVTKYTSSK	0.000000001.0
VLKQVHPDTGISSK	0.00100000000000.0
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VLKQVHPDTGISSK	0.00100000000000.0
AVTKYTSSK	0.000000001.0
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VLKQVHPDTGISSK	0.00100000000000.0
VLKQVHPDTGISSK	0.00100000000000.0
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AVTKYTSSK	0.000000001.0
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IMKAQALR	0.00100000.0
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ITITNDKGR	0.000000100.0
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VLDPSKFLK	0.000001000.0
VLDPSKFLK	0.000001000.0
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VLDPSKFLK	0.000001000.0
VLDPSKFLK	0.000001000.0
KGGPDDR	0.1000000.0
AYTSSK	0.000001.0
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SNKNGGNQEVEIAHCHKG	0.001000000000000000.0
SNKNGGNQEVEIAHCHKG	0.001000000000000000.0
SNKNGGNQEVEIAHCHKG	0.001000000000000000.0
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INNKANVVTSPK	0.000100000000.0
INNKANVVTSPK	0.000100000000.0
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GGGGGSSNSTHYQK	0.00000000000001.0
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GKGFSVVADTPELQR	0.010000000000000.0
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LDPWKLVSFGR	0.00001000000.0
LDPWKLVSFGR	0.00001000000.0
LDPWKLVSFGR	0.00001000000.0
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DTAVELGKGPEPK	0.0000000100000.0
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DFQEPLPQKGLEVER	0.000000001000000.0
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TSQVEKTPK	0.000001000.0
ESLKPATKPVASKSVR	0.0000000000001000.0
ESLKPATKPVASKSVR	0.0000000000001000.0
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ATKTTTTPEVK	0.00100000000.0
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DMSPLPESEVTLGKDVVILPETK	0.000000000000001000000000.0
DMSPLPESEVTLGKDVVILPETK	0.030000000000001000000000.0
TTPTVSKATSPSTLVSTGPSSR	0.000000100000000000000000.0
DMSPLPESEVTLGKDVVILPETK	0.000000000000001000000000.0
DMSPLPESEVTLGKDVVILPETK	0.000000000000001000000000.0
DMSPLPESEVTLGKDVVILPETK	0.000000000000001000000000.0
MTAKSASADLSR	0.000100000000.0
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DQGAVLLGPVKDLGPVAPAPIK	0.000000000100000000000.0
DQGAVLLGPVKDLGPVAPAPIK	0.000000000100000000000.0
GHDSVFVAPVKNQGPVIPEPVK	0.000000000100000000000.0
GHDSVFVAPVKNQGPVIPEPVK	0.000000000100000000000.0
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YLKGHDSVFVAPVK	0.00100000000000.0
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VKPTSDASKNR	0.00000000100.0
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VKPTSDASKNR	0.00000000100.0
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AGDSLMVMIAMKMEHTIK	0.000000000001000000.0
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MFTIDPKVYGEKR	0.0000001000000.0
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MFTIDPKVYGEKR	0.3000001000000.0
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TPGTPKSGILVPSEK	0.000001000000000.0
MFTIDPKVYGEKR	0.0000001000000.0
TPGTPKSGILVPSEK	0.000001000000000.0
TPGTPKSGILVPSEK	0.000001000000000.0
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IDSQKLNFR	0.000010000.0
EASPPTSADKSR	0.000000000100.0
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TPGTPKSGILVPSEK	0.000001000000000.0
TLGKVTSEPEAVSER	0.000100000000000.0
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YQPKGGQVQIVTK	0.0001000000000.0
GGQVQIVTKK	0.0000000001.0
TADKNKLEGAGSATIAEVEMPFYEDK	0.000100000000000000000000000.(
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INLIDKK	0.0000001.0
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IQEIQKAIELFSVGQGPAK	0.00000100000000000000.0
NKVVIAEK	0.01000000.0
NKVVIAEK	0.01000000.0
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DIEAMDPSILKGEPASGKR	0.000000000100000000.0
GAKEHGAVAVER	0.001000000000.0

GAKEHGAVAVER	0.001000000000.0
GAKEHGAVAVER	0.001000000000.0
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TVKHGAGAEISTVNPEQYSK	0.00100000000000000000.0
LLASGKVAQR	0.0000010000.0
LLASGKVAQR	0.0000010000.0
LLASGKVAQR	0.0000010000.0
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LLASGKVAQR	0.0000010000.0
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GQPLCVLSAMKMETVVTSPMEGTIRK	0.0000200000100000000000000.(
GQPLCVLSAMKMETVVTSPMEGTIR	0.000020000010000000300000.0
KMETVVTSPMEGTIR	0.100000000000000.0
GQPLCVLSAMKMETVVTSPMEGTIR	0.000020000010000000000000.0
SAMKMETVVTSPMEGTIR	0.000100000000000000.0
KMETVVTSPMEGTIR	0.100000000000000.0
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GQPLCVLSAMKMETVVTSPMEGTIR	0.000020000310000000000000.0
GQPLCVLSAMKMETVVTSPMEGTIR	0.000020000010000000300000.0
GQPLCVLSAMKMETVVTSPMEGTIR	0.000020000010000000300000.0
GQPLCVLSAMKMETVVTSPMEGTIR	0.000020000010000000000000.0
IDHYVVEVNKLIIR	0.00000000010000.0
IDHYVVEVNKLIIR	0.00000000010000.0
IDHYVVEVNKLIIR	0.00000000010000.0
IDHYVVEVNKLIIR	0.00000000010000.0
SSVSKVPLLLPNVSALESQIEMGNIVKPK	0.000010000000000000000000000
LSTEPSPEFSNYSEIAKFEK	0.00000000000000001000.0
SSVSKVPLLLPNVSALESQIEMGNIVKPK	0.000010000000000000000000000
SSVSKVPLLLPNVSALESQIEMGNIVKPK	0.000010000000000000000000000
LSTEPSPEFSNYSEIAKFEK	0.00000000000000000001.0
KGTEVQVDDIKR	0.100000000000.0
KGTEVQVDDIKR	0.100000000000.0
KGTEVQVDDIKR	0.100000000000.0
LSMINTMSKIR	0.00000000100.0
LSMINTMSKIR	0.00000000100.0
LSMINTMSKIR	0.00000000100.0
LSMINTMSKIR	0.00000000100.0
QGKIPDEELR	0.0010000000.0
SVKPGEGLELPVGAKSANLAPR	0.000000000000010000000.0
SVKPGEGLELPVGAKSANLAPR	0.000000000000010000000.0

SVKPGEGLELPVGAKSANLAPR	0.0000000000000010000000.0
GQMPENPYSEVGKIASK	0.00000000000010000.0
SVKPGEGLELPVGAKSANLAPR	0.0000000000000010000000.0
TGFLKWKPDYDSAASEYGK	0.00001000000000000000.0
TGFLKWKPDYDSAASEYGK	0.00001000000000000000.0
TGFLKWKPDYDSAASEYGK	0.00001000000000000000.0
SNKGGARPELVNNPR	0.001000000000000.0
AITFKNGWQMAR	0.000010000000.0
AITFKNGWQMAR	0.000010000000.0
AITFKNGWQMAR	0.000010000000.0
GFGGKFGVQMDR	0.000010000000.0
GFGGKFGVQTDR	0.000010000000.0
GFGGKFGVQMDR	0.000010000000.0
TVPIEAVTSKTSNIR	0.000000000100000.0
TGFGGKFGVQSER	0.0000010000000.0
GFGGKFGVQMDR	0.000010000000.0
GFGGKFGVQMDR	0.000010000000.0
GFGGKFGVQTDR	0.000010000000.0
GFGGKFGVQMDR	0.000010000000.0
GFGGKFGVQMDR	0.000010000000.0
GFGGKFGVQMDR	0.000010000000.0
ASHGYGGKFGVEQDR	0.000000010000000.0
TGFGGKFGVQSER	0.0000010000000.0
TGEVVVTSKK	0.0000000001.0
TGEVVVTSKK	0.0000000001.0
TGEVVVTSKK	0.0000000001.0
SKESVPDFPLSPPK	0.01000000000000.0
SKESVPDFPLSPPK	0.01000000000000.0
EAQMAAKLER	0.0000001000.0
SKESVPDFPLSPPK	0.01000000000000.0
SKESVPDFPLSPPK	0.01000000000000.0
EAQMAAKLER	0.0000001000.0
QASISGPAPTKASGAPPGGQQR	0.00000000001000000000000.0
SSILLIDKVSAPPSAASTFSR	0.000000010000000000000.0
EGVLYVGSKTK	0.00000000001.0
TKQGVAEAAGK	0.01000000000.0
TKEGVLYVGSKTK	0.0000000000100.0
TKQGVAEAAGK	0.01000000000.0
EGVLYVGSKTK	0.00000000001.0
TKQGVTEAAEK	0.01000000000.0
TKEGVLYVGSKTSGVVQGVASVAEK	0.00000000001000000000000000.0
TKEGVLYVGSKTSGVVQGVASVAEK	0.00000000001000000000000000.0
TKEGVLYVGSKTSGVVQGVASVAEK	0.00000000001000000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.0000000010000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.0000000010000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.0000000010000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.0000000010000000000000.0
TKEGVLYVGSKTSGVVQGVASVAEK	0.00000000001000000000000000.0

TKEGVLYVGSKTSGVVQGVASVAEK	0.000000000010000000000000.0
TKEGVLYVGSKTSGVVQGVASVAEK	0.000000000010000000000000.0
TKEGVLYVGSKTSGVVQGVASVAEK	0.000000000010000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.00000001000000000000000.0
TKQGVTEAAEK	0.01000000000.0
TKEGVLYVGSKTK	0.0000000000100.0
EGVLYVGSKTSGVVQGVASVAEK	0.00000001000000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.00000001000000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.00000001000000000000000.0
EGVLYVGSKTSGVVQGVASVAEK	0.00000001000000000000000.0
EGVLYVGSKTK	0.00000000001.0
TKQGVTEAAEK	0.01000000000.0
QGQNVIGLQMGSNKGASQAGMTGYGMPR	0.000000000000010000000000000
QGQNVIGLQMGSNKGASQAGMTGYGMPR	0.000000000000010000000000000
QGQNVIGLQMGSNKGASQAGMTGYGMPR	0.000000000000010000000000000
QGQNVIGLQMGSNKGASQAGMTGYGMPR	0.000000000000010000000000000
QGQNVIGLQMGSNKGASQAGMTGYGMPR	0.000000000000010000000000000
TTPFMGIIDKTAR	0.0000000001000.0
NSLKMLLTGGK	0.00010000000.0
TTPFMGIIDKTAR	0.0000000001000.0
IPAKTTPSPK	0.0001000000.0
VQSKIGSLDNITHVPGGGNK	0.00010000000000000000.0
KIETHKLTFR	0.0000010000.0
HVPGGGSVQIVYKPVDLSK	0.000000000001000000.0
IPAKTTPSPK	0.0001000000.0
VTSKCGSLGNIHHKPGGGQVEVK	0.00012000000000000000000.0
SKIGSTENLK	0.0100000000.0
IPAKTTPSPK	0.0001000000.0
VQSKIGSLDNITHVPGGGNK	0.00010000000000000000.0
VTSKCGSLGNIHHKPGGGQVEVK	0.00012000000000000000000.0
GTSNATRIPAKTTPSPK	0.00000000001000000.0
IPAKTTPSPK	0.0001000000.0
KLDLSNVQSK	0.1000000000.0
TPPKSPSASKSR	0.000000000100.0
VQSKIGSLDNITHVPGGGNK	0.00010000000000000000.0
KLDLSNVQSK	0.1000000000.0
TIGGGDDSFNTFFSETGAGKHVPR	0.00000000000000000010000.0
TIGGGDDSFNTFFSETGAGKHVPR	0.00000000000000000010000.0
TIGGGDDSFNTFFSETGAGKHVPR	0.00000000000000000010000.0
TIGGGDDSFNTFFSETGAGKHVPR	0.00000000000000000010000.0
TIGGGDDSFNTFFSETGAGKHVPR	0.00000000000000000010000.0
TIGGGDDSFNTFFSETGAGKHVPR	0.00000000000000000010000.0
TIGGGDDSFNTFFSETGAGKHVPR	0.00000000000000000010000.0
KMSATFIGNSTAIQELFKR	0.1000000000000000000.0
KMSATFIGNSTAIQELFKR	0.1000000000000000000.0
KMSATFIGNSTAIQELFKR	0.1000000000000000000.0
KMSATFIGNSTAIQELFKR	0.1000000000000000000.0
KMASTFIGNSTAIQELFKR	0.1000000000000000000.0

SKLGPYNEELR	0.01000000000.0
SKLGPYNEELR	0.01000000000.0
SKLGPYNEELR	0.01000000000.0
SKLGPYNEELR	0.01000000000.0
TKHKLDVMSVEDYK	0.01000000000000.0
VDLVDESGYVPGYKHAGTYDQK	0.000000000000000100000000.0
VNVDKVLER	0.000010000.0
VNVDKVLER	0.000010000.0
VNVDKVLER	0.000010000.0
VNVDKVLER	0.000010000.0
VNVDKVLER	0.000010000.0
VNVDKVLER	0.000010000.0
VGDVQGQELESQLPTKIILTGQK	0.00000000000000010000000.0
VGDVQGQELESQLPTKIILTGQK	0.00000000000000010000000.0
VGDVQGQELESQLPTKIILTGQK	0.00000000000000010000000.0
VGDVQGQELESQLPTKIILTGQK	0.00000000000000010000000.0
VGDVQGQELESQLPTKIILTGQK	0.00000000000000010000000.0
VGDVQGQELESQLPTKIILTGQK	0.00000000000000010000000.0
VGDVQGQELESQLPTKIILTGQK	0.00000000000000010000000.0
ANAPPTPLPLHSNKAQAYNR	0.0000000000001000000.0

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Table 10. **Biotinylated peptide list from cortex an**
Samples include neurons expressing BioID2-tau exp

AAV condition	Sample No.	Protein	Peptide Score
mycBioID2tau	5	41	40.78
mycBioID2tau	7	41	44.24
mycBioID2tau	9	41	52.83
mycBioID2tau	12	41	52.83
mycBioID2	*6*	41	56.03
mycBioID2tau	1	AAK1	52.2
mycBioID2tau	8	AAK1	47.74
mycBioID2tau	9	AAK1	54.15
mycBioID2tau	2	AFF2	43.99
mycBioID2tau	1	ALDOA	61.05
mycBioID2tau	3	ALDOA	66.33
mycBioID2tau	5	ALDOA	66.2
mycBioID2tau	5	ALDOA	63.17
mycBioID2tau	10	ALDOA	67.13
mycBioID2tau	10	ALDOA	50.88
mycBioID2	*8*	ALDOA	48.29
mycBioID2tau	1	ANK2	42.91
mycBioID2tau	2	ANK2	45.75
mycBioID2tau	3	ANK2	46.18
mycBioID2tau	4	ANK2	40.97
mycBioID2tau	6	ANK2	50.31
mycBioID2tau	6	ANK2	43.9
mycBioID2	*12*	ANS1B	51.63
mycBioID2tau	2	AP180	68.67
mycBioID2tau	5	AP180	41.17
mycBioID2tau	6	AP180	70.69
mycBioID2tau	8	AP180	79.7
mycBioID2	*12*	AP180	49.43
mycBioID2tau	10	ARBK1	52.22
mycBioID2tau	3	ASAP1	94.35
mycBioID2	*12*	ASAP1	41.27
mycBioID2tau	2	AT1B3	46.22
mycBioID2tau	1	AUXI	58.15
mycBioID2tau	3	AUXI	41.55
mycBioID2tau	1	BASP1	57.62
mycBioID2tau	1	BASP1	57.01
mycBioID2tau	2	BASP1	48.39
mycBioID2tau	6	BASP1	61.48
mycBioID2tau	8	BASP1	76.36
mycBioID2tau	8	BASP1	67.22
mycBioID2tau	8	BASP1	65.88
mycBioID2tau	1	BIN1	59.37
mycBioID2tau	3	BIN1	60.95
mycBioID2tau	6	BIN1	64.31

mycBioID2tau	6	BIN1	46.36
mycBioID2tau	8	BIN1	44.21
mycBioID2tau	8	BIN1	43.35
mycBioID2tau	10	BIN1	52.35
mycBioID2tau	1	BSN	47.85
mycBioID2tau	10	BSN	50.91
mycBioID2tau	10	BSN	50.19
mycBioID2tau	10	BSN	49.77
mycBioID2tau	1	CA123	55.17
mycBioID2tau	2	CA123	43.1
mycBioID2tau	3	CA123	40.74
mycBioID2tau	5	CA123	64.17
mycBioID2tau	6	CA123	68.16
mycBioID2tau	11	CA123	41.26
mycBioID2tau	1	CAMP3	76.83
mycBioID2tau	1	CAMP3	44.22
mycBioID2tau	2	CAMP3	63.96
mycBioID2tau	3	CAMP3	56.8
mycBioID2tau	5	CAMP3	57.55
mycBioID2tau	6	CAMP3	78.68
mycBioID2tau	8	CAMP3	69.13
mycBioID2tau	7	CAMP3	78.77
mycBioID2	*12*	CAMP3	65.65
mycBioID2tau	6	CC124	39.63
mycBioID2tau	1	CEND	46.8
mycBioID2tau	1	CEND	41.69
mycBioID2tau	1	CEND	38.12
mycBioID2tau	3	CEND	39.2
mycBioID2tau	6	CEND	42.76
mycBioID2tau	6	CEND	41.5
mycBioID2tau	8	CEND	42.07
mycBioID2tau	8	CEND	44.03
mycBioID2tau	10	CEND	44.54
mycBioID2tau	10	CEND	42.74
mycBioID2	*3*	CEND	48.24
mycBioID2	*3*	CEND	40.88
mycBioID2	*4*	CEND	53.79
mycBioID2	*12*	CEND	47.51
mycBioID2tau	1	CPLX1	54.72
mycBioID2tau	2	CPLX1	60.28
mycBioID2tau	3	CPLX1	48.1
mycBioID2tau	1	CPLX2	54.72
mycBioID2tau	8	CSKI1	64.63
mycBioID2tau	10	DC1L1	55.98
mycBioID2tau	3	DCLK1	56.47
mycBioID2tau	3	DCLK1	55.89
mycBioID2tau	8	DCLK1	59.23
mycBioID2tau	10	DCLK1	50.06

mycBioID2tau	10	DCLK1	49.62
mycBioID2tau	1	DCTN2	40.88
mycBioID2tau	6	DLGP3	47.39
mycBioID2	*7*	DLGP3	42.84
mycBioID2	*8*	DLGP3	80.75
mycBioID2	*10*	DLGP3	54.2
mycBioID2	*12*	DLGP3	89.4
mycBioID2tau	2	DNJB1	38.05
mycBioID2tau	3	DNJB1	46.03
mycBioID2tau	4	DNJB1	42.96
mycBioID2tau	5	DNJB1	42.28
mycBioID2tau	6	DNJB1	45.18
mycBioID2tau	8	DNJB1	41.55
mycBioID2tau	8	DNJB1	50
mycBioID2tau	7	DNJB1	49.87
mycBioID2tau	7	DNJB1	49.87
mycBioID2tau	7	DNJB1	49.87
mycBioID2tau	7	DNJB1	43.51
mycBioID2tau	10	DNJB1	43.82
mycBioID2tau	11	DNJB1	39.29
mycBioID2	*9*	DNJB1	52.63
mycBioID2	*12*	DNJB1	46.19
mycBioID2tau	1	DPYL2	78.42
mycBioID2tau	1	DPYL2	64.05
mycBioID2tau	2	DPYL2	83.05
mycBioID2tau	2	DPYL2	51.8
mycBioID2tau	3	DPYL2	86.14
mycBioID2tau	3	DPYL2	70.71
mycBioID2tau	4	DPYL2	58.26
mycBioID2tau	5	DPYL2	74.74
mycBioID2tau	5	DPYL2	63.61
mycBioID2tau	5	DPYL2	69.78
mycBioID2tau	5	DPYL2	45.77
mycBioID2tau	6	DPYL2	81.52
mycBioID2tau	6	DPYL2	72.8
mycBioID2tau	8	DPYL2	58.81
mycBioID2tau	8	DPYL2	59.55
mycBioID2tau	7	DPYL2	70.75
mycBioID2tau	7	DPYL2	61.81
mycBioID2tau	9	DPYL2	69.88
mycBioID2tau	12	DPYL2	69.88
mycBioID2tau	10	DPYL2	98.27
mycBioID2tau	10	DPYL2	59.69
mycBioID2tau	11	DPYL2	75.21
mycBioID2	*10*	DPYL2	62.72
mycBioID2	*12*	DPYL2	54.73
mycBioID2	*12*	DPYL2	53.06
mycBioID2tau	6	DYN1	67.68

mycBioID2tau	1	E41L1	61.33
mycBioID2tau	1	E41L1	56.98
mycBioID2tau	2	E41L1	40.8
mycBioID2tau	3	E41L1	57.64
mycBioID2tau	4	E41L1	40.32
mycBioID2tau	5	E41L1	64.48
mycBioID2tau	5	E41L1	47.93
mycBioID2tau	6	E41L1	45.54
mycBioID2tau	6	E41L1	52.19
mycBioID2tau	8	E41L1	59.74
mycBioID2tau	7	E41L1	57.88
mycBioID2tau	10	E41L1	70.98
mycBioID2tau	10	E41L1	59.64
mycBioID2tau	10	E41L1	45.52
mycBioID2tau	11	E41L1	45.4
mycBioID2tau	11	E41L1	44.25
mycBioID2	*2*	E41L1	55.14
mycBioID2	*3*	E41L1	51.32
mycBioID2	*4*	E41L1	53.04
mycBioID2	*5*	E41L1	41.7
mycBioID2	*5*	E41L1	41.7
mycBioID2	*5*	E41L1	41.7
mycBioID2	*6*	E41L1	49.14
mycBioID2	*6*	E41L1	49.14
mycBioID2	*8*	E41L1	55.18
mycBioID2	*9*	E41L1	51.62
mycBioID2	*10*	E41L1	65.87
mycBioID2	*11*	E41L1	53.18
mycBioID2	*12*	E41L1	69.58
mycBioID2	*12*	E41L1	56.57
mycBioID2	*4*	E41L2	49.4
mycBioID2	*8*	E41L2	69.84
mycBioID2tau	1	E41L3	69.54
mycBioID2tau	6	E41L3	63.34
mycBioID2tau	8	E41L3	48.97
mycBioID2tau	10	E41L3	68.15
mycBioID2tau	11	E41L3	48.4
mycBioID2	*8*	E41L3	69.84
mycBioID2	*8*	E41L3	69.84
mycBioID2	*12*	E41L3	57.75
mycBioID2	*12*	F169A	88.9
mycBioID2tau	9	G3P	69.33
mycBioID2tau	1	G3P	57.4
mycBioID2tau	6	GDIR1	50.74
mycBioID2tau	9	GDIR1	41.69
mycBioID2tau	12	GDIR1	41.69
mycBioID2tau	10	GDIR1	49.37
mycBioID2tau	5	GLNA	58.53

mycBioID2tau	5	GLNA	66.7
mycBioID2tau	6	GP158	43.54
mycBioID2tau	8	GP158	42.24
mycBioID2tau	10	GP158	47.57
mycBioID2tau	1	GRIN1	59.92
mycBioID2tau	1	GRIN1	43.56
mycBioID2tau	1	GRIN1	42.43
mycBioID2tau	3	GRIN1	54.69
mycBioID2tau	3	GRIN1	45.5
mycBioID2tau	8	GRIN1	47.44
mycBioID2tau	8	GRIN1	41.61
mycBioID2tau	8	GRIN1	39.88
mycBioID2tau	10	GRIN1	46.52
mycBioID2	*12*	GRIN1	50.87
mycBioID2tau	10	HAP28	75.28
mycBioID2tau	3	HS71A	62.05
mycBioID2tau	1	IF4B	66.13
mycBioID2tau	2	IF4B	56.08
mycBioID2tau	3	IF4B	71.51
mycBioID2tau	8	IF4B	62.99
mycBioID2tau	6	IF4G3	47.75
mycBioID2tau	10	IF4G3	61.85
mycBioID2	*7*	IF4G3	52.37
mycBioID2	*12*	IF4G3	48.4
mycBioID2tau	2	KCC2A	47.7
mycBioID2tau	3	KCC2A	51.23
mycBioID2tau	8	KCC2A	43.12
mycBioID2	*12*	KCC2A	55.81
mycBioID2tau	2	KCC2D	56.31
mycBioID2tau	8	KCC2D	53.96
mycBioID2tau	10	KI21A	42.48
mycBioID2tau	3	KPCB	46.75
mycBioID2tau	1	KT3K	56.52
mycBioID2tau	2	KT3K	57.04
mycBioID2tau	3	KT3K	61.55
mycBioID2tau	8	KT3K	64.25
mycBioID2tau	3	LASP1	58.95
mycBioID2tau	3	LASP1	44.48
mycBioID2tau	5	LASP1	76.69
mycBioID2tau	5	LASP1	51.54
mycBioID2tau	6	LASP1	72.11
mycBioID2tau	6	LASP1	44.73
mycBioID2tau	8	LASP1	77.74
mycBioID2tau	10	LASP1	99.21
mycBioID2tau	1	MAP1A	57.63
mycBioID2tau	1	MAP1A	50.91
mycBioID2tau	1	MAP1A	39.79
mycBioID2tau	2	MAP1A	60.78

mycBioID2tau	2	MAP1A	47.44
mycBioID2tau	3	MAP1A	61.67
mycBioID2tau	3	MAP1A	44.44
mycBioID2tau	3	MAP1A	41.34
mycBioID2tau	4	MAP1A	47.41
mycBioID2tau	4	MAP1A	40.75
mycBioID2tau	5	MAP1A	42.19
mycBioID2tau	5	MAP1A	41.16
mycBioID2tau	5	MAP1A	44.12
mycBioID2tau	6	MAP1A	96.96
mycBioID2tau	6	MAP1A	56.77
mycBioID2tau	6	MAP1A	49.19
mycBioID2tau	6	MAP1A	45.44
mycBioID2tau	8	MAP1A	49.05
mycBioID2tau	8	MAP1A	57.97
mycBioID2tau	8	MAP1A	50.94
mycBioID2tau	8	MAP1A	49.31
mycBioID2tau	8	MAP1A	45.43
mycBioID2tau	8	MAP1A	42.23
mycBioID2tau	8	MAP1A	41.95
mycBioID2tau	10	MAP1A	86.61
mycBioID2tau	10	MAP1A	58.7
mycBioID2tau	10	MAP1A	54.88
mycBioID2tau	10	MAP1A	53.23
mycBioID2tau	11	MAP1A	57.42
mycBioID2tau	11	MAP1A	46.36
mycBioID2	*3*	MAP1A	60.93
mycBioID2	*4*	MAP1A	57.16
mycBioID2	*4*	MAP1A	53.71
mycBioID2	*4*	MAP1A	53.25
mycBioID2	*6*	MAP1A	78.56
mycBioID2	*6*	MAP1A	39.16
mycBioID2	*9*	MAP1A	67.57
mycBioID2	*10*	MAP1A	60.96
mycBioID2	*12*	MAP1A	50.19
mycBioID2tau	1	MAP1B	79.14
mycBioID2tau	1	MAP1B	74.9
mycBioID2tau	2	MAP1B	46.77
mycBioID2tau	2	MAP1B	44.82
mycBioID2tau	3	MAP1B	61.54
mycBioID2tau	3	MAP1B	55.63
mycBioID2tau	3	MAP1B	52.14
mycBioID2tau	3	MAP1B	44.62
mycBioID2tau	6	MAP1B	54.28
mycBioID2tau	6	MAP1B	47.44
mycBioID2tau	8	MAP1B	39.93
mycBioID2tau	8	MAP1B	46.1
mycBioID2tau	7	MAP1B	42.84

mycBioID2tau	10	MAP1B	65.17
mycBioID2tau	11	MAP1B	50.54
mycBioID2tau	1	MAP4	43.99
mycBioID2tau	2	MAP4	46.13
mycBioID2tau	3	MAP4	101.14
mycBioID2tau	6	MAP4	52.49
mycBioID2tau	8	MAP4	54.39
mycBioID2tau	7	MAP4	45.26
mycBioID2tau	10	MAP4	60.94
mycBioID2tau	1	MAP6	58.86
mycBioID2tau	1	MAP6	53.56
mycBioID2tau	1	MAP6	45.91
mycBioID2tau	1	MAP6	42.13
mycBioID2tau	2	MAP6	73.81
mycBioID2tau	2	MAP6	65.53
mycBioID2tau	2	MAP6	61.76
mycBioID2tau	2	MAP6	59.44
mycBioID2tau	2	MAP6	48.41
mycBioID2tau	2	MAP6	47.93
mycBioID2tau	3	MAP6	63.7
mycBioID2tau	3	MAP6	50.03
mycBioID2tau	3	MAP6	43.79
mycBioID2tau	4	MAP6	67.17
mycBioID2tau	4	MAP6	61.18
mycBioID2tau	5	MAP6	43.38
mycBioID2tau	6	MAP6	60.05
mycBioID2tau	6	MAP6	57.08
mycBioID2tau	6	MAP6	50.27
mycBioID2tau	6	MAP6	77.78
mycBioID2tau	6	MAP6	59.81
mycBioID2tau	6	MAP6	56.54
mycBioID2tau	6	MAP6	55.65
mycBioID2tau	6	MAP6	46.84
mycBioID2tau	8	MAP6	64.93
mycBioID2tau	8	MAP6	58.83
mycBioID2tau	8	MAP6	50.85
mycBioID2tau	8	MAP6	71.75
mycBioID2tau	8	MAP6	63.06
mycBioID2tau	8	MAP6	59.22
mycBioID2tau	8	MAP6	51.44
mycBioID2tau	8	MAP6	46.8
mycBioID2tau	9	MAP6	45.04
mycBioID2tau	9	MAP6	58.74
mycBioID2tau	12	MAP6	58.74
mycBioID2tau	10	MAP6	63.79
mycBioID2tau	10	MAP6	62.94
mycBioID2tau	10	MAP6	57.24
mycBioID2tau	10	MAP6	56.12

mycBioID2tau	10	MAP6	52.05
mycBioID2tau	10	MAP6	47.68
mycBioID2tau	10	MAP6	44.14
mycBioID2tau	10	MAP6	43.64
mycBioID2tau	10	MAP6	39.98
mycBioID2tau	11	MAP6	58.21
mycBioID2tau	11	MAP6	55.56
mycBioID2tau	11	MAP6	50.5
mycBioID2tau	11	MAP6	50
mycBioID2	*4*	MAP6	46.38
mycBioID2tau	1	MARE1	63.43
mycBioID2tau	2	MARE1	56.54
mycBioID2tau	3	MARE1	66.31
mycBioID2tau	6	MARE1	59.14
mycBioID2tau	8	MARE1	57.17
mycBioID2tau	9	MARE1	41.05
mycBioID2tau	12	MARE1	41.05
mycBioID2tau	10	MARE1	64.55
mycBioID2tau	11	MARE1	53.2
mycBioID2tau	1	MARE2	44.96
mycBioID2tau	2	MARE2	44.76
mycBioID2tau	1	MARE3	50.74
mycBioID2tau	1	MARE3	47.04
mycBioID2tau	2	MARE3	38.37
mycBioID2tau	3	MARE3	46.21
mycBioID2tau	2	MCCA	39.68
mycBioID2tau	6	MCCA	41.77
mycBioID2tau	9	MCCA	41.35
mycBioID2tau	9	MCCA	50.47
mycBioID2tau	10	MCCA	45.42
mycBioID2	*2*	MCCA	65.9
mycBioID2	*4*	MCCA	54.6
mycBioID2	*4*	MCCA	54.6
mycBioID2	*6*	MCCA	60.01
mycBioID2tau	2	MK12	67.77
mycBioID2tau	3	MK12	41.03
mycBioID2tau	4	MK12	72.65
mycBioID2tau	5	MK12	72.57
mycBioID2tau	6	MK12	63.87
mycBioID2tau	7	MK12	69.29
mycBioID2tau	9	MK12	74.9
mycBioID2tau	12	MK12	74.9
mycBioID2	*1*	MK12	63.8
mycBioID2	*11*	MK12	82.63
mycBioID2tau	1	MTAP2	58.56
mycBioID2tau	1	MTAP2	57.9
mycBioID2tau	1	MTAP2	56.11
mycBioID2tau	1	MTAP2	50.51

mycBioID2tau	1	MTAP2	49.89
mycBioID2tau	1	MTAP2	45.64
mycBioID2tau	1	MTAP2	43.99
mycBioID2tau	1	MTAP2	43.25
mycBioID2tau	1	MTAP2	42.35
mycBioID2tau	1	MTAP2	39.8
mycBioID2tau	2	MTAP2	73.95
mycBioID2tau	2	MTAP2	64.94
mycBioID2tau	2	MTAP2	55.93
mycBioID2tau	2	MTAP2	54.08
mycBioID2tau	2	MTAP2	47.23
mycBioID2tau	2	MTAP2	46
mycBioID2tau	2	MTAP2	43.96
mycBioID2tau	2	MTAP2	40.77
mycBioID2tau	3	MTAP2	76.31
mycBioID2tau	3	MTAP2	68.73
mycBioID2tau	3	MTAP2	59.31
mycBioID2tau	3	MTAP2	54.65
mycBioID2tau	3	MTAP2	50.94
mycBioID2tau	3	MTAP2	43.88
mycBioID2tau	3	MTAP2	41.94
mycBioID2tau	3	MTAP2	39.99
mycBioID2tau	5	MTAP2	57.96
mycBioID2tau	5	MTAP2	54.1
mycBioID2tau	5	MTAP2	53.02
mycBioID2tau	5	MTAP2	51.88
mycBioID2tau	5	MTAP2	41.87
mycBioID2tau	5	MTAP2	53.36
mycBioID2tau	5	MTAP2	42.6
mycBioID2tau	6	MTAP2	51.22
mycBioID2tau	6	MTAP2	47.34
mycBioID2tau	6	MTAP2	40.71
mycBioID2tau	6	MTAP2	65.88
mycBioID2tau	6	MTAP2	62.81
mycBioID2tau	6	MTAP2	60.37
mycBioID2tau	6	MTAP2	57.87
mycBioID2tau	6	MTAP2	57.75
mycBioID2tau	6	MTAP2	53.38
mycBioID2tau	6	MTAP2	51.61
mycBioID2tau	6	MTAP2	45.57
mycBioID2tau	6	MTAP2	43.32
mycBioID2tau	6	MTAP2	38.85
mycBioID2tau	8	MTAP2	51.52
mycBioID2tau	8	MTAP2	84.56
mycBioID2tau	8	MTAP2	66.35
mycBioID2tau	8	MTAP2	58.1
mycBioID2tau	8	MTAP2	54.26
mycBioID2tau	8	MTAP2	52.58

mycBioID2tau	8	MTAP2	43.43
mycBioID2tau	7	MTAP2	50.94
mycBioID2tau	7	MTAP2	42.48
mycBioID2tau	9	MTAP2	55.78
mycBioID2tau	9	MTAP2	53.55
mycBioID2tau	9	MTAP2	46.44
mycBioID2tau	9	MTAP2	43.66
mycBioID2tau	12	MTAP2	43.66
mycBioID2tau	10	MTAP2	56.18
mycBioID2tau	10	MTAP2	55.64
mycBioID2tau	10	MTAP2	52.59
mycBioID2tau	10	MTAP2	51.33
mycBioID2tau	10	MTAP2	47.31
mycBioID2tau	10	MTAP2	45.68
mycBioID2tau	10	MTAP2	44.63
mycBioID2tau	10	MTAP2	43.22
mycBioID2tau	10	MTAP2	42.91
mycBioID2tau	10	MTAP2	41.34
mycBioID2tau	11	MTAP2	67.35
mycBioID2tau	11	MTAP2	58.96
mycBioID2tau	11	MTAP2	50.76
mycBioID2tau	11	MTAP2	43.25
mycBioID2	*2*	MTAP2	42.58
mycBioID2	*3*	MTAP2	49.39
mycBioID2	*4*	MTAP2	61.91
mycBioID2	*4*	MTAP2	57.87
mycBioID2	*4*	MTAP2	55.86
mycBioID2	*4*	MTAP2	48.19
mycBioID2	*5*	MTAP2	46.36
mycBioID2	*6*	MTAP2	58.3
mycBioID2	*6*	MTAP2	41.36
mycBioID2	*6*	MTAP2	39.21
mycBioID2	*7*	MTAP2	66.25
mycBioID2	*7*	MTAP2	47.59
mycBioID2	*8*	MTAP2	84.55
mycBioID2	*8*	MTAP2	53.69
mycBioID2	*8*	MTAP2	50.66
mycBioID2	*9*	MTAP2	55.85
mycBioID2	*10*	MTAP2	51.51
mycBioID2	*10*	MTAP2	44.16
mycBioID2	*10*	MTAP2	41.7
mycBioID2	*11*	MTAP2	41.37
mycBioID2	*12*	MTAP2	83.41
mycBioID2	*12*	MTAP2	48.43
mycBioID2	*12*	MTAP2	44.2
mycBioID2	*12*	MTAP2	41.46
mycBioID2	*12*	NACAM	45.72
mycBioID2tau	8	NCAM1	49.67

mycBioID2	*2*	NCAP	44.2
mycBioID2tau	1	NEUG	49.31
mycBioID2tau	2	NEUG	61.86
mycBioID2tau	3	NEUG	58.99
mycBioID2tau	5	NEUG	61.67
mycBioID2tau	6	NEUG	52.78
mycBioID2tau	8	NEUG	65.31
mycBioID2tau	8	NEUG	95.35
mycBioID2tau	7	NEUG	43.65
mycBioID2tau	9	NEUG	53.09
mycBioID2tau	12	NEUG	53.09
mycBioID2tau	11	NEUG	85.26
mycBioID2	*2*	NEUG	67.26
mycBioID2	*4*	NEUG	84
mycBioID2	*4*	NEUG	84
mycBioID2	*4*	NEUG	84
mycBioID2	*4*	NEUG	84
mycBioID2	*5*	NEUG	41.01
mycBioID2	*5*	NEUG	41.01
mycBioID2	*5*	NEUG	41.01
mycBioID2	*5*	NEUG	41.01
mycBioID2	*8*	NEUG	56.27
mycBioID2	*10*	NEUG	53.68
mycBioID2	*11*	NEUG	49.97
mycBioID2	*12*	NEUG	54.1
mycBioID2	*5*	NFAT5	43.07
mycBioID2	*6*	NFAT5	38.05
mycBioID2	*6*	NFAT5	38.05
mycBioID2tau	6	NFM	43.56
mycBioID2tau	10	NFM	46.68
mycBioID2	*8*	NFM	37.75
mycBioID2tau	1	NKTR	39.25
mycBioID2tau	2	NKTR	43
mycBioID2tau	3	NKTR	42.92
mycBioID2tau	4	NKTR	42.6
mycBioID2tau	5	NKTR	42.64
mycBioID2tau	8	NKTR	47.16
mycBioID2tau	7	NKTR	39.59
mycBioID2tau	9	NKTR	39.54
mycBioID2tau	12	NKTR	39.54
mycBioID2tau	10	NKTR	42.18
mycBioID2tau	11	NKTR	39.34
mycBioID2tau	3	NP1L4	43.57
mycBioID2tau	6	NP1L4	39.6
mycBioID2tau	9	NP1L4	38.12
mycBioID2tau	12	NP1L4	38.12
mycBioID2tau	10	NP1L4	66.63
mycBioID2tau	5	NSF	82.34

mycBioID2tau	8	NSF	59.6
mycBioID2tau	8	NSF	55.1
mycBioID2tau	12	NSF	58.1
mycBioID2	*4*	NSF1C	41.82
mycBioID2	*4*	NSF1C	41.82
mycBioID2	*4*	NSF1C	41.82
mycBioID2	*4*	NSF1C	41.82
mycBioID2	*10*	NSF1C	52.76
mycBioID2tau	1	PACS1	59.35
mycBioID2tau	6	PACS1	68.27
mycBioID2tau	8	PACS1	54.03
mycBioID2tau	10	PACS1	42.26
mycBioID2tau	6	PAK2	47.32
mycBioID2tau	10	PAK2	39.95
mycBioID2tau	1	PCCA	78.5
mycBioID2tau	2	PCCA	70.8
mycBioID2tau	3	PCCA	76.35
mycBioID2tau	5	PCCA	64.06
mycBioID2tau	6	PCCA	77.05
mycBioID2tau	8	PCCA	68.28
mycBioID2tau	8	PCCA	77.89
mycBioID2tau	9	PCCA	88.61
mycBioID2tau	9	PCCA	45.15
mycBioID2tau	10	PCCA	55.33
mycBioID2tau	11	PCCA	81.13
mycBioID2	*1*	PCCA	79.09
mycBioID2	*1*	PCCA	58.88
mycBioID2	*2*	PCCA	79.3
mycBioID2	*3*	PCCA	75.27
mycBioID2	*4*	PCCA	79.05
mycBioID2	*4*	PCCA	69.97
mycBioID2	*4*	PCCA	48.83
mycBioID2	*5*	PCCA	79.13
mycBioID2	*5*	PCCA	79.13
mycBioID2	*5*	PCCA	79.13
mycBioID2	*6*	PCCA	68.79
mycBioID2	*9*	PCCA	70.48
mycBioID2	*10*	PCCA	80.87
mycBioID2	*11*	PCCA	57.32
mycBioID2	*11*	PCCA	60.6
mycBioID2	*12*	PCCA	68.15
mycBioID2tau	1	PCLO	42.89
mycBioID2tau	3	PFD2	58.03
mycBioID2tau	10	PFD2	54.82
mycBioID2tau	1	PI42A	60.58
mycBioID2tau	8	PI42A	69.13
mycBioID2tau	1	PLEC	62.87
mycBioID2tau	2	PLEC	41.77

mycBioID2tau	3	PLEC	57.68
mycBioID2tau	4	PLEC	50.45
mycBioID2tau	5	PLEC	68.93
mycBioID2tau	6	PLEC	71
mycBioID2tau	8	PLEC	55.84
mycBioID2tau	8	PLEC	61.23
mycBioID2tau	7	PLEC	61.9
mycBioID2tau	7	PLEC	60.91
mycBioID2tau	9	PLEC	65.91
mycBioID2tau	9	PLEC	60.6
mycBioID2tau	9	PLEC	48.82
mycBioID2tau	12	PLEC	60.6
mycBioID2tau	10	PLEC	48.77
mycBioID2tau	11	PLEC	71.12
mycBioID2	2	PLEC	54.43
mycBioID2	3	PLEC	59.23
mycBioID2	4	PLEC	65.92
mycBioID2	6	PLEC	67.69
mycBioID2	7	PLEC	60.9
mycBioID2	8	PLEC	54.92
mycBioID2	9	PLEC	67.93
mycBioID2	10	PLEC	68.31
mycBioID2	12	PLEC	68.06
mycBioID2	12	PLEC	61.87
mycBioID2	12	PLEC	38.04
mycBioID2	12	PPR29	54.52
mycBioID2tau	1	PYC	103.79
mycBioID2tau	1	PYC	69.85
mycBioID2tau	2	PYC	81.61
mycBioID2tau	3	PYC	88.46
mycBioID2tau	4	PYC	107.23
mycBioID2tau	5	PYC	103.7
mycBioID2tau	5	PYC	48.42
mycBioID2tau	5	PYC	107.13
mycBioID2tau	5	PYC	63.96
mycBioID2tau	6	PYC	117.3
mycBioID2tau	6	PYC	95.15
mycBioID2tau	6	PYC	81.99
mycBioID2tau	6	PYC	74.78
mycBioID2tau	6	PYC	64.41
mycBioID2tau	6	PYC	49.82
mycBioID2tau	6	PYC	62.75
mycBioID2tau	8	PYC	83.58
mycBioID2tau	8	PYC	66.63
mycBioID2tau	8	PYC	52.55
mycBioID2tau	7	PYC	78.71
mycBioID2tau	7	PYC	54.84
mycBioID2tau	7	PYC	45.38

mycBioID2tau	7	PYC	43.34
mycBioID2tau	9	PYC	93.03
mycBioID2tau	9	PYC	93.03
mycBioID2tau	9	PYC	54.63
mycBioID2tau	9	PYC	54.63
mycBioID2tau	9	PYC	93.92
mycBioID2tau	9	PYC	65.27
mycBioID2tau	9	PYC	59.01
mycBioID2tau	9	PYC	57.37
mycBioID2tau	9	PYC	56.15
mycBioID2tau	10	PYC	88.68
mycBioID2tau	10	PYC	55.08
mycBioID2tau	10	PYC	49.39
mycBioID2tau	10	PYC	45.11
mycBioID2tau	10	PYC	42.09
mycBioID2tau	11	PYC	82.14
mycBioID2	*2*	PYC	95.52
mycBioID2	*2*	PYC	62.97
mycBioID2	*2*	PYC	44.55
mycBioID2	*4*	PYC	38.27
mycBioID2	*4*	PYC	38.27
mycBioID2	*5*	PYC	80.11
mycBioID2	*5*	PYC	80.11
mycBioID2	*6*	PYC	89.78
mycBioID2	*6*	PYC	89.78
mycBioID2	*6*	PYC	73.6
mycBioID2	*6*	PYC	73.6
mycBioID2	*6*	PYC	51.97
mycBioID2	*6*	PYC	51.97
mycBioID2	*8*	PYC	84.57
mycBioID2	*10*	PYC	77.9
mycBioID2	*11*	PYC	51.17
mycBioID2	*12*	PYC	87.28
mycBioID2tau	6	RBNS5	48.21
mycBioID2tau	10	RBNS5	68.81
mycBioID2tau	3	RTN3	38.49
mycBioID2tau	6	RTN3	38.46
mycBioID2	*8*	RTN3	48.73
mycBioID2tau	6	RTN4	46.81
mycBioID2	*12*	RTN4	44.69
mycBioID2tau	9	RUVB2	41.94
mycBioID2tau	12	RUVB2	41.94
mycBioID2tau	11	RUVB2	42.76
mycBioID2	*12*	RUVB2	60.07
mycBioID2tau	10	Sep5	59.12
mycBioID2tau	10	Sep5	59.12
mycBioID2tau	10	Sep5	45.16
mycBioID2tau	2	Sep7	41.55

mycBioID2tau	3	Sep7	62.34
mycBioID2tau	10	Sep7	54.79
mycBioID2	*12*	SET	51.69
mycBioID2tau	5	SH3G1	52.91
mycBioID2tau	1	SH3G2	44.62
mycBioID2tau	6	SH3G2	54.26
mycBioID2tau	8	SH3G2	57.74
mycBioID2	*12*	SH3G2	48.21
mycBioID2tau	8	SHAN2	53.5
mycBioID2tau	10	SHAN2	42.27
mycBioID2tau	2	SNP25	46.61
mycBioID2tau	3	SNP25	38.65
mycBioID2tau	11	SNP25	41.92
mycBioID2	*2*	SNP25	42.03
mycBioID2	*3*	SNP25	42.52
mycBioID2	*11*	SNP25	38.88
mycBioID2tau	2	SPAST	44
mycBioID2tau	1	SPTN1	65.59
mycBioID2tau	2	SPTN1	45.16
mycBioID2tau	5	SPTN1	43.91
mycBioID2tau	5	SPTN1	44.77
mycBioID2tau	11	SPTN1	56.92
mycBioID2	*4*	SPTN1	38.95
mycBioID2	*12*	SPTN1	41.34
mycBioID2tau	1	SRC8	52.84
mycBioID2tau	5	SRC8	68.71
mycBioID2tau	6	SRC8	68.84
mycBioID2tau	6	SRC8	53.09
mycBioID2tau	6	SRC8	41.92
mycBioID2tau	7	SRC8	40.41
mycBioID2tau	9	SRC8	78.41
mycBioID2tau	9	SRC8	78.41
mycBioID2tau	9	SRC8	78.41
mycBioID2	*4*	SRC8	78.79
mycBioID2	*6*	SRC8	49.23
mycBioID2	*10*	SRC8	63.21
mycBioID2	*12*	SRC8	45.19
mycBioID2tau	1	SRCN1	65.02
mycBioID2tau	1	SRCN1	44.98
mycBioID2tau	2	SRCN1	73.2
mycBioID2tau	5	SRCN1	52.47
mycBioID2tau	6	SRCN1	63.3
mycBioID2tau	8	SRCN1	84.08
mycBioID2tau	7	SRCN1	73.54
mycBioID2tau	9	SRCN1	77.88
mycBioID2tau	12	SRCN1	77.88
mycBioID2tau	10	SRCN1	85.38
mycBioID2tau	10	SRCN1	62.58

mycBioID2tau	10	SRCN1	48.06
mycBioID2tau	1	STMN1	63.4
mycBioID2tau	1	STMN1	61.32
mycBioID2tau	1	STMN1	45.83
mycBioID2tau	2	STMN1	66.34
mycBioID2tau	2	STMN1	60.6
mycBioID2tau	2	STMN1	42.73
mycBioID2tau	3	STMN1	56.77
mycBioID2tau	4	STMN1	54.7
mycBioID2tau	4	STMN1	42.23
mycBioID2tau	5	STMN1	59.94
mycBioID2tau	6	STMN1	71.64
mycBioID2tau	6	STMN1	52.73
mycBioID2tau	8	STMN1	107.89
mycBioID2tau	8	STMN1	44.44
mycBioID2tau	9	STMN1	46.79
mycBioID2tau	12	STMN1	46.79
mycBioID2tau	10	STMN1	82.2
mycBioID2tau	10	STMN1	75
mycBioID2tau	10	STMN1	38.06
mycBioID2	*10*	STMN1	50.13
mycBioID2tau	2	SV2A	40.2
mycBioID2tau	2	SV2A	40.2
mycBioID2tau	5	SV2A	40.2
mycBioID2tau	5	SV2A	40.2
mycBioID2tau	3	SYN1	50.7
mycBioID2tau	5	SYN1	48.82
mycBioID2tau	6	SYN1	44.1
mycBioID2	*12*	SYN1	48.43
mycBioID2tau	1	SYUA	95.48
mycBioID2tau	1	SYUA	86.29
mycBioID2tau	1	SYUA	43.94
mycBioID2tau	2	SYUA	58.17
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mycBioID2tau	2	SYUA	53.01
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mycBioID2tau	3	SYUA	87.07
mycBioID2tau	3	SYUA	81.64
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mycBioID2tau	3	SYUA	53.09
mycBioID2tau	3	SYUA	40.25
mycBioID2tau	4	SYUA	58.43
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mycBioID2tau	6	SYUA	64.69
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mycBioID2tau	6	SYUA	41.42
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mycBioID2tau	9	SYUA	53.84
mycBioID2tau	9	SYUA	42
mycBioID2tau	9	SYUA	41.05
mycBioID2tau	9	SYUA	40.45
mycBioID2tau	12	SYUA	55.47
mycBioID2tau	12	SYUA	53.84
mycBioID2tau	12	SYUA	42
mycBioID2tau	12	SYUA	41.05
mycBioID2tau	12	SYUA	40.45
mycBioID2tau	10	SYUA	61.67
mycBioID2tau	10	SYUA	52.32
mycBioID2tau	10	SYUA	46.49
mycBioID2tau	11	SYUA	67.53
mycBioID2	*6*	SYUA	40.13
mycBioID2	*6*	SYUA	40.13
mycBioID2	*10*	SYUA	51.45
mycBioID2	*12*	SYUA	50.05
mycBioID2	*12*	SYUA	40.26
mycBioID2tau	1	SYUB	88.24
mycBioID2tau	1	SYUB	86.29
mycBioID2tau	1	SYUB	44.16
mycBioID2tau	1	SYUB	43.94
mycBioID2tau	2	SYUB	72.17
mycBioID2tau	2	SYUB	76.79
mycBioID2tau	2	SYUB	58.17
mycBioID2tau	2	SYUB	46.73
mycBioID2tau	3	SYUB	87.07
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mycBioID2tau	3	SYUB	81.64
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mycBioID2tau	5	SYUB	39.51

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mycBioID2tau	6	SYUB	41.42
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mycBioID2tau	9	SYUB	41.05
mycBioID2tau	9	SYUB	40.45
mycBioID2tau	9	SYUB	96.76
mycBioID2tau	12	SYUB	42
mycBioID2tau	12	SYUB	41.05
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mycBioID2tau	10	SYUB	71.07
mycBioID2tau	10	SYUB	69.67
mycBioID2tau	10	SYUB	63.17
mycBioID2tau	10	SYUB	46.49
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mycBioID2tau	11	SYUB	75.51
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mycBioID2	*2*	SYUB	62.44
mycBioID2	*4*	SYUB	96.14
mycBioID2	*4*	SYUB	57.4
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mycBioID2	*6*	SYUB	68.56
mycBioID2	*8*	SYUB	42.22
mycBioID2	*8*	SYUB	40.56
mycBioID2	*9*	SYUB	46.65
mycBioID2	*10*	SYUB	59.9

mycBioID2	*11*	SYUB	57.19
mycBioID2	*12*	SYUB	73.34
mycBioID2	*12*	SYUB	48.59
mycBioID2	*12*	SYUB	41.92
mycBioID2tau	9	SYUG	46.63
mycBioID2tau	10	TAGL2	61.21
mycBioID2tau	1	TAGL3	109.71
mycBioID2tau	1	TAGL3	76.86
mycBioID2tau	1	TAGL3	58.31
mycBioID2tau	2	TAGL3	83.03
mycBioID2tau	5	TAGL3	107.49
mycBioID2tau	6	TAGL3	108.78
mycBioID2tau	8	TAGL3	54.03
mycBioID2tau	7	TAGL3	42.89
mycBioID2	*6*	TAGL3	85.34
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mycBioID2	*6*	TAGL3	85.34
mycBioID2	*6*	TAGL3	85.34
mycBioID2	*6*	TAGL3	85.34
mycBioID2	*6*	TAGL3	85.34
mycBioID2	*12*	TAGL3	96.71
mycBioID2tau	2	TAU	140.24
mycBioID2tau	2	TAU	140.24
mycBioID2	*2*	TAU	131.26
mycBioID2	*3*	TAU	48.58
mycBioID2	*4*	TAU	58.72
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mycBioID2	*4*	TAU	40.57
mycBioID2	*4*	TAU	38.8
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mycBioID2	*5*	TAU	42.2
mycBioID2	*8*	TAU	56.51
mycBioID2	*8*	TAU	41.4
mycBioID2	*12*	TAU	42.75
mycBioID2	*12*	TAU	39.53
mycBioID2	*12*	TAU	38.94
mycBioID2tau	5	TBB4A	47.1
mycBioID2tau	1	TBCB	61.61
mycBioID2tau	3	TBCB	49.06
mycBioID2tau	6	TBCB	43.54
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mycBioID2tau	1	TPPP	59.16
mycBioID2tau	1	TPPP	57.16
mycBioID2tau	1	TPPP	46.25
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mycBioID2tau	5	TPPP	43.74
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mycBioID2tau	8	TPPP	47.09
mycBioID2tau	8	TPPP	41.01
mycBioID2tau	2	VAMP1	52.24
mycBioID2tau	3	VAMP1	64.33
mycBioID2	*10*	VAMP1	63.36
mycBioID2	*12*	VAMP1	44.56
mycBioID2tau	1	VAMP2	56.96
mycBioID2tau	5	VAMP2	47.05
mycBioID2tau	6	VAMP2	61.05
mycBioID2tau	8	VAMP2	57.28
mycBioID2tau	10	VAMP2	42.91
mycBioID2tau	10	VAMP2	42.47
mycBioID2	*3*	VAMP2	46.39
mycBioID2	*4*	VAMP2	51.42
mycBioID2	*4*	VAMP2	51.42
mycBioID2	*4*	VAMP2	51.42
mycBioID2	*4*	VAMP2	51.42
mycBioID2	*4*	VAMP2	51.42
mycBioID2	*6*	VAMP2	46.32
mycBioID2	*6*	VAMP2	46.32
mycBioID2	*6*	VAMP2	46.32
mycBioID2	*6*	VAMP2	46.32
mycBioID2	*6*	VAMP2	46.32
mycBioID2tau	10	VCIP1	65.84
mycBioID2tau	8	WIPF2	50.91
mycBioID2tau	3	WIPF3	44.42
mycBioID2tau	1	ZC21A	42.3
mycBioID2tau	6	ZC21A	53.38
mycBioID2tau	8	ZC21A	66.37

d hippocampus of mice harvested at age P35.

erimental and BioID2 control.

Biotinylated Peptide Sequence
TVKGGISETR
TVKGGISETR
TVKGGISETR
TVKGGISETR
TVKGGISETR
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Table 11. **Biotinylated peptide list from hippoca**

Samples include neurons expressing BioID2-tau e

AAV condition	Sample No.	Protein	Peptide Score
mycBioID2tau	3	41	49.8
mycBioID2	3	2ABA	57.65
mycBioID2	1	AAK1	72.91
mycBioID2	1	AAK1	65.72
mycBioID2	3	AAK1	67.65
mycBioID2	3	AAK1	74.73
mycBioID2	3	AAK1	90.26
mycBioID2	3	AAK1	38
mycBioID2tau	1	AAK1	96.92
mycBioID2tau	1	AAK1	76.98
mycBioID2tau	1	AAK1	45.43
mycBioID2tau	2	AAK1	45.11
mycBioID2tau	2	AAK1	72.17
mycBioID2tau	2	AAK1	108.36
mycBioID2tau	2	AAK1	44.04
mycBioID2tau	4	AAK1	72.25
mycBioID2tau	4	AAK1	72.25
mycBioID2	2	ABD12	48.61
mycBioID2	3	ABI1	45.82
mycBioID2tau	2	ABI2	47.59
mycBioID2	1	ABLM3	56.47
mycBioID2	3	ABLM3	55.53
mycBioID2	2	ACAP2	46.85
mycBioID2	3	ACAP2	58.96
mycBioID2tau	1	ACAP2	50.63
mycBioID2	1	ACTA	90.52
mycBioID2tau	1	ACTA	70.69
mycBioID2	1	ACTB	90.52
mycBioID2	2	ACTB	77.95
mycBioID2	3	ACTB	45.17
mycBioID2	3	ACTB	62.97
mycBioID2tau	1	ACTB	70.69
mycBioID2tau	2	ACTB	73.71
mycBioID2	2	ACTC	77.95
mycBioID2tau	1	ACTC	70.69
mycBioID2	1	ADDA	43.78
mycBioID2	2	ADDA	54.41
mycBioID2	3	ADDA	39.1
mycBioID2	3	ADDB	44.08
mycBioID2	5	ADT1	69.08
mycBioID2	5	ADT1	52.77
mycBioID2	1	AFAD	43.26
mycBioID2	3	AFAD	39.67
mycBioID2	3	AFAD	57.37

mycBioID2	2	AGAP2	38.77
mycBioID2	1	AGFG1	56.81
mycBioID2	1	AGFG1	105.32
mycBioID2	2	AGFG1	87.96
mycBioID2	3	AGFG1	81.24
mycBioID2	3	AGFG1	73.77
mycBioID2	4	AGFG1	54.12
mycBioID2	5	AGFG1	68.28
mycBioID2tau	1	AGFG1	75.44
mycBioID2tau	2	AGFG1	50.06
mycBioID2tau	2	AGFG1	59.47
mycBioID2tau	4	AGFG1	85.63
mycBioID2tau	4	AGFG1	85.63
mycBioID2tau	4	AGFG1	85.63
mycBioID2tau	5	AGFG1	91.7
mycBioID2tau	5	AGFG1	91.7
mycBioID2tau	5	AGFG1	91.7
mycBioID2	2	AGFG2	76.2
mycBioID2	2	AGFG2	77.24
mycBioID2	3	AGFG2	88.44
mycBioID2	3	AGFG2	58.34
mycBioID2	3	AGFG2	82.97
mycBioID2tau	2	AHI1	49.62
mycBioID2	1	AINX	80.54
mycBioID2	1	AINX	67.59
mycBioID2	1	AINX	109.18
mycBioID2	1	AINX	98.25
mycBioID2	2	AINX	39.73
mycBioID2	2	AINX	78.75
mycBioID2	2	AINX	72.68
mycBioID2	2	AINX	111.15
mycBioID2	3	AINX	77.21
mycBioID2	3	AINX	73.75
mycBioID2	3	AINX	114.01
mycBioID2	3	AINX	112
mycBioID2	3	AINX	97.15
mycBioID2	3	AINX	45.88
mycBioID2	3	AINX	54.08
mycBioID2	4	AINX	96.18
mycBioID2	4	AINX	66.91
mycBioID2	5	AINX	102.62
mycBioID2tau	2	AINX	90.16
mycBioID2tau	2	AINX	98.26
mycBioID2tau	4	AINX	94.08
mycBioID2tau	5	AINX	68.9
mycBioID2	2	AKAP1	47.47
mycBioID2	3	AKAP1	40.57
mycBioID2	3	AKAP2	70.8

mycBioID2	1	ALDOA	59.18
mycBioID2	1	ALDOA	117.77
mycBioID2	2	ALDOA	97.44
mycBioID2	2	ALDOA	78.83
mycBioID2	3	ALDOA	134.92
mycBioID2	5	ALDOA	51.86
mycBioID2tau	1	ALDOA	42.48
mycBioID2tau	2	ALDOA	64.25
mycBioID2tau	2	ALDOA	107.62
mycBioID2tau	5	ALDOA	81.89
mycBioID2	3	AMPH	55.54
mycBioID2	3	ANK2	62
mycBioID2	3	ANK2	45.51
mycBioID2tau	1	ANK2	54.2
mycBioID2tau	2	ANK2	47.23
mycBioID2tau	2	ANK2	66.23
mycBioID2tau	2	ANK2	59.69
mycBioID2tau	2	ANK2	57.44
mycBioID2tau	4	ANK2	40.3
mycBioID2tau	5	ANK2	53.44
mycBioID2tau	5	ANK2	49.47
mycBioID2	3	ANK3	52.19
mycBioID2	1	ANS1B	52.61
mycBioID2	2	ANS1B	59.88
mycBioID2	3	ANS1B	63.38
mycBioID2	4	ANS1B	53.86
mycBioID2	5	ANS1B	54.27
mycBioID2	1	AP180	68.93
mycBioID2	2	AP180	58.95
mycBioID2	3	AP180	61.77
mycBioID2tau	1	AP180	57.49
mycBioID2tau	2	AP180	75.26
mycBioID2tau	4	AP180	65.13
mycBioID2tau	4	AP180	65.13
mycBioID2tau	4	AP180	65.13
mycBioID2tau	5	AP180	71.79
mycBioID2tau	5	AP180	71.79
mycBioID2tau	5	AP180	71.79
mycBioID2	2	AP2A1	43.56
mycBioID2	3	AP2A1	65.22
mycBioID2	3	AP2A1	57.16
mycBioID2	2	AP2A2	43.56
mycBioID2	3	AP2A2	65.22
mycBioID2	3	AP2A2	57.16
mycBioID2	2	AP2M1	58.59
mycBioID2	3	AP2M1	71.07
mycBioID2	3	AP2M1	46.89
mycBioID2tau	2	APC	50.61

mycBioID2	1	ARBK1	46.21
mycBioID2	1	ARBK1	89.96
mycBioID2	3	ARBK1	43.49
mycBioID2	3	ARBK1	63.6
mycBioID2tau	1	ARBK1	41.2
mycBioID2tau	2	ARBK1	60.37
mycBioID2	3	ARHG7	45.8
mycBioID2	3	ARP3	53.64
mycBioID2tau	1	ARP3	44.96
mycBioID2tau	2	ARP3	65.93
mycBioID2tau	1	ARP3B	46.47
mycBioID2tau	2	ARP3B	70.15
mycBioID2tau	5	ARP3B	55.67
mycBioID2	3	ARP5L	48.21
mycBioID2tau	2	ARP5L	51.66
mycBioID2	1	ARPC2	51.83
mycBioID2	2	ARPC2	69.81
mycBioID2	3	ARPC2	62.66
mycBioID2	3	ASAP1	48.15
mycBioID2tau	1	ASAP1	56.59
mycBioID2tau	2	ASAP1	69.46
mycBioID2tau	5	ASAP1	115.05
mycBioID2tau	5	ASAP1	115.05
mycBioID2	1	ASAP2	84.36
mycBioID2	2	ASAP2	79.26
mycBioID2	3	ASAP2	55.03
mycBioID2tau	1	ASAP2	52.75
mycBioID2tau	2	ASAP2	44.42
mycBioID2tau	2	ASAP2	70.27
mycBioID2	3	AT8A1	50.34
mycBioID2	1	AUXI	85.72
mycBioID2	2	AUXI	56.61
mycBioID2	3	AUXI	75.21
mycBioID2tau	1	AUXI	48.95
mycBioID2	2	BAIP2	39.75
mycBioID2	2	BAIP2	61.62
mycBioID2	3	BAIP2	55.89
mycBioID2tau	2	BAIP2	40.04
mycBioID2	1	BASP1	87.46
mycBioID2	1	BASP1	48.68
mycBioID2	1	BASP1	56.8
mycBioID2	1	BASP1	67
mycBioID2	2	BASP1	88.96
mycBioID2	2	BASP1	49.49
mycBioID2	2	BASP1	75.88
mycBioID2	3	BASP1	108.73
mycBioID2	3	BASP1	79.07
mycBioID2	3	BASP1	93.15

mycBioID2	3	BASP1	55.3
mycBioID2	3	BASP1	96.84
mycBioID2	5	BASP1	60.96
mycBioID2	5	BASP1	55.67
mycBioID2tau	1	BASP1	62.31
mycBioID2tau	2	BASP1	97.74
mycBioID2tau	2	BASP1	44.38
mycBioID2tau	2	BASP1	57.19
mycBioID2tau	2	BASP1	68.07
mycBioID2tau	2	BASP1	58.64
mycBioID2tau	5	BASP1	54.37
mycBioID2tau	5	BASP1	45.77
mycBioID2	2	BCLF1	50.43
mycBioID2	3	BEGIN	64.28
mycBioID2	1	BIN1	58.29
mycBioID2	2	BIN1	83.2
mycBioID2	3	BIN1	45.23
mycBioID2	3	BIN1	82.4
mycBioID2tau	2	BIN1	38.99
mycBioID2	3	BIRC6	53.02
mycBioID2	1	BSN	104.6
mycBioID2	2	BSN	48.86
mycBioID2	2	BSN	76.49
mycBioID2	2	BSN	68.98
mycBioID2	2	BSN	58.78
mycBioID2	2	BSN	46.79
mycBioID2	2	BSN	94.82
mycBioID2	2	BSN	39.48
mycBioID2	3	BSN	54
mycBioID2	3	BSN	96.78
mycBioID2	3	BSN	48.14
mycBioID2	3	BSN	41.02
mycBioID2	3	BSN	44.33
mycBioID2	3	BSN	75.08
mycBioID2	3	BSN	73.96
mycBioID2	3	BSN	57.88
mycBioID2	3	BSN	109.47
mycBioID2	3	BSN	43.56
mycBioID2	3	BSN	42.29
mycBioID2	3	BSN	45.95
mycBioID2	3	BSN	95.8
mycBioID2	3	BSN	52.25
mycBioID2	3	BSN	52.16
mycBioID2	3	BSN	67.5
mycBioID2	3	BSN	59.23
mycBioID2	4	BSN	72.65
mycBioID2tau	1	BSN	68.74
mycBioID2tau	2	BSN	65.45

mycBioID2tau	2	BSN	59.27
mycBioID2tau	2	BSN	55.47
mycBioID2tau	5	BSN	41.93
mycBioID2tau	5	BSN	44.39
mycBioID2	3	C170B	47.54
mycBioID2	3	C2C2L	56.9
mycBioID2	3	C2C4C	73.97
mycBioID2	1	CA021	64.35
mycBioID2	2	CAC1A	40.41
mycBioID2	3	CAC1A	46.22
mycBioID2	3	CACB1	44.03
mycBioID2	3	CACB1	85.82
mycBioID2	2	CALB1	39.37
mycBioID2tau	2	CALB2	38.52
mycBioID2tau	2	CALB2	42.3
mycBioID2	1	CALM	107.29
mycBioID2	2	CALM	98.73
mycBioID2	3	CALM	99.17
mycBioID2tau	1	CALM	100.7
mycBioID2tau	2	CALM	125.38
mycBioID2	2	CAMKV	58.78
mycBioID2	3	CAMKV	57.99
mycBioID2	3	CAMKV	70.29
mycBioID2tau	2	CAMKV	42.21
mycBioID2tau	5	CAMKV	44.52
mycBioID2	1	CAMP3	87.2
mycBioID2	2	CAMP3	78.45
mycBioID2	3	CAMP3	99.6
mycBioID2tau	1	CAMP3	75.66
mycBioID2tau	2	CAMP3	71.87
mycBioID2tau	2	CAMP3	73.1
mycBioID2tau	4	CAMP3	69.37
mycBioID2tau	4	CAMP3	69.37
mycBioID2tau	5	CAMP3	68.4
mycBioID2tau	5	CAMP3	68.4
mycBioID2	2	CAP1	40.25
mycBioID2	3	CAP1	69.57
mycBioID2	1	CAPS1	71.11
mycBioID2	2	CAPS1	51.57
mycBioID2	2	CAPS1	74.67
mycBioID2	3	CAPS1	125.25
mycBioID2	3	CAPS1	57.54
mycBioID2	3	CAPS1	51.01
mycBioID2	3	CAPS1	78.02
mycBioID2	3	CAPS1	78.02
mycBioID2tau	1	CAPS1	61.35
mycBioID2tau	1	CAPS1	53.94
mycBioID2tau	1	CAPS1	58.84

mycBioID2tau	1	CAPS1	67.59
mycBioID2tau	1	CAPS1	67.59
mycBioID2tau	2	CAPS1	77.7
mycBioID2tau	2	CAPS1	60.51
mycBioID2tau	2	CAPS1	42.32
mycBioID2tau	2	CAPS1	53.14
mycBioID2tau	2	CAPS1	53.14
mycBioID2tau	5	CAPS1	55.64
mycBioID2tau	5	CAPS1	55.64
mycBioID2tau	5	CAPS1	55.64
mycBioID2tau	2	CAPS2	55.6
mycBioID2tau	1	CC171	38.37
mycBioID2tau	2	CDV3	52.4
mycBioID2tau	5	CDV3	67.82
mycBioID2tau	2	CE170	58.33
mycBioID2tau	5	CE170	58.7
mycBioID2	1	CEND	53.39
mycBioID2	2	CEND	40.89
mycBioID2	2	CEND	42.96
mycBioID2	2	CEND	76.41
mycBioID2	2	CEND	39.08
mycBioID2	3	CEND	49.74
mycBioID2	3	CEND	54.01
mycBioID2	3	CEND	77.29
mycBioID2	3	CEND	49.65
mycBioID2	3	CEND	47.34
mycBioID2	3	CEND	41.43
mycBioID2	3	CEND	86.45
mycBioID2	3	CEND	39.11
mycBioID2	3	CEND	40.6
mycBioID2	3	CEND	88.65
mycBioID2	3	CEND	68.78
mycBioID2	4	CEND	63.3
mycBioID2	5	CEND	49.03
mycBioID2	5	CEND	42.5
mycBioID2tau	1	CEND	39.32
mycBioID2tau	2	CEND	39.08
mycBioID2tau	2	CEND	58.66
mycBioID2tau	2	CEND	49.2
mycBioID2tau	2	CEND	40.52
mycBioID2tau	2	CEND	41.42
mycBioID2tau	2	CEND	49.49
mycBioID2tau	4	CEND	63.38
mycBioID2tau	5	CEND	63.24
mycBioID2tau	5	CEND	53.8
mycBioID2tau	5	CEND	44.48
mycBioID2tau	2	CETN2	40.36
mycBioID2	1	CFA36	54.78

mycBioID2	3	CFA36	80.26
mycBioID2	2	CHM4B	97.25
mycBioID2	3	CHM4B	47.01
mycBioID2	3	CHM4B	91.05
mycBioID2tau	1	CHM4B	68.25
mycBioID2tau	2	CHM4B	91.2
mycBioID2	3	CKAP5	76
mycBioID2tau	1	CKAP5	55.83
mycBioID2	3	CLAP2	84.27
mycBioID2tau	1	CLAP2	88.71
mycBioID2tau	2	CLAP2	67.56
mycBioID2	2	CLH1	32.25
mycBioID2	3	CLH1	44.27
mycBioID2tau	2	CLH1	29.8
mycBioID2tau	2	CLIP2	48.09
mycBioID2tau	2	CNKR2	40.7
mycBioID2	3	COF1	49.48
mycBioID2	3	COF1	46.85
mycBioID2	2	CPLX1	69.62
mycBioID2	3	CPLX1	65.14
mycBioID2	5	CPLX1	46.36
mycBioID2tau	1	CPLX1	83.33
mycBioID2tau	1	CPLX1	57.47
mycBioID2tau	4	CPLX1	54.3
mycBioID2tau	4	CPLX1	54.3
mycBioID2tau	5	CPLX1	70.59
mycBioID2tau	5	CPLX1	70.59
mycBioID2tau	5	CPLX1	70.59
mycBioID2tau	5	CPLX1	70.59
mycBioID2	1	CPLX2	61.56
mycBioID2	3	CPLX2	65.14
mycBioID2	5	CPLX2	46.36
mycBioID2tau	1	CPLX2	83.33
mycBioID2tau	1	CPLX2	57.47
mycBioID2tau	2	CPLX2	68.72
mycBioID2	3	CPSF5	43.48
mycBioID2tau	5	CRKL	51.03
mycBioID2tau	5	CRKL	51.03
mycBioID2tau	5	CRKL	51.03
mycBioID2	2	CRTC1	48.21
mycBioID2	3	CRTC1	65.31
mycBioID2tau	1	CRTC1	44.18
mycBioID2tau	2	CRTC1	44.89
mycBioID2	2	CSDE1	48.95
mycBioID2	3	CSDE1	44.69
mycBioID2tau	2	CSDE1	47.7
mycBioID2	3	CSKI1	61.88
mycBioID2	3	CSN5	46.12

mycBioID2	3	CTND2	55.42
mycBioID2	3	CTTB2	38.25
mycBioID2	2	CYFP2	53.71
mycBioID2	3	CYFP2	50.85
mycBioID2tau	1	CYFP2	42.32
mycBioID2tau	2	CYFP2	42.07
mycBioID2tau	5	CYH1	49.97
mycBioID2tau	5	CYH1	49.97
mycBioID2tau	5	CYH1	49.97
mycBioID2tau	5	CYH1	49.97
mycBioID2tau	5	CYH2	49.97
mycBioID2tau	5	CYH2	49.97
mycBioID2tau	5	CYH2	49.97
mycBioID2tau	5	CYH2	49.97
mycBioID2tau	5	CYH2	49.97
mycBioID2tau	5	CYH3	49.97
mycBioID2tau	5	CYH3	49.97
mycBioID2tau	5	CYH3	49.97
mycBioID2	3	CYLD	78.47
mycBioID2	3	CZIB	67.47
mycBioID2tau	1	CZIB	67.32
mycBioID2tau	2	CZIB	70.2
mycBioID2tau	4	CZIB	54.68
mycBioID2tau	4	CZIB	54.68
mycBioID2tau	4	CZIB	54.68
mycBioID2tau	4	CZIB	54.68
mycBioID2tau	5	CZIB	67.07
mycBioID2tau	5	CZIB	67.07
mycBioID2tau	5	CZIB	67.07
mycBioID2tau	5	CZIB	67.07
mycBioID2	1	DBNL	61.93
mycBioID2	2	DBNL	105.13
mycBioID2	3	DBNL	82.64
mycBioID2	3	DBNL	80.32
mycBioID2tau	1	DBNL	54.12
mycBioID2tau	1	DBNL	51.15
mycBioID2tau	2	DBNL	46.78
mycBioID2	1	DCE2	89.97
mycBioID2	2	DCE2	90.06
mycBioID2	3	DCE2	77.39
mycBioID2tau	2	DCE2	58.17
mycBioID2tau	5	DCE2	65.04
mycBioID2	2	DCLK1	83.68
mycBioID2	3	DCLK1	99.63
mycBioID2tau	1	DCLK1	75.87
mycBioID2tau	2	DCLK1	64.76
mycBioID2tau	1	DCLK2	73.61
mycBioID2tau	2	DCLK2	62.35

mycBioID2tau	5	DCLK2	66.94
mycBioID2tau	5	DCLK2	66.94
mycBioID2tau	5	DCLK2	66.94
mycBioID2tau	5	DCLK2	66.94
mycBioID2	2	DCTN2	70.9
mycBioID2	3	DCTN2	41.67
mycBioID2tau	1	DCTN2	47.65
mycBioID2tau	2	DCTN2	72.64
mycBioID2tau	5	DCTN2	48.23
mycBioID2tau	5	DCTN2	48.23
mycBioID2	1	DEMA	70.6
mycBioID2	3	DEMA	73.72
mycBioID2	3	DEMA	44.19
mycBioID2	3	DEMA	58.73
mycBioID2tau	2	DEMA	43.9
mycBioID2tau	2	DEMA	48.24
mycBioID2	3	DEST	49.48
mycBioID2	3	DEST	46.85
mycBioID2	1	DGLA	42.6
mycBioID2	2	DGLA	46.58
mycBioID2	3	DGLA	42.48
mycBioID2	3	DLGP2	47.64
mycBioID2	3	DLGP2	48.78
mycBioID2	3	DLGP2	89.68
mycBioID2	1	DLGP3	47.11
mycBioID2	1	DLGP3	82.3
mycBioID2	1	DLGP3	86.33
mycBioID2	2	DLGP3	100.91
mycBioID2	2	DLGP3	52.82
mycBioID2	2	DLGP3	44.47
mycBioID2	2	DLGP3	77.91
mycBioID2	3	DLGP3	34.48
mycBioID2	3	DLGP3	89.38
mycBioID2	3	DLGP3	66.45
mycBioID2	3	DLGP3	71.12
mycBioID2	3	DLGP3	63.28
mycBioID2	4	DLGP3	79.07
mycBioID2tau	1	DLGP3	62.57
mycBioID2tau	2	DLGP3	95.48
mycBioID2	1	DMXL2	51.01
mycBioID2	2	DMXL2	44.03
mycBioID2	3	DMXL2	42.98
mycBioID2	3	DMXL2	39.27
mycBioID2	3	DMXL2	57.25
mycBioID2	4	DMXL2	38.99
mycBioID2	5	DMXL2	38.33
mycBioID2	2	DNJB1	52.12
mycBioID2	3	DNJB1	48.96

mycBioID2tau	1	DNJB1	49.14
mycBioID2tau	2	DNJB1	48.49
mycBioID2tau	3	DNJB1	43.69
mycBioID2tau	4	DNJB1	38.2
mycBioID2tau	4	DNJB1	38.2
mycBioID2tau	4	DNJB1	38.2
mycBioID2tau	5	DNJB1	53.94
mycBioID2tau	5	DNJB1	53.94
mycBioID2tau	5	DNJB1	53.94
mycBioID2	1	DNM1L	71.97
mycBioID2	2	DNM1L	50.93
mycBioID2	3	DNM1L	77.53
mycBioID2	3	DNM1L	48.04
mycBioID2tau	1	DNM1L	53.25
mycBioID2tau	2	DNM1L	53.21
mycBioID2	2	DPYL1	46.56
mycBioID2	3	DPYL1	87.83
mycBioID2	1	DPYL2	73.49
mycBioID2	1	DPYL2	72.6
mycBioID2	2	DPYL2	67.55
mycBioID2	2	DPYL2	81.19
mycBioID2	3	DPYL2	62.6
mycBioID2	3	DPYL2	66.17
mycBioID2	4	DPYL2	66.86
mycBioID2	5	DPYL2	90.16
mycBioID2	5	DPYL2	59.63
mycBioID2tau	1	DPYL2	64.69
mycBioID2tau	1	DPYL2	71.54
mycBioID2tau	2	DPYL2	66.46
mycBioID2tau	2	DPYL2	75.77
mycBioID2tau	3	DPYL2	51.48
mycBioID2tau	4	DPYL2	67.52
mycBioID2tau	4	DPYL2	77.29
mycBioID2tau	4	DPYL2	67.52
mycBioID2tau	4	DPYL2	77.29
mycBioID2tau	5	DPYL2	66.57
mycBioID2tau	5	DPYL2	66.57
mycBioID2	3	DPYL4	48.02
mycBioID2tau	2	DPYL4	41.51
mycBioID2tau	1	DRG2	57.73
mycBioID2tau	2	DRG2	69.64
mycBioID2	1	DYHC2	43.22
mycBioID2	1	DYN1	70.36
mycBioID2	1	DYN1	70.36
mycBioID2	3	DYN1	45.01
mycBioID2tau	1	DYN1	105.87
mycBioID2tau	2	DYN1	58.09
mycBioID2tau	2	DYN1	65.92

mycBioID2	1	E41L1	46.51
mycBioID2	1	E41L1	50.72
mycBioID2	1	E41L1	55.18
mycBioID2	1	E41L1	50.64
mycBioID2	2	E41L1	56.69
mycBioID2	2	E41L1	49.17
mycBioID2	2	E41L1	56.44
mycBioID2	2	E41L1	110.49
mycBioID2	2	E41L1	73.52
mycBioID2	3	E41L1	42.89
mycBioID2	3	E41L1	70.21
mycBioID2	3	E41L1	62.2
mycBioID2	3	E41L1	59.78
mycBioID2	3	E41L1	78.33
mycBioID2	3	E41L1	80.03
mycBioID2	3	E41L1	83.05
mycBioID2	3	E41L1	62.68
mycBioID2	5	E41L1	43
mycBioID2	5	E41L1	57.33
mycBioID2	5	E41L1	51.73
mycBioID2tau	1	E41L1	62.83
mycBioID2tau	1	E41L1	59.92
mycBioID2tau	1	E41L1	55.64
mycBioID2tau	1	E41L1	63.33
mycBioID2tau	1	E41L1	99.32
mycBioID2tau	2	E41L1	58.28
mycBioID2tau	2	E41L1	48.56
mycBioID2tau	2	E41L1	64.18
mycBioID2tau	2	E41L1	92.24
mycBioID2tau	2	E41L1	55.69
mycBioID2tau	4	E41L1	46.08
mycBioID2tau	5	E41L1	44.47
mycBioID2tau	5	E41L1	84.03
mycBioID2	3	E41L2	54.73
mycBioID2	3	E41L2	48.59
mycBioID2tau	1	E41L2	69.4
mycBioID2	1	E41L3	68.16
mycBioID2	1	E41L3	43.61
mycBioID2	1	E41L3	74.45
mycBioID2	1	E41L3	131.42
mycBioID2	1	E41L3	68.16
mycBioID2	1	E41L3	43.61
mycBioID2	2	E41L3	66.65
mycBioID2	2	E41L3	61.7
mycBioID2	3	E41L3	54.73
mycBioID2	3	E41L3	48.59
mycBioID2	3	E41L3	62.81
mycBioID2	3	E41L3	42.73

mycBioID2	3	E41L3	54.86
mycBioID2	3	E41L3	64.89
mycBioID2	3	E41L3	68.92
mycBioID2	4	E41L3	55.9
mycBioID2tau	1	E41L3	69.4
mycBioID2tau	1	E41L3	47.75
mycBioID2tau	1	E41L3	58.75
mycBioID2tau	2	E41L3	66.84
mycBioID2tau	2	E41L3	76.88
mycBioID2tau	2	E41L3	68.31
mycBioID2tau	4	E41L3	44.46
mycBioID2tau	5	E41L3	56.49
mycBioID2tau	5	EF1A2	51.58
mycBioID2tau	5	EF1A2	51.58
mycBioID2tau	5	EF1A2	51.58
mycBioID2tau	5	EF1A2	51.58
mycBioID2tau	5	EF1A2	51.58
mycBioID2	2	EF2	58.04
mycBioID2	3	EF2	69.97
mycBioID2tau	2	EF2	69
mycBioID2	3	ELAV1	62.81
mycBioID2	1	ELFN1	91.1
mycBioID2	1	ELOB	49.55
mycBioID2	2	ELOB	62.35
mycBioID2	3	ELOB	56.48
mycBioID2tau	1	ELOB	56.44
mycBioID2tau	2	ELOB	53.22
mycBioID2tau	2	ENSA	46.39
mycBioID2	3	EP15R	38.93
mycBioID2tau	2	F110B	43.31
mycBioID2	1	F1142	66.65
mycBioID2	1	F131B	84.49
mycBioID2	3	F131B	89.05
mycBioID2	3	F131B	44.69
mycBioID2	1	F169A	93.12
mycBioID2	2	F169A	83.55
mycBioID2	2	F169A	47.1
mycBioID2	2	F169A	64.09
mycBioID2	3	F169A	74.31
mycBioID2	3	F169A	77.2
mycBioID2	3	F169A	82.49
mycBioID2	3	F1712	58.42
mycBioID2	2	F171B	83.52
mycBioID2	3	F171B	44.79
mycBioID2	3	F171B	74.12
mycBioID2	3	F171B	42.13
mycBioID2	2	G3P	62.14
mycBioID2	3	G3P	70.92

mycBioID2	4	G3P	69.09
mycBioID2tau	1	G3P	55.2
mycBioID2tau	2	G3P	50.57
mycBioID2	2	GAK	43.55
mycBioID2	3	GAK	53.69
mycBioID2	1	GAMT	42.29
mycBioID2	1	GBRA1	75.05
mycBioID2	2	GBRA1	41.62
mycBioID2	2	GBRA1	76.03
mycBioID2	3	GBRA1	73.52
mycBioID2	4	GBRA1	56.54
mycBioID2	5	GBRA1	57.42
mycBioID2tau	2	GBRA1	47.62
mycBioID2tau	2	GDIR1	43.09
mycBioID2	1	GP158	49.77
mycBioID2	1	GP158	97.57
mycBioID2	2	GP158	67.44
mycBioID2	2	GP158	107.79
mycBioID2	3	GP158	57.4
mycBioID2	3	GP158	49.26
mycBioID2	3	GP158	57.3
mycBioID2	5	GP158	43.13
mycBioID2tau	1	GP158	50.38
mycBioID2tau	2	GP158	55.32
mycBioID2tau	2	GP158	86.49
mycBioID2tau	4	GP158	35.2
mycBioID2tau	4	GP158	35.2
mycBioID2tau	5	GP158	39.59
mycBioID2tau	5	GP158	39.59
mycBioID2	1	GRIN1	85.62
mycBioID2	1	GRIN1	81.15
mycBioID2	1	GRIN1	93.45
mycBioID2	1	GRIN1	107.62
mycBioID2	2	GRIN1	48.96
mycBioID2	2	GRIN1	41.2
mycBioID2	2	GRIN1	86.93
mycBioID2	2	GRIN1	70.85
mycBioID2	2	GRIN1	79.34
mycBioID2	2	GRIN1	80.88
mycBioID2	2	GRIN1	95.15
mycBioID2	2	GRIN1	44.19
mycBioID2	2	GRIN1	79.14
mycBioID2	2	GRIN1	73.14
mycBioID2	2	GRIN1	76.36
mycBioID2	3	GRIN1	62.24
mycBioID2	3	GRIN1	47.02
mycBioID2	3	GRIN1	83.18
mycBioID2	3	GRIN1	57.58

mycBioID2	3	GRIN1	55.45
mycBioID2	3	GRIN1	41.93
mycBioID2	3	GRIN1	95.71
mycBioID2	3	GRIN1	55.92
mycBioID2	3	GRIN1	42.33
mycBioID2	3	GRIN1	90.57
mycBioID2	3	GRIN1	49.29
mycBioID2	3	GRIN1	60.31
mycBioID2	3	GRIN1	72.38
mycBioID2	3	GRIN1	71.25
mycBioID2	3	GRIN1	44.91
mycBioID2	3	GRIN1	54.11
mycBioID2	4	GRIN1	61.97
mycBioID2	4	GRIN1	53.8
mycBioID2	4	GRIN1	46.85
mycBioID2	5	GRIN1	71.43
mycBioID2	5	GRIN1	56.35
mycBioID2tau	1	GRIN1	81.51
mycBioID2tau	1	GRIN1	92.18
mycBioID2tau	1	GRIN1	90.94
mycBioID2tau	1	GRIN1	64.87
mycBioID2tau	1	GRIN1	86.68
mycBioID2tau	2	GRIN1	110.34
mycBioID2tau	2	GRIN1	47.96
mycBioID2tau	2	GRIN1	84.28
mycBioID2tau	2	GRIN1	120.64
mycBioID2tau	2	GRIN1	63.63
mycBioID2tau	2	GRIN1	46.92
mycBioID2tau	2	GRIN1	53.95
mycBioID2tau	5	GRIN1	70.75
mycBioID2tau	5	GRIN1	48.08
mycBioID2tau	5	GRIN1	49.56
mycBioID2tau	5	GRIN1	53.37
mycBioID2tau	5	GRIN1	47.14
mycBioID2	2	GRIN3	55.33
mycBioID2	3	GRIN3	65.49
mycBioID2	3	GRIN3	62.96
mycBioID2tau	2	GSDME	70.61
mycBioID2	3	GSK3A	67.03
mycBioID2tau	1	GSK3A	71.97
mycBioID2tau	2	GSK3A	43.25
mycBioID2tau	2	GSK3B	77.94
mycBioID2	3	H2B1C	64.26
mycBioID2	3	H2B1F	64.26
mycBioID2	3	H3C	46.96
mycBioID2	3	HABP4	45.5
mycBioID2tau	2	HAP28	49.72
mycBioID2	2	HNRPC	46.46

mycBioID2	3	HNRPC	43.84
mycBioID2	3	HNRPK	58.14
mycBioID2	2	HNRPL	56.44
mycBioID2	3	HNRPL	67.16
mycBioID2	3	HNRPM	95.08
mycBioID2	3	HPCA	41.73
mycBioID2	1	HS90A	43.54
mycBioID2	1	HS90A	43.54
mycBioID2tau	2	HS90A	44.13
mycBioID2	1	HS90B	43.54
mycBioID2tau	2	HS90B	44.13
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mycBioID2	3	HSP7C	52.48
mycBioID2	1	IF4B	48.05
mycBioID2	2	IF4B	52.31
mycBioID2	3	IF4B	57.18
mycBioID2tau	1	IF4B	49.57
mycBioID2tau	2	IF4B	89.03
mycBioID2tau	2	IF4B	53.09
mycBioID2tau	4	IF4B	61.44
mycBioID2tau	5	IF4B	51.85
mycBioID2tau	2	IF4G1	44.66
mycBioID2	2	IF4G3	58.92
mycBioID2	3	IF4G3	52.56
mycBioID2	3	IF4G3	41.69
mycBioID2	3	IF4G3	104.6
mycBioID2tau	1	IF4G3	61.23
mycBioID2tau	2	IF4G3	52.18
mycBioID2	3	IF4H	38.51
mycBioID2	3	IGBP1	50.74
mycBioID2	3	INT12	50.62
mycBioID2	1	IQEC1	48.82
mycBioID2	2	IQEC1	43.97
mycBioID2	3	IQEC1	53.04
mycBioID2	2	IQEC3	43.42
mycBioID2	3	IQEC3	39.84
mycBioID2tau	1	IQEC3	113.73
mycBioID2tau	2	IQEC3	98.78
mycBioID2	3	ITSN1	43.91
mycBioID2	3	ITSN1	54.18
mycBioID2	2	JIP4	42.69
mycBioID2	3	JIP4	58.47
mycBioID2	5	JIP4	40.91
mycBioID2tau	5	JUPI1	45.82
mycBioID2tau	1	K1107	43.57
mycBioID2tau	2	K1107	77.61
mycBioID2tau	5	K1107	75.33
mycBioID2	1	K1549	68.69

mycBioID2	1	K1671	50.72
mycBioID2	3	K1671	46.72
mycBioID2	3	KAP2	50.52
mycBioID2tau	1	KAP2	45.33
mycBioID2	2	KAPCA	45.38
mycBioID2	3	KAPCA	57.74
mycBioID2tau	2	KAPCA	46.55
mycBioID2tau	5	KAPCA	50.67
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mycBioID2tau	5	KAPCA	50.67
mycBioID2tau	5	KAPCA	50.67
mycBioID2tau	1	KC1E	41.54
mycBioID2tau	2	KC1E	65.88
mycBioID2	1	KCC2A	44.34
mycBioID2	1	KCC2A	52.48
mycBioID2	1	KCC2A	38.55
mycBioID2	2	KCC2A	42.12
mycBioID2	3	KCC2A	47.84
mycBioID2	3	KCC2A	55.89
mycBioID2	3	KCC2A	72.63
mycBioID2	3	KCC2A	44.29
mycBioID2	3	KCC2A	50.41
mycBioID2	4	KCC2A	48.76
mycBioID2	5	KCC2A	39.84
mycBioID2tau	1	KCC2A	41.17
mycBioID2tau	1	KCC2A	45.39
mycBioID2tau	2	KCC2A	50.69
mycBioID2tau	2	KCC2A	72.75
mycBioID2tau	2	KCC2A	41.7
mycBioID2tau	2	KCC2A	41.96
mycBioID2tau	4	KCC2A	51.33
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mycBioID2tau	5	KCC2A	51.07
mycBioID2tau	5	KCC2A	65.22
mycBioID2tau	5	KCC2A	51.07
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mycBioID2tau	5	KCC2A	51.07
mycBioID2tau	5	KCC2A	65.22

mycBioID2tau	5	KCC2A	51.07
mycBioID2tau	5	KCC2A	65.22
mycBioID2	1	KCC2B	38.55
mycBioID2	1	KCC2B	83.43
mycBioID2	1	KCC2B	56.46
mycBioID2	1	KCC2B	111.19
mycBioID2	2	KCC2B	48.58
mycBioID2	2	KCC2B	116.57
mycBioID2	3	KCC2B	41.51
mycBioID2	3	KCC2B	72.28
mycBioID2	3	KCC2B	50.41
mycBioID2	3	KCC2B	44.39
mycBioID2	3	KCC2B	43.36
mycBioID2	3	KCC2B	52.39
mycBioID2	3	KCC2B	118.95
mycBioID2	3	KCC2B	57.76
mycBioID2	3	KCC2B	80.68
mycBioID2tau	1	KCC2B	45.39
mycBioID2tau	1	KCC2B	68.73
mycBioID2tau	2	KCC2B	41.96
mycBioID2tau	2	KCC2B	64.37
mycBioID2tau	2	KCC2B	43.25
mycBioID2tau	2	KCC2B	77.74
mycBioID2tau	2	KCC2B	68.99
mycBioID2tau	2	KCC2B	51.34
mycBioID2tau	4	KCC2B	49.92
mycBioID2tau	4	KCC2B	49.92
mycBioID2tau	5	KCC2B	45.64
mycBioID2tau	5	KCC2B	53.89
mycBioID2tau	5	KCC2B	39.7
mycBioID2tau	5	KCC2B	45.64
mycBioID2tau	5	KCC2B	53.89
mycBioID2tau	5	KCC2B	39.7
mycBioID2	1	KCC2D	62.05
mycBioID2	1	KCC2D	38.55
mycBioID2	2	KCC2D	41.79
mycBioID2	3	KCC2D	86.17
mycBioID2	3	KCC2D	50.41
mycBioID2tau	1	KCC2D	60.21
mycBioID2tau	1	KCC2D	45.39
mycBioID2tau	2	KCC2D	76.89
mycBioID2tau	2	KCC2D	41.96
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mycBioID2tau	4	KCC2D	44.49
mycBioID2	1	KCNJ3	48.25
mycBioID2	3	KCNJ3	52.5
mycBioID2	3	KI21A	40.58
mycBioID2	3	KI21A	55.85

mycBioID2tau	5	KI21A	45.39
mycBioID2	3	KIF5C	67.54
mycBioID2tau	2	KIF5C	44.14
mycBioID2tau	5	KIF5C	64.48
mycBioID2	3	KPCA	78.97
mycBioID2	1	KPCB	51.41
mycBioID2	2	KPCB	55.93
mycBioID2	3	KPCB	49.66
mycBioID2	4	KPCB	51.1
mycBioID2tau	1	KPCB	63.29
mycBioID2tau	2	KPCG	47.39
mycBioID2	2	KT3K	69.22
mycBioID2	3	KT3K	58.41
mycBioID2tau	1	KT3K	56.48
mycBioID2tau	2	KT3K	77.61
mycBioID2tau	4	KT3K	50.79
mycBioID2tau	5	KT3K	97.02
mycBioID2	2	LASP1	75.42
mycBioID2	3	LASP1	61.07
mycBioID2	3	LASP1	76.51
mycBioID2tau	1	LASP1	66.34
mycBioID2tau	1	LASP1	88.46
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mycBioID2tau	2	LASP1	66.03
mycBioID2tau	2	LASP1	43.9
mycBioID2tau	2	LASP1	89.22
mycBioID2tau	4	LASP1	57.05
mycBioID2tau	4	LASP1	57.05
mycBioID2tau	4	LASP1	57.05
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mycBioID2tau	4	LASP1	57.05
mycBioID2	5	LDHA	82.72
mycBioID2	1	LNEBL	90.71
mycBioID2	1	LNEBL	73.41
mycBioID2	2	LNEBL	66.28
mycBioID2	3	LNEBL	64.41
mycBioID2	3	LNEBL	63.82
mycBioID2	3	LNEBL	78.54
mycBioID2	3	LNEBL	65.44
mycBioID2tau	1	LNEBL	70.91
mycBioID2tau	2	LNEBL	47.8
mycBioID2	3	LNP	42.13
mycBioID2	1	LRRC7	90.72
mycBioID2	1	LRRC7	40.79
mycBioID2	1	LRRC7	40.43
mycBioID2	1	LRRC7	72.48
mycBioID2	2	LRRC7	50.01
mycBioID2	2	LRRC7	75.21

mycBioID2	2	LRRC7	41.75
mycBioID2	2	LRRC7	45.96
mycBioID2	3	LRRC7	60.5
mycBioID2	3	LRRC7	50.62
mycBioID2	3	LRRC7	72.43
mycBioID2	3	LRRC7	67.3
mycBioID2	3	LRRC7	40.67
mycBioID2	3	LRRC7	44.82
mycBioID2	3	LRRC7	67.83
mycBioID2	2	LUZP1	43.41
mycBioID2	3	LUZP1	43.84
mycBioID2tau	1	LUZP1	68.16
mycBioID2tau	2	LUZP1	44.16
mycBioID2	3	LYRIC	61.52
mycBioID2	3	M3K10	51.73
mycBioID2	2	M4K4	91.56
mycBioID2tau	5	M4K4	54.55
mycBioID2tau	5	M4K4	54.55
mycBioID2	3	MA7D2	60.54
mycBioID2tau	2	MA7D2	70.31
mycBioID2tau	2	MA7D2	64.66
mycBioID2tau	2	MA7D2	41.79
mycBioID2tau	2	MA7D2	42.35
mycBioID2tau	2	MA7D2	37.73
mycBioID2	1	MAP1A	64.64
mycBioID2	1	MAP1A	52.29
mycBioID2	1	MAP1A	57.34
mycBioID2	1	MAP1A	51.6
mycBioID2	1	MAP1A	66.91
mycBioID2	1	MAP1A	45.15
mycBioID2	1	MAP1A	58.63
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mycBioID2	2	MAP1A	61.24
mycBioID2	2	MAP1A	56.82
mycBioID2	2	MAP1A	59.82
mycBioID2	2	MAP1A	49.23
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mycBioID2	2	MAP1A	49.85
mycBioID2	2	MAP1A	72.77
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mycBioID2	3	MAP1A	43.98
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mycBioID2	3	MAP1A	46.21

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mycBioID2	3	MAP1A	74.44
mycBioID2	3	MAP1A	79.76
mycBioID2	3	MAP1A	44.27
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mycBioID2	4	MAP1A	44.49
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mycBioID2tau	1	MAP1A	40.03
mycBioID2tau	1	MAP1A	61.45
mycBioID2tau	1	MAP1A	61.3
mycBioID2tau	1	MAP1A	43.39
mycBioID2tau	1	MAP1A	42.2
mycBioID2tau	1	MAP1A	47.29
mycBioID2tau	1	MAP1A	76.89
mycBioID2tau	1	MAP1A	50.83
mycBioID2tau	1	MAP1A	69.52
mycBioID2tau	1	MAP1A	51.29
mycBioID2tau	1	MAP1A	57.43
mycBioID2tau	2	MAP1A	42.27
mycBioID2tau	2	MAP1A	41.23
mycBioID2tau	2	MAP1A	64.99
mycBioID2tau	2	MAP1A	58.92
mycBioID2tau	2	MAP1A	80.41
mycBioID2tau	2	MAP1A	49.01
mycBioID2tau	2	MAP1A	46.32
mycBioID2tau	2	MAP1A	42.88
mycBioID2tau	2	MAP1A	48.84
mycBioID2tau	2	MAP1A	58.31
mycBioID2tau	2	MAP1A	59.09
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mycBioID2tau	2	MAP1A	64.62
mycBioID2tau	2	MAP1A	43.59
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mycBioID2tau	4	MAP1A	46.79
mycBioID2tau	4	MAP1A	50.22
mycBioID2tau	4	MAP1A	60.68
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mycBioID2tau	5	MAP1A	47.27
mycBioID2tau	5	MAP1A	47.13
mycBioID2tau	5	MAP1A	63.87
mycBioID2tau	5	MAP1A	49.82
mycBioID2tau	5	MAP1A	47.62

mycBioID2tau	5	MAP1A	45.3
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mycBioID2tau	5	MAP1A	42.68
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mycBioID2	1	MAP1B	43.57
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mycBioID2	1	MAP1B	77.32
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mycBioID2	2	MAP1B	50.76
mycBioID2	2	MAP1B	83.13
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mycBioID2	2	MAP1B	50.57
mycBioID2	2	MAP1B	62.84
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mycBioID2	2	MAP1B	91.94
mycBioID2	2	MAP1B	65.04
mycBioID2	3	MAP1B	42.62
mycBioID2	3	MAP1B	51.8
mycBioID2	3	MAP1B	43.49
mycBioID2	3	MAP1B	81
mycBioID2	3	MAP1B	53.9
mycBioID2	3	MAP1B	40.95
mycBioID2	3	MAP1B	75.47
mycBioID2	5	MAP1B	84.81
mycBioID2	5	MAP1B	38.39
mycBioID2tau	1	MAP1B	62.59
mycBioID2tau	1	MAP1B	53.74
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mycBioID2tau	1	MAP1B	41.47
mycBioID2tau	1	MAP1B	55.08
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mycBioID2tau	2	MAP1B	51.29
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mycBioID2tau	2	MAP1B	41.27
mycBioID2tau	2	MAP1B	75.53
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mycBioID2tau	2	MAP1B	47.86
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mycBioID2tau	2	MAP1B	55.27
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mycBioID2tau	2	MAP1B	54.38
mycBioID2tau	2	MAP1B	52.81

mycBioID2tau	2	MAP1B	46.79
mycBioID2tau	2	MAP1B	76.8
mycBioID2tau	2	MAP1B	45.27
mycBioID2tau	2	MAP1B	55.21
mycBioID2tau	2	MAP1B	86.45
mycBioID2tau	2	MAP1B	48.14
mycBioID2tau	2	MAP1B	50.46
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mycBioID2tau	4	MAP1B	48.66
mycBioID2tau	4	MAP1B	54.43
mycBioID2tau	4	MAP1B	62.53
mycBioID2tau	4	MAP1B	38.07
mycBioID2tau	5	MAP1B	41.12
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mycBioID2tau	5	MAP1B	68.47
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mycBioID2tau	5	MAP1B	73.75
mycBioID2tau	5	MAP1B	76.49
mycBioID2tau	5	MAP1B	47.88
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mycBioID2tau	5	MAP1B	86.86
mycBioID2	3	MAP4	71.97
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mycBioID2tau	1	MAP4	94.93
mycBioID2tau	1	MAP4	54.22
mycBioID2tau	1	MAP4	57.95
mycBioID2tau	1	MAP4	48.82
mycBioID2tau	1	MAP4	51.41
mycBioID2tau	2	MAP4	86.6
mycBioID2tau	2	MAP4	53.43
mycBioID2tau	2	MAP4	79.1
mycBioID2tau	2	MAP4	51.74
mycBioID2tau	3	MAP4	47.49
mycBioID2tau	4	MAP4	60.23
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mycBioID2tau	5	MAP4	43.08
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mycBioID2	1	MAP6	65.43
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mycBioID2	1	MAP6	55.42

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mycBioID2	1	MAP6	62.02
mycBioID2	1	MAP6	36.94
mycBioID2	1	MAP6	79
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mycBioID2	2	MAP6	61.96
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mycBioID2	2	MAP6	52.88
mycBioID2	2	MAP6	37.65
mycBioID2	2	MAP6	44.68
mycBioID2	3	MAP6	51.05
mycBioID2	3	MAP6	46.82
mycBioID2	3	MAP6	57.05
mycBioID2	3	MAP6	56.27
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mycBioID2	3	MAP6	57.13
mycBioID2	3	MAP6	58.07
mycBioID2	3	MAP6	49.59
mycBioID2	3	MAP6	72.91
mycBioID2	3	MAP6	48.43
mycBioID2tau	1	MAP6	67.44
mycBioID2tau	1	MAP6	58.19
mycBioID2tau	1	MAP6	48.13
mycBioID2tau	1	MAP6	71.68
mycBioID2tau	1	MAP6	54.56
mycBioID2tau	1	MAP6	64.17
mycBioID2tau	1	MAP6	84.29
mycBioID2tau	1	MAP6	38.71
mycBioID2tau	1	MAP6	73.77
mycBioID2tau	1	MAP6	57.6
mycBioID2tau	1	MAP6	79.77
mycBioID2tau	1	MAP6	109.86
mycBioID2tau	1	MAP6	53.31
mycBioID2tau	1	MAP6	46.3
mycBioID2tau	1	MAP6	55.32
mycBioID2tau	1	MAP6	45.03
mycBioID2tau	1	MAP6	71.26
mycBioID2tau	1	MAP6	40.27
mycBioID2tau	1	MAP6	50.82
mycBioID2tau	1	MAP6	38.28
mycBioID2tau	1	MAP6	63.78
mycBioID2tau	1	MAP6	41.24
mycBioID2tau	1	MAP6	37.81
mycBioID2tau	1	MAP6	52.93
mycBioID2tau	2	MAP6	57.2
mycBioID2tau	2	MAP6	51.03
mycBioID2tau	2	MAP6	60.69
mycBioID2tau	2	MAP6	62.63

mycBioID2tau	2	MAP6	73.4
mycBioID2tau	2	MAP6	57.26
mycBioID2tau	2	MAP6	75.57
mycBioID2tau	2	MAP6	58.81
mycBioID2tau	2	MAP6	38.47
mycBioID2tau	2	MAP6	54.49
mycBioID2tau	2	MAP6	73.23
mycBioID2tau	2	MAP6	52.72
mycBioID2tau	2	MAP6	75.59
mycBioID2tau	2	MAP6	76.17
mycBioID2tau	2	MAP6	96.23
mycBioID2tau	2	MAP6	68.18
mycBioID2tau	2	MAP6	103.23
mycBioID2tau	2	MAP6	43.29
mycBioID2tau	2	MAP6	45.72
mycBioID2tau	2	MAP6	46.05
mycBioID2tau	2	MAP6	49.26
mycBioID2tau	2	MAP6	45.57
mycBioID2tau	2	MAP6	52.74
mycBioID2tau	2	MAP6	58.74
mycBioID2tau	2	MAP6	52.46
mycBioID2tau	2	MAP6	52.81
mycBioID2tau	2	MAP6	60.96
mycBioID2tau	2	MAP6	77.9
mycBioID2tau	2	MAP6	43.84
mycBioID2tau	3	MAP6	54.57
mycBioID2tau	4	MAP6	56.61
mycBioID2tau	4	MAP6	91.45
mycBioID2tau	4	MAP6	41.61
mycBioID2tau	4	MAP6	61.46
mycBioID2tau	4	MAP6	61.17
mycBioID2tau	4	MAP6	64.81
mycBioID2tau	4	MAP6	60.46
mycBioID2tau	5	MAP6	45.43
mycBioID2tau	5	MAP6	42.63
mycBioID2tau	5	MAP6	61.43
mycBioID2tau	5	MAP6	90.52
mycBioID2tau	5	MAP6	85.11
mycBioID2tau	5	MAP6	111.09
mycBioID2tau	5	MAP6	80.41
mycBioID2tau	5	MAP6	65.75
mycBioID2tau	5	MAP6	38.76
mycBioID2tau	5	MAP6	81.96
mycBioID2tau	5	MAP6	63.95
mycBioID2tau	5	MAP6	47.57
mycBioID2	3	MARE1	50.48
mycBioID2tau	1	MARE1	55.44
mycBioID2tau	2	MARE1	66.05

mycBioID2tau	4	MARE1	65.92
mycBioID2tau	4	MARE1	65.92
mycBioID2	2	MARE3	69.45
mycBioID2	3	MARE3	89.05
mycBioID2	3	MARE3	56.92
mycBioID2tau	1	MARE3	57.07
mycBioID2tau	1	MARE3	83.54
mycBioID2tau	1	MARE3	73.53
mycBioID2tau	2	MARE3	49.15
mycBioID2tau	2	MARE3	92.18
mycBioID2tau	4	MARE3	55.04
mycBioID2tau	4	MARE3	55.04
mycBioID2tau	4	MARE3	55.04
mycBioID2tau	5	MARE3	51.34
mycBioID2tau	5	MARE3	51.34
mycBioID2tau	5	MARE3	51.34
mycBioID2	1	MCCA	48.02
mycBioID2	3	MCCA	48.85
mycBioID2	3	MCCA	56.17
mycBioID2tau	2	MCCA	42.95
mycBioID2tau	4	MCCA	56.53
mycBioID2tau	4	MCCA	56.53
mycBioID2tau	4	MCCA	56.53
mycBioID2tau	5	MCCA	50.35
mycBioID2tau	5	MCCA	50.35
mycBioID2tau	5	MCCA	50.35
mycBioID2	5	MDHM	40.55
mycBioID2	1	MECP2	54.84
mycBioID2	3	MECP2	63.3
mycBioID2	1	MINK1	92.33
mycBioID2	2	MINK1	40.77
mycBioID2	2	MINK1	41.56
mycBioID2	2	MINK1	91.56
mycBioID2	3	MINK1	45.04
mycBioID2	3	MINK1	89.75
mycBioID2	3	MINK1	65.11
mycBioID2tau	1	MINK1	91.27
mycBioID2tau	2	MINK1	116
mycBioID2tau	5	MINK1	54.55
mycBioID2tau	5	MINK1	54.55
mycBioID2tau	5	MINK1	54.55
mycBioID2	1	MTAP2	71.66
mycBioID2	1	MTAP2	60.28
mycBioID2	1	MTAP2	55.8
mycBioID2	1	MTAP2	43.39
mycBioID2	1	MTAP2	60.15
mycBioID2	1	MTAP2	46.02
mycBioID2	1	MTAP2	73.92

mycBioID2	1	MTAP2	53.2
mycBioID2	1	MTAP2	74.35
mycBioID2	1	MTAP2	67.95
mycBioID2	1	MTAP2	75.59
mycBioID2	1	MTAP2	44.21
mycBioID2	1	MTAP2	57.73
mycBioID2	2	MTAP2	55.28
mycBioID2	2	MTAP2	62.4
mycBioID2	2	MTAP2	42.67
mycBioID2	2	MTAP2	39.77
mycBioID2	2	MTAP2	56.98
mycBioID2	2	MTAP2	76.85
mycBioID2	2	MTAP2	91.89
mycBioID2	2	MTAP2	37.1
mycBioID2	2	MTAP2	46.75
mycBioID2	2	MTAP2	53.44
mycBioID2	2	MTAP2	63.42
mycBioID2	2	MTAP2	72
mycBioID2	2	MTAP2	41.81
mycBioID2	2	MTAP2	48.76
mycBioID2	2	MTAP2	41.48
mycBioID2	3	MTAP2	24.71
mycBioID2	3	MTAP2	40.94
mycBioID2	3	MTAP2	42.49
mycBioID2	3	MTAP2	64.51
mycBioID2	3	MTAP2	45.08
mycBioID2	3	MTAP2	42.77
mycBioID2	3	MTAP2	64.33
mycBioID2	3	MTAP2	62.86
mycBioID2	3	MTAP2	79.44
mycBioID2	3	MTAP2	47.77
mycBioID2	3	MTAP2	46.1
mycBioID2	3	MTAP2	70.31
mycBioID2	3	MTAP2	52.59
mycBioID2	3	MTAP2	60.11
mycBioID2	3	MTAP2	64.64
mycBioID2	3	MTAP2	43.96
mycBioID2	3	MTAP2	56.29
mycBioID2	3	MTAP2	52.97
mycBioID2	3	MTAP2	71.09
mycBioID2	3	MTAP2	47.39
mycBioID2	3	MTAP2	41.87
mycBioID2	4	MTAP2	72.28
mycBioID2	4	MTAP2	54.57
mycBioID2	4	MTAP2	46.99
mycBioID2	4	MTAP2	44.68
mycBioID2	4	MTAP2	42.68
mycBioID2	4	MTAP2	42.04

mycBioID2	4	MTAP2	40.81
mycBioID2	5	MTAP2	71.59
mycBioID2	5	MTAP2	53.45
mycBioID2	5	MTAP2	52.34
mycBioID2	5	MTAP2	45.76
mycBioID2	5	MTAP2	42.61
mycBioID2	5	MTAP2	40.74
mycBioID2tau	1	MTAP2	41.66
mycBioID2tau	1	MTAP2	47.69
mycBioID2tau	1	MTAP2	44.39
mycBioID2tau	1	MTAP2	56.22
mycBioID2tau	1	MTAP2	64.51
mycBioID2tau	1	MTAP2	61.08
mycBioID2tau	1	MTAP2	50.1
mycBioID2tau	1	MTAP2	43.47
mycBioID2tau	1	MTAP2	44.13
mycBioID2tau	1	MTAP2	56.66
mycBioID2tau	1	MTAP2	59.45
mycBioID2tau	1	MTAP2	54.58
mycBioID2tau	1	MTAP2	79.04
mycBioID2tau	1	MTAP2	43.9
mycBioID2tau	1	MTAP2	59.71
mycBioID2tau	1	MTAP2	55.75
mycBioID2tau	1	MTAP2	48.94
mycBioID2tau	1	MTAP2	43.22
mycBioID2tau	1	MTAP2	89.92
mycBioID2tau	1	MTAP2	77.88
mycBioID2tau	1	MTAP2	70.26
mycBioID2tau	1	MTAP2	40.58
mycBioID2tau	2	MTAP2	25.72
mycBioID2tau	2	MTAP2	31.93
mycBioID2tau	2	MTAP2	41.61
mycBioID2tau	2	MTAP2	65.44
mycBioID2tau	2	MTAP2	41.41
mycBioID2tau	2	MTAP2	43.31
mycBioID2tau	2	MTAP2	66.69
mycBioID2tau	2	MTAP2	50.4
mycBioID2tau	2	MTAP2	42.09
mycBioID2tau	2	MTAP2	42.82
mycBioID2tau	2	MTAP2	45.42
mycBioID2tau	2	MTAP2	55.44
mycBioID2tau	2	MTAP2	44.88
mycBioID2tau	2	MTAP2	74.91
mycBioID2tau	2	MTAP2	42.07
mycBioID2tau	2	MTAP2	91.52
mycBioID2tau	2	MTAP2	64.81
mycBioID2tau	2	MTAP2	48.66
mycBioID2tau	2	MTAP2	84.05

mycBioID2tau	2	MTAP2	65.01
mycBioID2tau	2	MTAP2	43.02
mycBioID2tau	2	MTAP2	52.84
mycBioID2tau	2	MTAP2	57.7
mycBioID2tau	2	MTAP2	46.66
mycBioID2tau	2	MTAP2	91.59
mycBioID2tau	2	MTAP2	64.16
mycBioID2tau	2	MTAP2	60.86
mycBioID2tau	2	MTAP2	78.65
mycBioID2tau	2	MTAP2	71.7
mycBioID2tau	2	MTAP2	51.3
mycBioID2tau	3	MTAP2	46.92
mycBioID2tau	4	MTAP2	54.42
mycBioID2tau	4	MTAP2	45.69
mycBioID2tau	4	MTAP2	44.16
mycBioID2tau	4	MTAP2	40.84
mycBioID2tau	4	MTAP2	41.39
mycBioID2tau	4	MTAP2	50.29
mycBioID2tau	4	MTAP2	52.36
mycBioID2tau	4	MTAP2	39.95
mycBioID2tau	5	MTAP2	49.83
mycBioID2tau	5	MTAP2	44.17
mycBioID2tau	5	MTAP2	46.42
mycBioID2tau	5	MTAP2	44.88
mycBioID2tau	5	MTAP2	46.55
mycBioID2tau	5	MTAP2	60.48
mycBioID2tau	5	MTAP2	64.14
mycBioID2tau	5	MTAP2	41.48
mycBioID2tau	5	MTAP2	43.22
mycBioID2tau	5	MTAP2	51.09
mycBioID2tau	5	MTAP2	69.78
mycBioID2tau	5	MTAP2	46.39
mycBioID2tau	5	MTAP2	59.67
mycBioID2tau	5	MTAP2	55.69
mycBioID2tau	5	MTAP2	46.32
mycBioID2tau	5	MTAP2	67.63
mycBioID2tau	5	MTAP2	43.12
mycBioID2tau	2	MYO5A	37.72
mycBioID2	2	NAC1	44.56
mycBioID2	1	NACA	83.25
mycBioID2	3	NACA	81.03
mycBioID2tau	2	NACAM	78.41
mycBioID2	3	NBEA	56.32
mycBioID2	3	NBEA	89.3
mycBioID2	3	NCALD	41.73
mycBioID2	1	NCAM1	62.84
mycBioID2	3	NCAM1	86.57
mycBioID2	2	NCDN	69.57

mycBioID2	3	NCDN	42.12
mycBioID2	1	NDST3	38.52
mycBioID2	2	NEB2	46.2
mycBioID2	3	NEB2	46.51
mycBioID2	2	NECP1	43.66
mycBioID2	2	NECP1	44.89
mycBioID2	3	NECP1	47.13
mycBioID2	3	NECP1	44.51
mycBioID2	3	NECP1	43.57
mycBioID2tau	2	NECP1	56.31
mycBioID2tau	2	NECP1	40.13
mycBioID2tau	5	NECP1	43.81
mycBioID2tau	5	NECP1	39.4
mycBioID2tau	5	NECP1	43.81
mycBioID2tau	5	NECP1	39.4
mycBioID2	1	NEUG	87.34
mycBioID2	2	NEUG	85.47
mycBioID2	3	NEUG	85.82
mycBioID2	5	NEUG	67.96
mycBioID2tau	1	NEUG	92.1
mycBioID2tau	2	NEUG	61.91
mycBioID2tau	4	NEUG	88.17
mycBioID2tau	4	NEUG	88.17
mycBioID2tau	4	NEUG	88.17
mycBioID2tau	4	NEUG	88.17
mycBioID2tau	5	NEUG	84.15
mycBioID2tau	5	NEUG	84.15
mycBioID2tau	5	NEUG	84.15
mycBioID2tau	5	NEUG	84.15
mycBioID2	2	NFH	43.28
mycBioID2	1	NFM	58.09
mycBioID2	1	NFM	68.96
mycBioID2	1	NFM	64.7
mycBioID2	2	NFM	56.09
mycBioID2	2	NFM	50.21
mycBioID2	2	NFM	47.28
mycBioID2	2	NFM	60.39
mycBioID2	3	NFM	41.75
mycBioID2	3	NFM	47.93
mycBioID2	3	NFM	52.96
mycBioID2	3	NFM	49.79
mycBioID2	3	NFM	61.73
mycBioID2	3	NFM	52.6
mycBioID2	3	NFM	47.73
mycBioID2tau	1	NFM	61.44
mycBioID2tau	1	NFM	60.86
mycBioID2tau	2	NFM	52.74
mycBioID2tau	2	NFM	49.51

mycBioID2tau	2	NFM	62.08
mycBioID2tau	2	NFM	43.55
mycBioID2tau	2	NFM	85.71
mycBioID2tau	4	NFM	41.27
mycBioID2tau	5	NFM	55.34
mycBioID2tau	5	NFM	69.01
mycBioID2tau	1	NKTR	38.95
mycBioID2tau	4	NKTR	40.44
mycBioID2	2	NMDE1	58.21
mycBioID2	3	NMDE1	44.86
mycBioID2	3	NMDE1	83.34
mycBioID2	1	NMDE2	56.07
mycBioID2	2	NMDE2	40.63
mycBioID2	3	NMDE2	68.62
mycBioID2	3	NMDE2	44.84
mycBioID2tau	2	NP1L4	41.48
mycBioID2tau	4	NP1L4	43.16
mycBioID2tau	4	NP1L4	43.16
mycBioID2	1	NSF	54.61
mycBioID2	1	NSF	69.12
mycBioID2	2	NSF	65.26
mycBioID2	2	NSF	63.53
mycBioID2	3	NSF	43.49
mycBioID2	3	NSF	66.79
mycBioID2	3	NSF	48.6
mycBioID2	3	NSF	67.16
mycBioID2tau	2	NSF	70.47
mycBioID2tau	2	NSF	58.94
mycBioID2tau	5	NSF	65.41
mycBioID2tau	5	NSF	61.47
mycBioID2tau	5	NSF	43.28
mycBioID2	1	NSF1C	64.67
mycBioID2	1	NSF1C	60.51
mycBioID2	2	NSF1C	63.35
mycBioID2	2	NSF1C	47.66
mycBioID2	3	NSF1C	70.04
mycBioID2	3	NSF1C	52.07
mycBioID2	3	NSF1C	45.94
mycBioID2	3	NSF1C	64.62
mycBioID2	3	NSF1C	67.02
mycBioID2tau	2	NSF1C	41.35
mycBioID2	3	OGA	65.76
mycBioID2tau	5	OGA	40.85
mycBioID2tau	5	OGA	40.85
mycBioID2tau	5	OGA	40.85
mycBioID2	1	OXR1	57.86
mycBioID2	2	OXR1	52.55
mycBioID2	3	OXR1	67.35

mycBioID2	3	OXR1	59.58
mycBioID2	3	OXR1	72.75
mycBioID2tau	1	OXR1	48.2
mycBioID2tau	2	OXR1	82.37
mycBioID2tau	2	OXR1	43.33
mycBioID2tau	5	OXR1	43.1
mycBioID2tau	5	OXR1	72.43
mycBioID2	3	P33MX	50.7
mycBioID2tau	2	P33MX	44.29
mycBioID2	1	PACS1	87.17
mycBioID2	2	PACS1	88.15
mycBioID2	3	PACS1	72.83
mycBioID2	3	PACS1	80.15
mycBioID2	3	PACS1	53.38
mycBioID2	3	PACS1	56.56
mycBioID2tau	1	PACS1	83.61
mycBioID2tau	1	PACS1	68.1
mycBioID2tau	2	PACS1	45.81
mycBioID2	3	PAK2	67.58
mycBioID2tau	2	PAK2	81.52
mycBioID2	1	PALM	53.84
mycBioID2	2	PALM	41.91
mycBioID2	2	PALM	61.86
mycBioID2	3	PALM	60.65
mycBioID2	2	PALM2	53.12
mycBioID2	3	PALM2	49.42
mycBioID2	1	PCBP1	63.74
mycBioID2	2	PCBP1	48.22
mycBioID2	2	PCBP1	87.4
mycBioID2	3	PCBP1	91.49
mycBioID2	3	PCBP1	71.59
mycBioID2tau	2	PCBP1	55.16
mycBioID2	1	PCCA	85.32
mycBioID2	1	PCCA	71.03
mycBioID2	1	PCCA	69.06
mycBioID2	2	PCCA	57.02
mycBioID2	2	PCCA	88.56
mycBioID2	2	PCCA	62.02
mycBioID2	2	PCCA	46.51
mycBioID2	2	PCCA	50.83
mycBioID2	2	PCCA	45.81
mycBioID2	3	PCCA	74.58
mycBioID2	3	PCCA	57.63
mycBioID2	3	PCCA	44.72
mycBioID2	4	PCCA	50.09
mycBioID2	5	PCCA	76.22
mycBioID2	5	PCCA	73.84
mycBioID2	5	PCCA	55.09

mycBioID2	5	PCCA	53.46
mycBioID2tau	1	PCCA	63.48
mycBioID2tau	1	PCCA	43.51
mycBioID2tau	1	PCCA	42.73
mycBioID2tau	1	PCCA	43.97
mycBioID2tau	1	PCCA	65.95
mycBioID2tau	2	PCCA	50.9
mycBioID2tau	2	PCCA	50.07
mycBioID2tau	2	PCCA	45.75
mycBioID2tau	3	PCCA	42.99
mycBioID2tau	3	PCCA	56.68
mycBioID2tau	4	PCCA	52.25
mycBioID2tau	4	PCCA	85.15
mycBioID2tau	4	PCCA	48.88
mycBioID2tau	4	PCCA	47.75
mycBioID2tau	4	PCCA	51.07
mycBioID2tau	4	PCCA	52.25
mycBioID2tau	4	PCCA	85.15
mycBioID2tau	4	PCCA	48.88
mycBioID2tau	4	PCCA	47.75
mycBioID2tau	4	PCCA	51.07
mycBioID2tau	4	PCCA	52.25
mycBioID2tau	4	PCCA	85.15
mycBioID2tau	4	PCCA	48.88
mycBioID2tau	4	PCCA	47.75
mycBioID2tau	4	PCCA	51.07
mycBioID2tau	5	PCCA	46.69
mycBioID2tau	5	PCCA	73.65
mycBioID2tau	5	PCCA	50.26
mycBioID2tau	5	PCCA	37.83
mycBioID2tau	5	PCCA	44.43
mycBioID2tau	5	PCCA	42.86
mycBioID2tau	5	PCCA	46.23
mycBioID2tau	5	PCCA	59.22
mycBioID2tau	5	PCCA	46.69
mycBioID2tau	5	PCCA	73.65
mycBioID2tau	5	PCCA	50.26
mycBioID2tau	5	PCCA	37.83
mycBioID2tau	5	PCCA	44.43
mycBioID2tau	5	PCCA	42.86
mycBioID2tau	5	PCCA	46.23
mycBioID2tau	5	PCCA	59.22
mycBioID2tau	5	PCCA	46.69
mycBioID2tau	5	PCCA	73.65
mycBioID2tau	5	PCCA	50.26
mycBioID2tau	5	PCCA	37.83
mycBioID2tau	5	PCCA	44.43
mycBioID2tau	5	PCCA	42.86

mycBioID2tau	5	PCCA	46.23
mycBioID2tau	5	PCCA	59.22
mycBioID2	3	PCDH1	88.15
mycBioID2	1	PCLO	57.2
mycBioID2	1	PCLO	43.23
mycBioID2	2	PCLO	46.78
mycBioID2	2	PCLO	73.75
mycBioID2	3	PCLO	52.72
mycBioID2	3	PCLO	75.29
mycBioID2	3	PCLO	61.36
mycBioID2	3	PCLO	50.19
mycBioID2	3	PCLO	66.94
mycBioID2	3	PCLO	52.72
mycBioID2tau	2	PCLO	44.51
mycBioID2tau	2	PCLO	53.49
mycBioID2tau	2	PCLO	61.55
mycBioID2tau	2	PCLO	43.21
mycBioID2	3	PCNP	51.78
mycBioID2	5	PCP	35.64
mycBioID2	3	PDE1A	57.26
mycBioID2	1	PEA15	50.94
mycBioID2	3	PEA15	79.57
mycBioID2	1	PEBP1	101.52
mycBioID2	1	PEX5R	41.5
mycBioID2	1	PFD2	62.09
mycBioID2	2	PFD2	55.59
mycBioID2	3	PFD2	41.48
mycBioID2	3	PFD2	67.12
mycBioID2tau	2	PFD2	55.56
mycBioID2tau	4	PFD2	73.2
mycBioID2tau	5	PFD2	88.27
mycBioID2	1	PGAM1	60.9
mycBioID2	2	PGAM1	56.19
mycBioID2	3	PGAM1	67.43
mycBioID2	5	PGAM1	59.94
mycBioID2tau	1	PGAM1	59.39
mycBioID2tau	2	PGAM1	62.84
mycBioID2tau	4	PGAM1	46.35
mycBioID2tau	4	PGAM1	66.5
mycBioID2tau	4	PGAM1	46.35
mycBioID2tau	4	PGAM1	66.5
mycBioID2tau	5	PGAM1	47.32
mycBioID2tau	5	PGAM1	54.27
mycBioID2tau	5	PGAM1	47.32
mycBioID2tau	5	PGAM1	54.27
mycBioID2tau	2	PI42A	67.74
mycBioID2	3	PI42B	71.8
mycBioID2tau	5	PI42B	67.93

mycBioID2tau	5	PI42B	67.93
mycBioID2tau	5	PI42B	67.93
mycBioID2tau	2	PI42C	68.39
mycBioID2	1	PI51C	45.58
mycBioID2	2	PKP4	50.71
mycBioID2	2	PKP4	44.19
mycBioID2	2	PLCL2	69.58
mycBioID2	3	PLCL2	78.64
mycBioID2tau	1	PLCL2	45.38
mycBioID2tau	2	PLCL2	49.67
mycBioID2tau	1	PLCX3	50.08
mycBioID2	1	PLEC	84.36
mycBioID2	1	PLEC	90.66
mycBioID2	2	PLEC	74.49
mycBioID2	2	PLEC	69.7
mycBioID2	2	PLEC	55.1
mycBioID2	3	PLEC	44.86
mycBioID2	3	PLEC	84.36
mycBioID2	3	PLEC	50.66
mycBioID2	3	PLEC	64.53
mycBioID2	4	PLEC	48.04
mycBioID2	4	PLEC	43.41
mycBioID2	5	PLEC	62.36
mycBioID2	5	PLEC	56.73
mycBioID2	5	PLEC	48.82
mycBioID2tau	1	PLEC	74.39
mycBioID2tau	1	PLEC	73.84
mycBioID2tau	2	PLEC	40.22
mycBioID2tau	2	PLEC	70.73
mycBioID2tau	2	PLEC	41.1
mycBioID2tau	2	PLEC	81.9
mycBioID2tau	4	PLEC	57.24
mycBioID2tau	4	PLEC	57.24
mycBioID2tau	5	PLEC	62.68
mycBioID2tau	5	PLEC	62.68
mycBioID2	1	PLPR4	42.33
mycBioID2	1	PLPR4	82.97
mycBioID2	2	PLPR4	51.54
mycBioID2	2	PLPR4	54.22
mycBioID2	2	PLPR4	61.74
mycBioID2	3	PLPR4	56.12
mycBioID2	3	PLPR4	40.65
mycBioID2	3	PLPR4	61.54
mycBioID2	3	PLPR4	42.95
mycBioID2tau	2	PLPR4	46.62
mycBioID2	3	PLXA4	74.06
mycBioID2tau	5	PP1RB	42.78
mycBioID2tau	5	PP1RB	42.78

mycBioID2tau	5	PP1RB	42.78
mycBioID2tau	5	PP1RB	42.78
mycBioID2tau	5	PP1RB	42.78
mycBioID2	1	PP2BA	114.62
mycBioID2	2	PP2BA	47.85
mycBioID2	3	PP2BA	55.98
mycBioID2	2	PPR29	81.4
mycBioID2	2	PPR29	74.04
mycBioID2	3	PPR29	51.96
mycBioID2	3	PPR29	67.08
mycBioID2	2	PRAF3	48.02
mycBioID2	3	PRAF3	43.68
mycBioID2tau	1	PRAF3	46.32
mycBioID2tau	2	PRAF3	50.07
mycBioID2	1	PRRT2	54.16
mycBioID2	3	PRRT2	64.23
mycBioID2	2	PSD1	72.17
mycBioID2	3	PSMD2	42.24
mycBioID2	2	PURA2	55.25
mycBioID2	3	PURA2	50.74
mycBioID2tau	1	PURA2	53.78
mycBioID2tau	2	PURA2	65.61
mycBioID2tau	5	PURA2	65.58
mycBioID2tau	5	PURA2	65.58
mycBioID2tau	5	PURA2	65.58
mycBioID2tau	5	PURA2	65.58
mycBioID2	1	PURB	48.07
mycBioID2	3	PURB	55.88
mycBioID2tau	1	PURB	38.97
mycBioID2tau	2	PURB	60.14
mycBioID2	1	PYC	58.12
mycBioID2	1	PYC	89.35
mycBioID2	1	PYC	57.25
mycBioID2	1	PYC	44.47
mycBioID2	1	PYC	75.95
mycBioID2	1	PYC	47.58
mycBioID2	1	PYC	59.43
mycBioID2	1	PYC	44.19
mycBioID2	1	PYC	76.09
mycBioID2	1	PYC	42.24
mycBioID2	1	PYC	63.02
mycBioID2	1	PYC	65.02
mycBioID2	1	PYC	79.5
mycBioID2	1	PYC	92.26
mycBioID2	1	PYC	54.75
mycBioID2	2	PYC	85.31
mycBioID2	2	PYC	60.62
mycBioID2	2	PYC	86.1

mycBioID2	3	PYC	96.32
mycBioID2	3	PYC	56.17
mycBioID2	3	PYC	48.46
mycBioID2	3	PYC	67.68
mycBioID2	3	PYC	71.45
mycBioID2	3	PYC	110.8
mycBioID2	3	PYC	69.17
mycBioID2	3	PYC	41.72
mycBioID2	3	PYC	50.76
mycBioID2	3	PYC	65.28
mycBioID2	3	PYC	52.33
mycBioID2	3	PYC	57.08
mycBioID2	3	PYC	66.47
mycBioID2	4	PYC	66.22
mycBioID2	5	PYC	74.35
mycBioID2tau	1	PYC	61.86
mycBioID2tau	1	PYC	51.92
mycBioID2tau	1	PYC	72.15
mycBioID2tau	1	PYC	83.95
mycBioID2tau	1	PYC	67.46
mycBioID2tau	1	PYC	44.87
mycBioID2tau	1	PYC	41.24
mycBioID2tau	1	PYC	74.76
mycBioID2tau	1	PYC	56.78
mycBioID2tau	1	PYC	79.04
mycBioID2tau	1	PYC	64.67
mycBioID2tau	1	PYC	51.23
mycBioID2tau	1	PYC	68.32
mycBioID2tau	1	PYC	46.8
mycBioID2tau	1	PYC	50.26
mycBioID2tau	1	PYC	55.4
mycBioID2tau	1	PYC	55.75
mycBioID2tau	1	PYC	53.12
mycBioID2tau	1	PYC	47.72
mycBioID2tau	1	PYC	44.09
mycBioID2tau	1	PYC	83.68
mycBioID2tau	1	PYC	44.11
mycBioID2tau	1	PYC	54.91
mycBioID2tau	2	PYC	55.83
mycBioID2tau	2	PYC	80.61
mycBioID2tau	2	PYC	51.11
mycBioID2tau	2	PYC	88.74
mycBioID2tau	2	PYC	51.36
mycBioID2tau	2	PYC	75.13
mycBioID2tau	2	PYC	126.98
mycBioID2tau	2	PYC	48.06
mycBioID2tau	2	PYC	61.92
mycBioID2tau	2	PYC	63.04

mycBioID2tau	2	PYC	57.66
mycBioID2tau	2	PYC	42.14
mycBioID2tau	4	PYC	81.23
mycBioID2tau	4	PYC	72.56
mycBioID2tau	4	PYC	70.4
mycBioID2tau	4	PYC	89.48
mycBioID2tau	4	PYC	64.93
mycBioID2tau	4	PYC	47.73
mycBioID2tau	4	PYC	53.46
mycBioID2tau	4	PYC	44.78
mycBioID2tau	4	PYC	81.23
mycBioID2tau	4	PYC	72.56
mycBioID2tau	4	PYC	70.4
mycBioID2tau	4	PYC	89.48
mycBioID2tau	4	PYC	64.93
mycBioID2tau	4	PYC	47.73
mycBioID2tau	4	PYC	53.46
mycBioID2tau	4	PYC	44.78
mycBioID2tau	5	PYC	76.92
mycBioID2tau	5	PYC	75.2
mycBioID2tau	5	PYC	65.03
mycBioID2tau	5	PYC	68.1
mycBioID2tau	5	PYC	51.83
mycBioID2tau	5	PYC	61.1
mycBioID2tau	5	PYC	55.58
mycBioID2tau	5	PYC	50.69
mycBioID2tau	5	PYC	72.09
mycBioID2tau	5	PYC	76.92
mycBioID2tau	5	PYC	75.2
mycBioID2tau	5	PYC	65.03
mycBioID2tau	5	PYC	68.1
mycBioID2tau	5	PYC	51.83
mycBioID2tau	5	PYC	61.1
mycBioID2tau	5	PYC	55.58
mycBioID2tau	5	PYC	50.69
mycBioID2tau	5	PYC	72.09
mycBioID2	3	R7BP	51.85
mycBioID2tau	2	RANG	55.2
mycBioID2	1	RASL1	43.01
mycBioID2	2	RASL1	58.03
mycBioID2	3	RASL1	61.57
mycBioID2tau	1	RASL1	64.59
mycBioID2tau	2	RASL1	56.18
mycBioID2tau	5	RASL1	45.94
mycBioID2tau	1	RBNS5	44.49
mycBioID2tau	2	RBNS5	49.32
mycBioID2	2	REPS1	48
mycBioID2	3	RGRF1	67.37

mycBioID2tau	1	RGRF1	52.44
mycBioID2	3	RHG20	56.57
mycBioID2	3	RHG32	73.78
mycBioID2	3	RHG35	44.22
mycBioID2	3	RHG39	46.21
mycBioID2	1	RIMKA	90.27
mycBioID2	3	RIMKA	87.9
mycBioID2tau	1	RIMKA	63.49
mycBioID2tau	2	RIMKA	40.25
mycBioID2tau	2	RIMKA	64.24
mycBioID2	2	RL24	42.53
mycBioID2	3	RL24	42.31
mycBioID2tau	2	RL24	42.92
mycBioID2	2	RL29	44.33
mycBioID2	2	RL29	57.43
mycBioID2	3	RL29	44.17
mycBioID2	3	RL29	52.94
mycBioID2tau	1	RL29	49.3
mycBioID2tau	2	RL29	44.29
mycBioID2tau	2	RL29	44.68
mycBioID2tau	5	RL29	46.91
mycBioID2	3	RN214	62.56
mycBioID2tau	1	RN214	68.19
mycBioID2tau	2	RN214	53.13
mycBioID2	2	ROA1	67.64
mycBioID2	2	RP3A	46.85
mycBioID2	3	RP3A	63.33
mycBioID2	2	RS20	69.52
mycBioID2	3	RS20	49.35
mycBioID2tau	2	RS20	47.43
mycBioID2tau	2	RTN1	50.6
mycBioID2	1	RTN3	42.79
mycBioID2	1	RTN3	52.29
mycBioID2	1	RTN3	69.76
mycBioID2	2	RTN3	40.39
mycBioID2	2	RTN3	60.21
mycBioID2	2	RTN3	45.53
mycBioID2	2	RTN3	54.4
mycBioID2	2	RTN3	125.95
mycBioID2	3	RTN3	56.19
mycBioID2	3	RTN3	52.19
mycBioID2	3	RTN3	59.22
mycBioID2	3	RTN3	77.81
mycBioID2tau	1	RTN3	43.2
mycBioID2tau	1	RTN3	62.42
mycBioID2tau	2	RTN3	49.16
mycBioID2tau	2	RTN3	34.92
mycBioID2tau	2	RTN3	62.2

mycBioID2tau	2	RTN3	84.89
mycBioID2tau	2	RTN3	81.28
mycBioID2tau	4	RTN3	70.37
mycBioID2tau	5	RTN3	73.92
mycBioID2	1	RTN4	85.72
mycBioID2	2	RTN4	60.95
mycBioID2	2	RTN4	68.74
mycBioID2	3	RTN4	57.92
mycBioID2	3	RTN4	46.53
mycBioID2	3	RTN4	74.83
mycBioID2	3	RTN4	49.22
mycBioID2	3	RTN4	122.84
mycBioID2tau	1	RTN4	51.79
mycBioID2tau	1	RTN4	45.41
mycBioID2tau	2	RTN4	52.63
mycBioID2tau	2	RTN4	62.09
mycBioID2tau	2	RTN4	60.37
mycBioID2tau	5	RTN4	38.61
mycBioID2	2	RU2A	61.25
mycBioID2	3	RU2A	56.77
mycBioID2	3	RU2A	38.79
mycBioID2tau	2	RUFY3	43.88
mycBioID2	3	RUVB2	93.93
mycBioID2	5	RUVB2	51.54
mycBioID2	3	RYR2	38.92
mycBioID2tau	1	S10A6	66
mycBioID2tau	2	S10A6	63.84
mycBioID2	2	S12A5	45.6
mycBioID2	3	S12A5	57.69
mycBioID2	1	S6A17	68.44
mycBioID2	3	S6A17	48.25
mycBioID2	3	S7A14	84.04
mycBioID2	3	SC6A7	42.85
mycBioID2	2	SEP5	48.31
mycBioID2	2	SEP5	66.66
mycBioID2	3	SEP5	56.86
mycBioID2	3	SEP5	60.13
mycBioID2tau	1	SEP5	62.76
mycBioID2tau	1	SEP5	53.76
mycBioID2tau	2	SEP5	61.4
mycBioID2tau	2	SEP5	49.08
mycBioID2tau	2	SEP5	56.77
mycBioID2	1	SEP7	60.01
mycBioID2	1	SEP7	41.04
mycBioID2	2	SEP7	56.61
mycBioID2	2	SEP7	45.4
mycBioID2tau	1	SEP7	72.57
mycBioID2tau	1	SEP7	70.37

mycBioID2tau	2	SEP7	62.67
mycBioID2tau	2	SEP7	71.05
mycBioID2tau	4	SEP7	46.59
mycBioID2tau	4	SEP7	46.59
mycBioID2tau	4	SEP7	46.59
mycBioID2tau	4	SEP7	46.59
mycBioID2tau	4	SEP7	46.59
mycBioID2tau	4	SEP7	46.59
mycBioID2tau	5	SEP7	56.12
mycBioID2tau	5	SEP7	56.12
mycBioID2tau	5	SEP7	56.12
mycBioID2tau	5	SEP7	56.12
mycBioID2tau	5	SEP7	56.12
mycBioID2tau	5	SEP7	56.12
mycBioID2tau	1	SEP9	60.22
mycBioID2tau	2	SEP9	60.79
mycBioID2	2	SETLP	65.43
mycBioID2	3	SETLP	67.79
mycBioID2	3	SGIP1	33.6
mycBioID2	3	SGIP1	62.01
mycBioID2	1	SH3G1	61.89
mycBioID2	2	SH3G1	52.19
mycBioID2	2	SH3G1	52.45
mycBioID2	3	SH3G1	63.5
mycBioID2	3	SH3G1	60.19
mycBioID2	3	SH3G1	46.04
mycBioID2	3	SH3G1	39.6
mycBioID2	1	SH3G2	61.89
mycBioID2	1	SH3G2	79.62
mycBioID2	2	SH3G2	52.19
mycBioID2	2	SH3G2	86.82
mycBioID2	3	SH3G2	63.5
mycBioID2	3	SH3G2	60.19
mycBioID2	3	SH3G2	82.18
mycBioID2	4	SH3G2	51.58
mycBioID2	5	SH3G2	50.64
mycBioID2tau	1	SH3G2	60.6
mycBioID2tau	1	SH3G2	58.55
mycBioID2tau	2	SH3G2	75.01
mycBioID2tau	4	SH3G2	60.25
mycBioID2tau	4	SH3G2	46.41
mycBioID2tau	4	SH3G2	60.25
mycBioID2tau	4	SH3G2	46.41
mycBioID2tau	4	SH3G2	60.25
mycBioID2tau	4	SH3G2	46.41
mycBioID2tau	5	SH3G2	50.57
mycBioID2tau	5	SH3G2	70.01
mycBioID2tau	5	SH3G2	50.57

mycBioID2tau	5	SH3G2	70.01
mycBioID2tau	5	SH3G2	50.57
mycBioID2tau	5	SH3G2	70.01
mycBioID2	3	SH3K1	44.16
mycBioID2	3	SHAN1	51.07
mycBioID2	3	SHAN1	78.94
mycBioID2	1	SHAN2	68.73
mycBioID2	1	SHAN2	63.16
mycBioID2	1	SHAN2	73.22
mycBioID2	1	SHAN2	42.41
mycBioID2	2	SHAN2	63.15
mycBioID2	3	SHAN2	43.57
mycBioID2	3	SHAN2	52.15
mycBioID2	3	SHAN2	41.49
mycBioID2	3	SHAN2	38.54
mycBioID2	3	SHAN2	64.46
mycBioID2	3	SHAN2	58.55
mycBioID2	3	SHAN2	39.98
mycBioID2	3	SHAN2	48.15
mycBioID2	3	SHAN2	69.14
mycBioID2tau	2	SHAN2	47.42
mycBioID2tau	2	SHAN2	62.98
mycBioID2tau	4	SHAN2	69.65
mycBioID2tau	4	SHAN2	69.65
mycBioID2tau	5	SHAN2	50.91
mycBioID2tau	5	SHAN2	50.91
mycBioID2	2	SHRM2	53.06
mycBioID2tau	1	SHRM2	44.42
mycBioID2tau	2	SHRM2	42.48
mycBioID2	3	SHSA6	64.79
mycBioID2	2	SI1L1	70.8
mycBioID2	2	SI1L1	48.49
mycBioID2	3	SI1L1	64.24
mycBioID2	2	SKT	68.11
mycBioID2	2	SKT	57.07
mycBioID2	3	SKT	100.16
mycBioID2	3	SKT	68.32
mycBioID2	3	SKT	38.06
mycBioID2tau	1	SKT	42.3
mycBioID2tau	1	SKT	59.87
mycBioID2tau	2	SKT	49.66
mycBioID2	1	SLIK5	65.75
mycBioID2	3	SLIK5	85.5
mycBioID2	3	SMAP1	47.93
mycBioID2tau	1	SMAP1	41.78
mycBioID2tau	2	SMAP1	36.53
mycBioID2	1	SMHD1	60.35
mycBioID2	2	SMHD1	76.43

mycBioID2	3	SMHD1	74.61
mycBioID2	4	SMHD1	41.91
mycBioID2	1	SNAG	72.45
mycBioID2	3	SNAG	56.64
mycBioID2tau	1	SNAG	89.21
mycBioID2tau	2	SNAG	79.29
mycBioID2	1	SNP25	40.6
mycBioID2	1	SNP25	39.53
mycBioID2	1	SNP25	44.26
mycBioID2	2	SNP25	41.53
mycBioID2	3	SNP25	53.8
mycBioID2	3	SNP25	68.62
mycBioID2	3	SNP25	51.07
mycBioID2tau	4	SPAST	42.51
mycBioID2tau	4	SPAST	42.51
mycBioID2tau	5	SPAST	48.81
mycBioID2tau	5	SPAST	48.81
mycBioID2	3	SPEG	42.18
mycBioID2	2	SPKAP	48
mycBioID2	3	SPKAP	58.33
mycBioID2	1	SPTB2	59.13
mycBioID2	1	SPTB2	71.2
mycBioID2	2	SPTB2	70.95
mycBioID2	2	SPTB2	81.28
mycBioID2	3	SPTB2	86.69
mycBioID2	3	SPTB2	78.69
mycBioID2tau	2	SPTB2	38.82
mycBioID2	1	SPTN1	69.61
mycBioID2	2	SPTN1	41.34
mycBioID2	2	SPTN1	53.44
mycBioID2	2	SPTN1	67.54
mycBioID2	3	SPTN1	53.31
mycBioID2	3	SPTN1	49.44
mycBioID2	3	SPTN1	82.47
mycBioID2	4	SPTN1	50.47
mycBioID2	4	SPTN1	44.65
mycBioID2	5	SPTN1	44.77
mycBioID2tau	1	SPTN1	45.48
mycBioID2tau	2	SPTN1	57.68
mycBioID2tau	2	SPTN1	51.18
mycBioID2tau	2	SPTN1	44.32
mycBioID2tau	2	SPTN1	69.21
mycBioID2tau	4	SPTN1	40.6
mycBioID2tau	5	SPTN1	52.68
mycBioID2tau	5	SPTN1	47.07
mycBioID2tau	5	SPTN1	63.67
mycBioID2	1	SRBS1	64.45
mycBioID2	2	SRBS1	60.31

mycBioID2	2	SRBS1	46.78
mycBioID2	3	SRBS1	43.4
mycBioID2	3	SRBS1	57.27
mycBioID2tau	5	SRBS1	47.28
mycBioID2tau	5	SRBS1	47.28
mycBioID2	3	SRBS2	73.6
mycBioID2	1	SRC8	76.14
mycBioID2	1	SRC8	48.23
mycBioID2	1	SRC8	65.36
mycBioID2	1	SRC8	102.48
mycBioID2	1	SRC8	57.32
mycBioID2	1	SRC8	46.57
mycBioID2	2	SRC8	76.77
mycBioID2	2	SRC8	63.45
mycBioID2	2	SRC8	50.4
mycBioID2	2	SRC8	63.86
mycBioID2	2	SRC8	44.81
mycBioID2	2	SRC8	62.65
mycBioID2	2	SRC8	107.66
mycBioID2	2	SRC8	43.11
mycBioID2	2	SRC8	54.13
mycBioID2	3	SRC8	43.92
mycBioID2	3	SRC8	72.77
mycBioID2	3	SRC8	64.53
mycBioID2	3	SRC8	64.98
mycBioID2	3	SRC8	43.47
mycBioID2	3	SRC8	51.62
mycBioID2	3	SRC8	51.85
mycBioID2	3	SRC8	69.44
mycBioID2	3	SRC8	63.95
mycBioID2	3	SRC8	115.83
mycBioID2	3	SRC8	62.26
mycBioID2	3	SRC8	53.41
mycBioID2	3	SRC8	49.16
mycBioID2	3	SRC8	54.82
mycBioID2	3	SRC8	62.7
mycBioID2	3	SRC8	39.66
mycBioID2	3	SRC8	76.83
mycBioID2	4	SRC8	55.13
mycBioID2	4	SRC8	44.4
mycBioID2	4	SRC8	40.58
mycBioID2tau	1	SRC8	42.73
mycBioID2tau	1	SRC8	80.4
mycBioID2tau	1	SRC8	68.76
mycBioID2tau	1	SRC8	69.02
mycBioID2tau	1	SRC8	51.2
mycBioID2tau	1	SRC8	44.98
mycBioID2tau	1	SRC8	65.41

mycBioID2tau	2	SRC8	70.13
mycBioID2tau	2	SRC8	87.29
mycBioID2tau	2	SRC8	74.44
mycBioID2tau	2	SRC8	46.75
mycBioID2tau	2	SRC8	95.73
mycBioID2tau	2	SRC8	111.37
mycBioID2tau	2	SRC8	47.95
mycBioID2tau	2	SRC8	70.52
mycBioID2tau	2	SRC8	51.1
mycBioID2tau	2	SRC8	50.72
mycBioID2tau	5	SRC8	58.29
mycBioID2tau	5	SRC8	52.87
mycBioID2tau	5	SRC8	115.96
mycBioID2tau	5	SRC8	58.29
mycBioID2tau	5	SRC8	52.87
mycBioID2tau	5	SRC8	115.96
mycBioID2	1	SRCN1	58.26
mycBioID2	1	SRCN1	68.44
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mycBioID2	1	SRCN1	68.44
mycBioID2	2	SRCN1	50.91
mycBioID2	2	SRCN1	42.99
mycBioID2	2	SRCN1	81.1
mycBioID2	2	SRCN1	63.68
mycBioID2	3	SRCN1	56.39
mycBioID2	3	SRCN1	85.25
mycBioID2	3	SRCN1	68.12
mycBioID2	3	SRCN1	56.82
mycBioID2	3	SRCN1	40.25
mycBioID2	3	SRCN1	42.67
mycBioID2	4	SRCN1	59.65
mycBioID2	5	SRCN1	81.01
mycBioID2tau	1	SRCN1	43.24
mycBioID2tau	1	SRCN1	73.15
mycBioID2tau	1	SRCN1	57.61
mycBioID2tau	2	SRCN1	53.9
mycBioID2tau	2	SRCN1	58.35
mycBioID2tau	2	SRCN1	54.06
mycBioID2tau	4	SRCN1	64.55
mycBioID2tau	4	SRCN1	64.55
mycBioID2tau	4	SRCN1	64.55
mycBioID2tau	5	SRCN1	85.03
mycBioID2tau	5	SRCN1	85.03
mycBioID2tau	5	SRCN1	85.03
mycBioID2	1	SRRM2	66.25
mycBioID2	3	STAM1	63.96
mycBioID2tau	2	STAM1	50.8
mycBioID2tau	2	STAR5	41.92

mycBioID2	3	STAT1	101.6
mycBioID2tau	2	STAT1	71.15
mycBioID2	1	STAU2	58.42
mycBioID2	3	STAU2	66.25
mycBioID2	1	STIP1	77.03
mycBioID2	2	STIP1	68.26
mycBioID2	1	STMN1	54.52
mycBioID2	1	STMN1	55.3
mycBioID2	1	STMN1	58.77
mycBioID2	2	STMN1	51.93
mycBioID2	2	STMN1	85.76
mycBioID2	3	STMN1	42.48
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mycBioID2	3	STMN1	41.16
mycBioID2	3	STMN1	94.16
mycBioID2	4	STMN1	43.7
mycBioID2tau	1	STMN1	42.5
mycBioID2tau	1	STMN1	83.76
mycBioID2tau	1	STMN1	59.07
mycBioID2tau	2	STMN1	46.2
mycBioID2tau	2	STMN1	52.58
mycBioID2tau	2	STMN1	112.44
mycBioID2tau	4	STMN1	44.08
mycBioID2tau	4	STMN1	44.08
mycBioID2tau	4	STMN1	44.08
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mycBioID2tau	5	STMN1	54.32
mycBioID2	3	STRN	86.54
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mycBioID2	1	SYGP1	43.78
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mycBioID2	2	SYGP1	147.9
mycBioID2	3	SYGP1	41.71
mycBioID2	3	SYGP1	46.85
mycBioID2	3	SYGP1	89.07
mycBioID2	3	SYGP1	45.93
mycBioID2	3	SYGP1	112.51
mycBioID2	3	SYGP1	71.74
mycBioID2	2	SYN1	42.09
mycBioID2	2	SYN1	66.93
mycBioID2	2	SYN1	70.8
mycBioID2	2	SYN1	96.12

mycBioID2	3	SYN1	63.85
mycBioID2	3	SYN1	74.03
mycBioID2	3	SYN1	134.92
mycBioID2	3	SYN1	70.98
mycBioID2	4	SYN1	64.45
mycBioID2tau	2	SYN1	55.86
mycBioID2tau	2	SYN1	55.6
mycBioID2	2	SYN2	49.89
mycBioID2	2	SYN2	44.74
mycBioID2	3	SYN2	56.18
mycBioID2	3	SYN2	50.97
mycBioID2tau	1	SYN2	39.71
mycBioID2tau	2	SYN2	42.03
mycBioID2tau	2	SYNC	42.13
mycBioID2	3	SYNJ1	48.39
mycBioID2tau	1	SYNJ1	72.69
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mycBioID2tau	2	SYNJ1	41.36
mycBioID2	1	SYNPO	73.94
mycBioID2	1	SYNPO	64
mycBioID2	1	SYNPO	42.84
mycBioID2	1	SYNPO	49.66
mycBioID2	1	SYNPO	51.19
mycBioID2	2	SYNPO	64.03
mycBioID2	3	SYNPO	43.45
mycBioID2	3	SYNPO	53.33
mycBioID2tau	1	SYNPO	44.41
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mycBioID2	2	SYUA	71.58
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mycBioID2	3	SYUA	74.86
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mycBioID2	3	SYUA	41
mycBioID2	4	SYUA	48.55
mycBioID2	4	SYUA	47.91
mycBioID2	5	SYUA	62.62
mycBioID2	5	SYUA	45.86
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mycBioID2tau	1	SYUA	63.74
mycBioID2tau	1	SYUA	81.05
mycBioID2tau	2	SYUA	52.26
mycBioID2tau	2	SYUA	48.55

mycBioID2tau	2	SYUA	79.29
mycBioID2tau	2	SYUA	78.01
mycBioID2tau	2	SYUA	50.56
mycBioID2tau	5	SYUA	56.68
mycBioID2tau	5	SYUA	56.68
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mycBioID2	1	SYUB	156.93
mycBioID2	1	SYUB	109.56
mycBioID2	2	SYUB	44.2
mycBioID2	2	SYUB	82.65
mycBioID2	2	SYUB	41.46
mycBioID2	2	SYUB	78.15
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mycBioID2	3	SYUB	81.77
mycBioID2	3	SYUB	75.93
mycBioID2	3	SYUB	102.7
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mycBioID2	5	SYUB	62.62
mycBioID2tau	1	SYUB	68.29
mycBioID2tau	1	SYUB	52.44
mycBioID2tau	1	SYUB	63.74
mycBioID2tau	1	SYUB	114.57
mycBioID2tau	1	SYUB	127
mycBioID2tau	1	SYUB	80.24
mycBioID2tau	2	SYUB	48.55
mycBioID2tau	2	SYUB	50.48
mycBioID2tau	2	SYUB	52.08
mycBioID2tau	2	SYUB	55.01
mycBioID2tau	2	SYUB	79.29
mycBioID2tau	2	SYUB	43.15
mycBioID2tau	2	SYUB	65.19
mycBioID2tau	2	SYUB	40.37
mycBioID2tau	2	SYUB	79.9
mycBioID2tau	2	SYUB	41.66
mycBioID2tau	2	SYUB	49.58
mycBioID2tau	4	SYUB	89.75

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mycBioID2tau	4	SYUB	58.15
mycBioID2tau	5	SYUB	72.1
mycBioID2tau	5	SYUB	41.27
mycBioID2tau	5	SYUB	102.89
mycBioID2tau	5	SYUB	80.72
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mycBioID2	3	SYVC	59.35
mycBioID2	1	TAGL3	106.76
mycBioID2	1	TAGL3	73.78
mycBioID2	2	TAGL3	78.39
mycBioID2	3	TAGL3	118.62
mycBioID2	3	TAGL3	83.85
mycBioID2	3	TAGL3	99.35
mycBioID2	3	TAGL3	62.94
mycBioID2tau	1	TAGL3	111.12
mycBioID2tau	1	TAGL3	48.16
mycBioID2tau	1	TAGL3	64.71
mycBioID2tau	1	TAGL3	78.24
mycBioID2tau	1	TAGL3	41.97
mycBioID2tau	2	TAGL3	108.73
mycBioID2tau	2	TAGL3	44.46
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mycBioID2tau	4	TAGL3	77.65
mycBioID2tau	4	TAGL3	77.65
mycBioID2tau	4	TAGL3	77.65
mycBioID2tau	4	TAGL3	77.65
mycBioID2tau	5	TAGL3	68.75
mycBioID2tau	5	TAGL3	42.85
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mycBioID2tau	5	TAGL3	68.75
mycBioID2tau	5	TAGL3	42.85
mycBioID2tau	5	TAGL3	68.75
mycBioID2tau	5	TAGL3	42.85
mycBioID2	2	TANC1	46
mycBioID2	2	TANC1	69.94
mycBioID2	3	TANC1	63.17
mycBioID2tau	1	TANC1	49.82
mycBioID2tau	2	TANC1	50.87
mycBioID2	1	TANC2	50.97
mycBioID2	2	TANC2	50.76
mycBioID2	3	TANC2	60.41
mycBioID2	3	TANC2	45.59
mycBioID2tau	1	TANC2	67.47

mycBioID2tau	1	TANC2	46.15
mycBioID2tau	2	TANC2	62.84
mycBioID2	6	TB10B	37.82
mycBioID2	6	TB10B	38.27
mycBioID2tau	5	TB10B	36.33
mycBioID2tau	5	TB10B	51.44
mycBioID2	1	TB182	78.14
mycBioID2	3	TB182	64.67
mycBioID2	3	TB182	81.16
mycBioID2	4	TB182	34.53
mycBioID2	6	TB182	84.24
mycBioID2	6	TB182	47.66
mycBioID2	6	TB182	89.72
mycBioID2tau	4	TB182	79.99
mycBioID2tau	4	TB182	41.61
mycBioID2tau	5	TBA1A	52.27
mycBioID2tau	4	TBC21	44.74
mycBioID2tau	4	TBC21	44.74
mycBioID2tau	5	TBC21	40.24
mycBioID2tau	5	TBC21	40.5
mycBioID2tau	5	TBC21	40.5
mycBioID2	3	TBCB	41.27
mycBioID2	6	TBCB	60.78
mycBioID2tau	5	TBCB	60.33
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mycBioID2	6	TCOF	39.76
mycBioID2	3	TCP4	80.67
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mycBioID2	6	TCP4	71.66
mycBioID2	6	TCPE	82.27
mycBioID2	1	TM1L2	66.85
mycBioID2	6	TM1L2	60.94
mycBioID2tau	4	TM1L2	48.06
mycBioID2tau	5	TM1L2	49.04
mycBioID2tau	5	TMOD2	40.15
mycBioID2	3	TNR6B	63.3
mycBioID2	6	TNR6B	50.28
mycBioID2	1	TPPP	55.15
mycBioID2	1	TPPP	46.45
mycBioID2	3	TPPP	64.85
mycBioID2	6	TPPP	50.95
mycBioID2	6	TPPP	81.58
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mycBioID2tau	4	TPPP	65.33
mycBioID2tau	4	TPPP	53.97
mycBioID2tau	4	TPPP	40.63
mycBioID2tau	4	TPPP	99.89
mycBioID2tau	4	TPPP	45.48

mycBioID2tau	5	TPPP	36.18
mycBioID2tau	5	TPPP	55.02
mycBioID2tau	5	TPPP	60.75
mycBioID2tau	5	TPPP	43.77
mycBioID2tau	5	TPPP	64.46
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mycBioID2tau	5	TPPP	40.99
mycBioID2tau	5	TPPP	40.3
mycBioID2tau	5	TPPP	46.6
mycBioID2tau	5	TPPP	79.95
mycBioID2tau	5	TPPP	42.37
mycBioID2	3	TR150	79.22
mycBioID2	1	TRIM9	39.62
mycBioID2	3	TRIM9	48.95
mycBioID2	1	VAMP1	60.94
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mycBioID2	3	VAMP2	53.21
mycBioID2	3	VAMP2	52.21
mycBioID2	4	VAMP2	56.78
mycBioID2	4	VAMP2	55.03
mycBioID2	5	VAMP2	50.57
mycBioID2	6	VAMP2	61.19
mycBioID2	6	VAMP2	44.87
mycBioID2	6	VAMP2	53.09
mycBioID2	6	VAMP2	50.36
mycBioID2	6	VAMP2	46.19
mycBioID2tau	4	VAMP2	61.37
mycBioID2tau	5	VAMP2	51.83
mycBioID2tau	5	VAMP2	58.89
mycBioID2tau	5	VAMP2	47.59
mycBioID2tau	5	VAMP2	47.59
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mycBioID2	6	VAPB	87.82
mycBioID2	6	VATC1	58.37
mycBioID2	3	VATF	48.04
mycBioID2tau	5	VATF	45.52
mycBioID2	1	VCIP1	75.67
mycBioID2	1	VCIP1	120.74
mycBioID2	6	VCIP1	55.47
mycBioID2tau	4	VCIP1	51.11
mycBioID2tau	5	VCIP1	57.9
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mycBioID2	3	VIAAT	70.69
mycBioID2	3	VIAAT	64.93
mycBioID2	3	VIAAT	48.44
mycBioID2	4	VIAAT	43.53

mycBioID2	6	VIAAT	42.27
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mycBioID2tau	4	VIAAT	88.69
mycBioID2tau	4	VIAAT	79.83
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mycBioID2tau	5	VIAAT	80.19
mycBioID2	6	VIGLN	66.11
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mycBioID2tau	5	VMA5A	40.5
mycBioID2tau	5	VMA5A	46.14
mycBioID2	6	VP13C	46.61
mycBioID2tau	4	VP13C	63.15
mycBioID2tau	5	VPS25	43.95
mycBioID2	3	VPS36	43.27
mycBioID2	6	VPS36	56.87
mycBioID2tau	4	VPS36	64.22
mycBioID2	6	WASC5	67.37
mycBioID2tau	5	WASC5	57.11
mycBioID2	3	WIPF2	73.46
mycBioID2	6	WIPF2	94.33
mycBioID2tau	5	WIPF2	65.76
mycBioID2tau	5	WIPF2	41.86
mycBioID2tau	5	WIPF2	59.61
mycBioID2	3	WIPF3	36.33
mycBioID2	6	WIPF3	83.33
mycBioID2	6	WIPF3	89.22
mycBioID2tau	4	WIPF3	92.6
mycBioID2tau	5	WIPF3	63.29
mycBioID2tau	5	WIPF3	108.36
mycBioID2	3	WNK2	55.13
mycBioID2	3	XRN1	54.98
mycBioID2	3	ZCH18	44.66
mycBioID2	6	ZCH18	59.54

ampus of tau knock-out (-/-) mice harvest

xperimental and BioID2 control.

Biotinylated Peptide Sequence
TVKGGISETR
VVIFQQEQENKIQSHSR
VAEDEFDPIPVLITKNTQGGHSR
VAEDEFDPIPVLITKNTQGGHSR
VAEDEFDPIPVLITKNTQGGHSR
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VAEDEFDPIPVLITKNTQGGHSR
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TLEPVKPPTVPNDYMTSPAR
VSTQNMKMGGLPR
VDNEILNYKDLAALPK
SHYLADSDPLISKSASLPAYR
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EYFTFPASKSQDR
WKTPAAVLPTPVAVSQPIR

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GPSYSKGSVSATPVQGSVPEGKPIR
KGQEGFFPANHVASETLYR
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ILSSTASKVSSAGLSLK
KTGKSATEESTSSSQK
VGEGFEETLGEAVISTKK
KVFGDSSR
TGKSATEESTSSSQK
KTGKSATEESTSSSQK
KTGKSATEESTSSSQK
ILSSTASKVSSAGLSLK
ILSSTASKVSSAGLSLK
KTGKSATEESTSSSQK
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TSKVGEGFEETLGEAVISTK
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SSTSSKAER
TPEKPAPGSATGKHEK
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:ed at age 6 m.o.

Biotinylated Lysine (K = '1')
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Table 12 **High recovery of biotinylated proteins with probable e**
Three representative MS samples showing a total of 78 identified

Sample	AAV condition	MWM biotin	Protein
1	pRAM-MiniTtauWT	d1-6	AAK1_MOUSE
2	pSyn1-MnTid	d1-6	AAK1_MOUSE
1	pRAM-MiniTtauWT	d1-6	ANR35_MOUSE
2	pSyn1-MnTid	d1-6	CFTR_MOUSE
1	pRAM-MiniTtauWT	d1-6	CLAP2_MOUSE
3	pRAM-MiniTtauWT	d3-6	F16B1_MOUSE
1	pRAM-MiniTtauWT	d1-6	F16B1_MOUSE
3	pRAM-MiniTtauWT	d3-6	HIBCH_MOUSE
3	pRAM-MiniTtauWT	d3-6	ICAM1_MOUSE
1	pRAM-MiniTtauWT	d1-6	ICAM1_MOUSE
2	pSyn1-MnTid	d1-6	ICAM1_MOUSE
3	pRAM-MiniTtauWT	d3-6	MAP6_MOUSE
3	pRAM-MiniTtauWT	d3-6	MAP6_MOUSE
3	pRAM-MiniTtauWT	d3-6	MAP6_MOUSE
3	pRAM-MiniTtauWT	d3-6	MAP6_MOUSE
3	pRAM-MiniTtauWT	d3-6	MAP6_MOUSE
1	pRAM-MiniTtauWT	d1-6	MAP6_MOUSE
1	pRAM-MiniTtauWT	d1-6	MAP6_MOUSE
1	pRAM-MiniTtauWT	d1-6	MAP6_MOUSE
1	pRAM-MiniTtauWT	d1-6	MAP6_MOUSE
1	pRAM-MiniTtauWT	d1-6	MAP6_MOUSE
1	pRAM-MiniTtauWT	d1-6	MAP6_MOUSE
1	pRAM-MiniTtauWT	d1-6	MCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	MCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	MCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	MCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	MCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	MCCA_MOUSE
2	pSyn1-MnTid	d1-6	MCCA_MOUSE
2	pSyn1-MnTid	d1-6	MCCA_MOUSE
2	pSyn1-MnTid	d1-6	MCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	MINK1_MOUSE
1	pRAM-MiniTtauWT	d1-6	MINK1_MOUSE
2	pSyn1-MnTid	d1-6	MINK1_MOUSE
2	pSyn1-MnTid	d1-6	MINK1_MOUSE
3	pRAM-MiniTtauWT	d3-6	MTAP2_MOUSE
3	pRAM-MiniTtauWT	d3-6	MTAP2_MOUSE
3	pRAM-MiniTtauWT	d3-6	MTAP2_MOUSE
1	pRAM-MiniTtauWT	d1-6	MTAP2_MOUSE
1	pRAM-MiniTtauWT	d1-6	MTAP2_MOUSE
1	pRAM-MiniTtauWT	d1-6	MTAP2_MOUSE
1	pRAM-MiniTtauWT	d1-6	MTAP2_MOUSE
1	pRAM-MiniTtauWT	d1-6	MTAP2_MOUSE
1	pRAM-MiniTtauWT	d1-6	MTAP2_MOUSE

2	pSyn1-MnTid	d1-6	MTAP2_MOUSE
1	pRAM-MiniTtauWT	d1-6	NFM_MOUSE
1	pRAM-MiniTtauWT	d1-6	NFM_MOUSE
1	pRAM-MiniTtauWT	d1-6	NFM_MOUSE
3	pRAM-MiniTtauWT	d3-6	PCCA_MOUSE
3	pRAM-MiniTtauWT	d3-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PCCA_MOUSE
2	pSyn1-MnTid	d1-6	PCCA_MOUSE
2	pSyn1-MnTid	d1-6	PCCA_MOUSE
2	pSyn1-MnTid	d1-6	PCCA_MOUSE
1	pRAM-MiniTtauWT	d1-6	PLAP_MOUSE
1	pRAM-MiniTtauWT	d1-6	PLAP_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
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3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
3	pRAM-MiniTtauWT	d3-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE

1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
1	pRAM-MiniTtauWT	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	PYC_MOUSE
2	pSyn1-MnTid	d1-6	SHAN2_MOUSE
2	pSyn1-MnTid	d1-6	SHAN2_MOUSE
2	pSyn1-MnTid	d1-6	SHAN2_MOUSE
1	pRAM-MiniTtauWT	d1-6	SPTN1_MOUSE
2	pSyn1-MnTid	d1-6	SPTN1_MOUSE
2	pSyn1-MnTid	d1-6	SUGP2_MOUSE
2	pSyn1-MnTid	d1-6	SYNC_MOUSE
2	pSyn1-MnTid	d1-6	SYNC_MOUSE
2	pSyn1-MnTid	d1-6	SYNC_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUA_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUA_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUA_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUA_MOUSE
1	pRAM-MiniTtauWT	d1-6	SYUA_MOUSE
1	pRAM-MiniTtauWT	d1-6	SYUA_MOUSE
2	pSyn1-MnTid	d1-6	SYUA_MOUSE
2	pSyn1-MnTid	d1-6	SYUA_MOUSE
2	pSyn1-MnTid	d1-6	SYUA_MOUSE
2	pSyn1-MnTid	d1-6	SYUA_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE

3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
3	pRAM-MiniTtauWT	d3-6	SYUB_MOUSE
1	pRAM-MiniTtauWT	d1-6	SYUB_MOUSE
1	pRAM-MiniTtauWT	d1-6	SYUB_MOUSE
1	pRAM-MiniTtauWT	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE
2	pSyn1-MnTid	d1-6	SYUB_MOUSE

ndogenous origin.

biotinylated peptides (grey) with mitochondrial origin (grey) from 161 peptide hits (48.4%)

Protein description
AP2-associated protein kinase 1 OS=Mus musculus OX=10090 GN=Aak1 PE=1 SV=2
AP2-associated protein kinase 1 OS=Mus musculus OX=10090 GN=Aak1 PE=1 SV=2
Ankyrin repeat domain-containing protein 35 OS=Homo sapiens OX=9606 GN=ANKRD35 PI
Cystic fibrosis transmembrane conductance regulator OS=Sus scrofa OX=9823 GN=CFTR PI
CLIP-associating protein 2 OS=Mus musculus OX=10090 GN=Clasp2 PE=1 SV=1
Protein FAM160B1 OS=Homo sapiens OX=9606 GN=FAM160B1 PE=1 SV=1
Protein FAM160B1 OS=Homo sapiens OX=9606 GN=FAM160B1 PE=1 SV=1
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Bos taurus OX=9913 GN=HIBCH PE=
Intercellular adhesion molecule 1 OS=Rattus norvegicus OX=10116 GN=Icam1 PE=2 SV=1
Intercellular adhesion molecule 1 OS=Rattus norvegicus OX=10116 GN=Icam1 PE=2 SV=1
Intercellular adhesion molecule 1 OS=Rattus norvegicus OX=10116 GN=Icam1 PE=2 SV=1
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Microtubule-associated protein 6 OS=Mus musculus OX=10090 GN=Map6 PE=1 SV=2
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Mus musculus OX=1009
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Mus musculus OX=1009
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Rattus norvegicus OX=1(
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Rattus norvegicus OX=1(
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens OX=9606
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens OX=9606
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Mus musculus OX=1009
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens OX=9606
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Rattus norvegicus OX=1(
Misshapen-like kinase 1 OS=Mus musculus OX=10090 GN=Mink1 PE=1 SV=3
Misshapen-like kinase 1 OS=Rattus norvegicus OX=10116 GN=Mink1 PE=1 SV=2
Misshapen-like kinase 1 OS=Mus musculus OX=10090 GN=Mink1 PE=1 SV=3
Misshapen-like kinase 1 OS=Rattus norvegicus OX=10116 GN=Mink1 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
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Microtubule-associated protein 2 OS=Mus musculus OX=10090 GN=Map2 PE=1 SV=2
Neurofilament medium polypeptide OS=Mus musculus OX=10090 GN=Nefm PE=1 SV=4
Neurofilament medium polypeptide OS=Rattus norvegicus OX=10116 GN=Nefm PE=1 SV=4
Neurofilament medium polypeptide OS=Bos taurus OX=9913 GN=NEFM PE=1 SV=3
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus OX=10090 GN=Pc
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Rattus norvegicus OX=10116 GN
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus OX=10090 GN=Pc
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens OX=9606 GN=PC
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Sus scrofa OX=9823 GN=PCCA
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Rattus norvegicus OX=10116 GN
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus OX=10090 GN=Pc
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens OX=9606 GN=PC
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Sus scrofa OX=9823 GN=PCCA
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Rattus norvegicus OX=10116 GN
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus OX=10090 GN=Pc
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus OX=10090 GN=Pc
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus OX=10090 GN=Pc
Phospholipase A-2-activating protein OS=Mus musculus OX=10090 GN=Plaa PE=1 SV=4
Phospholipase A-2-activating protein OS=Rattus norvegicus OX=10116 GN=Plaa PE=1 SV=
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
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Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
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Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
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Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1

Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
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Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
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Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Mus musculus OX=10090 GN=Pc PE=1 SV=1
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
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Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=2
SH3 and multiple ankyrin repeat domains protein 2 OS=Mus musculus OX=10090 GN=Shan
SH3 and multiple ankyrin repeat domains protein 2 OS=Homo sapiens OX=9606 GN=SHANI
SH3 and multiple ankyrin repeat domains protein 2 OS=Rattus norvegicus OX=10116 GN=SI
Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus OX=10090 GN=Sptan1 PE=1 SV
Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus OX=10090 GN=Sptan1 PE=1 SV
SURP and G-patch domain-containing protein 2 OS=Mus musculus OX=10090 GN=Sugp2 P
Asparagine--tRNA ligase, cytoplasmic OS=Mus musculus OX=10090 GN=NARS1 PE=1 SV=
Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=NARS1 PE=1 SV=1
Asparagine--tRNA ligase, cytoplasmic OS=Macaca fascicularis OX=9541 GN=NARS1 PE=2
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca PE=1 SV=2
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca PE=1 SV=2
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Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca PE=1 SV=2
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Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=Snca PE=1 SV=1
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=Snca PE=1 SV=1
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb PE=1 SV=1
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb PE=1 SV=1

Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb PE=1 SV=1
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=1 SV=1
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Beta-synuclein OS=Rattus norvegicus OX=10116 GN=Sncb PE=1 SV=1

Peptide Score	Biotinylated Peptide Sequence	PTM modifi	Biotinylated Lysine (K
55.86	VAEDEFDPIPVLITKNTQGGHSR	Biotin (K)	0.00000000000000100
82.58	VAEDEFDPIPVLITKNTQGGHSR	Biotin (K)	0.00000000000000100
40.09	LASRKSARPTK	Biotin (K)	0.00000000001.0
39.45	ACLVVLCLLKK	Biotin (K)	0.00000000001.0
77.73	AGGDAADGSQPALDNKASLLHSI	Biotin (K)	0.00000000000000010
39.61	SPKALEK	Biotin (K)	0.0010000.0
39.37	SPKALEK	Biotin (K)	0.0010000.0
47.92	QLKKWEQDPK	Biotin (K)	0.0010000000.0
45.76	LQKAQEEALKLKVQA	Biotin (K)	0.000000000001000.0
44.88	LQKAQEEALKLKVQA	Biotin (K)	0.000000000001000.0
49.12	LQKAQEEALKLKVQA	Biotin (K)	0.000000000001000.0
40.7	PIIPVPLKGQDPLVPAPTK	Biotin (K)	0.00000001000000000
58.64	DQGAVLLGPVKDLGPVAPAPIK	Biotin (K)	0.00000000001000000
96.1	DQGAVLLGPVKDLGPVAPAPIK	Biotin (K)	0.00000000001000000
41.63	NQDPIIPVPLKGQDPLVPAPTK	Biotin (K)	0.00000000001000000
51.1	NQDPIIPVPLKGQDPLVPAPTK	Biotin (K)	0.00000000001000000
48.21	YLKGHDSVFVAPVK	Biotin (K)	0.00100000000000.0
34.67	PIIPVPLKGQDPLVPAPTK	Biotin (K)	0.00000001000000000
110.85	DQGAVLLGPVKDLGPVAPAPIK	Biotin (K)	0.00000000001000000
64.57	DQGAVLLGPVKDLGPVAPAPIK	Biotin (K)	0.00000000001000000
50.74	DQGAVLLGPVKDLGPVAPAPIK	Biotin (K)	0.00000000001000000
76.58	GHDSVFVAPVKNQGPVIPEPVK	Biotin (K)	0.00000000001000000
43.94	KMEHTIK	Biotin (K)	0.1000000.0
68.35	IAMKMEHTIK	Biotin (K)	0.0001000000.0
43.94	KMEHTIK	Biotin (K)	0.1000000.0
68.35	IAMKMEHTIK	Biotin (K)	0.0001000000.0
43.94	KMEHTIK	Biotin (K)	0.1000000.0
68.35	IAMKMEHTIK	Biotin (K)	0.0001000000.0
63.27	IAMKMEHTIK	Biotin (K)	0.0001000000.0
63.27	IAMKMEHTIK	Biotin (K)	0.0001000000.0
63.27	IAMKMEHTIK	Biotin (K)	0.0001000000.0
54.7	GINPADKPAWAR	Biotin (K)	0.000000100000.0
54.7	GINPADKPAWAR	Biotin (K)	0.000000100000.0
56.9	GINPADKPAWAR	Biotin (K)	0.000000100000.0
56.9	GINPADKPAWAR	Biotin (K)	0.000000100000.0
37.89	KLILKPAIK	2 Biotin (K)	0.100010000.0
27.68	LILKPAIK	Biotin (K)	0.00010000.0
48.95	KLILKPAIK	Biotin (K)	0.000010000.0
34.88	KLILKPAIK	2 Biotin (K)	0.100010000.0
37.28	LILKPAIK	Biotin (K)	0.00010000.0
52.12	KLILKPAIK	Biotin (K)	0.000010000.0
22.99	KLILKPAIK	Biotin (K)	0.000010000.0
24.03	KLILKPAIK	Biotin (K)	0.000010000.0
42.82	TPGTPKSGILVPSEK	Biotin (K)	0.000001000000000.0

56.55	VSDFGQMASGMNVDAGKAIELK	Biotin (K)	0.00000000000000001
49.17	YITKSVTVTQK	Biotin (K)	0.00010000000.0
49.17	YITKSVTVTQK	Biotin (K)	0.00010000000.0
49.17	YITKSVTVTQK	Biotin (K)	0.00010000000.0
51.04	KMQNSMTAGK	Biotin (K); C	0.1000030000.0
51.04	KMQNSMTAGK	Biotin (K); C	0.1000030000.0
88.75	KMQNSMTAGK	Biotin (K)	0.1000000000.0
88.75	KMQNSMTAGK	Biotin (K)	0.1000000000.0
88.75	KMQNSMTAGK	Biotin (K)	0.1000000000.0
88.75	KMQNSMTAGK	Biotin (K)	0.1000000000.0
75.88	KMQNSMTAGK	Biotin (K); C	0.1300000000.0
75.88	KMQNSMTAGK	Biotin (K); C	0.1300000000.0
75.88	KMQNSMTAGK	Biotin (K); C	0.1300000000.0
75.88	KMQNSMTAGK	Biotin (K); C	0.1300000000.0
88.29	KMQNSMTAGK	Biotin (K)	0.1000000000.0
50.02	KMQNSMTAGK	Biotin (K); C	0.1300000000.0
48.21	KMQNSMTAGK	Biotin (K); C	0.1300000000.0
65.67	SAASKTVNIYFPK	Biotin (K)	0.0000100000000.0
65.67	SAASKTVNIYFPK	Biotin (K)	0.0000100000000.0
82.99	KMETVVTSPMEGTIR	Biotin (K)	0.100000000000000.0
82.99	KMETVVTSPMEGTIR	Biotin (K)	0.100000000000000.0
58.23	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
75.78	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
97.14	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
47.2	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
58.23	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
75.78	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
97.14	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
47.2	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
50.5	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000
50.5	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000
56.25	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031000000
51.53	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
45.41	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
56.25	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031000000
51.53	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
45.41	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
77.3	KMETVVTSPMEGTIR	Biotin (K)	0.100000000000000.0
47.46	SAMKMETVVTSPMEGTIR	Biotin (K)	0.00010000000000000
77.3	KMETVVTSPMEGTIR	Biotin (K)	0.100000000000000.0
47.46	SAMKMETVVTSPMEGTIR	Biotin (K)	0.00010000000000000
45.43	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
55.46	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
45.43	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
55.46	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
45.91	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000
53.23	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
60.7	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000

45.91	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000
53.23	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
60.7	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000
46.12	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
45.7	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
47.53	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
46.12	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
45.7	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
47.53	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
45.14	KMETVVTSPMEGTIRK	Biotin (K)	0.1000000000000000.(
60.14	SAMKMETVVTSPMEGTIR	Biotin (K)	0.00010000000000000
45.14	KMETVVTSPMEGTIRK	Biotin (K)	0.1000000000000000.(
60.14	SAMKMETVVTSPMEGTIR	Biotin (K)	0.00010000000000000
58.95	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
68.74	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
58.95	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
68.74	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
79.41	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000
79.41	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031300000
59.48	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031000000
70.11	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031000000
63.79	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
51.71	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
59.48	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031000000
70.11	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000031000000
63.79	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001000000
51.71	GQPLCVLSAMKMETVVTSPMEG	Biotin (K); C	0.00002000001300000
60.27	IASKAVYVPAKPAR	Biotin (K)	0.00010000000000.0
60.27	IASKAVYVPAKPAR	Biotin (K)	0.00010000000000.0
60.27	IASKAVYVPAKPAR	Biotin (K)	0.00010000000000.0
40.68	TASPWKSAR	Biotin (K)	0.000001000.0
39.8	TASPWKSAR	Biotin (K)	0.000001000.0
56.21	LTDKNVGFQMLQK	Biotin (K)	0.0001000000000.0
44.75	KNLMFLVLR	Biotin (K)	0.100000000.0
44.75	KNLMFLVLR	Biotin (K)	0.100000000.0
44.75	KNLMFLVLR	Biotin (K)	0.100000000.0
51.39	EGVLYVGSKTK	Biotin (K)	0.00000000001.0
64.82	TKEGVLYVGSKTK	Biotin (K)	0.0000000000100.0
51.39	EGVLYVGSKTK	Biotin (K)	0.00000000001.0
64.82	TKEGVLYVGSKTK	Biotin (K)	0.0000000000100.0
73.57	TKEGVLYVGSK	Biotin (K)	0.01000000000.0
73.57	TKEGVLYVGSK	Biotin (K)	0.01000000000.0
47.72	QGVAEAAGKTK	Biotin (K)	0.00000000100.0
54.81	TKEGVLYVGSKTK	Biotin (K)	0.0000000000001.0
47.72	QGVAEAAGKTK	Biotin (K)	0.00000000100.0
54.81	TKEGVLYVGSKTK	Biotin (K)	0.0000000000001.0
72.8	QGVTEAAEKTK	Biotin (K)	0.00000000100.0
76.21	TKQGVTEAAEKTK	Biotin (K)	0.0000000000100.0

48.5	EGVLYVGSKTSGVVQGVASVAEK	Biotin (K)	0.000000001000000000
72.8	QGVTEAAEKTK	Biotin (K)	0.00000000100.0
51.39	EGVLYVGSKTK	Biotin (K)	0.00000000001.0
76.21	TKQGVTEAAEKTK	Biotin (K)	0.0000000000100.0
64.82	TKEGVLYVGSKTK	Biotin (K)	0.0000000000100.0
72.8	QGVTEAAEKTK	Biotin (K)	0.00000000100.0
51.39	EGVLYVGSKTK	Biotin (K)	0.00000000001.0
76.21	TKQGVTEAAEKTK	Biotin (K)	0.0000000000100.0
64.82	TKEGVLYVGSKTK	Biotin (K)	0.0000000000100.0
45.6	QGVTEAAEKTK	Biotin (K)	0.00000000100.0
73.57	TKEGVLYVGSK	Biotin (K)	0.01000000000.0
81.4	TKQGVTEAAEKTK	Biotin (K)	0.0000000000001.0
70.61	QGVTEAAEKTK	Biotin (K)	0.00000000100.0
73.79	TKQGVTEAAEKTK	Biotin (K)	0.0000000000100.0
73.41	EGVLYVGSKTSGVVQGVASVAEK	Biotin (K)	0.000000001000000000
70.61	QGVTEAAEKTK	Biotin (K)	0.00000000100.0
73.79	TKQGVTEAAEKTK	Biotin (K)	0.0000000000100.0
54.81	TKEGVLYVGSKTK	Biotin (K)	0.0000000000001.0
70.61	QGVTEAAEKTK	Biotin (K)	0.00000000100.0
73.79	TKQGVTEAAEKTK	Biotin (K)	0.0000000000100.0
54.81	TKEGVLYVGSKTK	Biotin (K)	0.0000000000001.0

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Table 13 **Lower recovery of biotinylated proteins with endogenous origin from cytosolic fr**

Representative cytosolic fraction MS sample showing a total of 10 (grey) identified biotinylated peptide

MS Sample	AAV condition	MWM biotin	Protein	tein descrip	Peptide Scor
F004707-3	RAM-MiniTid cytosolic	ALBU_MOUSE	Albumin OS=	45.96	0.026
F004707-3	RAM-MiniTid cytosolic	ALBU_MOUSE	Albumin OS=	45.61	0.03
F004707-3	RAM-MiniTid cytosolic	ALBU_MOUSE	Albumin OS=	41.61	0.067
F004707-3	RAM-MiniTid cytosolic	ALBU_MOUSE	Albumin OS=	66.74	0.00024
F004707-3	RAM-MiniTid cytosolic	E41L1_MOUSE	Band 4.1-like	83.79	4.10E-06
F004707-3	RAM-MiniTid cytosolic	E41L1_MOUSE	Band 4.1-like	54.15	0.0032
F004707-3	RAM-MiniTid cytosolic	H90B3_MOUSE	Putative heat	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS904_MOUSE	Putative heat	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90A_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90A_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90A_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90B_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90B_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90B_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90B_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90B_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90B_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	HS90B_MOUSE	Heat shock p	46.79	0.0069
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	63.2	0.0003
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	54.23	0.0019
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	96.72	1.60E-07
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	63.27	0.0003
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	60.6	0.00076
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	54.23	0.0019
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	54.23	0.0019
F004707-3	RAM-MiniTid cytosolic	PEA15_MOUSE	Astrocytic ph	63.42	0.00033
F004707-3	RAM-MiniTid cytosolic	PEA15_MOUSE	Astrocytic ph	40.11	0.073
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	68.64	0.00015
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	68.64	0.00015
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	67.96	0.00012
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	67.96	0.00012
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	66.23	0.00027
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	66.23	0.00027
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	64.99	0.00035
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	64.99	0.00035
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	46.93	0.021
F004707-3	RAM-MiniTid cytosolic	PYC_MOUSE	Pyruvate car	46.93	0.021
F004707-3	RAM-MiniTid cytosolic	SYUA_MOUSE	Alpha-synucl	42.24	0.033
F004707-3	RAM-MiniTid cytosolic	SYUA_MOUSE	Alpha-synucl	42.24	0.033
F004707-3	RAM-MiniTid cytosolic	SYUA_MOUSE	Alpha-synucl	42.24	0.033
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	153.2	4.00E-13
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	153.2	4.00E-13
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	153.2	4.00E-13
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	67.01	0.00016
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	52.39	0.0035
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	52.39	0.0035
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	52.39	0.0035
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	45.76	0.021

F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	45.76	0.021
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	45.76	0.021
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	37.42	0.13
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	37.42	0.13
F004707-3	RAM-MiniTid cytosolic	SYUB_MOUSE	Beta-synucle	37.42	0.13
F004707-3	RAM-MiniTid cytosolic	AT1A2_MOUSE	Sodium/potas	40.01	0.0091
F004707-3	RAM-MiniTid cytosolic	AT1A2_PIG	Sodium/potas	40.01	0.0091
F004707-3	RAM-MiniTid cytosolic	MTAP2_HUMAN	Microtubule-a	39.97	0.037
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	39.97	0.037
F004707-3	RAM-MiniTid cytosolic	MTAP2_MOUSE	Microtubule-a	39.97	0.037

raction.

s with mitochondrial origin (grey) from 58 peptide hits (17.2%)

Biotinylated	PTM modifi	Biotinylated Lysine (K = '1')
RHPYFYAPE	Biotin (K)	0.00000000000000000100.0
RHPYFYAPE	Biotin (K)	0.00000000000000000100.0
RHPYFYAPE	Biotin (K)	0.00000000000000000100.0
CIAEVEKDA	Biotin (K); 2 (	0.2000001000000000000000000000020.0
SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IMKAQALR	Biotin (K)	0.00100000.0
IEGVGAATS	Biotin (K); Ox	0.000000000000300000100000.0
NKDDLTLSF	Biotin (K)	0.010000000.0
NKLEGAGS/	Biotin (K); Ox	0.000000000000000000000100300.0
LEGAGSAT\	Biotin (K); Ox	0.000000000000300000100000.0
TADKNKLEG	Biotin (K); Ox	0.000000000000000000000000100300.0
NKDDLTLSF	Biotin (K)	0.010000000.0
NKDDLTLSF	Biotin (K)	0.010000000.0
ISEEEELDTI	Biotin (K)	0.0000000001000.0
ISEEEELDTI	Biotin (K)	0.0000000001000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000.0
KMETVVTSF	Biotin (K); 2 (	0.130000000300000.0
KMETVVTSF	Biotin (K); 2 (	0.130000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000300000.0
QGVAEAAG	Biotin (K)	0.00000000100.0
QGVAEAAG	Biotin (K)	0.00000000100.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKEQASHLC	Biotin (K)	0.010000000000000000000000000.0
TKEQASHLC	Biotin (K)	0.010000000000000000000000000.0
TKEQASHLC	Biotin (K)	0.010000000000000000000000000.0
EGVLYVGSI	Biotin (K)	0.000000001000000000000.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
GLSMAKEG\	Biotin (K); Ox	0.000301000000000.0

GLSMAKEG'	Biotin (K); O›	0.000301000000000.0
GLSMAKEG'	Biotin (K); O›	0.000301000000000.0
GLSMAKEG'	Biotin (K); O›	0.000301000000000.0
GLSMAKEG'	Biotin (K); O›	0.000301000000000.0
GLSMAKEG'	Biotin (K); O›	0.000301000000000.0
VMKGAPER	Biotin (K); O›	0.0300000000000000000001.0
VMKGAPER	Biotin (K); O›	0.0300000000000000000001.0
DLHSKNKDI	Biotin (K)	0.00001000000000.0
DLHSKNKDI	Biotin (K)	0.00001000000000.0
DLHSKNKDI	Biotin (K)	0.00001000000000.0

Table 14 **Maximal recovery of biotinyla**

Representative mitochondrial fraction MS s

MS Sample	AV conditio	MWM biotin
F004706-2	RAM-MnTid	PYC_MOUSE
F004706-2	RAM-MnTid	PYC_MOUSE
F004706-2	RAM-MnTid	PYC_MOUSE
F004706-2	RAM-MnTid	PYC_MOUSE
F004706-2	RAM-MnTid	PCCA_MOUSE
F004706-2	RAM-MnTid	PCCA_MOUSE
F004706-2	RAM-MnTid	PYC_MOUSE
F004706-2	RAM-MnTid	PYC_MOUSE
F004706-2	RAM-MnTid	PYC_MOUSE
F004706-2	RAM-MnTid	TRI41_MOUSE
F004706-2	RAM-MnTid	TRI41_MOUSE
F004706-2	RAM-MnTid	PYC_MOUSE

ıted proteins with endogenous origin from mitochondrial fraction.

sample showing a total of 10 (grey) identified biotinylated peptides with mitochondı

Protein	tein descrip	eptide Scor
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	62.86	0.0004
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	58.41	0.0016
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	47.95	0.018
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	45.27	0.035
Propionyl-CoA carboxylase alpha chain, mitochondrial OS	42.87	0.021
Propionyl-CoA carboxylase alpha chain, mitochondrial OS	42.87	0.021
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	22.99	5.5
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	21.45	8.4
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	18.75	11
E3 ubiquitin-protein ligase TRIM41 OS=Homo sapiens OX	17.31	14
E3 ubiquitin-protein ligase TRIM41 OS=Mus musculus OX	17.31	14
Pyruvate carboxylase, mitochondrial OS=Rattus norvegicı	14.21	42

rial origin (grey) from 12 peptide hits (83.3%)

Biotinylate	PTM modifi	Biotinylated Lysine (K = '1')
KMETVVTS	Biotin (K)	0.100000000000000.0
GQPLCVLS	Biotin (K); C	0.000020000013000000000000.0
GQPLCVLS	Biotin (K); C	0.000020000313000000000000.0
GQPLCVLS	Biotin (K); C	0.0000200000100000000000000.0
KMQNSMT/	Biotin (K)	0.1000000000.0
KMQNSMT/	Biotin (K)	0.1000000000.0
GQPLCVLS	Biotin (K); C	0.000020000013000000000000.0
GQPLCVLS	Biotin (K); C	0.0000200000100000000000000.0
KMETVVTS	Biotin (K)	0.100000000000000.0
VVPLEEVV	Biotin (K)	0.000000000001.0
VVPLEEVV	Biotin (K)	0.000000000001.0
GQPLCVLS	Biotin (K); C	0.000020000013000000000000.0

Table 15 **Total peptides list for AAV.RAM-MiniTid-tau rAAVs in the encoding-consolidatio**

n=12, pep = 536, pro = 100, non-overlapping = 62

rAAV	Sample	Biotin	Protein Accession	Protein Des	Peptide Scor	ptide Sequer
RAM-MiniTid	8	d1-4	AAK1_MOUSE	AP2-associa	116.12	VAEDEFDPI
RAM-MiniTid	9	d1-4	AAK1_MOUSE	AP2-associa	77.87	VAEDEFDPI
RAM-MiniTid	12	d1-4	AAK1_MOUSE	AP2-associa	80.38	VAEDEFDPI
RAM-MiniTid	12	d1-4	AAK1_MOUSE	AP2-associa	68.67	VAEDEFDPI
RAM-MiniTid	8	d1-4	ABLM2_MOUSE	Actin-binding	65.44	TTWLLLKGI
RAM-MiniTid	8	d1-4	ABLM2_MOUSE	Actin-binding	65.44	TTWLLLKGI
RAM-MiniTid	3	d1-4	ACSM5_MOUSE	Acyl-coenzy	39.19	QSRKAAN
RAM-MiniTid	2	d1-4	ACTH_MOUSE	Actin, gamma	41.23	EETTALVCD
RAM-MiniTid	2	d1-4	ACTH_MOUSE	Actin, gamma	41.23	EETTALVCD
RAM-MiniTid	8	d1-4	ADDB_MOUSE	Beta-adducir	77.71	ADEVEKSSS
RAM-MiniTid	8	d1-4	ADDB_MOUSE	Beta-adducir	77.71	ADEVEKSSS
RAM-MiniTid	8	d1-4	ADDB_MOUSE	Beta-adducir	77.71	ADEVEKSSS
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP tra	98.43	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP tra	98.43	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP tra	98.43	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP tra	83.43	LAADVGKGS
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP tra	83.43	LAADVGKGS
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP tra	67.63	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP tra	67.63	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	54.74	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	54.74	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	54.74	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	54.74	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	54.74	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	46.82	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	46.82	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	46.82	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	46.82	LLLQVQHAS
RAM-MiniTid	8	d1-4	ADT2_MOUSE	ADP/ATP tra	46.82	LLLQVQHAS
RAM-MiniTid	8	d1-4	AGFG1_MOUSE	Arf-GAP dom	155.08	AGLQTADK
RAM-MiniTid	8	d1-4	AGFG1_MOUSE	Arf-GAP dom	155.08	AGLQTADK
RAM-MiniTid	8	d1-4	AGFG1_MOUSE	Arf-GAP dom	155.08	AGLQTADK
RAM-MiniTid	10	d1-4	AGFG1_MOUSE	Arf-GAP dom	102.66	AGLQTADK
RAM-MiniTid	10	d1-4	AGFG1_MOUSE	Arf-GAP dom	102.66	AGLQTADK
RAM-MiniTid	10	d1-4	AGFG1_MOUSE	Arf-GAP dom	102.66	AGLQTADK
RAM-MiniTid	8	d1-4	AINX_MOUSE	Alpha-interne	116.41	ILSSTASKVS
RAM-MiniTid	1	d1-4	ANR35_MOUSE	Ankyrin repe	40.23	LASRKSARF
RAM-MiniTid	1	d1-4	ANR35_MOUSE	Ankyrin repe	40.23	LASRKSARF
RAM-MiniTid	8	d1-4	AP180_MOUSE	Clathrin coat	47.65	KPPAKDPLA
RAM-MiniTid	8	d1-4	AP180_MOUSE	Clathrin coat	47.65	KPPAKDPLA
RAM-MiniTid	8	d1-4	ATPB_MOUSE	ATP synthas	78.49	AAQASAAPK
RAM-MiniTid	8	d1-4	ATPB_MOUSE	ATP synthas	60.72	ASAAPKAGT
RAM-MiniTid	8	d1-4	AUXI_MOUSE	Putative tyro	82.38	QKAADFEDI
RAM-MiniTid	7	d1-4	BASP1_MOUSE	Brain acid so	75.01	GEAKKTEAF
RAM-MiniTid	10	d1-4	BD1L1_MOUSE	Biorientation	37.83	TDVSTDK
RAM-MiniTid	8	d1-4	CAPS1_MOUSE	Calcium-dep	43.37	LNAKGGNVI
RAM-MiniTid	8	d1-4	CEND_MOUSE	Cell cycle ex	47.99	GKSASSPKF
RAM-MiniTid	8	d1-4	CH10_MOUSE	10 kDa heat	85.64	SAAETVTKG
RAM-MiniTid	8	d1-4	CH10_MOUSE	10 kDa heat	85.64	SAAETVTKG
RAM-MiniTid	8	d1-4	CH10_MOUSE	10 kDa heat	58.15	SAAETVTKG
RAM-MiniTid	8	d1-4	CH10_MOUSE	10 kDa heat	58.15	SAAETVTKG

RAM-MiniTid	8	d1-4	CLAP2_MOUSE	CLIP-associa	94.88	AGGDAADG
RAM-MiniTid	10	d1-4	CLAP2_MOUSE	CLIP-associa	48.87	AGGDAADG
RAM-MiniTid	8	d1-4	CMTR1_MOUSE	Cap-specific	43.62	LMAKMGFR
RAM-MiniTid	8	d1-4	CMTR1_MOUSE	Cap-specific	43.62	LMAKMGFR
RAM-MiniTid	8	d1-4	CMTR1_MOUSE	Cap-specific	43.62	LMAKMGFR
RAM-MiniTid	8	d1-4	CMTR1_MOUSE	Cap-specific	43.62	LMAKMGFR
RAM-MiniTid	8	d1-4	CMTR1_MOUSE	Cap-specific	43.62	LMAKMGFR
RAM-MiniTid	6	d1-4	CPLX1_MOUSE	Complexin-1	51.54	QALGGATK
RAM-MiniTid	6	d1-4	CPLX1_MOUSE	Complexin-1	51.54	QALGGATK
RAM-MiniTid	8	d1-4	CPLX1_MOUSE	Complexin-1	81.8	QALGGATK
RAM-MiniTid	8	d1-4	CPLX1_MOUSE	Complexin-1	81.8	QALGGATK
RAM-MiniTid	8	d1-4	CPLX1_MOUSE	Complexin-1	67.15	QALGGATK
RAM-MiniTid	8	d1-4	CPLX1_MOUSE	Complexin-1	67.15	QALGGATK
RAM-MiniTid	8	d1-4	CPLX1_MOUSE	Complexin-1	60.01	YLPGPLQD
RAM-MiniTid	8	d1-4	CPLX1_MOUSE	Complexin-1	60.01	YLPGPLQD
RAM-MiniTid	8	d1-4	DDX46_MOUSE	Probable ATI	56.63	INAKLNYVP
RAM-MiniTid	8	d1-4	DDX46_MOUSE	Probable ATI	56.63	INAKLNYVP
RAM-MiniTid	8	d1-4	DDX46_MOUSE	Probable ATI	56.63	INAKLNYVP
RAM-MiniTid	8	d1-4	DDX46_MOUSE	Probable ATI	56.63	INAKLNYVP
RAM-MiniTid	8	d1-4	DLG2_MOUSE	Disks large h	63.66	FNAKPGVID
RAM-MiniTid	8	d1-4	DLG2_MOUSE	Disks large h	63.66	FNAKPGVID
RAM-MiniTid	8	d1-4	DLGP2_MOUSE	Disks large-a	41.91	AVLASKAEE
RAM-MiniTid	7	d1-4	DNJC5_MOUSE	DnaJ homolo	44.3	GLLTCCYC
RAM-MiniTid	12	d1-4	DPYL2_MOUSE	Dihydropyrim	53.43	GLYDGPVC
RAM-MiniTid	12	d1-4	DPYL2_MOUSE	Dihydropyrim	53.43	GLYDGPVC
RAM-MiniTid	8	d1-4	E41L1_MOUSE	Band 4.1-like	132.1	SLSPIIGKDV
RAM-MiniTid	8	d1-4	E41L1_MOUSE	Band 4.1-like	132.1	SLSPIIGKDV
RAM-MiniTid	8	d1-4	E41L1_MOUSE	Band 4.1-like	132.1	SLSPIIGKDV
RAM-MiniTid	8	d1-4	E41L1_MOUSE	Band 4.1-like	54.81	LQHPDMLV
RAM-MiniTid	8	d1-4	E41L1_MOUSE	Band 4.1-like	54.81	LQHPDMLV
RAM-MiniTid	8	d1-4	E41L1_MOUSE	Band 4.1-like	54.81	LQHPDMLV
RAM-MiniTid	7	d1-4	EEA1_MOUSE	Early endosc	38.12	QAAVTELTA
RAM-MiniTid	8	d1-4	ELFN1_MOUSE	Protein ELFN	108.91	SGAVSAAEF
RAM-MiniTid	8	d1-4	ELFN1_MOUSE	Protein ELFN	39.35	YIEKSSPVPE
RAM-MiniTid	12	d1-4	ENOA_MOUSE	Alpha-enolas	51.66	YSDKVVIGM
RAM-MiniTid	11	d1-4	ENOB_MOUSE	Beta-enolase	41.88	GANAILGVS
RAM-MiniTid	11	d1-4	FKBP4_MOUSE	Peptidyl-proly	54.16	KPEYAYGAA
RAM-MiniTid	8	d1-4	GBRA1_MOUSE	Gamma-amir	44.45	GDPGLATIA
RAM-MiniTid	8	d1-4	GBRA1_MOUSE	Gamma-amir	44.45	GDPGLATIA
RAM-MiniTid	8	d1-4	GBRA1_MOUSE	Gamma-amir	44.45	GDPGLATIA
RAM-MiniTid	8	d1-4	GBRA1_MOUSE	Gamma-amir	44.45	GDPGLATIA
RAM-MiniTid	8	d1-4	GBRA1_MOUSE	Gamma-amir	44.45	GDPGLATIA
RAM-MiniTid	8	d1-4	GBRA1_MOUSE	Gamma-amir	44.45	GDPGLATIA
RAM-MiniTid	12	d1-4	GGA1_MOUSE	ADP-ribosyla	61.84	NVIFEDEEK
RAM-MiniTid	12	d1-4	GGA1_MOUSE	ADP-ribosyla	61.84	NVIFEDEEK
RAM-MiniTid	8	d1-4	GIT1_MOUSE	ARF GTPase	54.31	QAFSMYEP
RAM-MiniTid	7	d1-4	GLD2_MOUSE	Poly(A) RNA	38.21	KVPIVK
RAM-MiniTid	8	d1-4	HNRPM_MOUSE	Heterogeneo	100.74	RGEIIAKQG
RAM-MiniTid	5	d1-4	HXK1_MOUSE	Hexokinase-	40.53	KTHPQYSR
RAM-MiniTid	5	d1-4	HXK1_MOUSE	Hexokinase-	40.53	KTHPQYSR
RAM-MiniTid	5	d1-4	HXK1_MOUSE	Hexokinase-	40.53	KTHPQYSR
RAM-MiniTid	4	d1-4	HYALP_MOUSE	Hyaluronidas	41.19	LGYYPYIDS
RAM-MiniTid	5	d1-4	IL7RA_MOUSE	Interleukin-7	37.13	KLQPAAMYE
RAM-MiniTid	8	d1-4	ISCU_MOUSE	Iron-sulfur cl	74.15	TVEEALTIKN
RAM-MiniTid	8	d1-4	ISCU_MOUSE	Iron-sulfur cl	74.15	TVEEALTIKN
RAM-MiniTid	8	d1-4	JIP4_MOUSE	C-Jun-amino	61.35	GTDTSNKSE

RAM-MiniTid	8	d1-4	KCC2A_MOUSE	Calcium/calm	62.19	LKGAILTTMI
RAM-MiniTid	8	d1-4	KCC2A_MOUSE	Calcium/calm	62.19	LKGAILTTMI
RAM-MiniTid	8	d1-4	KCC2A_MOUSE	Calcium/calm	62.19	LKGAILTTMI
RAM-MiniTid	8	d1-4	KCC2A_MOUSE	Calcium/calm	62.19	LKGAILTTMI
RAM-MiniTid	8	d1-4	KCC2B_MOUSE	Calcium/calm	62.19	LKGAILTTMI
RAM-MiniTid	8	d1-4	KCC2B_MOUSE	Calcium/calm	62.19	LKGAILTTMI
RAM-MiniTid	8	d1-4	KCC2B_MOUSE	Calcium/calm	62.19	LKGAILTTMI
RAM-MiniTid	8	d1-4	LAS1L_MOUSE	Ribosomal bi	53.18	TKCSNLPLK
RAM-MiniTid	8	d1-4	LNEBL_MOUSE	LIM zinc-binc	79.43	STQVVSDAA
RAM-MiniTid	8	d1-4	MAP1A_MOUSE	Microtubule-a	139.59	SPQAQDTLC
RAM-MiniTid	8	d1-4	MAP1A_MOUSE	Microtubule-a	87.04	SPWASDFKI
RAM-MiniTid	8	d1-4	MAP1A_MOUSE	Microtubule-a	72.57	TRHDEYLEV
RAM-MiniTid	8	d1-4	MAP1A_MOUSE	Microtubule-a	69.63	DFQEPLPQI
RAM-MiniTid	8	d1-4	MAP1A_MOUSE	Microtubule-a	53.62	DFQEPLPQI
RAM-MiniTid	9	d1-4	MAP1A_MOUSE	Microtubule-a	65.39	DFQEPLPQI
RAM-MiniTid	10	d1-4	MAP1A_MOUSE	Microtubule-a	71.76	DFQEPLPQI
RAM-MiniTid	10	d1-4	MAP1A_MOUSE	Microtubule-a	59.18	SPWASDFKI
RAM-MiniTid	12	d1-4	MAP1A_MOUSE	Microtubule-a	72.4	DFQEPLPQI
RAM-MiniTid	12	d1-4	MAP1A_MOUSE	Microtubule-a	44.84	EGEGGAGA
RAM-MiniTid	12	d1-4	MAP1A_MOUSE	Microtubule-a	60.48	DFQEPLPQI
RAM-MiniTid	12	d1-4	MAP1B_MOUSE	Microtubule-a	80.11	ITKTPQAST
RAM-MiniTid	6	d1-4	MAP4_MOUSE	Microtubule-a	38.71	CGSKDNIK
RAM-MiniTid	6	d1-4	MAP4_MOUSE	Microtubule-a	38.71	CGSKDNIK
RAM-MiniTid	12	d1-4	MAP4_MOUSE	Microtubule-a	53.89	CGSKDNIK
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-a	109.04	DQGAVLLGI
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-a	79.3	DQGAVLLGI
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-a	70.08	RGDHPWIPI
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-a	62.72	NQDPIIPVPL
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-a	50.56	NQDPIIPVPL
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-a	47.56	NQSPVVLGI
RAM-MiniTid	9	d1-4	MAP6_MOUSE	Microtubule-a	117.11	DQGAVLLGI
RAM-MiniTid	9	d1-4	MAP6_MOUSE	Microtubule-a	57.45	GHDSVFVAI
RAM-MiniTid	9	d1-4	MAP6_MOUSE	Microtubule-a	56.46	NQDPIIPVPL
RAM-MiniTid	9	d1-4	MAP6_MOUSE	Microtubule-a	50.91	DQGAVLLGI
RAM-MiniTid	9	d1-4	MAP6_MOUSE	Microtubule-a	37.93	DQGAVLLGI
RAM-MiniTid	10	d1-4	MAP6_MOUSE	Microtubule-a	117.17	DQGAVLLGI
RAM-MiniTid	10	d1-4	MAP6_MOUSE	Microtubule-a	67.88	GHDSVFVAI
RAM-MiniTid	10	d1-4	MAP6_MOUSE	Microtubule-a	67.21	NQDPIIPVPL
RAM-MiniTid	10	d1-4	MAP6_MOUSE	Microtubule-a	63.21	DQGAVLLGI
RAM-MiniTid	11	d1-4	MAP6_MOUSE	Microtubule-a	71.69	DQGAVLLGI
RAM-MiniTid	11	d1-4	MAP6_MOUSE	Microtubule-a	54.01	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	61.47	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	97.99	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	79.83	GHDSVFVAI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	71.96	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	54.31	YLKGHDSVI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	54.06	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	53.93	NQDPIIPVPL
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	52.76	NKDSVPLAI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	46.81	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	44.55	RGDHPWIPI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	91.52	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	65.52	NQDPIIPVPL
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	64	DQGAVLLGI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	59	GHDSVFVAI
RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	48.15	NQDPIIPVPL

RAM-MiniTid	12	d1-4	MAP6_MOUSE	Microtubule-a	45.97	DQGAVLLG
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	66.13	IAMKMEHTI
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	66.13	IAMKMEHTI
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	66.13	IAMKMEHTI
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	66.13	IAMKMEHTI
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	41.9	KMEHTIK
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	41.9	KMEHTIK
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	41.9	KMEHTIK
RAM-MiniTid	1	d1-4	MCCA_MOUSE	Methylcroton	41.9	KMEHTIK
RAM-MiniTid	2	d1-4	MCCA_MOUSE	Methylcroton	41.93	KMEHTIK
RAM-MiniTid	2	d1-4	MCCA_MOUSE	Methylcroton	41.93	KMEHTIK
RAM-MiniTid	10	d1-4	MCCA_MOUSE	Methylcroton	66.61	AGDSLMVM
RAM-MiniTid	10	d1-4	MCCA_MOUSE	Methylcroton	66.61	AGDSLMVM
RAM-MiniTid	10	d1-4	MCCA_MOUSE	Methylcroton	52.16	IAMKMEHTI
RAM-MiniTid	10	d1-4	MCCA_MOUSE	Methylcroton	52.16	IAMKMEHTI
RAM-MiniTid	10	d1-4	MCCA_MOUSE	Methylcroton	39.93	KMEHTIK
RAM-MiniTid	10	d1-4	MCCA_MOUSE	Methylcroton	39.93	KMEHTIK
RAM-MiniTid	11	d1-4	MCCA_MOUSE	Methylcroton	46.17	IAMKMEHTI
RAM-MiniTid	11	d1-4	MCCA_MOUSE	Methylcroton	46.17	IAMKMEHTI
RAM-MiniTid	11	d1-4	MCCA_MOUSE	Methylcroton	46.17	IAMKMEHTI
RAM-MiniTid	11	d1-4	MCCA_MOUSE	Methylcroton	41.81	KMEHTIK
RAM-MiniTid	11	d1-4	MCCA_MOUSE	Methylcroton	41.81	KMEHTIK
RAM-MiniTid	11	d1-4	MCCA_MOUSE	Methylcroton	41.81	KMEHTIK
RAM-MiniTid	12	d1-4	MCCA_MOUSE	Methylcroton	39.78	KMEHTIK
RAM-MiniTid	12	d1-4	MCCA_MOUSE	Methylcroton	39.78	KMEHTIK
RAM-MiniTid	12	d1-4	MCCA_MOUSE	Methylcroton	39.78	KMEHTIK
RAM-MiniTid	12	d1-4	MCCA_MOUSE	Methylcroton	55.78	IAMKMEHTI
RAM-MiniTid	12	d1-4	MCCA_MOUSE	Methylcroton	55.78	IAMKMEHTI
RAM-MiniTid	12	d1-4	MCCA_MOUSE	Methylcroton	55.78	IAMKMEHTI
RAM-MiniTid	8	d1-4	MECP2_MOUSE	Methyl-CpG-	44.38	LVVKMPFQA
RAM-MiniTid	5	d1-4	MTAP2_MOUSE	Microtubule-a	48.04	LILKPAIK
RAM-MiniTid	5	d1-4	MTAP2_MOUSE	Microtubule-a	48.04	LILKPAIK
RAM-MiniTid	6	d1-4	MTAP2_MOUSE	Microtubule-a	38.71	CGSKDNIK
RAM-MiniTid	6	d1-4	MTAP2_MOUSE	Microtubule-a	38.71	TPGTPKSGI
RAM-MiniTid	6	d1-4	MTAP2_MOUSE	Microtubule-a	38.71	TPGTPKSGI
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	140.45	VSDFGQMA
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	122.13	TADKNKLEG
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	91.31	LEGAGSATI
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	87.78	TADKNKLEG
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	76.65	VSDFGQMA
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	74.4	EASPPTSAD
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	70.91	TLGKVTSEF
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	43.27	NKDDLTLSR
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	43.67	LILKPAIK
RAM-MiniTid	8	d1-4	MTAP2_MOUSE	Microtubule-a	40.65	KLILKPAIK
RAM-MiniTid	9	d1-4	MTAP2_MOUSE	Microtubule-a	78.99	VSDFGQMA
RAM-MiniTid	9	d1-4	MTAP2_MOUSE	Microtubule-a	50.91	EASPPTSAD
RAM-MiniTid	9	d1-4	MTAP2_MOUSE	Microtubule-a	40.99	KLILKPAIK
RAM-MiniTid	9	d1-4	MTAP2_MOUSE	Microtubule-a	40.78	KLILKPAIK
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	136.53	VSDFGQMA
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	99.33	VSEGPRPFA
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	82.89	EASPPTSAD
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	79.62	VSDFGQMA
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	52.53	LEGAGSATI
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	49.32	TPGTPKSGI
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	48.35	KLILKPAIK

RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	38.98	KLILKPAIK
RAM-MiniTid	10	d1-4	MTAP2_MOUSE	Microtubule-a	41.48	LILKPAIK
RAM-MiniTid	11	d1-4	MTAP2_MOUSE	Microtubule-a	47.57	EASPPTSAD
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	114.17	VSDFGQMA
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	62.29	TPGTPKSGI
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	60.25	VSDFGQMA
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	48.02	LRDDKTGVI
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	44.07	ADQGLDFA
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	43.94	EASPPTSAD
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	42.42	KLILKPAIK
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	41.23	LILKPAIK
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	38.97	KLILKPAIK
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	77.85	EASPPTSAD
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	64.03	VSDFGQMA
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	38.99	KLILKPAIK
RAM-MiniTid	12	d1-4	MTAP2_MOUSE	Microtubule-a	38.42	KLILKPAIK
RAM-MiniTid	1	d1-4	MYCPP_MOUSE	C-myc prom	40.45	QRLLLGLTS
RAM-MiniTid	1	d1-4	MYCPP_MOUSE	C-myc prom	40.45	QRLLLGLTS
RAM-MiniTid	8	d1-4	NFH_MOUSE	Neurofilamer	53.59	IGFGPSPFS
RAM-MiniTid	8	d1-4	NFH_MOUSE	Neurofilamer	43.4	VKSEEMIK
RAM-MiniTid	8	d1-4	NFM_MOUSE	Neurofilamer	64.43	YITKSVTVT
RAM-MiniTid	8	d1-4	NFM_MOUSE	Neurofilamer	64.43	YITKSVTVT
RAM-MiniTid	8	d1-4	NMDE2_MOUSE	Glutamate re	55.59	ALVTNKPVV
RAM-MiniTid	8	d1-4	NMDE2_MOUSE	Glutamate re	55.59	ALVTNKPVV
RAM-MiniTid	7	d1-4	NSF_MOUSE	Vesicle-fusin	110.78	DIEAMDPSIL
RAM-MiniTid	7	d1-4	NSF_MOUSE	Vesicle-fusin	88.39	DIEAMDPSIL
RAM-MiniTid	8	d1-4	ODP2_MOUSE	Dihydrolipoyl	76.31	LAAEKGIDL
RAM-MiniTid	8	d1-4	PAK2_MOUSE	Serine/threor	61.22	NKIISIFSGTI
RAM-MiniTid	8	d1-4	PAK2_MOUSE	Serine/threor	61.22	NKIISIFSGTI
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	88.8	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-Co	73.3	KMQNSMTA
RAM-MiniTid	2	d1-4	PCCA_MOUSE	Propionyl-Co	93.52	KMQNSMTA
RAM-MiniTid	2	d1-4	PCCA_MOUSE	Propionyl-Co	93.52	KMQNSMTA
RAM-MiniTid	2	d1-4	PCCA_MOUSE	Propionyl-Co	73.54	KMQNSMTA
RAM-MiniTid	2	d1-4	PCCA_MOUSE	Propionyl-Co	73.54	KMQNSMTA
RAM-MiniTid	2	d1-4	PCCA_MOUSE	Propionyl-Co	69.02	KMQNSMTA
RAM-MiniTid	2	d1-4	PCCA_MOUSE	Propionyl-Co	69.02	KMQNSMTA
RAM-MiniTid	3	d1-4	PCCA_MOUSE	Propionyl-Co	46.63	KMQNSMTA
RAM-MiniTid	3	d1-4	PCCA_MOUSE	Propionyl-Co	46.63	KMQNSMTA
RAM-MiniTid	6	d1-4	PCCA_MOUSE	Propionyl-Co	92.9	KMQNSMTA
RAM-MiniTid	6	d1-4	PCCA_MOUSE	Propionyl-Co	85.29	KMQNSMTA
RAM-MiniTid	6	d1-4	PCCA_MOUSE	Propionyl-Co	73.02	KMQNSMTA

RAM-MiniTid	6	d1-4	PCCA_MOUSE	Propionyl-Co	61.44	KMQNSMTA
RAM-MiniTid	6	d1-4	PCCA_MOUSE	Propionyl-Co	55.4	KMQNSMTA
RAM-MiniTid	6	d1-4	PCCA_MOUSE	Propionyl-Co	49.2	KMQNSMTA
RAM-MiniTid	7	d1-4	PCCA_MOUSE	Propionyl-Co	72.92	KMQNSMTA
RAM-MiniTid	7	d1-4	PCCA_MOUSE	Propionyl-Co	67.05	KMQNSMTA
RAM-MiniTid	7	d1-4	PCCA_MOUSE	Propionyl-Co	58.03	KMQNSMTA
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-Co	54.13	KMQNSMTA
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-Co	54.13	KMQNSMTA
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-Co	49.8	KMQNSMTA
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-Co	49.8	KMQNSMTA
RAM-MiniTid	9	d1-4	PCCA_MOUSE	Propionyl-Co	84.95	KMQNSMTA
RAM-MiniTid	9	d1-4	PCCA_MOUSE	Propionyl-Co	84.95	KMQNSMTA
RAM-MiniTid	10	d1-4	PCCA_MOUSE	Propionyl-Co	68.65	KMQNSMTA
RAM-MiniTid	10	d1-4	PCCA_MOUSE	Propionyl-Co	59.99	KMQNSMTA
RAM-MiniTid	11	d1-4	PCCA_MOUSE	Propionyl-Co	76.51	KMQNSMTA
RAM-MiniTid	11	d1-4	PCCA_MOUSE	Propionyl-Co	76.51	KMQNSMTA
RAM-MiniTid	11	d1-4	PCCA_MOUSE	Propionyl-Co	45.28	KMQNSMTA
RAM-MiniTid	11	d1-4	PCCA_MOUSE	Propionyl-Co	45.28	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	66.15	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	66.15	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	67.23	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	67.23	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	48.99	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	48.99	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	44.24	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	44.24	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	63.33	KMQNSMTA
RAM-MiniTid	12	d1-4	PCCA_MOUSE	Propionyl-Co	63.33	KMQNSMTA
RAM-MiniTid	5	d1-4	PDZD8_MOUSE	PDZ domain-	38.98	EPHLVEEVS
RAM-MiniTid	8	d1-4	PLAP_MOUSE	Phospholipas	87.78	SAASKTVNI
RAM-MiniTid	8	d1-4	PLAP_MOUSE	Phospholipas	87.78	SAASKTVNI
RAM-MiniTid	12	d1-4	PLAP_MOUSE	Phospholipas	65.75	SAASKTVNI
RAM-MiniTid	12	d1-4	PLAP_MOUSE	Phospholipas	65.75	SAASKTVNI
RAM-MiniTid	8	d1-4	PLEC_MOUSE	Plectin, Gene	43.42	SAEVELQSK
RAM-MiniTid	5	d1-4	PP2BA_MOUSE	Serine/threor	41.95	NDGKPRVD
RAM-MiniTid	5	d1-4	PP2BA_MOUSE	Serine/threor	41.95	NDGKPRVD
RAM-MiniTid	5	d1-4	PP2BA_MOUSE	Serine/threor	41.95	NDGKPRVD
RAM-MiniTid	5	d1-4	PRR11_MOUSE	Proline-rich p	40.3	KKEAAVVSP
RAM-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate car	60.74	GQPLCVLSA
RAM-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate car	50.65	GQPLCVLSA
RAM-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate car	44.26	GQPLCVLSA
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate car	71.19	GQPLCVLSA
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate car	58.98	GQPLCVLSA
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate car	45.2	GQPLCVLSA
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate car	89	KMETVVTSF
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate car	65.67	KMETVVTSF
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate car	62.36	GQPLCVLSA
RAM-MiniTid	9	d1-4	PYC_MOUSE	Pyruvate car	75.15	KMETVVTSF
RAM-MiniTid	9	d1-4	PYC_MOUSE	Pyruvate car	49.56	KMETVVTSF
RAM-MiniTid	10	d1-4	PYC_MOUSE	Pyruvate car	111.81	GQPLCVLSA
RAM-MiniTid	10	d1-4	PYC_MOUSE	Pyruvate car	92.56	GQPLCVLSA
RAM-MiniTid	10	d1-4	PYC_MOUSE	Pyruvate car	76.2	VVKGQPLC
RAM-MiniTid	10	d1-4	PYC_MOUSE	Pyruvate car	44.36	GQPLCVLSA
RAM-MiniTid	11	d1-4	PYC_MOUSE	Pyruvate car	83.43	KMETVVTSF
RAM-MiniTid	11	d1-4	PYC_MOUSE	Pyruvate car	83.39	KMETVVTSF
RAM-MiniTid	11	d1-4	PYC_MOUSE	Pyruvate car	50.39	GQPLCVLSA

RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	110.52	GQPLCVLSA
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	80.06	KMETVVTSF
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	67.25	KMETVVTSF
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	50.71	GQPLCVLSA
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	50	GQPLCVLSA
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	46.98	VVKGQPLCV
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	44.51	GQPLCVLSA
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	105.32	KMETVVTSF
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	71.22	SAMKMETVV
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	63.5	MKMETVVTS
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	60.3	KMETVVTSF
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	56.85	SAMKMETVV
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	46.58	GQPLCVLSA
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	63.68	GQPLCVLSA
RAM-MiniTid	12	d1-4	PYC_MOUSE	Pyruvate car	62.95	GQPLCVLSA
RAM-MiniTid	10	d1-4	QCR2_MOUSE	Cytochrome	44.44	ELEFTKLPN
RAM-MiniTid	8	d1-4	RELCH_MOUSE	RAB11-bindi	66.07	QSPAVNSSD
RAM-MiniTid	8	d1-4	RHG35_MOUSE	Rho GTPase	93.68	NEEENIYSVI
RAM-MiniTid	8	d1-4	RHG35_MOUSE	Rho GTPase	93.68	NEEENIYSVI
RAM-MiniTid	8	d1-4	RHG35_MOUSE	Rho GTPase	93.68	NEEENIYSVI
RAM-MiniTid	8	d1-4	RHG35_MOUSE	Rho GTPase	93.68	NEEENIYSVI
RAM-MiniTid	4	d1-4	RIMS1_MOUSE	Regulating sy	38.63	TMPKDSGAI
RAM-MiniTid	4	d1-4	RT23_MOUSE	28S ribosoma	37.36	EAGKALLAE
RAM-MiniTid	4	d1-4	RT23_MOUSE	28S ribosoma	41.22	EAGKALLAE
RAM-MiniTid	4	d1-4	RT23_MOUSE	28S ribosoma	40.46	EAGKALLAE
RAM-MiniTid	4	d1-4	RT23_MOUSE	28S ribosoma	40.21	EAGKALLAE
RAM-MiniTid	9	d1-4	RT31_MOUSE	28S ribosoma	49.23	QTTKSELLR
RAM-MiniTid	9	d1-4	RT31_MOUSE	28S ribosoma	49.23	QTTKSELLR
RAM-MiniTid	12	d1-4	RT31_MOUSE	28S ribosoma	54.1	QTTKSELLR
RAM-MiniTid	12	d1-4	RT31_MOUSE	28S ribosoma	54.1	QTTKSELLR
RAM-MiniTid	8	d1-4	RTN3_MOUSE	Reticulon-3,	51.98	IADFKNTLPV
RAM-MiniTid	8	d1-4	SET_MOUSE	Protein SET,	43.85	LEDKSASPG
RAM-MiniTid	8	d1-4	SET_MOUSE	Protein SET,	43.85	LEDKSASPG
RAM-MiniTid	8	d1-4	SH3G2_MOUSE	Endophilin-A	51.44	QGKIPDEEL
RAM-MiniTid	8	d1-4	SH3G2_MOUSE	Endophilin-A	51.44	QGKIPDEEL
RAM-MiniTid	8	d1-4	SH3G2_MOUSE	Endophilin-A	51.44	QGKIPDEEL
RAM-MiniTid	8	d1-4	SHAN2_MOUSE	SH3 and mul	76.25	IASKAVYVPA
RAM-MiniTid	8	d1-4	SHAN2_MOUSE	SH3 and mul	76.25	IASKAVYVPA
RAM-MiniTid	8	d1-4	SHAN2_MOUSE	SH3 and mul	76.25	IASKAVYVPA
RAM-MiniTid	8	d1-4	SHAN2_MOUSE	SH3 and mul	47.12	ADLNKPLYID
RAM-MiniTid	8	d1-4	SHAN2_MOUSE	SH3 and mul	47.12	ADLNKPLYID
RAM-MiniTid	8	d1-4	SHAN2_MOUSE	SH3 and mul	47.12	ADLNKPLYID
RAM-MiniTid	12	d1-4	SHAN2_MOUSE	SH3 and mul	42.02	IASKAVYVPA
RAM-MiniTid	12	d1-4	SHAN2_MOUSE	SH3 and mul	42.02	IASKAVYVPA
RAM-MiniTid	12	d1-4	SHAN2_MOUSE	SH3 and mul	42.02	IASKAVYVPA
RAM-MiniTid	4	d1-4	SMC4_MOUSE	Structural ma	41.37	TKSVAVNPK
RAM-MiniTid	4	d1-4	SMC4_MOUSE	Structural ma	41.37	TKSVAVNPK
RAM-MiniTid	4	d1-4	SMC4_MOUSE	Structural ma	41.37	TKSVAVNPK
RAM-MiniTid	4	d1-4	SMC4_MOUSE	Structural ma	40.94	NITKSVAVNI
RAM-MiniTid	4	d1-4	SMC4_MOUSE	Structural ma	40.94	NITKSVAVNI
RAM-MiniTid	4	d1-4	SMC4_MOUSE	Structural ma	40.26	NITKSVAVNI
RAM-MiniTid	4	d1-4	SMC4_MOUSE	Structural ma	40.26	NITKSVAVNI
RAM-MiniTid	8	d1-4	SPTN1_MOUSE	Spectrin alph	72.68	DEADSKTAS
RAM-MiniTid	8	d1-4	SPTN1_MOUSE	Spectrin alph	72.68	DEADSKTAS
RAM-MiniTid	8	d1-4	SPTN1_MOUSE	Spectrin alph	52.74	TASPWKSAF
RAM-MiniTid	8	d1-4	SPTN1_MOUSE	Spectrin alph	52.74	TASPWKSAF

RAM-MiniTid	12	d1-4	SPTN1_MOUSE	Spectrin alph	40.42	TASPWKSAF
RAM-MiniTid	8	d1-4	SRC8_MOUSE	Src substrate	59.89	GFGGKFGV
RAM-MiniTid	8	d1-4	SRC8_MOUSE	Src substrate	59.89	GFGGKFGV
RAM-MiniTid	8	d1-4	SRC8_MOUSE	Src substrate	59.89	GFGGKFGV
RAM-MiniTid	8	d1-4	SRC8_MOUSE	Src substrate	54	VDKSAVGFD
RAM-MiniTid	8	d1-4	SRC8_MOUSE	Src substrate	54	VDKSAVGFD
RAM-MiniTid	8	d1-4	SRC8_MOUSE	Src substrate	54	VDKSAVGFD
RAM-MiniTid	8	d1-4	SRCN1_MOUSE	SRC kinase s	90.62	AALTQYSAK
RAM-MiniTid	8	d1-4	SRCN1_MOUSE	SRC kinase s	90.62	AALTQYSAK
RAM-MiniTid	8	d1-4	SRCN1_MOUSE	SRC kinase s	90.62	AALTQYSAK
RAM-MiniTid	4	d1-4	SRPK2_MOUSE	SRSF proteir	41.28	AKTRAAD
RAM-MiniTid	8	d1-4	SUGP2_MOUSE	SURP and G	73.13	LTDKNVGFC
RAM-MiniTid	4	d1-4	SYNE4_MOUSE	Nesprin-4 OS	37.47	VGGLGPSG
RAM-MiniTid	4	d1-4	SYNE4_MOUSE	Nesprin-4 OS	37.47	VGGLGPSG
RAM-MiniTid	8	d1-4	SYNRG_MOUSE	Synergin gan	100.59	ASDKYEALR
RAM-MiniTid	8	d1-4	SYNRG_MOUSE	Synergin gan	93.81	GISTDKPSE
RAM-MiniTid	8	d1-4	SYNRG_MOUSE	Synergin gan	49.46	ASTDKYAVF
RAM-MiniTid	12	d1-4	SYNRG_MOUSE	Synergin gan	58.74	ASDKYEALR
RAM-MiniTid	12	d1-4	SYNRG_MOUSE	Synergin gan	43.5	ASTDKYAVF
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	39.64	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	39.64	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	39.64	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	39.64	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	39.64	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	39.64	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUA_MOUSE	Alpha-synucl	39.64	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUA_MOUSE	Alpha-synucl	43.21	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUA_MOUSE	Alpha-synucl	43.21	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUA_MOUSE	Alpha-synucl	43.21	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUA_MOUSE	Alpha-synucl	43.21	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUA_MOUSE	Alpha-synucl	43.21	TKEGVLYVG
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synucl	75.25	TKEGVLYVG
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synucl	75.25	TKEGVLYVG
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synucl	60.87	QGVAEAAG
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synucl	60.87	QGVAEAAG
RAM-MiniTid	12	d1-4	SYUA_MOUSE	Alpha-synucl	75.48	TKEGVLYVG
RAM-MiniTid	12	d1-4	SYUA_MOUSE	Alpha-synucl	75.48	TKEGVLYVG
RAM-MiniTid	12	d1-4	SYUA_MOUSE	Alpha-synucl	55.64	TKEGVLYVG
RAM-MiniTid	12	d1-4	SYUA_MOUSE	Alpha-synucl	55.64	TKEGVLYVG
RAM-MiniTid	12	d1-4	SYUA_MOUSE	Alpha-synucl	52.92	QGVAEAAG
RAM-MiniTid	12	d1-4	SYUA_MOUSE	Alpha-synucl	52.92	QGVAEAAG
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	57.97	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	40.28	QGVTEAAEK
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	40.28	QGVTEAAEK
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	40.28	QGVTEAAEK
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	38.92	TKQGVTEA
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	38.92	TKQGVTEA
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	38.92	TKQGVTEA

RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	39.64	TKEGVLYVG
RAM-MiniTid	4	d1-4	SYUB_MOUSE	Beta-synucle	39.64	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	71.07	TKQGVTEA/
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	71.07	TKQGVTEA/
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	71.07	TKQGVTEA/
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	65.3	QGVTEAAEI
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	65.3	QGVTEAAEI
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	65.3	QGVTEAAEI
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	43.21	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	43.21	TKEGVLYVG
RAM-MiniTid	6	d1-4	SYUB_MOUSE	Beta-synucle	43.21	TKEGVLYVG
RAM-MiniTid	7	d1-4	SYUB_MOUSE	Beta-synucle	38.07	QGVTEAAEI
RAM-MiniTid	7	d1-4	SYUB_MOUSE	Beta-synucle	38.07	QGVTEAAEI
RAM-MiniTid	7	d1-4	SYUB_MOUSE	Beta-synucle	38.07	QGVTEAAEI
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	137.85	EGVLYVGSI
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	137.68	TKEQASHLC
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	137.68	TKEQASHLC
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	137.68	TKEQASHLC
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	91.97	TKEGVLYVG
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	78.3	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	78.3	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	78.3	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	76.47	EGVLYVGSI
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	75.25	TKEGVLYVG
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	75.25	TKEGVLYVG
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	61.38	QGVTEAAEI
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	61.38	QGVTEAAEI
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	61.38	QGVTEAAEI
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	60.57	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	60.57	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	60.57	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	49.81	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	49.81	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	49.81	TKQGVTEA/
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	47.2	GLSMAKEG'
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	47.2	GLSMAKEG'
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synucle	47.2	GLSMAKEG'
RAM-MiniTid	9	d1-4	SYUB_MOUSE	Beta-synucle	97.4	EGVLYVGSI
RAM-MiniTid	9	d1-4	SYUB_MOUSE	Beta-synucle	73.05	TKEGVLYVG
RAM-MiniTid	9	d1-4	SYUB_MOUSE	Beta-synucle	72.22	TKQGVTEA/
RAM-MiniTid	9	d1-4	SYUB_MOUSE	Beta-synucle	63.54	QGVTEAAEI
RAM-MiniTid	10	d1-4	SYUB_MOUSE	Beta-synucle	64.41	TKQGVTEA/
RAM-MiniTid	10	d1-4	SYUB_MOUSE	Beta-synucle	63.51	QGVTEAAEI
RAM-MiniTid	10	d1-4	SYUB_MOUSE	Beta-synucle	59.59	TKEGVLYVG
RAM-MiniTid	10	d1-4	SYUB_MOUSE	Beta-synucle	47.93	TKQGVTEA/
RAM-MiniTid	11	d1-4	SYUB_MOUSE	Beta-synucle	65.66	QGVTEAAEI
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	120.58	EGVLYVGSI
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	100.74	TKEGVLYVG
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	78.13	TKQGVTEA/
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	73.43	TKQGVTEA/
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	66.68	QGVTEAAEI
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	55.64	TKEGVLYVG
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	51.47	TKQGVTEA/
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	47.68	EGVLYVGSI
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	86.55	EGVLYVGSI
RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	63.61	QGVTEAAEI

RAM-MiniTid	12	d1-4	SYUB_MOUSE	Beta-synucle	62.9	TKQGVTEA
RAM-MiniTid	4	d1-4	SYUG_MOUSE	Gamma-syn	40.28	QGVTEAAE
RAM-MiniTid	4	d1-4	SYUG_MOUSE	Gamma-syn	38.92	TKQGVTEA
RAM-MiniTid	6	d1-4	SYUG_MOUSE	Gamma-syn	71.07	TKQGVTEA
RAM-MiniTid	6	d1-4	SYUG_MOUSE	Gamma-syn	65.3	QGVTEAAE
RAM-MiniTid	7	d1-4	SYUG_MOUSE	Gamma-syn	38.07	QGVTEAAE
RAM-MiniTid	5	d1-4	TCPH_MOUSE	T-complex pr	39.5	AIKNDSVVA
RAM-MiniTid	5	d1-4	TCPH_MOUSE	T-complex pr	39.5	AIKNDSVVA
RAM-MiniTid	8	d1-4	TCPQ_MOUSE	T-complex pr	61.11	GTVLIKTAE
RAM-MiniTid	3	d1-4	TEP1_MOUSE	Telomerase	41.74	HVNSKCLF
RAM-MiniTid	3	d1-4	TIM44_MOUSE	Mitochondria	51.76	LGKTAAFK
RAM-MiniTid	3	d1-4	TIM44_MOUSE	Mitochondria	51.76	LGKTAAFK
RAM-MiniTid	8	d1-4	TIM44_MOUSE	Mitochondria	74.37	ESLDEVSKS
RAM-MiniTid	8	d1-4	TIM44_MOUSE	Mitochondria	51.05	LGKTAAFK
RAM-MiniTid	3	d1-4	TMM62_MOUSE	Transmembr	39.59	KMEELLLLA
RAM-MiniTid	8	d1-4	TRAP1_MOUSE	Heat shock p	81	MQQLAKTQ
RAM-MiniTid	8	d1-4	TRAP1_MOUSE	Heat shock p	81	MQQLAKTQ
RAM-MiniTid	8	d1-4	TRAP1_MOUSE	Heat shock p	81	MQQLAKTQ
RAM-MiniTid	3	d1-4	UD3A2_MOUSE	UDP-glucuro	38.01	KSAAVAASV
RAM-MiniTid	3	d1-4	UD3A2_MOUSE	UDP-glucuro	40.02	KSAAVAASV
RAM-MiniTid	11	d1-4	VA0D2_MOUSE	V-type proto	58.14	EGLVRGCK
RAM-MiniTid	11	d1-4	VA0D2_MOUSE	V-type proto	58.14	EGLVRGCK
RAM-MiniTid	8	d1-4	VAMP2_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP2_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP2_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP2_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP2_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP2_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP2_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP3_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP3_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP3_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP3_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	8	d1-4	VAMP3_MOUSE	Vesicle-asso	50.54	VNVDKVLER
RAM-MiniTid	3	d1-4	WEE1_MOUSE	Wee1-like pr	41.79	CVKRLDGC
RAM-MiniTid	3	d1-4	WEE1_MOUSE	Wee1-like pr	41.79	CVKRLDGC
RAM-MiniTid	3	d1-4	ZN345_MOUSE	Zinc finger pr	46.93	KDFSFVSVL

n (EC) spatial memory phase

Peptide Mod	Position of peptide modification	RMT-EC
Biotin (K)	0.00000000000000100000000.0	AAK1_MOUSE
Biotin (K)	0.00000000000000100000000.0	ABLM2_MOUSE
Biotin (K)	0.00000000000000100000000.0	ACSM5_MOUSE
Biotin (K)	0.00000000000000100000000.0	ACTH_MOUSE
Biotin (K)	0.0000001000000.0	ADDB_MOUSE
Biotin (K)	0.0000001000000.0	ADT1_MOUSE
Biotin (K)	0.0001000.0	ADT2_MOUSE
Biotin (K)	0.00000000000000010000000000.0	AGFG1_MOUSE
Biotin (K)	0.00000000000000010000000000.0	AINX_MOUSE
Biotin (K)	0.00000100000000.0	ANR35_MOUSE
Biotin (K)	0.00000100000000.0	AP180_MOUSE
Biotin (K)	0.00000100000000.0	ATPB_MOUSE
Biotin (K)	0.0000000001000000.0	AUXI_MOUSE
Biotin (K)	0.0000000001000000.0	BASP1_MOUSE
Biotin (K)	0.0000000001000000.0	BD1L1_MOUSE
Biotin (K)	0.000000100000.0	CAPS1_MOUSE
Biotin (K)	0.000000100000.0	CEND_MOUSE
Biotin (K)	0.0000000001000000.0	CH10_MOUSE
Biotin (K)	0.0000000001000000.0	CLAP2_MOUSE
Biotin (K)	0.0000000001000000.0	CMTR1_MOUSE
Biotin (K)	0.0000000001000000.0	CPLX1_MOUSE
Biotin (K)	0.0000000001000000.0	DDX46_MOUSE
Biotin (K)	0.0000000001000000.0	DLG2_MOUSE
Biotin (K)	0.0000000001000000.0	DLGP2_MOUSE
Biotin (K)	0.0000000001000000.0	DNJC5_MOUSE
Biotin (K)	0.0000000001000000.0	DPYL2_MOUSE
Biotin (K)	0.0000000001000000.0	E41L1_MOUSE
Biotin (K)	0.0000000001000000.0	EEA1_MOUSE
Biotin (K)	0.0000000001000000.0	ELFN1_MOUSE
Biotin (K)	0.00000001000000000000000000000000000.0	ENOA_MOUSE
Biotin (K)	0.00000001000000000000000000000000000.0	ENOB_MOUSE
Biotin (K)	0.00000001000000000000000000000000000.0	FKBP4_MOUSE
Biotin (K)	0.00000001000000000000000000000000000.0	GBRA1_MOUSE
Biotin (K)	0.00000001000000000000000000000000000.0	GGA1_MOUSE
Biotin (K)	0.00000001000000000000000000000000000.0	GIT1_MOUSE
Biotin (K)	0.00000001000000000.0	GLD2_MOUSE
Biotin (K)	0.00000000001.0	HNRPM_MOUSE
Biotin (K)	0.00000000001.0	HXK1_MOUSE
Biotin (K)	0.00001000000000000.0	HYALP_MOUSE
Biotin (K)	0.00001000000000000.0	IL7RA_MOUSE
Biotin (K)	0.0000000010000000.0	ISCU_MOUSE
Biotin (K)	0.0000010000000.0	JIP4_MOUSE
Biotin (K)	0.0100000000000000000.0	KCC2A_MOUSE
2 Biotin (K)	0.000010000000000010000000000000000000000.0	KCC2B_MOUSE
Biotin (K)	0.0000001.0	LAS1L_MOUSE
Biotin (K)	0.00010000000000000000.0	LNEBL_MOUSE
Biotin (K)	0.010000000000.0	MAP1A_MOUSE
Biotin (K)	0.0000000100000000.0	MAP1B_MOUSE
Biotin (K)	0.0000000100000000.0	MAP4_MOUSE
Biotin (K)	0.0000000100000000.0	MAP6_MOUSE
Biotin (K)	0.0000000100000000.0	MCCA_MOUSE

Biotin (K)	0.000000000000001000000000000.0	MECP2_MOUSE
Biotin (K)	0.000000000000001000000000000.0	MTAP2_MOUSE
Biotin (K)	0.00010000.0	MYCPP_MOUSE
Biotin (K)	0.00010000.0	NFH_MOUSE
Biotin (K)	0.00010000.0	NFM_MOUSE
Biotin (K)	0.00010000.0	NMDE2_MOUSE
Biotin (K)	0.00010000.0	NSF_MOUSE
Biotin (K)	0.000000010000.0	ODP2_MOUSE
Biotin (K)	0.000000010000.0	PAK2_MOUSE
Biotin (K)	0.000000010000.0	PCCA_MOUSE
Biotin (K)	0.000000010000.0	PDZD8_MOUSE
Biotin (K); O›	0.000000010300.0	PLAP_MOUSE
Biotin (K); O›	0.000000010300.0	PLEC_MOUSE
Biotin (K)	0.000000000001.0	PP2BA_MOUSE
Biotin (K)	0.000000000001.0	PRR11_MOUSE
Biotin (K)	0.000100000000.0	PYC_MOUSE
Biotin (K)	0.000100000000.0	QCR2_MOUSE
Biotin (K)	0.000100000000.0	RELCH_MOUSE
Biotin (K)	0.000100000000.0	RHG35_MOUSE
Biotin (K)	0.000000000010000000000000.0	RIMS1_MOUSE
Biotin (K)	0.000000000010000000000000.0	RT23_MOUSE
Biotin (K)	0.000001000000.0	RT31_MOUSE
2 Biotin (K); 1	0.000000022202220022200210100000000000000000(	RTN3_MOUSE
Biotin (K)	0.000000020000001000000000.0	SET_MOUSE
Biotin (K)	0.000000020000001000000000.0	SH3G2_MOUSE
Biotin (K)	0.000000010000000000000000000000000.0	SHAN2_MOUSE
Biotin (K)	0.000000010000000000000000000000000.0	SMC4_MOUSE
Biotin (K)	0.000000010000000000000000000000000.0	SPTN1_MOUSE
Biotin (K)	0.000000000100000.0	SRC8_MOUSE
Biotin (K)	0.000000000100000.0	SRCN1_MOUSE
Biotin (K)	0.000000000100000.0	SRPK2_MOUSE
Biotin (K)	0.00000000001.0	SUGP2_MOUSE
Biotin (K)	0.000000000000000000001000000000.0	SYNE4_MOUSE
Biotin (K)	0.000100000000000000000000.0	SYNRG_MOUSE
Biotin (K)	0.000100003000000000.0	SYUA_MOUSE
2 Biotin (K)	0.000000000000210000010000000000000000000000(	SYUB_MOUSE
Biotin (K)	0.10000000000000.0	SYUG_MOUSE
Biotin (K)	0.000000000010000000.0	TCPH_MOUSE
Biotin (K)	0.000000000010000000.0	TCPQ_MOUSE
Biotin (K)	0.000000000010000000.0	TEP1_MOUSE
Biotin (K)	0.000000000010000000.0	TIM44_MOUSE
Biotin (K)	0.000000000010000000.0	TMM62_MOUSE
Biotin (K)	0.000000000010000000.0	TRAP1_MOUSE
Biotin (K)	0.00000000001.0	UD3A2_MOUSE
Biotin (K)	0.00000000001.0	VA0D2_MOUSE
Biotin (K)	0.000000000000010000000000000.0	VAMP2_MOUSE
Biotin (K)	0.000001.0	VAMP3_MOUSE
Biotin (K)	0.000000100000000000000.0	WEE1_MOUSE
Biotin (K)	0.10000000.0	ZN345_MOUSE
Biotin (K)	0.10000000.0	TAU_MOUSE
Biotin (K)	0.10000000.0	
Biotin (K)	0.000000000000000000000010.0	
Biotin (K)	0.100000000000.0	
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Final list after background is subtracted

RMT-EC		62	STRING gene names and description
ABLM2_MOUSE	Ablim2		Ablim2 - Actin-binding LIM protein 2; May act as scaff
ACSM5_MOUSE	Acsm5		Acsm5 - Acyl-coa synthetase medium-chain family m
ACTH_MOUSE	Actg2		Actg2 - Actin, gamma 2, smooth muscle, enteric; Acti
ADT2_MOUSE	Slc25a5		Slc25a5 - Solute carrier family 25 (mitochondrial carri
AP180_MOUSE	Snap91		Snap91 - Adaptins are components of the adaptor cor
ATPB_MOUSE	Atp5b		Atp5b - Atp synthase, h+ transporting mitochondrial f1
AUXI_MOUSE	Dnajc6		Dnajc6 - Dnaj heat shock protein family (hsp40) mem
BASP1_MOUSE	Basp1		Basp1 - Brain abundant, membrane attached signal pr
BD1L1_MOUSE	Bod1l		Bod1l - Biorientation of chromosomes in cell division p
CAPS1_MOUSE	Cadps		Cadps - Calcium-dependent secretion activator 1; Ca
CLAP2_MOUSE	Clasp2		Clasp2 - Clip-associating protein 1/2; Microtubule plus
CMTR1_MOUSE	Cmtr1		Cmtr1 - Cap-specific mRNA (nucleoside-2'-O-)-methy
DDX46_MOUSE	Ddx46		Ddx46 - Probable ATP-dependent RNA helicase DDX
DLG2_MOUSE	Dlg2		Dlg2 - Discs large maguk scaffold protein 2; Disks lar
DLGP2_MOUSE	Dlgap2		Dlgap2 - Disks large-associated protein 2; May play a
DNJC5_MOUSE	Dnajc5		Dnajc5 - Dnaj heat shock protein family (hsp40) mem
EEA1_MOUSE	Eea1		Eea1 - Early endosome antigen 1; Binds phospholipid
FKBP4_MOUSE	Fkbp4		Fkbp4 - Peptidyl-prolyl cis-trans isomerase FKBP4; Ir
GIT1_MOUSE	Git1		Git1 - ARF GTPase-activating protein GIT1; GTPase-
GLD2_MOUSE	Papd4		Papd4 - Terminal nucleotidyltransferase 2; Poly(A) RN
HNRPM_MOUSE	Hnrnpm		Hnrnpm - Heterogeneous nuclear ribonucleoprotein M
HXK1_MOUSE	Hk1		Hk1 - Hexokinase-1; Hexokinase 1; Belongs to the he
HYALP_MOUSE	Spam1		Spam1 - Hyaluronoglucosaminidase; Hyaluronidase P
IL7RA_MOUSE	Il7r		Il7r - Interleukin-7 receptor subunit alpha; Receptor fo
JIP4_MOUSE	Spag9		Spag9 - C-Jun-amino-terminal kinase-interacting prot
KCC2A_MOUSE	Camk2a		Camk2a - Calcium/calmodulin-dependent protein kina
KCC2B_MOUSE	Camk2b		Camk2b - Calcium/calmodulin-dependent protein kina
LAS1L_MOUSE	Las1l		Las1l - Ribosomal biogenesis protein LAS1L; Involved
MAP4_MOUSE	Map4		Map4 - Microtubule-associated protein 4; Non-neuron
MECP2_MOUSE	Mecp2		Mecp2 - Methyl-CpG-binding protein 2; Chromosomal
NFM_MOUSE	Nefm		Nefm - Neurofilament medium polypeptide (neurofilam
NMDE2_MOUSE	Grin2b		Grin2b - Glutamate receptor, ionotropic, nmda2b (eps
NSF_MOUSE	Nsf		Nsf - N-ethylmaleimide sensitive fusion protein; Vesicl
PAK2_MOUSE	Pak2		Pak2 - Serine/threonine-protein kinase PAK 2; Serine/
PDZD8_MOUSE	Pdzd8		Pdzd8 - PDZ domain-containing protein 8; Molecular t
PLEC_MOUSE	Plec		Plec - Plectin; Interlinks intermediate filaments with mi
PP2BA_MOUSE	Ppp3ca		Ppp3ca - Serine/threonine-protein phosphatase 2B ca
PRR11_MOUSE	Prr11		Prr11 - Proline-rich protein 11; Plays a critical role in c
QCR2_MOUSE	Uqcrc2		Uqcrc2 - Cytochrome b-c1 complex subunit 2, mitoch
RELCH_MOUSE	Relch		Relch - RAB11 binding and LisH domain, coiled-coil ar
RHG35_MOUSE	Arhgap35		Arhgap35 - Glucocorticoid receptor dna-binding factor
RIMS1_MOUSE	Rims1		Rims1 - Regulating synaptic membrane exocytosis pr
RT23_MOUSE	Mrps23		Mrps23 - Mitochondrial ribosomal protein S23; Belong
RTN3_MOUSE	Rtn3		Rtn3 - Reticulon-3; May be involved in membrane traf
SET_MOUSE	Set		Set - Protein SET; Multitasking protein, involved in apo
SH3G2_MOUSE	Sh3gl2		Sh3gl2 - SH3-domain GRB2-like 2; Endophilin-A1; Imp
SMC4_MOUSE	Smc4		Smc4 - Structural maintenance of chromosomes prot
SRC8_MOUSE	Cttn		Cttn - Src substrate cortactin; Contributes to the orga
SRCN1_MOUSE	Srcin1		Srcin1 - Src kinase signaling inhibitor 1; Acts as a neg
SRPK2_MOUSE	Srpk2		Srpk2 - SRSF protein kinase 2; Serine/arginine-rich pr
SYNE4_MOUSE	Syne4		Syne4 - Spectrin repeat containing, nuclear envelope

SYUG_MOUSE	Sncg	Sncg - Gamma-synuclein; Plays a role in neurofilame
TAU_MOUSE	Mapt	Mapt - Microtubule-associated protein tau; Promotes
TCPH_MOUSE	Cct7	Cct7 - T-complex protein 1 subunit eta; Molecular cha
TCPQ_MOUSE	Cct8	Cct8 - Chaperonin containing tcp1, subunit 8 (theta);
TEP1_MOUSE	Tep1	Tep1 - Telomerase associated protein 1; Telomerase
TMM62_MOUSE	Tmem62	Tmem62 - Transmembrane protein 62 [a.k.a. NP_780
TRAP1_MOUSE	Trap1	Trap1 - Heat shock protein 75 kDa, mitochondrial; Ch
UD3A2_MOUSE	Ugt3a2	Ugt3a2 - UDP-glucuronosyltransferase 3A2; UDP-glu
VA0D2_MOUSE	Atp6v0d2	Atp6v0d2 - Atpase, h+ transporting, lysosomal v0 sub
VAMP3_MOUSE	Vamp3	Vamp3 - Vesicle-associated membrane protein 3; SN
WEE1_MOUSE	Wee1	Wee1 - Wee 1 homolog 1 (s. pombe); Wee1-like prote

Network Properties

number of nodes:	62
number of edges:	89
average node degree:	2.87
avg. local clustering coefficient:	0.353
expected number of edges:	34
PPI enrichment p-value:	4E-15

old protein. May stimulate ABRA activity and ABRA-dependent SRF transcriptional activity [a.k.
ember 5; Acyl-coenzyme A synthetase ACSM5, mitochondrial; Has medium-chain fatty acid:C
n, gamma-enteric smooth muscle; Actins are highly conserved proteins that are involved in var
er, adenine nucleotide translocator), member 5; ADP/ATP translocase 2; Catalyzes the exchan
mplexes which link clathrin to receptors in coated vesicles. Clathrin-associated protein comple
complex, beta subunit; ATP synthase subunit beta, mitochondrial; Mitochondrial membrane A
ber c6; Putative tyrosine-protein phosphatase auxilin; Recruits HSPA8/HSC70 to clathrin-coate
rotein 1 [a.k.a. Nap22, mmu:70350, Basp1-201, BASP1_MOUSE]
rotein 1-like 1; Component of the fork protection machinery required to protect stalled/damage
lcium-binding protein involved in exocytosis of vesicles filled with neurotransmitters and neurop
-end tracking protein that promotes the stabilization of dynamic microtubules. Involved in the n
yltransferase 1; S-adenosyl-L-methionine-dependent methyltransferase that mediates mRNA c
46; Plays an essential role in splicing, either prior to, or during A complex formation [a.k.a. Kiaa
ge homolog 2; Required for perception of chronic pain through NMDA receptor signaling. Regu
role in the molecular organization of synapses and neuronal cell signaling. Could be an adapte
ber c5; DnaJ homolog subfamily C member 5; Acts as a co-chaperone for the SNARE protein
vesicles containing phosphatidylinositol 3-phosphate and participates in endosomal trafficking
mmunophilin protein with PPIase and co-chaperone activities. Component of steroid receptors h
-activating protein for the ADP ribosylation factor family. May serve as a scaffold to bring togeth
NA polymerase GLD2; Cytoplasmic poly(A) RNA polymerase that adds successive AMP monc
1; Pre-mRNA binding protein in vivo, binds avidly to poly(G) and poly(U) RNA homopolymers in
exokinase family [a.k.a. OTTMUST00000086517, uc007fgy.2, Q61659, HXK1_MOUSE]
PH-20; Involved in sperm-egg adhesion. Upon fertilization sperm must first penetrate a layer of
r interleukin-7. Also acts as a receptor for thymic stromal lymphopoietin (TSLP) [a.k.a. CD127,
ein 4; The JNK-interacting protein (JIP) group of scaffold proteins selectively mediates JNK sig
se type II subunit alpha; CaM-kinase II (CAMK2) is a prominent kinase in the central nervous s
se type II subunit beta; Calcium/calmodulin-dependent protein kinase that functions autonomou
l in the biogenesis of the 60S ribosomal subunit. Required for maturation of the 28S rRNA (By s
al microtubule-associated protein. Promotes microtubule assembly [a.k.a. Mtap4, XP_006512C
l protein that binds to methylated DNA. It can bind specifically to a single methyl-CpG pair. It is
ent 3); Neurofilament medium polypeptide; Neurofilaments usually contain three intermediate fil
silon 2); Component of NMDA receptor complexes that function as heterotetrameric, ligand-gate
le-fusing ATPase; Required for vesicle-mediated transport. Catalyzes the fusion of transport ve
'threonine protein kinase that plays a role in a variety of different signaling pathways including c
ethering protein that connects endoplasmic reticulum and mitochondria membranes. PDZD8- c
crotubules and microfilaments and anchors intermediate filaments to desmosomes or hemides
talytic subunit alpha isoform; Calcium-dependent, calmodulin-stimulated protein phosphatase.
cell cycle progression [a.k.a. OTTMUSG00000001219, ENSMUSP00000060803, B930067F20
ondrial; This is a component of the ubiquinol-cytochrome c reductase complex (complex III or
nd HEAT repeat containing; LisH domain and HEAT repeat-containing protein KIAA1468; RIKE
r 1; Rho GTPase-activating protein 35; Rho GTPase-activating protein (GAP), binds several ac
rotein 1; Rab effector involved in exocytosis . May act as scaffold protein that regulates neurotr
s to the mitochondrion-specific ribosomal protein mS23 family [a.k.a. Mrps23-004, OTTMUSP0
fficking in the early secretory pathway. Inhibits BACE1 activity and amyloid precursor protein pr
optosis, transcription, nucleosome assembly and histone chaperoning. Isoform 2 anti-apoptotic
plicated in synaptic vesicle endocytosis. May recruit other proteins to membranes with high cur
ein 4; Central component of the condensin complex, a complex required for conversion of inter
nization of the actin cytoskeleton and cell shape. Plays a role in the formation of lamellipodia an
gative regulator of SRC by activating CSK which inhibits SRC activity and downstream signaling
rotein-specific kinase which specifically phosphorylates its substrates at serine residues locate
family member 4; Nesprin-4; As a component of the LINC (LInker of Nucleoskeleton and Cytos

nt network integrity. May be involved in modulating axonal architecture during development and
microtubule assembly and stability, and might be involved in the establishment and maintenanc
aperone; assists the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in th
T-complex protein 1 subunit theta; Molecular chaperone; assists the folding of proteins upon AT
protein component 1; Component of the telomerase ribonucleoprotein complex that is essentia
)494, OTTMUST00000037990, ENSMUSP00000118808, TMM62_MOUSE]
aperone that expresses an ATPase activity. Involved in maintaining mitochondrial function and
curonosyltransferases catalyze phase II biotransformation reactions in which lipophilic substra
unit d2; V-type proton ATPase subunit d 2; Subunit of the integral membrane V0 complex of va
ARE involved in vesicular transport from the late endosomes to the trans-Golgi network [a.k.a.
ein kinase; Acts as a negative regulator of entry into mitosis (G2 to M transition) by protecting th

a. ENSMUST00000114206, CCDS51477.1, NP_001171170.1, ABLM2_MOUSE]
oA ligase activity with broad substrate specificity (in vitro). Acts on acids from C(4) to C(11) an
ious types of cell motility and are ubiquitously expressed in all eukaryotic cells [a.k.a. Actsg, Ac
ıge of cytoplasmic ADP with mitochondrial ATP across the mitochondrial inner membrane. As p
kes are believed to interact with the cytoplasmic tails of membrane proteins, leading to their sel
TP synthase (F(1)F(0) ATP synthase or Complex V) produces ATP from ADP in the presence
ed vesicles and promotes uncoating of clathrin-coated vesicles. Plays a role in clathrin-mediate

d replication forks from uncontrolled DNA2- dependent resection. Acts by stabilizing RAD51 at
eptides. Probably acts upstream of fusion in the biogenesis or maintenance of mature secreto
ucleation of noncentrosomal microtubules originating from the trans-Golgi network (TGN). Req
ap1 2'-O-ribose methylation to the 5'-cap structure of mRNAs. Methylates the ribose of the firs
0801, ENSMUST00000172272, Probable ATP-dependent RNA helicase DDX46, DDX46_MOU
lates surface expression of NMDA receptors in dorsal horn neurons of the spinal cord. Interac
r protein linking ion channel to the subsynaptic cytoskeleton. May induce enrichment of PSD-9
SNAP-25. Involved in the calcium-mediated control of a late stage of exocytosis. Acts as a gen
[a.k.a. XM_006513522, XM_006513525, BC075637, EEA1_MOUSE]
heterocomplexes through interaction with heat-shock protein 90 (HSP90). May play a role in th
her molecules to form signaling modules controlling vesicle trafficking, adhesion and cytoskelet
mers to the 3'-end of specific RNAs, forming a poly(A) tail. In contrast to the canonical nuclear
vitro. Involved in splicing. Acts as a receptor for carcinoembryonic antigen in Kupffer cells, ma

cumulus cells that surrounds the egg before reaching the zona pellucida. The cumulus cells ar
MGI:96562, UPI0000020D9F, IL7RA_MOUSE]
naling by aggregating specific components of the MAPK cascade to form a functional JNK sign
ystem that may function in long-term potentiation and neurotransmitter release. Member of the
ısly after Ca(2+)/calmodulin-binding and autophosphorylation, and is involved in dendritic spine
similarity). Functions as a component of the Five Friends of Methylated CHTOP (5FMC) compl
018.1, XM_006511956.1, MAP4_MOUSE]
not influenced by sequences flanking the methyl-CpGs. Mediates transcriptional repression thr
ament proteins: L, M, and H which are involved in the maintenance of neuronal caliber [a.k.a. N
ed ion channels with high calcium permeability and voltage-dependent sensitivity to magnesium
esicles within the Golgi cisternae. Is also required for transport from the endoplasmic reticulum
ytoskeleton regulation, cell motility, cell cycle progression, apoptosis or proliferation. Acts as d
lependent endoplasmic reticulum-mitochondria membrane tethering is essential for endoplasmi
mosomes. May be involved not only in the cross-linking and stabilization of cytoskeletal interme
Many of the substrates contain a PxIxIT motif. This subunit may have a role in the calmodulin a
Rik, PRR11_MOUSE]
cytochrome b-c1 complex), which is part of the mitochondrial respiratory chain. The core prote
N cDNA 2310035C23 gene [a.k.a. 2310035C23Rik, RP24-353D23.1-011, ENSMUST00000172
cidic phospholipids which inhibits the Rho GAP activity to promote the Rac GAP activity. This b
ransmitter release at the active zone. Essential for maintaining normal probability of neurotransı
)0000001431, CCDS25227.1, RT23_MOUSE]
rocessing. May induce caspase-8 cascade and apoptosis. May favor BCL2 translocation to the
activity is mediated by inhibition of the GZMA-activated DNase, NME1. In the course of cytoto
vature. Required for BDNF-dependent dendrite outgrowth. Cooperates with SH3GL2 to mediat
phase chromatin into mitotic-like condense chromosomes. The condensin complex probably in
d in cell migration (By similarity). Plays a role in the regulation of neuron morphology, axon grov
g, leading to impaired cell spreading and migration. Regulates dendritic spine morphology. Involv
ed in regions rich in arginine/serine dipeptides, known as RS domains and is involved in the phc
skeleton) complex, involved in the connection between the nuclear lamina and the cytoskeleton

l in the adult. In vitro, increases the susceptibility of neurofilament-H to calcium-dependent prot
e of neuronal polarity. The C-terminus binds axonal microtubules while the N- terminus binds n
e folding of actin and tubulin; Belongs to the TCP-1 chaperonin family [a.k.a. Ccth, chaperonin c
TP hydrolysis. As part of the BBS/CCT complex may play a role in the assembly of BBSome, a
ıl for the replication of chromosome termini. Also component of the ribonucleoprotein vaults par

polarization, downstream of PINK1 and mitochondrial complex I. Is a negative regulator of mitc
ıtes are conjugated with glucuronic acid to increase water solubility and enhance excretion. The
ıcuolar ATPase. Vacuolar ATPase is responsible for acidifying a variety of intracellular compart
Syb3, D130027G05Rik, AK169087, VAMP3_MOUSE]
ıe nucleus from cytoplasmically activated cyclin B1-complexed CDK1 before the onset of mitos

d on the corresponding 3-hydroxy- and 2,3- or 3,4- unsaturated acids (in vitro) (By similarity) [
cta3, M26689, ACTH_MOUSE]
art of the mitotic spindle-associated MMXD complex it may play a role in chromosome segrega
ection and concentration. Binding of AP180 to clathrin triskelia induces their assembly into 60- 7
of a proton gradient across the membrane which is generated by electron transport complexes
d endocytosis in neurons [a.k.a. Kiaa0473, AK147570, uc008tvt.1, AUXI_MOUSE]

stalled replication forks and protecting RAD51 nucleofilaments from the antirecombinogenic act
y vesicles. Regulates catecholamine loading of DCVs. May specifically mediate the Ca(2+)-de
uired for the polarization of the cytoplasmic microtubule arrays in migrating cells towards the le
t nucleotide of a m(7)GpppG-capped mRNA and small nuclear RNA (snRNA) to produce m(7)
ISE]
ts with the cytoplasmic tail of NMDA receptor subunits as well as inward rectifying potassium c
5/SAP90 at the plasma membrane [a.k.a. Dap2, Dlgap2-002, uc009kyy.2, DLGP2_MOUSE]
neral chaperone in regulated exocytosis (By similarity). May have an important role in presynap

e intracellular trafficking of heterooligomeric forms of steroid hormone receptors between cytop
al organization. Increases the speed of cell migration, as well as the size and rate of formation
poly(A) RNA polymerase, it only adds poly(A) to selected cytoplasmic mRNAs. Does not play
y initiate a series of signaling events leading to tyrosine phosphorylation of proteins and inducti

e embedded in a matrix containing hyaluronic acid which is formed prior to ovulation. This prote

naling module [a.k.a. Mapk8ip4, Jsap2, Jip4, JIP4_MOUSE]
NMDAR signaling complex in excitatory synapses it may regulate NMDAR-dependent potentia
and synapse formation, neuronal plasticity and regulation of sarcoplasmic reticulum Ca(2+) tra
ex; the 5FMC complex is recruited to ZNF148 by methylated CHTOP, leading to desumoylation

ough interaction with histone deacetylase and the corepressor SIN3. Binds both 5-methylcytos
lef3, Nfm, ENSMUSP00000022638, NFM_MOUSE]
. Channel activation requires binding of the neurotransmitter glutamate to the epsilon subunit, g
to the Golgi stack. Seems to function as a fusion protein required for the delivery of cargo prot
ownstream effector of the small GTPases CDC42 and RAC1. Activation by the binding of active
c reticulum-mitochondria Ca(2+) transfer. In neurons, involved in the regulation of dendritic Ca(
ediate filaments network, but also in the regulation of their dynamics; Belongs to the plakin or cy
nctivation of calcineurin. Dephosphorylates DNM1L and HSPB1 (By similarity). Dephosphorylat

ein 2 is required for the assembly of the complex (By similarity); Belongs to the peptidase M16 f
039, RELCH_MOUSE]
inding is inhibited by phosphorylation by PRKCA (By similarity). Involved in cell differentiation as
mitter release and for regulating release during short-term synaptic plasticity . Plays a role in de

e mitochondria upon endoplasmic reticulum stress (By similarity). Induces the formation of endo
xic T- lymphocyte (CTL)-induced apoptosis, GZMA cleaves SET, disrupting its binding to NME
e BDNF-NTRK2 early endocytic trafficking and signaling from early endosomes [a.k.a. Sh3d2a
ntroduces positive supercoils into relaxed DNA in the presence of type I topoisomerases and co
wth and formation of neuronal growth cones (By similarity). Through its interaction with CTTNB
ved in calcium-dependent exocytosis. May play a role in neurotransmitter release or synapse r
sphorylation of SR splicing factors and the regulation of splicing. Promotes neuronal apoptosis
n. The nucleocytoplasmic interactions established by the LINC complex play an important role in

eases. May also function in modulating the keratin network in skin. Activates the MAPK and Elk
eural plasma membrane components, suggesting that tau functions as a linker protein betweer
containing Tcp1, subunit 7 (eta), BAA81878.1, TCPH_MOUSE]
complex involved in ciliogenesis regulating transports vesicles to the cilia. Known to play a role
ticle, a multi- subunit structure involved in nucleo-cytoplasmic transport. Responsible for the lo

chondrial respiration able to modulate the balance between oxidative phosphorylation and aerc
ey are of major importance in the conjugation and subsequent elimination of potentially toxic xer
ments in eukaryotic cells, thus providing most of the energy required for transport processes i

sis by mediating phosphorylation of CDK1 on 'Tyr-15'. Specifically phosphorylates and inactivat

a.k.a. Macs3, 6.2.1.2, AK149591, ACSM5_MOUSE]

ation (By similarity); Belongs to the mitochondrial carrier (TC 2.A.29) family [a.k.a. Ant2, ADT2_
70 nm coats [a.k.a. Snap91-001, OTTMUST00000120811, ENSMUSP00000128738, AP180_M
s of the respiratory chain. F-type ATPases consist of two structural domains, F(1) - containing

tivities of FBXO18/FBH1 and BLM. Does not regulate spindle orientation [a.k.a. Kiaa1327, ENSI
pendent exocytosis of large dense-core vesicles (DCVs) and other dense-core vesicles by ac
ading edge of the cell. May act at the cell cortex to enhance the frequency of rescue of depolyr
GpppRm (cap1). Displays a preference for cap0 transcripts. Cap1 modification is linked to high

hannels. Involved in regulation of synaptic stability at cholinergic synapses. Part of the postsyn

tic function (By similarity). May be involved in calcium-dependent neurotransmitter release at n

lasm and nuclear compartments. The isomerase activity controls neuronal growth cones via re
of protrusions, possibly by targeting PAK1 to adhesions and the leading edge of lamellipodia. Se
a role in replication-dependent histone mRNA degradation (By similarity) [a.k.a. Gld2, Tent2, X
on of IL-1 alpha, IL-6, IL-10 and tumor necrosis factor alpha cytokines (By similarity) [a.k.a. Hn

ein aids in penetrating the layer of cumulus cells by digesting hyaluronic acid [a.k.a. Spam, Ph2

ation of the AMPAR and synaptic plasticity. Phosphorylates transcription factor FOXO3 on 'Ser·
nsport in skeletal muscle. In neurons, plays an essential structural role in the reorganization of
n of ZNF148 and subsequent transactivation of ZNF148 target genes; Belongs to the LAS1 fam

sine (5mC) and 5-hydroxymethylcytosine (5hmC)-containing DNA, with a preference for 5-metl

lycine binding to the zeta subunit, plus membrane depolarization to eliminate channel inhibition b
eins to all compartments of the Golgi stack GRIA2 leads to influence GRIA2 membrane cycling
e CDC42 and RAC1 results in a conformational change and a subsequent autophosphorylation
2+) dynamics by regulating mitochondrial Ca(2+) uptake in neurons [a.k.a. AAI41372.1, PDZ d
tolinker family [a.k.a. Plec1, NP_958793, NM_201389, PLEC_MOUSE]
es SSH1; Belongs to the PPP phosphatase family. PP-2B subfamily [a.k.a. Calna, 19055, EC 3

amily. UQCRC2/QCR2 subfamily [

s well as cell adhesion and migration, plays an important role in retinal tissue morphogenesis, n
endrite formation by melanocytes (By similarity) [a.k.a. MGI:2152971, UPI0000D8ABB2, Rab-3·

oplasmic reticulum tubules [a.k.a. AF195940, Q8CCU2, uc008gle.2, RTN3_MOUSE]
1 and releasing NME1 inhibition. Isoform 1 and isoform 2 are potent inhibitors of protein phosph
a, Een1, A830014P03, SH3G2_MOUSE]
onverts nicked DNA into positive knotted forms in the presence of type II topoisomerases (By s
P2, involved in the regulation of neuronal spine density. Plays a role in the invasiveness of canc
naintenance (By similarity) [a.k.a. P140, UPI000059DCDF, XP_006533843.1, SRCN1_MOUSE
by up-regulating cyclin-D1 (CCND1) expression. This is done by the phosphorylation of SRSF
n the transmission of mechanical forces across the nuclear envelope and in nuclear movemen

:-1 signal transduction pathway (By similarity); Belongs to the synuclein family [a.k.a. Persyn, 2
ı both. Axonal polarity is predetermined by tau localization (in the neuronal cell) in the domain of

, in vitro, in the folding of actin and tubulin (By similarity) [a.k.a. Cctq, Cct8-009, OTTMUST000
calizing and stabilizing vault RNA (vRNA) association in the vault ribonucleoprotein particle. Bin

bic glycolysis. The impact of TRAP1 on mitochondrial respiration is probably mediated by modu
nobiotics and endogenous compounds (By similarity); Belongs to the UDP-glycosyltransferase
n the vacuolar system (By similarity). May play a role in coupling of proton transport and ATP h

tes cyclin B1-complexed CDK1 reaching a maximum during G2 phase and a minimum as cells

MOUSE, ENSMUSG00000016319]
OUSE]
the extramembraneous catalytic core, and F(0) - containing the membrane proton channel, lin

MUSG00000061755, Q80TF0, BD1L1_MOUSE]
ting as a PtdIns(4,5)P2-binding protein that acts at prefusion step following ATP-dependent pri
merizing microtubules by attaching their plus-ends to cortical platforms composed of ERC1 and
ner levels of translation. May be involved in the interferon response pathway [a.k.a. Ftsjd2, Kiaa

aptic protein scaffold of excitatory synapses [a.k.a. Dlgh2, XP_006507851, XP_006507850, DI

erve endings (By similarity) [a.k.a. OTTMUST00000040588, NM_016775.3, Csp, DNJC5_MO

egulation of TRPC1 channel opening. Acts also as a regulator of microtubule dynamics by inhib
equesters inactive non-tyrosine- phosphorylated paxillin in cytoplasmic complexes (By similarit
M_017315331.1, GLD2_MOUSE]
irpm, Hnrnpm-002, ENSMUSP00000084864, HNRPM_MOUSE]

0, uc009bby.2, HYALP_MOUSE]

-298' (By similarity). Activates FOXO3 transcriptional activity [a.k.a. ENSMUSP00000048325, F
the actin cytoskeleton during plasticity by binding and bundling actin filaments in a kinase-indep
ily [a.k.a. A2BE30, LAS1-like (S. cerevisiae), 76130, LAS1L_MOUSE]

hylcytosine (5mC) [a.k.a. ENSMUSP00000033770, OTTMUST00000043832, NM_010788.4, M

by Mg(2+) . Sensitivity to glutamate and channel kinetics depend on the subunit composition . In
(By similarity) [a.k.a. Skd2, AU020090, ENSMUST00000127813, NSF_MOUSE]
on several serine and/or threonine residues. Full-length PAK2 stimulates cell survival and cell
omain containing 8, 107368, PDZD8_MOUSE]

.1.3.16, PP2BA_MOUSE]

eural tube fusion, midline fusion of the cerebral hemispheres and mammary gland branching m
-interacting molecule 1, RIMS1_MOUSE]

natase 2A. Isoform 1 and isoform 2 inhibit EP300/CREBBP and PCAF-mediated acetylation of h

similarity) [a.k.a. Smc4l1, Capc, OTTMUST00000060030, SMC4_MOUSE]
cer cells, and the formation of metastases (By similarity). Plays a role in focal adhesion assemb
E]
F2, leading to the suppression of p53/TP53 phosphorylation thereby relieving the repressive eff
t and positioning (By similarity). Behaves as a kinesin cargo, providing a functional binding site

:0618, C530045H03, SYUG_MOUSE]
f the cell body defined by the centrosome. The short isoforms allow plasticity of the cytoskeletc

00104334, TCPQ_MOUSE]
ds to TERC (By similarity) [a.k.a. Tp1, XP_006518861.1, XM_006518798, TEP1_MOUSE]

ulation of mitochondrial SRC and inhibition of SDHA [a.k.a. Hsp75, AAH22912.1, NM_026508.2
family [a.k.a. C730018P11, ENSMUST00000090378, UDPGT 3A2, UD3A2_MOUSE]
ıydrolysis. Regulator of osteoclast fusion and bone formation; Belongs to the V-ATPase V0D/A

enter M phase. Phosphorylation of cyclin B1-CDK1 occurs exclusively on 'Tyr-15' and phosph

ked together by a central stalk and a peripheral stalk. During catalysis, ATP synthesis in t [...] [

ming and participates in DCVs-membrane fusion. However, it may also participate in [...] [a.k.a.
l PHLDB2. This cortical microtubule stabilizing activity is regulated at [...] [a.k.a. NM_00111434
a0082, I830119C20, CMTR1_MOUSE]

LG2_MOUSE]

USE]

iting MAPT/TAU ability to promote microtubule assembly. May have a protective role a [...] [a.k
y). Involved in the regulation of cytokinesis; the function may invo [...] [a.k.a. OTTMUST00000

P11798, Q61284, KCC2A_MOUSE]
pendent manner. This structural function is required for correct targeti [...] [a.k.a. Camk2d, Can

MECP2_MOUSE]

n concert with DAPK1 at extrasynaptic sites, acts as a central mediator for [...] [a.k.a. OTTMUS

growth. Phosphorylates MAPK4 and MAPK6 and activates the downstream targ [...] [a.k.a. PA

orphogenesis. Transduces signals from p21-ras to the nucleus, acting via the r [...] [a.k.a. Grlf

istones (HAT) and nucleosomes, most probably by masking the accessibility of lysi [...] [a.k.a.

oly and turnover (By similarity). In complex with ABL1 and M [...] [a.k.a. Ems1, BAE38252.1, XM

ect of p53/TP53 on cyclin-D1 (CCND1) expression. Phosphorylates ACIN1, and [...] [a.k.a. 71
for kinesin-1 at the nuclear envelope. Hence may contribute to the establishment of [...] [a.k.a.

›n whereas the longer isoforms may preferentially play a role in its stabil [...] [a.k.a. Tau, Mtapt,

, TRAP1_MOUSE]

C39 subunit family [a.k.a. BAC40907.1, OTTMUST00000014513, ENSMUSG00000028238, VA

ıorylation of monomeric CDK1 does not occur. Its activity increases during S and G2 phases [.

a.k.a. I420029F15, AAH18392.1, AK145684, ATPB_MOUSE]

Kiaa1121, Caps1, Caps, CAPS1_MOUSE]
7, ENSMUST00000084888, ENSMUST00000035088, CLAP2_MOUSE]

.a. Fkpb52, p59, HBI, FKBP4_MOUSE]
018576, ENSMUST00000152428, ENSMUSG00000011877, GIT1_MOUSE]

nk2b-010, NP_031621.3, KCC2B_MOUSE]

ST00000118422, Grin2b-002, CCDS20648.1, NMDE2_MOUSE]

K2_MOUSE, NM_177326.2, XM_006522072]

1, P190A, p190ARHOGAP, RHG35_MOUSE]

Set-003, Template-activating factor I, ENSMUST00000102866, SET_MOUSE]

1_006508472, SRC8_MOUSE]

20479J06, Srpk2-201, XP_006535727.1, SRPK2_MOUSE]
ENSMUSG00000019737, 233066, mmu:233066, SYNE4_MOUSE]

ENSMUSP00000102600, TAU_MOUSE]

\0D2_MOUSE]

..] [a.k.a. Q9EPL7, WEE1_MOUSE, Wee1-201]

Table 16 **Total peptides list for three control rAAVs in the encoding-consolida**
n=8, pep = 440, pro = 51

rAAV	Sample	Biotin	Protein Accession	Protein Description
SYN-MiniTid	1	d1-4	ANR35_MOUSE	Ankyrin repeat domain-contain
SYN-MiniTid	1	d1-4	ANR35_MOUSE	Ankyrin repeat domain-contain
SYN-MiniTid	1	d1-4	ICAM1_MOUSE	Intercellular adhesion molecule
SYN-MiniTid	1	d1-4	ICAM1_MOUSE	Intercellular adhesion molecule
SYN-MiniTid	1	d1-4	MAP6_MOUSE	Microtubule-associated protein
SYN-MiniTid	1	d1-4	MAP6_MOUSE	Microtubule-associated protein
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Ateles ge
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Lagothrix
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Mus mus
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Rattus no
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Ateles ge
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Lagothrix
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Mus mus
SYN-MiniTid	1	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Rattus no
SYN-MiniTid	1	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
SYN-MiniTid	1	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
SYN-MiniTid	1	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
SYN-MiniTid	1	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
RAM-MiniTid	2	d1-4	ICAM1_MOUSE	Intercellular adhesion molecule
RAM-MiniTid	2	d1-4	ICAM1_MOUSE	Intercellular adhesion molecule
RAM-MiniTid	2	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid	2	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho

RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	2	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	2	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid	2	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid	2	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid	2	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SNP25_MOUSE	Synaptosomal-associated prot
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Bos taurus
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Homo sap
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Rattus nor
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Bos taurus
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Homo sap
RAM-MiniTid	2	d1-4	SYUB_MOUSE	Beta-synuclein OS=Rattus nor
RAM-MiniTid 3		d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid 3		d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 3		d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 3		d1-4	SYUB_MOUSE	Beta-synuclein Gene: Sncb
RAM-MiniTid 3		d1-4	SYUB_MOUSE	Beta-synuclein Gene: Sncb
RAM-MiniTid 3		d1-4	SYUB_MOUSE	Beta-synuclein Gene: Sncb
RAM-MiniTid 3		d1-4	SYUB_MOUSE	Beta-synuclein Gene: Sncb
RAM-MiniTid 3		d1-4	SYUB_MOUSE	Beta-synuclein Gene: Sncb
RAM-MiniTid 3		d1-4	TIM44_MOUSE	Mitochondrial import inner mem
RAM-MiniTid 3		d1-4	VAMP1_MOUSE	Vesicle-associated membrane
RAM-MiniTid 3		d1-4	AAK1_MOUSE	AP2-associated protein kinase
RAM-MiniTid 3		d1-4	AAK1_MOUSE	AP2-associated protein kinase
RAM-MiniTid 3		d1-4	BIN1_MOUSE	Myc box-dependent-interacting
RAM-MiniTid 3		d1-4	BRAF_MOUSE	Serine/threonine-protein kinase
RAM-MiniTid 3		d1-4	BRAF_MOUSE	Serine/threonine-protein kinase
RAM-MiniTid 3		d1-4	CH10_MOUSE	10 kDa heat shock protein, mit
RAM-MiniTid 3		d1-4	CH10_MOUSE	10 kDa heat shock protein, mit
RAM-MiniTid 3		d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
RAM-MiniTid 3		d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
RAM-MiniTid 3		d1-4	CPLX2_MOUSE	Complexin-2 Gene: CPLX2

RAM-MiniTid 3	d1-4	CPLX2_MOUSE	Complexin-2, Gene: CPLX2
RAM-MiniTid 3	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr
RAM-MiniTid 3	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr
RAM-MiniTid 3	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 3	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 3	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 3	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 3	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 3	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 3	d1-4	GRIN1_MOUSE	G protein-regulated inducer of
RAM-MiniTid 3	d1-4	ISCU_MOUSE	Iron-sulfur cluster assembly en
RAM-MiniTid 3	d1-4	ISCU_MOUSE	Iron-sulfur cluster assembly en
RAM-MiniTid 3	d1-4	MAP1A_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP1B_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MCCA_MOUSE	Methylcrotonoyl-CoA carboxyl
RAM-MiniTid 3	d1-4	MCCA_MOUSE	Methylcrotonoyl-CoA carboxyl
RAM-MiniTid 3	d1-4	MCCA_MOUSE	Methylcrotonoyl-CoA carboxyl
RAM-MiniTid 3	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 3	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 3	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 3	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 3	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 3	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 3	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 3	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 3	d1-4	RT31_MOUSE	28S ribosomal protein S31, mit
RAM-MiniTid 3	d1-4	RT31_MOUSE	28S ribosomal protein S31, mit
RAM-MiniTid 3	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 3	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 3	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 3	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 3	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 3	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 3	d1-4	SPTN1_MOUSE	Spectrin alpha chain, non-eryth
RAM-MiniTid 3	d1-4	SPTN1_MOUSE	Spectrin alpha chain, non-eryth
RAM-MiniTid 3	d1-4	SUGP2_MOUSE	SURP and G-patch domain-co
RAM-MiniTid 3	d1-4	SYNRG_MOUSE	Synergin gamma, Gene: Synrg
RAM-MiniTid 3	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca

RAM-MiniTid 3	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 3	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 3	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 3	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 3	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 3	d1-4	TIM44_MOUSE	Mitochondrial import inner mem
RAM-MiniTid 3	d1-4	TIM44_MOUSE	Mitochondrial import inner mem
SYN-MiniTid 4	d1-4	CPLX1_MOUSE	Complexin-1, Gene: Cplx1
SYN-MiniTid 4	d1-4	CPLX1_MOUSE	Complexin-1, Gene: Cplx1
SYN-MiniTid 4	d1-4	CPLX1_MOUSE	Complexin-1, Gene: CPLX1
SYN-MiniTid 4	d1-4	CPLX1_MOUSE	Complexin-1, Gene: CPLX1
SYN-MiniTid 4	d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
SYN-MiniTid 4	d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
SYN-MiniTid 4	d1-4	CPLX2_MOUSE	Complexin-2, Gene: CPLX2
SYN-MiniTid 4	d1-4	CPLX2_MOUSE	Complexin-2, Gene: CPLX2
SYN-MiniTid 4	d1-4	MAP6_MOUSE	Microtubule-associated protein
SYN-MiniTid 4	d1-4	MAP6_MOUSE	Microtubule-associated protein
SYN-MiniTid 4	d1-4	MTAP2_MOUSE	Microtubule-associated protein
SYN-MiniTid 4	d1-4	MTAP2_MOUSE	Microtubule-associated protein
SYN-MiniTid 4	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid 4	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid 4	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
SYN-MiniTid 4	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid 4	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid 4	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid 4	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid 4	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid 4	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid 4	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
SYN-MiniTid 4	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
SYN-MiniTid 4	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
SYN-MiniTid 4	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 5	d1-4	ADDB_MOUSE	Beta-adducin, Gene: Add2
RAM-MiniTid 5	d1-4	AGFG1_MOUSE	Arf-GAP domain and FG repea
RAM-MiniTid 5	d1-4	AGFG1_MOUSE	Arf-GAP domain and FG repea
RAM-MiniTid 5	d1-4	AGFG1_MOUSE	Arf-GAP domain and FG repea
RAM-MiniTid 5	d1-4	BSN_MOUSE	Protein bassoon, Gene: Bsn
RAM-MiniTid 5	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr
RAM-MiniTid 5	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr
RAM-MiniTid 5	d1-4	E41L1_MOUSE	Band 4.1-like protein 1, Gene:
RAM-MiniTid 5	d1-4	E41L1_MOUSE	Band 4.1-like protein 1, Gene:
RAM-MiniTid 5	d1-4	E41L1_MOUSE	Band 4.1-like protein 1, Gene:
RAM-MiniTid 5	d1-4	ELFN1_MOUSE	Protein ELFN1, Gene: Elfn1
RAM-MiniTid 5	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 5	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 5	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 5	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 5	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec

RAM-MiniTid 5	d1-4	GBRA1_MOUSE	Gamma-aminobutyric acid rec
RAM-MiniTid 5	d1-4	LNEBL_MOUSE	LIM zinc-binding domain-conta
RAM-MiniTid 5	d1-4	MAP1A_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MAP1A_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MAP1A_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MAP1B_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 5	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 5	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 5	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 5	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 5	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 5	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 5	d1-4	S12A5_MOUSE	Solute carrier family 12 membe
RAM-MiniTid 5	d1-4	S12A5_MOUSE	Solute carrier family 12 membe
RAM-MiniTid 5	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 5	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 5	d1-4	SPTN1_MOUSE	Spectrin alpha chain, non-eryth
RAM-MiniTid 5	d1-4	SUGP2_MOUSE	SURP and G-patch domain-co
RAM-MiniTid 5	d1-4	SYNRG_MOUSE	Synergin gamma, Gene: Synrg
RAM-MiniTid 5	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 5	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 5	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 5	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 5	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 5	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 5	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 5	d1-4	VAMP2_MOUSE	Vesicle-associated membrane
RAM-MiniTid 5	d1-4	VAMP2_MOUSE	Vesicle-associated membrane
RAM-MiniTid 5	d1-4	VAMP2_MOUSE	Vesicle-associated membrane
RAM-MiniTid 5	d1-4	VCIP1_MOUSE	Deubiquitinating protein VCIP1
RAM-MiniTid 6	d1-4	AAK1_MOUSE	AP2-associated protein kinase
RAM-MiniTid 6	d1-4	CH10_MOUSE	10 kDa heat shock protein, mit
RAM-MiniTid 6	d1-4	CH10_MOUSE	10 kDa heat shock protein, mit
RAM-MiniTid 6	d1-4	CH10_MOUSE	10 kDa heat shock protein, mit
RAM-MiniTid 6	d1-4	CH10_MOUSE	10 kDa heat shock protein, mit
RAM-MiniTid 6	d1-4	CPLX1_MOUSE	Complexin-1, Gene: Cplx1
RAM-MiniTid 6	d1-4	CPLX1_MOUSE	Complexin-1, Gene: Cplx1
RAM-MiniTid 6	d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
RAM-MiniTid 6	d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
RAM-MiniTid 6	d1-4	CPLX2_MOUSE	Complexin-2, Gene: CPLX2
RAM-MiniTid 6	d1-4	CPLX2_MOUSE	Complexin-2, Gene: CPLX2
RAM-MiniTid 6	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr
RAM-MiniTid 6	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr

RAM-MiniTid 6	d1-4	ELFN1_MOUSE	Protein ELFN1, Gene: Elfn1
RAM-MiniTid 6	d1-4	GGA1_MOUSE	ADP-ribosylation factor-bindinç
RAM-MiniTid 6	d1-4	GGA1_MOUSE	ADP-ribosylation factor-bindinç
RAM-MiniTid 6	d1-4	MAP1A_MOUSE	Microtubule-associated protein
RAM-MiniTid 6	d1-4	MAP1B_MOUSE	Microtubule-associated protein
RAM-MiniTid 6	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 6	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 6	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 6	d1-4	NFH_MOUSE	Neurofilament heavy polypepti
RAM-MiniTid 6	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 6	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 6	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 6	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 6	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 6	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 6	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 6	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 6	d1-4	SUGP2_MOUSE	SURP and G-patch domain-co
RAM-MiniTid 6	d1-4	SYNRG_MOUSE	Synergin gamma, Gene: Synrg
RAM-MiniTid 6	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 6	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 6	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 6	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 6	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 6	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 6	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 6	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 6	d1-4	VCIP1_MOUSE	Deubiquitinating protein VCIP1
RAM-MiniTid 7	d1-4	AAK1_MOUSE	AP2-associated protein kinase
RAM-MiniTid 7	d1-4	AGFG1_MOUSE	Arf-GAP domain and FG repea
RAM-MiniTid 7	d1-4	AGFG1_MOUSE	Arf-GAP domain and FG repea
RAM-MiniTid 7	d1-4	AGFG1_MOUSE	Arf-GAP domain and FG repea
RAM-MiniTid 7	d1-4	AINX_MOUSE	Alpha-internexin, Gene: Ina

RAM-MiniTid 7	d1-4	BRAF_MOUSE	Serine/threonine-protein kinase
RAM-MiniTid 7	d1-4	BRAF_MOUSE	Serine/threonine-protein kinase
RAM-MiniTid 7	d1-4	CEND_MOUSE	Cell cycle exit and neuronal dif
RAM-MiniTid 7	d1-4	CPLX1_MOUSE	Complexin-1, Gene: Cplx1
RAM-MiniTid 7	d1-4	CPLX1_MOUSE	Complexin-1, Gene: Cplx1
RAM-MiniTid 7	d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
RAM-MiniTid 7	d1-4	CPLX2_MOUSE	Complexin-2, Gene: Cplx2
RAM-MiniTid 7	d1-4	CPLX2_MOUSE	Complexin-2, Gene: CPLX2
RAM-MiniTid 7	d1-4	CPLX2_MOUSE	Complexin-2, Gene: CPLX2
RAM-MiniTid 7	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr
RAM-MiniTid 7	d1-4	DPYL2_MOUSE	Dihydropyrimidinase-related pr
RAM-MiniTid 7	d1-4	E41L1_MOUSE	Band 4.1-like protein 1, Gene:
RAM-MiniTid 7	d1-4	E41L1_MOUSE	Band 4.1-like protein 1, Gene:
RAM-MiniTid 7	d1-4	E41L1_MOUSE	Band 4.1-like protein 1, Gene:
RAM-MiniTid 7	d1-4	GGA1_MOUSE	ADP-ribosylation factor-binding
RAM-MiniTid 7	d1-4	GGA1_MOUSE	ADP-ribosylation factor-binding
RAM-MiniTid 7	d1-4	GRIN1_MOUSE	G protein-regulated inducer of
RAM-MiniTid 7	d1-4	MAP1A_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP1A_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	MTAP2_MOUSE	Microtubule-associated protein
RAM-MiniTid 7	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid 7	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid 7	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid 7	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid 7	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid 7	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 7	d1-4	PLAP_MOUSE	Phospholipase A-2-activating p
RAM-MiniTid 7	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 7	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 7	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 7	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid 7	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 7	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 7	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 7	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th

RAM-MiniTid 7	d1-4	RAF1_MOUSE	RAF proto-oncogene serine/th
RAM-MiniTid 7	d1-4	RT31_MOUSE	28S ribosomal protein S31, mit
RAM-MiniTid 7	d1-4	RT31_MOUSE	28S ribosomal protein S31, mit
RAM-MiniTid 7	d1-4	RTN4_MOUSE	Reticulon-4, Gene: Rtn4
RAM-MiniTid 7	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 7	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 7	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 7	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 7	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 7	d1-4	SHAN2_MOUSE	SH3 and multiple ankyrin repea
RAM-MiniTid 7	d1-4	SPTN1_MOUSE	Spectrin alpha chain, non-eryth
RAM-MiniTid 7	d1-4	SPTN1_MOUSE	Spectrin alpha chain, non-eryth
RAM-MiniTid 7	d1-4	SUGP2_MOUSE	SURP and G-patch domain-co
RAM-MiniTid 7	d1-4	SYNRG_MOUSE	Synergin gamma, Gene: Synrg
RAM-MiniTid 7	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 7	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 7	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 7	d1-4	SYUA_MOUSE	Alpha-synuclein, Gene: Snca
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: SNCB
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: SNCB
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: SNCB
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: SNCB
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: Sncb
RAM-MiniTid 7	d1-4	SYUB_MOUSE	Beta-synuclein, Gene: SNCB
RAM-MiniTid 7	d1-4	TBB2A_MOUSE	Tubulin beta-2A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB2A_MOUSE	Tubulin beta-2A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB2A_MOUSE	Tubulin beta-2A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB2A_MOUSE	Tubulin beta-2A chain, OX=954
RAM-MiniTid 7	d1-4	TBB2A_MOUSE	Tubulin beta-2A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB2B_MOUSE	Tubulin beta-2B chain, Gene: T
RAM-MiniTid 7	d1-4	TBB2B_MOUSE	Tubulin beta-2B chain, Gene: T
RAM-MiniTid 7	d1-4	TBB2B_MOUSE	Tubulin beta-2B chain, Gene: T
RAM-MiniTid 7	d1-4	TBB2B_MOUSE	Tubulin beta-2B chain, Gene: T
RAM-MiniTid 7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, OX=954
RAM-MiniTid 7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, Gene: T
RAM-MiniTid 7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, Gene: T

RAM-MiniTid	7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, Gene: T
RAM-MiniTid	7	d1-4	TBB4A_MOUSE	Tubulin beta-4A chain, OX=954
RAM-MiniTid	7	d1-4	TBB4B_MOUSE	Tubulin beta-4B chain, Gene: T
RAM-MiniTid	7	d1-4	TBB4B_MOUSE	Tubulin beta-4B chain, Gene: T
RAM-MiniTid	7	d1-4	TBB4B_MOUSE	Tubulin beta-4B chain, Gene: T
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta-5 chain, Gene: TU
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta-5 chain, Gene: Tu
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta-5 chain, Gene: Tu
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta-5 chain, Gene: TU
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta chain, Gene: TUB
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta chain, Gene: TUB
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta chain, Gene: TUB
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta chain, Gene: TUB
RAM-MiniTid	7	d1-4	TBB5_MOUSE	Tubulin beta chain, Gene: TUB
RAM-MiniTid	7	d1-4	TIM44_MOUSE	Mitochondrial import inner mem
RAM-MiniTid	7	d1-4	TIM44_MOUSE	Mitochondrial import inner mem
RAM-MiniTid	7	d1-4	VCIP1_MOUSE	Deubiquitinating protein VCIP13
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP translocase 1 OS=M
RAM-MiniTid	8	d1-4	ADT1_MOUSE	ADP/ATP translocase 1 OS=R
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid	8	d1-4	MAP6_MOUSE	Microtubule-associated protein
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid	8	d1-4	PCCA_MOUSE	Propionyl-CoA carboxylase alp
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	8	d1-4	PYC_MOUSE	Pyruvate carboxylase, mitocho
RAM-MiniTid	8	d1-4	SYNRG_MOUSE	Synergin gamma OS=Mus mus
RAM-MiniTid	8	d1-4	SYNRG_MOUSE	Synergin gamma OS=Mus mus
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Erythroce
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Gorilla go
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Macaca r
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Homo sap
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Macaca f
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Saguinus
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Pan panis
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Pan troglo
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Erythroce
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Gorilla go
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Macaca r
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Homo sap
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Macaca f
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Saguinus
RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Pan panis

RAM-MiniTid	8	d1-4	SYUA_MOUSE	Alpha-synuclein OS=Pan troglo
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Bos taurus
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Rattus nor
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Bos taurus
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Rattus nor
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Bos taurus
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Rattus nor
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Bos taurus
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Mus musc
RAM-MiniTid	8	d1-4	SYUB_MOUSE	Beta-synuclein OS=Rattus nor

ıtion (EC) spatial memory phase

Peptide Scor	ptide Sequer	Peptide Mo	Position of peptide modification
39.99	LASRKSARF	Biotin (K)	0.00000000001.0
39.99	LASRKSARF	Biotin (K)	0.00000000001.0
52.85	LQKAQEEAL	Biotin (K)	0.000000000001000.0
52.85	LQKAQEEAL	Biotin (K)	0.000000000001000.0
39.6	NQDPIIPVPL	Biotin (K)	0.0000000000100000000000.0
39.6	NQDPIIPVPL	Biotin (K)	0.0000000000100000000000.0
93.48	KMQNSMTA	Biotin (K)	0.1000000000.0
93.48	KMQNSMTA	Biotin (K)	0.1000000000.0
93.48	KMQNSMTA	Biotin (K)	0.1000000000.0
52.31	KMQNSMTA	Biotin (K); Ox	0.1300000000.0
52.31	KMQNSMTA	Biotin (K); Ox	0.1300000000.0
52.31	KMQNSMTA	Biotin (K); Ox	0.1300000000.0
48.8	KMQNSMTA	Biotin (K); Ox	0.1000030000.0
48.8	KMQNSMTA	Biotin (K); Ox	0.1000030000.0
78.11	GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
66.22	GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
54.32	KMETVVTSF	Biotin (K); Ox	0.130000000000000.0
54.32	KMETVVTSF	Biotin (K); Ox	0.130000000000000.0
49.49	GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
48.72	GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
48.72	GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
44.05	GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
44.05	GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.34	TKEGVLYVG	Biotin (K)	0.01000000000.0
50.19	QGVTEAAEI	Biotin (K)	0.00000000100.0
50.19	QGVTEAAEI	Biotin (K)	0.00000000100.0
45.62	LQKAQEEAL	Biotin (K)	0.000000000001000.0
45.62	LQKAQEEAL	Biotin (K)	0.000000000001000.0
61.33	DQGAVLLGI	Biotin (K)	0.0000000000100000000000.0
61.33	DQGAVLLGI	Biotin (K)	0.0000000000100000000000.0
95.2	KMETVVTSF	Biotin (K)	0.100000000000000.0
95.2	KMETVVTSF	Biotin (K)	0.100000000000000.0
71.35	GQPLCVLSA	Biotin (K); Ca	0.000020000010000000000000000.0
65.62	GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
63.18	GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0

59.52	GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000.0
44.98	GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
44.89	IASKAVYVP/	Biotin (K)	0.00010000000000.0
44.89	IASKAVYVP/	Biotin (K)	0.00010000000000.0
44.89	IASKAVYVP/	Biotin (K)	0.00010000000000.0
44.89	IASKAVYVP/	Biotin (K)	0.00010000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
87.9	AYKKAWGN	2 Biotin (K)	0.0011000000000000000.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
52.08	QGVTEAAEI	Biotin (K)	0.00000000100.0
66.54	KMQNSMTA	Biotin (K); Ox	0.1300000000.0
63.19	KMETVVTSF	Biotin (K)	0.100000000000000.0
38.96	IASKAVYVP/	Biotin (K)	0.00010000000000.0
67.9	TKQGVTEA/	Biotin (K)	0.0000000000001.0
56.24	EGVLYVGSI	Biotin (K)	0.00000000001.0
41.41	QGVTEAAEI	Biotin (K)	0.00000000100.0
41.41	QGVTEAAEI	Biotin (K)	0.00000000100.0
41.02	QGVTEAAEI	Biotin (K)	0.00000000100.0
48.73	LGKTAAFK	Biotin (K)	0.00100000.0
47.96	VNVDKVLEF	Biotin (K)	0.000010000.0
100.56	VAEDEFDPI	Biotin (K)	0.00000000000000100000000.0
100.56	VAEDEFDPI	Biotin (K)	0.00000000000000100000000.0
38.28	IAKPVSLLEK	Biotin (K)	0.0010000000.0
44.76	VFLPNKQR	Biotin (K)	0.00000100.0
44.76	VFLPNKQR	Biotin (K)	0.00000100.0
50.97	SAAETVTKG	Biotin (K)	0.0000000100000000.0
50.97	SAAETVTKG	Biotin (K)	0.0000000100000000.0
72.62	QALGGATKI	Biotin (K)	0.000000010000.0
72.62	QALGGATKI	Biotin (K)	0.000000010000.0
72.62	QALGGATKI	Biotin (K)	0.000000010000.0

Exc

72.62	QALGGATK	Biotin (K)	0.000000010000.0
48.12	GLYDGPVC	Biotin (K)	0.00000002000000100000000.0
48.12	GLYDGPVC	Biotin (K)	0.00000002000000100000000.0
51.76	GDPGLATIA	Biotin (K)	0.00000000010000000.0
51.76	GDPGLATIA	Biotin (K)	0.00000000010000000.0
51.76	GDPGLATIA	Biotin (K)	0.00000000010000000.0
51.76	GDPGLATIA	Biotin (K)	0.00000000010000000.0
51.76	GDPGLATIA	Biotin (K)	0.00000000010000000.0
51.76	GDPGLATIA	Biotin (K)	0.00000000010000000.0
44.24	AETVSPGE\	Biotin (K)	0.000000000000000100000000.0
58.31	TVEEALTIKN	Biotin (K)	0.000000001000000.0
58.31	TVEEALTIKN	Biotin (K)	0.000000001000000.0
55.99	SPWASDFKI	Biotin (K)	0.000000000000000001000000.0
75.88	ITKTPQAST`	Biotin (K)	0.00100000000000000.0
105.35	DQGAVLLGI	Biotin (K)	0.000000000100000000000.0
73.74	GQSPTAPG	Biotin (K)	0.000000000000000000000100000000000.0
59.92	RGDHPWIPI	Biotin (K)	0.000000001000000000000000000.0
58.84	RGDHPWIPI	Biotin (K)	0.000000001000000000000000000.0
52.46	NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
42.83	NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
40.85	DQGAVLLGI	Biotin (K)	0.000000000100000000000.0
41.33	KMEHTIK	Biotin (K)	0.1000000.0
41.33	KMEHTIK	Biotin (K)	0.1000000.0
41.33	KMEHTIK	Biotin (K)	0.1000000.0
59.02	VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
35.42	KLILKPAIK	Biotin (K)	0.000010000.0
39.88	LILKPAIK	Biotin (K)	0.00010000.0
38.02	KLILKPAIK	Biotin (K)	0.000010000.0
66.11	SAASKTVNI`	Biotin (K)	0.0000100000000.0
66.11	SAASKTVNI`	Biotin (K)	0.0000100000000.0
44.76	VFLPNKQR	Biotin (K)	0.00000100.0
44.76	VFLPNKQR	Biotin (K)	0.00000100.0
44.76	VFLPNKQR	Biotin (K)	0.00000100.0
44.76	VFLPNKQR	Biotin (K)	0.00000100.0
44.76	VFLPNKQR	Biotin (K)	0.00000100.0
46.85	QTTKSELLR	Biotin (K)	0.000100000.0
46.85	QTTKSELLR	Biotin (K)	0.000100000.0
59.71	SVKPGEGLE	Biotin (K)	0.000000000000010000000.0
59.71	SVKPGEGLE	Biotin (K)	0.000000000000010000000.0
54.59	IASKAVYVP/	Biotin (K)	0.00010000000000.0
54.59	IASKAVYVP/	Biotin (K)	0.00010000000000.0
45.32	IASKAVYVP/	Biotin (K)	0.00010000000000.0
45.32	IASKAVYVP/	Biotin (K)	0.00010000000000.0
41.84	DEADSKTAS	Biotin (K)	0.000001000000.0
40.77	TASPWKSAF	Biotin (K)	0.000001000.0
68.47	LTDKNVGF(	Biotin (K)	0.0001000000000.0
47.8	ASDKYEALR	Biotin (K)	0.00000000000000000000000000000000000001.0
57.1	QGVAEAAG	Biotin (K)	0.00000000100.0

57.1	QGVAEAAG	Biotin (K)	0.00000000100.0
101.71	TKEGVLYVG	Biotin (K)	0.000000000010000000000000.0
78.2	TKQGVTEA/	Biotin (K)	0.0000000000100.0
58.42	QGVTEAAEI	Biotin (K)	0.00000000100.0
55.23	TKQGVTEA/	Biotin (K)	0.0000000000100.0
47.68	LGKTAAFK	Biotin (K)	0.00100000.0
47.68	LGKTAAFK	Biotin (K)	0.00100000.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
55.25	QALGGATKI	Biotin (K); O›	0.000000010300.0
110.4	DQGAVLLGI	Biotin (K)	0.000000000100000000000.0
72	DQGAVLLGI	Biotin (K)	0.000000000100000000000.0
59.99	VSDFGQMA	Biotin (K)	0.000000000000000100000.0
58.09	EASPPTSAD	Biotin (K)	0.000000000100.0
39.79	KMQNSMTA	Biotin (K); O›	0.1300000000.0
39.79	KMQNSMTA	Biotin (K); O›	0.1300000000.0
39.79	KMQNSMTA	Biotin (K); O›	0.1300000000.0
125.42	GQPLCVLSA	Biotin (K); Ca	0.000020000010000000000000.0
82.93	KMETVVTSF	Biotin (K)	0.100000000000000.0
82.93	KMETVVTSF	Biotin (K)	0.100000000000000.0
82.17	KMETVVTSF	Biotin (K); O›	0.100000000300000.0
55.79	KMETVVTSF	Biotin (K)	0.100000000000000.0
55.79	KMETVVTSF	Biotin (K)	0.100000000000000.0
54.95	GQPLCVLSA	Biotin (K); Ca	0.000020000010000000000000.0
52.25	QGVAEAAG	Biotin (K)	0.00000000100.0
52.25	QGVAEAAG	Biotin (K)	0.00000000100.0
81.15	TKQGVTEA/	Biotin (K)	0.0000000000001.0
59.58	ADEVEKSSS	Biotin (K)	0.00000100000000.0
96.77	AGLQTADK	Biotin (K)	0.000000010000000000000000000000000000.0
96.77	AGLQTADK	Biotin (K)	0.000000010000000000000000000000000000.0
96.77	AGLQTADK	Biotin (K)	0.000000010000000000000000000000000000.0
48.59	GLAGPTTVF	Biotin (K)	0.00000000000100000.0
45.15	GLYDGPVCI	Biotin (K)	0.000000020000001000000000.0
45.15	GLYDGPVCI	Biotin (K)	0.000000020000001000000000.0
115.05	SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
115.05	SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
115.05	SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
100.47	SGAVSAAEF	Biotin (K)	0.000000000000000000001000000000.0
56.03	GDPGLATIA	Biotin (K)	0.00000000010000000.0
56.03	GDPGLATIA	Biotin (K)	0.00000000010000000.0
56.03	GDPGLATIA	Biotin (K)	0.00000000010000000.0
56.03	GDPGLATIA	Biotin (K)	0.00000000010000000.0
56.03	GDPGLATIA	Biotin (K)	0.00000000010000000.0

56.03	GDPGLATIA	Biotin (K)	0.00000000010000000.0
57.23	STQVVSDA/	Biotin (K)	0.000000000100000000000.0
71.57	DFQEPLPQI	Biotin (K)	0.000000001000000.0
68.61	SPWASDFKI	Biotin (K)	0.000000000000000001000000.0
65.38	SPQAQDTL(	Biotin (K)	0.0000000000000000020000000001000000000000000
90.71	ITKTPQAST	Biotin (K)	0.00100000000000000.0
104.67	DQGAVLLGI	Biotin (K)	0.000000000100000000000.0
46.62	NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
41.75	DQGAVLLGI	Biotin (K)	0.000000000100000000000.0
63.32	EASPPTSAD	Biotin (K)	0.000000000100.0
38.62	LILKPAIK	Biotin (K)	0.00010000.0
63.99	SAASKTVNI	Biotin (K)	0.0000100000000.0
63.99	SAASKTVNI	Biotin (K)	0.0000100000000.0
64.37	GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
56.95	KMETVVTSF	Biotin (K)	0.100000000300000.0
52.28	GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
49.73	KMETVVTSF	Biotin (K)	0.130000000000000.0
45.98	NKGPSPVS:	Biotin (K)	0.0100000000000.0
45.98	NKGPSPVS:	Biotin (K)	0.0100000000000.0
60.63	SVKPGEGLE	Biotin (K)	0.000000000000010000000.0
60.63	SVKPGEGLE	Biotin (K)	0.000000000000010000000.0
40.2	TASPWKSAF	Biotin (K)	0.000001000.0
57.17	LTDKNVGF(	Biotin (K)	0.0001000000000.0
67.67	GISTDKPSE	Biotin (K)	0.000000000000000000100000.0
73.44	TKEGVLYVG	Biotin (K)	0.0000000000001.0
73.44	TKEGVLYVG	Biotin (K)	0.0000000000001.0
66.07	QGVAEAAG	Biotin (K)	0.00000000100.0
66.07	QGVAEAAG	Biotin (K)	0.00000000100.0
81.17	TKQGVTEA/	Biotin (K)	0.0000000000001.0
54.22	TKQGVTEA/	Biotin (K)	0.01000000000.0
51.61	EGVLYVGSI	Biotin (K)	0.000000001000000000000000.0
50.54	VNVDKVLEF	Biotin (K)	0.000010000.0
50.54	VNVDKVLEF	Biotin (K)	0.000010000.0
50.54	VNVDKVLEF	Biotin (K)	0.000010000.0
70.39	VGDVQGQE	Biotin (K)	0.000000000000010000000.0
109.33	VAEDEFDPI	Biotin (K)	0.000000000000100000000.0
69.02	SAAETVTKG	Biotin (K)	0.0000000100000000.0
69.02	SAAETVTKG	Biotin (K)	0.0000000100000000.0
69.02	SAAETVTKG	Biotin (K)	0.0000000100000000.0
69.02	SAAETVTKG	Biotin (K)	0.0000000100000000.0
73.26	QALGGATK	Biotin (K)	0.000000010000.0
73.26	QALGGATK	Biotin (K)	0.000000010000.0
73.26	QALGGATK	Biotin (K)	0.000000010000.0
73.26	QALGGATK	Biotin (K)	0.000000010000.0
73.26	QALGGATK	Biotin (K)	0.000000010000.0
73.26	QALGGATK	Biotin (K)	0.000000010000.0
55.21	GLYDGPVC	Biotin (K)	0.00000002000000100000000.0
55.21	GLYDGPVC	Biotin (K)	0.00000002000000100000000.0

84.59	SGAVSAAEF	Biotin (K)	0.0000000000000000000001000000000.0
41.97	NVIFEDEEK	Biotin (K)	0.00000000001.0
41.97	NVIFEDEEK	Biotin (K)	0.00000000001.0
63.76	DFQEPLPQI	Biotin (K)	0.000000001000000.0
75.14	ITKTPQAST	Biotin (K)	0.00100000000000000.0
50.04	NQDPIIPVPL	Biotin (K)	0.00000000001000000000000.0
58.07	EASPPTSAD	Biotin (K)	0.000000000100.0
42.87	KLILKPAIK	Biotin (K)	0.000010000.0
44.7	IGFGPSPFS	Biotin (K)	0.0000000000000001000000000.0
79.27	SAASKTVNI	Biotin (K)	0.0000100000000.0
79.27	SAASKTVNI	Biotin (K)	0.0000100000000.0
119.27	GQPLCVLSA	Biotin (K)	0.000020000010000000000000000.0
90.1	KGQPLCVLS	Biotin (K)	0.0000020000010000000000000000.0
87.83	MKMETVVTS	Biotin (K)	0.0100000000000000.0
84.85	GQPLCVLSA	Biotin (K)	0.000020000010000000000000000.0
82.83	KMETVVTSF	Biotin (K)	0.100000000000000.0
78.87	SAMKMETV	Biotin (K)	0.000100000000000000.0
77.17	KMETVVTSF	Biotin (K)	0.100000000000000.0
68.19	GQPLCVLSA	Biotin (K)	0.000020000010000000000000000.0
64.38	GQPLCVLSA	Biotin (K)	0.000020000313000000000000000.0
62.39	GQPLCVLSA	Biotin (K)	0.000020000010000000000000000.0
55.25	GQPLCVLSA	Biotin (K)	0.000020000310000000000000000.0
49.23	GQPLCVLSA	Biotin (K)	0.000020000013000000030000000.0
46.03	KMETVVTSF	Biotin (K)	0.1000000000000000.0
43.97	GQPLCVLSA	Biotin (K)	0.000020000313000000000000000.0
42.47	SAMKMETV	Biotin (K)	0.000100000000000000.0
48.73	IASKAVYVPA	Biotin (K)	0.00010000000000.0
48.73	IASKAVYVPA	Biotin (K)	0.00010000000000.0
48.73	IASKAVYVPA	Biotin (K)	0.00010000000000.0
38.13	IASKAVYVPA	Biotin (K)	0.00010000000000.0
38.13	IASKAVYVPA	Biotin (K)	0.00010000000000.0
38.13	IASKAVYVPA	Biotin (K)	0.00010000000000.0
63.71	LTDKNVGFC	Biotin (K)	0.0001000000000.0
88.97	GISTDKPSE	Biotin (K)	0.00000000000000000000100000.0
58.33	QGVAEAAG	Biotin (K)	0.00000000100.0
58.33	QGVAEAAG	Biotin (K)	0.00000000100.0
47.89	EGVLYVGSK	Biotin (K)	0.00000000001.0
47.89	EGVLYVGSK	Biotin (K)	0.00000000001.0
75.52	TKEGVLYVG	Biotin (K)	0.000000000010000000000000.0
58.82	TKQGVTEA	Biotin (K)	0.0000000000100.0
54.71	QGVTEAAEK	Biotin (K)	0.00000000100.0
49.37	TKQGVTEA	Biotin (K)	0.01000000000.0
68.63	VGDVQGQE	Biotin (K)	0.00000000000000010000000.0
92.12	VAEDEFDPI	Biotin (K)	0.00000000000000100000000.0
125.02	AGLQTADK	Biotin (K)	0.000000010000000000000000000000000000.0
125.02	AGLQTADK	Biotin (K)	0.000000010000000000000000000000000000.0
125.02	AGLQTADK	Biotin (K)	0.000000010000000000000000000000000000.0
78.87	ILSSTASKVS	Biotin (K)	0.00000001000000000.0

52.46	VFLPNKQR	Biotin (K)	0.00000100.0
52.46	VFLPNKQR	Biotin (K)	0.00000100.0
52.07	GKSASSPKF	Biotin (K)	0.010000000000.0
80.96	QALGGATK	Biotin (K)	0.000000010000.0
80.96	QALGGATK	Biotin (K)	0.000000010000.0
80.96	QALGGATK	Biotin (K)	0.000000010000.0
80.96	QALGGATK	Biotin (K)	0.000000010000.0
80.96	QALGGATK	Biotin (K)	0.000000010000.0
80.96	QALGGATK	Biotin (K)	0.000000010000.0
49.73	GLYDGPVC	Biotin (K)	0.00000002000000100000000000.0
49.73	GLYDGPVC	Biotin (K)	0.00000002000000100000000000.0
119.16	SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
119.16	SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
119.16	SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
42.17	NVIFEDEEK	Biotin (K)	0.00000000001.0
42.17	NVIFEDEEK	Biotin (K)	0.00000000001.0
46.09	AETVSPGEV	Biotin (K)	0.000000000000000100000000.0
62.84	DFQEPLPQ	Biotin (K)	0.000000001000000.0
42.93	SSFLEDKST	Biotin (K)	0.000000100000.0
122.01	DQGAVLLG	Biotin (K)	0.0000000000100000000000.0
66.92	DQGAVLLG	Biotin (K)	0.0000000000100000000000.0
66.71	DQGAVLLG	Biotin (K)	0.0000000000100000000000.0
63.51	NQDPIIPVPL	Biotin (K)	0.0000000000100000000000.0
62.34	DQGAVLLG	Biotin (K)	0.0000000000100000000000.0
61.37	RGDHPWIP	Biotin (K)	0.000000001000000000000000000000.0
50.52	RGDHPWIP	Biotin (K)	0.000000001000000000000000000000.0
38.7	NQDPIIPVPL	Biotin (K)	0.0000000000100000000000.0
110.04	TADKNKLEC	Biotin (K)	0.00000000000000000000000000100000.0
78.51	TADKNKLEC	Biotin (K)	0.00000000000000000000000000100000.0
70.9	EASPPTSAD	Biotin (K)	0.000000000100.0
64.87	NKLEGAGSA	Biotin (K)	0.00000000000000000000000100000.0
39.79	KLILKPAIK	Biotin (K)	0.000010000.0
38.21	LILKPAIK	Biotin (K)	0.00010000.0
80.82	KMQNSMTA	Biotin (K)	0.1000000000.0
80.82	KMQNSMTA	Biotin (K)	0.1000000000.0
48.7	KMQNSMTA	Biotin (K)	0.1300030000.0
48.7	KMQNSMTA	Biotin (K)	0.1300030000.0
48.7	KMQNSMTA	Biotin (K)	0.1300030000.0
74.8	SAASKTVNI	Biotin (K)	0.0000100000000.0
74.8	SAASKTVNI	Biotin (K)	0.0000100000000.0
104.98	GQPLCVLSA	Biotin (K)	0.000020000010000000000000000.0
73.79	GQPLCVLSA	Biotin (K)	0.000020000010000000000000000.0
70.88	GQPLCVLSA	Biotin (K)	0.000020000010000000000000000.0
45.18	GQPLCVLSA	Biotin (K)	0.000020000313000000000000000.0
52.46	VFLPNKQR	Biotin (K)	0.00000100.0
52.46	VFLPNKQR	Biotin (K)	0.00000100.0
52.46	VFLPNKQR	Biotin (K)	0.00000100.0
52.46	VFLPNKQR	Biotin (K)	0.00000100.0

52.46	VFLPNKQR	Biotin (K)	0.00000100.0
50.59	QTTKSELLR	Biotin (K)	0.000100000.0
50.59	QTTKSELLR	Biotin (K)	0.000100000.0
56.29	SSVSKVPLL	Biotin (K)	0.000010000000000000000000000000.0
43.06	IASKAVYVP/	Biotin (K)	0.00010000000000.0
43.06	IASKAVYVP/	Biotin (K)	0.00010000000000.0
43.06	IASKAVYVP/	Biotin (K)	0.00010000000000.0
39.89	IASKAVYVP/	Biotin (K)	0.00010000000000.0
39.89	IASKAVYVP/	Biotin (K)	0.00010000000000.0
39.89	IASKAVYVP/	Biotin (K)	0.00010000000000.0
55.8	DEADSKTAS	Biotin (K)	0.000001000000.0
40.84	TASPWKSAF	Biotin (K)	0.000001000.0
46.77	LTDKNVGF(	Biotin (K)	0.0001000000000.0
54.52	ASDKYEALR	Biotin (K)	0.00000000000000000000000000000000100000.0
69.26	TKEGVLYVG	Biotin (K)	0.0000000000001.0
69.26	TKEGVLYVG	Biotin (K)	0.0000000000001.0
52.9	QGVAEAAG	Biotin (K)	0.00000000100.0
52.9	QGVAEAAG	Biotin (K)	0.00000000100.0
75.68	EGVLYVGSI	Biotin (K)	0.00000001000000000000.0
69.26	TKEGVLYVG	Biotin (K)	0.0000000000001.0
69.26	TKEGVLYVG	Biotin (K)	0.0000000000001.0
65.21	TKQGVTEA/	Biotin (K)	0.0000000000100.0
65.21	TKQGVTEA/	Biotin (K)	0.0000000000100.0
65.21	TKQGVTEA/	Biotin (K)	0.0000000000100.0
62.95	QGVTEAAEI	Biotin (K)	0.00000000100.0
62.95	QGVTEAAEI	Biotin (K)	0.00000000100.0
62.95	QGVTEAAEI	Biotin (K)	0.00000000100.0
58.96	TKQGVTEA/	Biotin (K)	0.01000000000.0
58.96	TKQGVTEA/	Biotin (K)	0.01000000000.0
58.96	TKQGVTEA/	Biotin (K)	0.01000000000.0
56.47	TKQGVTEA/	Biotin (K)	0.0000000000100.0
56.47	TKQGVTEA/	Biotin (K)	0.0000000000100.0
56.47	TKQGVTEA/	Biotin (K)	0.0000000000100.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
68.18	SGPFGQIFF	Biotin (K)	0.00000000000000000000000001000000000000000(
68.18	SGPFGQIFF	Biotin (K)	0.00000000000000000000000001000000000000000(

68.18	SGPFGQIFF	Biotin (K)	0.0000000000000000000000000100000000000000000
68.18	SGPFGQIFF	Biotin (K)	0.0000000000000000000000000100000000000000000
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
131.86	YDICFRTLK	Biotin (K); 2 (	0.000200001000000000000000000000000200.0
41.29	ESLDEVSKS	Biotin (K)	0.0000000100000.0
41.29	ESLDEVSKS	Biotin (K)	0.0000000100000.0
69.18	VGDVQGQE	Biotin (K)	0.00000000000000010000000.0
38.99	LAADVGKG	Biotin (K)	0.000000100000.0
38.99	LAADVGKG	Biotin (K)	0.000000100000.0
85.84	DQGAVLLG	Biotin (K)	0.00000000010000000000.0
46.14	RGDHPWIP	Biotin (K)	0.000000010000000000000000000.0
81.46	KMQNSMTA	Biotin (K)	0.1000000000.0
81.46	KMQNSMTA	Biotin (K)	0.1000000000.0
51.75	KMQNSMTA	Biotin (K)	0.1000000000.0
51.75	KMQNSMTA	Biotin (K)	0.1000000000.0
40.9	KMQNSMTA	Biotin (K)	0.1000000000.0
79.63	KMETVVTSF	Biotin (K)	0.100000000000000.0
72.97	KMETVVTSF	Biotin (K)	0.100000000000000.0
72.54	GQPLCVLS/	Biotin (K); Ca	0.000020000310000000300000.0
66.49	GQPLCVLS/	Biotin (K); Ca	0.00002000031000000000000000.0
59.35	SAMKMETV	Biotin (K)	0.000100000000000000.0
76.12	GISTDKPSE	Biotin (K)	0.000000000000000000100000.0
44.2	ASDKYEALR	Biotin (K)	0.000000000000000000000000000000000100000.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSI	Biotin (K)	0.00000000001.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0

40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
51.48	EGVLYVGSK	Biotin (K)	0.00000000001.0
51.48	EGVLYVGSK	Biotin (K)	0.00000000001.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
40.12	TKEGVLYVG	Biotin (K)	0.01000000000.0
37.96	QGVTEAAEK	Biotin (K)	0.00000000100.0
37.96	QGVTEAAEK	Biotin (K)	0.00000000100.0
37.96	QGVTEAAEK	Biotin (K)	0.00000000100.0
46.27	TKQGVTEAA	Biotin (K)	0.0000000000100.0
46.27	TKQGVTEAA	Biotin (K)	0.0000000000100.0
46.27	TKQGVTEAA	Biotin (K)	0.0000000000100.0

Protein Accession
AAK1_MOUSE
ADDB_MOUSE
ADT1_MOUSE
AGFG1_MOUSE
AINX_MOUSE
ANR35_MOUSE
BIN1_MOUSE
BRAF_MOUSE
BSN_MOUSE
CEND_MOUSE
CH10_MOUSE
CPLX1_MOUSE
CPLX2_MOUSE
DPYL2_MOUSE
E41L1_MOUSE
ELFN1_MOUSE
GBRA1_MOUSE
GGA1_MOUSE
GRIN1_MOUSE
ICAM1_MOUSE
ISCU_MOUSE
LNEBL_MOUSE
MAP1A_MOUSE
MAP1B_MOUSE
MAP6_MOUSE
MCCA_MOUSE
MTAP2_MOUSE
NFH_MOUSE
PCCA_MOUSE
PLAP_MOUSE
PYC_MOUSE
RAF1_MOUSE
RT31_MOUSE
RTN4_MOUSE
S12A5_MOUSE
SHAN2_MOUSE
SNP25_MOUSE
SPTN1_MOUSE
SUGP2_MOUSE
SYNRG_MOUSE
SYUA_MOUSE
SYUB_MOUSE
TBB2A_MOUSE
TBB2B_MOUSE

51 ***Biological Process***

#term ID	term description	observed ger
GO:0035493	SNARE complex assembly	2
GO:0048680	Positive regulation of axon regeneratio	2
GO:0090174	Organelle membrane fusion	3
GO:0050772	Positive regulation of axonogenesis	3
GO:0099504	Synaptic vesicle cycle	3
GO:0000278	Mitotic cell cycle	6
GO:0000226	Microtubule cytoskeleton organization	5
GO:0007017	Microtubule-based process	6
GO:0061024	Membrane organization	5
GO:0007010	Cytoskeleton organization	6
GO:0048699	Generation of neurons	8
GO:0051128	Regulation of cellular component orga	10
GO:0022607	Cellular component assembly	8
GO:0007399	Nervous system development	9
GO:0006996	Organelle organization	11
GO:0016043	Cellular component organization	15
GO:0030154	Cell differentiation	10
GO:0048731	System development	11
GO:0051179	Localization	11

Molecular Function

#term ID	term description	observed ger
GO:0031434	Mitogen-activated protein kinase kinas	2
GO:0005200	Structural constituent of cytoskeleton	5
GO:0004709	MAP kinase kinase kinase activity	2
GO:0005484	SNAP receptor activity	2
GO:0003924	GTPase activity	5
GO:0005525	GTP binding	5
GO:0005198	Structural molecule activity	6
GO:0044877	Protein-containing complex binding	6
GO:0035639	Purine ribonucleoside triphosphate bin	7
GO:0032555	Purine ribonucleotide binding	7
GO:0043168	Anion binding	8
GO:0005515	Protein binding	12
GO:0005488	Binding	15

TBB4A_MOUSE
TBB4B_MOUSE
TBB5_MOUSE
TIM44_MOUSE
VAMP1_MOUSE
VAMP2_MOUSE
VCIP1_MOUSE

clusive to background

BIN1_MOUSE
BRAF_MOUSE
BSN_MOUSE
GRIN1_MOUSE
ICAM1_MOUSE
RAF1_MOUSE
RTN4_MOUSE
S12A5_MOUSE
SNP25_MOUSE
TBB2A_MOUSE
TBB2B_MOUSE
TBB4A_MOUSE
TBB4B_MOUSE
TBB5_MOUSE
VAMP1_MOUSE
VCIP1_MOUSE

)000000000.0

)00000000.0
)00000000.0

)00000000.0
)00000000.0

background g	strength	false discove	matching pro	matching proteins in your network (labe
12	2.36	0.0407	10090.ENSM	Snap25,Vamp1
15	2.26	0.0407	10090.ENSM	Braf,Rtn4
79	1.72	0.0314	10090.ENSM	Snap25,Vamp1,Vcpip1
104	1.6	0.0407	10090.ENSM	Braf,Tubb2b,Rtn4
125	1.52	0.0478	10090.ENSM	Bin1,Snap25,Vamp1
527	1.2	0.0038	10090.ENSM	Tubb5,Tubb4b,Vcpip1,Tubb2a,Tubb4a,T
484	1.15	0.0241	10090.ENSM	Tubb5,Tubb4b,Tubb2a,Tubb4a,Tubb2b
722	1.06	0.0164	10090.ENSM	Tubb5,Bsn,Tubb4b,Tubb2a,Tubb4a,Tubb
603	1.06	0.0407	10090.ENSM	Bin1,Snap25,Vamp1,Vcpip1,Rtn4
1064	0.89	0.0407	10090.ENSM	Raf1,Tubb5,Tubb4b,Tubb2a,Tubb4a,Tub
1660	0.82	0.0164	10090.ENSM	Braf,Bin1,Snap25,Tubb2a,Tubb2b,Slc12
2438	0.75	0.0038	10090.ENSM	Raf1,Tubb5,Braf,Bin1,Snap25,Vamp1,Tu
1983	0.75	0.0314	10090.ENSM	Raf1,Tubb5,Bin1,Snap25,Vamp1,Bsn,Vc
2358	0.72	0.0169	10090.ENSM	Braf,Bin1,Snap25,Bsn,Tubb2a,Tubb2b,S
3066	0.69	0.0036	10090.ENSM	Raf1,Tubb5,Bin1,Snap25,Vamp1,Tubb4b
4769	0.64	1.78E-05	10090.ENSM	Raf1,Tubb5,Bin1,Snap25,Vamp1,Bsn,Tu
3674	0.57	0.0407	10090.ENSM	Raf1,Braf,Bin1,Snap25,Tubb2a,Tubb2b,
4350	0.54	0.0314	10090.ENSM	Raf1,Braf,Bin1,Snap25,Bsn,Tubb2a,Tubb
4646	0.51	0.0407	10090.ENSM	Raf1,Braf,Bin1,Snap25,Vamp1,Bsn,Tubb

background g	strength	false discove	matching pro	matching proteins in your network (labe
19	2.16	0.0284	10090.ENSM	Raf1,Braf
62	2.05	3.05E-06	10090.ENSM	Tubb5,Tubb4b,Tubb2a,Tubb4a,Tubb2b
25	2.04	0.0302	10090.ENSM	Raf1,Braf
34	1.91	0.0437	10090.ENSM	Snap25,Vamp1
270	1.41	0.0012	10090.ENSM	Tubb5,Tubb4b,Tubb2a,Tubb4a,Tubb2b
342	1.3	0.0029	10090.ENSM	Tubb5,Tubb4b,Tubb2a,Tubb4a,Tubb2b
483	1.23	0.0012	10090.ENSM	Tubb5,Bsn,Tubb4b,Tubb2a,Tubb4a,Tubb
1411	0.77	0.0437	10090.ENSM	Raf1,Tubb5,Braf,Bin1,Icam1,Rtn4
1704	0.75	0.0284	10090.ENSM	Raf1,Tubb5,Braf,Tubb4b,Tubb2a,Tubb4a
1773	0.74	0.0302	10090.ENSM	Raf1,Tubb5,Braf,Tubb4b,Tubb2a,Tubb4a
2678	0.61	0.0382	10090.ENSM	Raf1,Tubb5,Braf,Bin1,Tubb4b,Tubb2a,Tu
6764	0.39	0.0437	10090.ENSM	Raf1,Tubb5,Braf,Bin1,Snap25,Vamp1,Bs
11199	0.27	0.0437	10090.ENSM	Raf1,Tubb5,Braf,Bin1,Snap25,Vamp1,Bs

els)

ubb2b

b2b

bb2b
a5,Rtn4,Gprin1
ubb4a,Tubb2b,Icam1,Rtn4
pip1,Rtn4
lc12a5,Rtn4,Gprin1
b,Vcpip1,Tubb2a,Tubb4a,Tubb2b,Rtn4
bb4b,Vcpip1,Tubb2a,Tubb4a,Tubb2b,Icam1,Slc12a5,Rtn4,Gprin1
Icam1,Slc12a5,Rtn4,Gprin1
b2b,Icam1,Slc12a5,Rtn4,Gprin1
b2a,Tubb2b,Icam1,Slc12a5,Rtn4

els)

b2b

a,Tubb2b
a,Tubb2b
ubb4a,Tubb2b
sn,Tubb2b,Icam1,Slc12a5,Rtn4,Gprin1
sn,Tubb4b,Tubb2a,Tubb4a,Tubb2b,Icam1,Slc12a5,Rtn4,Gprin1

Subcellular compartment

#term ID	term descrip	observed ger	background g	strength
GOCC:01500	Primary denc	2	2	2.65
GOCC:00700	Synaptobrevi	3	4	2.53
GOCC:00700	Synaptobrevi	3	4	2.53
GOCC:19905	Dendritic lam	2	3	2.48
GOCC:00991	Postsynaptic	2	4	2.35
GOCC:00443	Dendritic bra	2	5	2.26
GOCC:00700	Synaptobrevi	2	5	2.26
GOCC:00058	Neurofilame	3	10	2.13
GOCC:00974	Basal dendri	3	10	2.13
GOCC:00452	Tubulin com	2	9	2
GOCC:00057	Mitochondria	2	10	1.95
GOCC:19906	Proximal der	2	11	1.91
GOCC:00431	Axon initial s	3	18	1.88
GOCC:00442	Dendritic gro	2	12	1.88
GOCC:00431	Varicosity	2	16	1.75
GOCC:00312	SNARE comp	5	45	1.7
GOCC:00974	Apical dendri	3	28	1.68
GOCC:00443	Main axon	6	81	1.52
GOCC:00443	Calyx of held	2	27	1.52
GOCC:00432	Myelin sheat	6	88	1.49
GOCC:00431	Terminal bou	4	88	1.31
GOCC:00431	Dendritic sha	3	66	1.31
GOCC:00443	Neuron proje	8	193	1.27
GOCC:00436	Axon terminu	7	174	1.26
GOCC:00058	Microtubule	8	204	1.25
GOCC:00304	Growth cone	7	176	1.25
GOCC:00017	Photorecepto	3	79	1.23
GOCC:00162	Inclusion boc	3	81	1.22
GOCC:00986	Schaffer colla	3	82	1.22
GOCC:00487	Presynaptic a	3	84	1.21
GOCC:01500	Distal axon	12	337	1.2
GOCC:00995	Polymeric cy	12	346	1.19
GOCC:00989	Glutamaterg	8	244	1.17
GOCC:00430	Neuronal cel	12	377	1.16
GOCC:00306	Transport ve	4	129	1.14
GOCC:00304	Dendrite	15	495	1.13
GOCC:00322	Asymmetric	9	297	1.13
GOCC:00306	Synaptic vesi	3	102	1.12
GOCC:00304	Axon	16	554	1.11
GOCC:00140	Postsynaptic	8	288	1.1
GOCC:00057	Mitochondria	7	249	1.1
GOCC:00995	Postsynaptic	9	329	1.09
GOCC:00080	Synaptic vesi	5	185	1.08

GOCC:00442	Cell body	13	493	1.07
GOCC:00364	Somatodend	18	711	1.06
GOCC:00987	Postsynapse	14	563	1.05
GOCC:00995	Supramolecu	14	564	1.05
GOCC:00452	Synapse	24	1032	1.02
GOCC:00301	Transport ve	6	260	1.02
GOCC:00987	Presynapse	11	487	1.01
GOCC:00430	Neuron proje	21	1054	0.95
GOCC:00987	Mitochondria	5	270	0.92
GOCC:00300	Cell junction	25	1453	0.89
GOCC:00057	Mitochondria	5	309	0.86
GOCC:00306	Cytoplasmic	5	321	0.85
GOCC:00156	Actin cytoske	5	351	0.81
GOCC:00995	Secretory ves	7	501	0.8
GOCC:00429	Cell projectic	23	1794	0.76
GOCC:00058	Cytoskeleton	18	1397	0.76
GOCC:01200	Plasma mem	22	1774	0.75
GOCC:00156	Microtubule	9	855	0.68
GOCC:00319	Organelle en	8	760	0.68
GOCC:00057	Mitochondric	12	1178	0.66
GOCC:00987	Membrane p	12	1221	0.65
GOCC:00319	Vesicle	13	1396	0.62
GOCC:00314	Cytoplasmic	11	1298	0.58
GOCC:00432	Intracellular	20	2950	0.48
GOCC:00058	Cytosol	11	1784	0.44
GOCC:00057	Cytoplasm	36	6579	0.39
GOCC:00329	Protein-conta	24	4654	0.37
GOCC:00160	Membrane	24	4741	0.36
GOCC:00432	Intracellular	39	8073	0.34
GOCC:00432	Organelle	41	8565	0.33
GOCC:00056	Intracellular	43	9943	0.29
GOCC:00432	Membrane-b	29	7176	0.26
GOCC:01101	Cellular anat	48	12108	0.25
GOCC:00432	Intracellular	25	6320	0.25

false discove	matching prc	matching proteins in your network (labels)
0.0012	10090.ENSM	Map2,Map1a
2.03E-05	10090.ENSM	Vamp2,Snap25,Cplx1
2.03E-05	10090.ENSM	Vamp2,Cplx2,Snap25
0.0019	10090.ENSM	Sncb,Snca
0.0027	10090.ENSM	Ina,Nefh
0.0037	10090.ENSM	Map2,Map1a
0.0037	10090.ENSM	Vamp2,Snap25
0.00015	10090.ENSM	Ina,Nefh,Shank2
0.00015	10090.ENSM	Map1b,Map2,Nefh
0.0085	10090.ENSM	Tubb5,Tubb4b
0.0097	10090.ENSM	Slc25a4,Snca
0.0111	10090.ENSM	Map2,Nefh
0.0006	10090.ENSM	Bin1,Map2,Map1a
0.0128	10090.ENSM	Map2,Rtn4
0.0203	10090.ENSM	Bin1,Map1b
5.61E-06	10090.ENSM	Vamp2,Cplx2,Snap25,Vamp1,Cplx1
0.0018	10090.ENSM	Map1b,Map2,Nefh
2.95E-06	10090.ENSM	Bin1,Map1b,Tubb4a,Map2,Map1a,Sptan1
0.0436	10090.ENSM	Cplx2,Cplx1
4.25E-06	10090.ENSM	Snap25,Ina,Tubb4a,Nefh,Sptan1,Rtn4
0.002	10090.ENSM	Bsn,Sncb,Aak1,Snca
0.014	10090.ENSM	Map2,Map1a,Slc12a5
1.16E-06	10090.ENSM	Vamp2,Bin1,Cplx2,Bsn,Cplx1,Sncb,Aak1,Snca
9.01E-06	10090.ENSM	Bin1,Cplx2,Bsn,Cplx1,Sncb,Aak1,Snca
1.68E-06	10090.ENSM	Tubb5,Tubb4b,Tubb2a,Map6,Map1b,Tubb4a,Tubb2b,Map1a
9.44E-06	10090.ENSM	Dpysl2,Snap25,Sncb,Map1b,Map2,Rtn4,Snca
0.022	10090.ENSM	Map1b,Map1a,Shank2
0.0224	10090.ENSM	Sncb,Nefh,Snca
0.023	10090.ENSM	Bsn,Cplx1,Tubb2b
0.024	10090.ENSM	Snap25,Bsn,Shank2
2.15E-09	10090.ENSM	Dpysl2,Bin1,Cplx2,Snap25,Bsn,Cplx1,Sncb,Map1b,Map2,Aak1,Rtn4,
2.64E-09	10090.ENSM	Tubb5,Ina,Tubb4b,Tubb2a,Map6,Map1b,Tubb4a,Tubb2b,Map2,Nef
5.22E-06	10090.ENSM	Bin1,Cplx2,Snap25,Vamp1,Bsn,Cplx1,Rtn4,Shank2
5.20E-09	10090.ENSM	Dpysl2,Snap25,Bsn,Sncb,Map1b,Tubb4a,Map2,Nefh,Map1a,Slc12a
0.0071	10090.ENSM	Vamp2,Bin1,Synrg,Snca
6.33E-11	10090.ENSM	Dpysl2,Bin1,Cplx2,Bsn,Cplx1,Sncb,Elfn1,Map1b,Map2,Nefh,Map1a,
1.69E-06	10090.ENSM	Add2,Bsn,Map1b,Map2,Nefh,Map1a,Epb4.1l1,Rtn4,Shank2
0.039	10090.ENSM	Vamp2,Bin1,Snca
2.06E-11	10090.ENSM	Dpysl2,Bin1,Cplx2,Snap25,Bsn,Cplx1,Sncb,Map1b,Tubb4a,Map2,Aa
1.55E-05	10090.ENSM	Add2,Bsn,Map1b,Map2,Nefh,Map1a,Epb4.1l1,Rtn4
7.92E-05	10090.ENSM	Timm44,Mccc1,Mrps31,Pcca,Pcx,Hspe1,Snca
3.57E-06	10090.ENSM	Gabra1,Add2,Bsn,Map1b,Map2,Nefh,Map1a,Epb4.1l1,Rtn4
0.0024	10090.ENSM	Vamp2,Bin1,Snap25,Bsn,Snca

6.44E-09	10090.ENSM	Braf,Dpysl2,Snap25,Bsn,Sncb,Map1b,Tubb4a,Map2,Nefh,Map1a,Sl
4.18E-12	10090.ENSM	Dpysl2,Bin1,Cplx2,Snap25,Bsn,Cplx1,Sncb,Elfn1,Map1b,Tubb4a,Ma
2.84E-09	10090.ENSM	Gabra1,Cplx2,Snap25,Add2,Bsn,Cplx1,Ina,Map1b,Map2,Nefh,Map1
2.84E-09	10090.ENSM	Tubb5,Ina,Tubb4b,Tubb2a,Map6,Map1b,Tubb4a,Tubb2b,Map2,Nef
6.80E-16	10090.ENSM	Gabra1,Vamp2,Dpysl2,Bin1,Cplx2,Snap25,Add2,Vamp1,Bsn,Cplx1,I
0.0011	10090.ENSM	Vamp2,Bin1,Snap25,Bsn,Synrg,Snca
8.28E-07	10090.ENSM	Vamp2,Dpysl2,Bin1,Cplx2,Snap25,Bsn,Cplx1,Sncb,Aak1,Shank2,Snc
1.70E-12	10090.ENSM	Braf,Vamp2,Dpysl2,Bin1,Cplx2,Snap25,Bsn,Cplx1,Sncb,Elfn1,Map1
0.0107	10090.ENSM	Mccc1,Mrps31,Slc25a4,Ina,Snca
5.07E-14	10090.ENSM	Gabra1,Vamp2,Dpysl2,Bin1,Cplx2,Snap25,Add2,Vamp1,Bsn,Cplx1,I
0.0183	10090.ENSM	Timm44,Slc25a4,Ina,Pcx,Snca
0.0211	10090.ENSM	Vamp2,Bin1,Vamp1,Synrg,Snca
0.028	10090.ENSM	Snap25,Add2,Map2,Sptan1,Snca
0.004	10090.ENSM	Vamp2,Bin1,Snap25,Vamp1,Bsn,Sncb,Snca
1.88E-10	10090.ENSM	Raf1,Braf,Vamp2,Dpysl2,Bin1,Cplx2,Snap25,Bsn,Cplx1,Sncb,Elfn1,N
5.47E-08	10090.ENSM	Tubb5,Snap25,Add2,Bsn,Ina,Tubb4b,Tubb2a,Map6,Map1b,Tubb4a,
1.29E-09	10090.ENSM	Raf1,Braf,Vamp2,Dpysl2,Bin1,Cplx2,Snap25,Bsn,Cplx1,Sncb,Elfn1,N
0.0037	10090.ENSM	Tubb5,Tubb4b,Tubb2a,Map6,Map1b,Tubb4a,Tubb2b,Map2,Map1a
0.0085	10090.ENSM	Tubb5,Timm44,Bin1,Slc25a4,Ina,Pcx,Rtn4,Snca
0.00039	10090.ENSM	Braf,Timm44,Iscu,Mccc1,Mrps31,Slc25a4,Pcca,Ina,Pcx,Hspe1,Nefh
0.00054	10090.ENSM	Gabra1,Vamp2,Cplx2,Snap25,Vamp1,Slc25a4,Cplx1,Ina,Synrg,Icam
0.00039	10090.ENSM	Vamp2,Bin1,Snap25,Vamp1,Bsn,Gga1,Sncb,Synrg,Icam1,Aak1,Pla
0.0038	10090.ENSM	Vamp2,Bin1,Snap25,Vamp1,Bsn,Gga1,Sncb,Synrg,Aak1,Snca,Agfg
0.0001	10090.ENSM	Tubb5,Timm44,Snap25,Add2,Mrps31,Bsn,Ina,Tubb4b,Tubb2a,Map
0.0385	10090.ENSM	Raf1,Tubb5,Braf,Dpysl2,Bin1,Iscu,Snap25,Sncb,Map1b,Map1a,Snc
4.56E-08	10090.ENSM	Raf1,Tubb5,Braf,Timm44,Vamp2,Dpysl2,Bin1,Iscu,Cplx2,Snap25,M
0.00063	10090.ENSM	Tubb5,Gabra1,Vamp2,Bin1,Iscu,Cplx2,Snap25,Mccc1,Add2,Vamp1,
0.00086	10090.ENSM	Braf,Timm44,Gabra1,Vamp2,Bin1,Cplx2,Snap25,Add2,Vamp1,Slc2
9.92E-08	10090.ENSM	Raf1,Tubb5,Braf,Timm44,Vamp2,Bin1,Iscu,Snap25,Mccc1,Add2,Va
1.84E-08	10090.ENSM	Raf1,Tubb5,Braf,Timm44,Gabra1,Vamp2,Bin1,Iscu,Snap25,Mccc1,
6.21E-08	10090.ENSM	Raf1,Tubb5,Braf,Timm44,Vamp2,Dpysl2,Bin1,Iscu,Cplx2,Snap25,M
0.0039	10090.ENSM	Raf1,Tubb5,Braf,Timm44,Vamp2,Bin1,Iscu,Snap25,Mccc1,Vamp1,
1.64E-09	10090.ENSM	Raf1,Tubb5,Braf,Timm44,Gabra1,Vamp2,Dpysl2,Bin1,Iscu,Cplx2,Sn
0.022	10090.ENSM	Raf1,Tubb5,Braf,Timm44,Vamp2,Bin1,Iscu,Snap25,Mccc1,Mrps31,

,Snca
h,Map1a,Shank2

5,Rtn4,Agfg1

,Slc12a5,Rtn4,Shank2,Snca

k1,Nefh,Map1a,Sptan1,Rtn4,Snca

lc12a5,Rtn4,Agfg1
p2,Nefh,Map1a,Slc12a5,Rtn4,Shank2,Snca,Agfg1
La,Epb4.1l1,Rtn4,Shank2
h,Map1a,Sptan1,Shank2,Snca
na,Sncb,Elfn1,Map1b,Tubb2b,Map2,Aak1,Nefh,Map1a,Epb4.1l1,Rtn4,Shank2,Plaa,Snca

a
b,Tubb4a,Map2,Aak1,Nefh,Map1a,Slc12a5,Sptan1,Rtn4,Shank2,Snca

na,Sncb,Elfn1,Map1b,Tubb2b,Map2,Aak1,Nefh,Map1a,Sptan1,Epb4.1l1,Rtn4,Shank2,Plaa,Snc

Map1b,Tubb4a,Map2,Aak1,Nefh,Map1a,Slc12a5,Sptan1,Rtn4,Shank2,Snca,Agfg1
Tubb2b,Map2,Nefh,Map1a,Sptan1,Epb4.1l1,Shank2,Snca
Map1b,Tubb4a,Map2,Aak1,Nefh,Map1a,Slc12a5,Sptan1,Rtn4,Shank2,Snca

,Snca
1,Aak1,Snca
a,Snca,Agfg1
1
6,Map1b,Tubb4a,Tubb2b,Map2,Nefh,Map1a,Sptan1,Epb4.1l1,Shank2,Snca
a
lccc1,Vamp1,Mrps31,Slc25a4,Bsn,Gga1,Cplx1,Pcca,Ina,Sncb,Vcpip1,Synrg,Pcx,Map1b,Tubb4a,
,Mrps31,Slc25a4,Cplx1,Ina,Tubb4b,Vcpip1,Synrg,Map1b,Map2,Icam1,Aak1,Map1a,Sptan1,Snc
5a4,Bsn,Cplx1,Ina,Synrg,Pcx,Map2,Icam1,Aak1,Slc12a5,Sptan1,Epb4.1l1,Rtn4,Snca,Gprin1
amp1,Mrps31,Slc25a4,Bsn,Gga1,Pcca,Ina,Tubb4b,Sncb,Synrg,Tubb2a,Pcx,Map6,Map1b,Tubb4a
Add2,Vamp1,Mrps31,Slc25a4,Bsn,Gga1,Pcca,Ina,Tubb4b,Sncb,Synrg,Tubb2a,Pcx,Map6,Map1b
lccc1,Add2,Vamp1,Mrps31,Slc25a4,Bsn,Gga1,Cplx1,Pcca,Ina,Tubb4b,Sncb,Vcpip1,Synrg,Tubb2
Mrps31,Slc25a4,Bsn,Gga1,Pcca,Ina,Sncb,Synrg,Pcx,Hspe1,Map2,Icam1,Aak1,Nefh,Sugp2,Rtn4
nap25,Mccc1,Add2,Vamp1,Mrps31,Slc25a4,Bsn,Gga1,Cplx1,Pcca,Ina,Tubb4b,Sncb,Vcpip1,Elfn
,Slc25a4,Bsn,Gga1,Pcca,Ina,Synrg,Pcx,Hspe1,Map2,Nefh,Sugp2,Rtn4,Plaa,Snca,Agfg1

a

Hspe1,Map2,Aak1,Nefh,Map1a,Sptan1,Rtn4,Shank2,Plaa,Snca,Agfg1
a

a,Hspe1,Tubb2b,Map2,Aak1,Nefh,Sugp2,Map1a,Sptan1,Epb4.1l1,Rtn4,Shank2,Plaa,Snca,Agfg1
o,Tubb4a,Hspe1,Tubb2b,Map2,Icam1,Aak1,Nefh,Sugp2,Map1a,Sptan1,Epb4.1l1,Rtn4,Shank2,P
a,Pcx,Map6,Map1b,Tubb4a,Hspe1,Tubb2b,Map2,Aak1,Nefh,Sugp2,Map1a,Sptan1,Epb4.1l1,Rt
,Plaa,Snca,Agfg1
1,Synrg,Tubb2a,Pcx,Map6,Map1b,Tubb4a,Hspe1,Tubb2b,Map2,Icam1,Aak1,Nefh,Sugp2,Map1

1
Plaa,Snca,Agfg1
n4,Shank2,Plaa,Snca,Agfg1

a,Slc12a5,Sptan1,Epb4.1l1,Rtn4,Shank2,Plaa,Snca,Gprin1,Agfg1

Table 17 **GO for tau interactome from encoding-consolidation (EC) spatial memory p**

Biological Process			
#term ID	**term description**	**observed ge**	**background**
GO:0098989	***NMDA selective glutamate receptor signalin***	***2***	***4***
GO:0016191	Synaptic vesicle uncoating	2	5
GO:0050432	Catecholamine secretion	2	5
GO:1904851	Positive regulation of establishment of protein lo	2	10
GO:2000369	Regulation of clathrin-dependent endocytosis	3	16
GO:0035865	Cellular response to potassium ion	2	11
GO:0099645	Neurotransmitter receptor localization to postsy	3	19
GO:0099558	Maintenance of synapse structure	3	30
GO:0060996	Dendritic spine development	3	36
GO:0048169	Regulation of long-term neuronal synaptic plasti	3	37
GO:0031113	Regulation of microtubule polymerization	4	55
GO:0060291	***Long-term synaptic potentiation***	***4***	***57***
GO:0017156	***Calcium-ion regulated exocytosis***	***3***	***45***
GO:0048488	Synaptic vesicle endocytosis	3	51
GO:0043954	Cellular component maintenance	4	69
GO:0048168	Regulation of neuronal synaptic plasticity	4	70
GO:0043624	Cellular protein complex disassembly	3	52
GO:0061001	Regulation of dendritic spine morphogenesis	3	55
GO:0060998	Regulation of dendritic spine development	4	94
GO:0099504	Synaptic vesicle cycle	5	125
GO:0007338	Single fertilization	5	126
GO:0099173	Postsynapse organization	4	106
GO:0007163	Establishment or maintenance of cell polarity	7	199
GO:0006457	Protein folding	5	146
GO:0048814	Regulation of dendrite morphogenesis	4	117
GO:0048259	Regulation of receptor-mediated endocytosis	4	118
GO:0098693	Regulation of synaptic vesicle cycle	5	150
GO:0099175	Regulation of postsynapse organization	4	130
GO:0008037	Cell recognition	4	131
GO:0050770	Regulation of axonogenesis	6	203
GO:0018105	Peptidyl-serine phosphorylation	5	181
GO:0007268	Chemical synaptic transmission	9	335
GO:0048167	Regulation of synaptic plasticity	6	221
GO:0010769	Regulation of cell morphogenesis involved in dif	9	343
GO:0050808	Synapse organization	8	303
GO:0050773	Regulation of dendrite development	5	193
GO:1990778	Protein localization to cell periphery	6	247
GO:0001505	Regulation of neurotransmitter levels	6	255
GO:0017157	Regulation of exocytosis	6	255
GO:0031345	Negative regulation of cell projection organizatio	5	212
GO:0022604	Regulation of cell morphogenesis	12	528
GO:0032271	Regulation of protein polymerization	5	223
GO:0050807	Regulation of synapse organization	6	275
GO:0030100	Regulation of endocytosis	5	228
GO:0034329	Cell junction assembly	5	228
GO:0031334	Positive regulation of protein-containing complex	5	230
GO:0034330	Cell junction organization	10	481
GO:0010975	Regulation of neuron projection development	12	607
GO:0050804	Modulation of chemical synaptic transmission	10	521
GO:1902903	Regulation of supramolecular fiber organization	7	364

GO:0010976	Positive regulation of neuron projection develop	7	366
GO:1901214	Regulation of neuron death	7	375
GO:0060627	Regulation of vesicle-mediated transport	11	600
GO:0120035	Regulation of plasma membrane bounded cell p	14	788
GO:1903047	Mitotic cell cycle process	8	454
GO:0032940	Secretion by cell	7	391
GO:0045666	Positive regulation of neuron differentiation	8	465
GO:0051640	Organelle localization	8	465
GO:0045664	Regulation of neuron differentiation	13	774
GO:0072657	Protein localization to membrane	7	427
GO:0034622	Cellular protein-containing complex assembly	11	683
GO:0048858	Cell projection morphogenesis	8	490
GO:0043254	Regulation of protein-containing complex assem	7	437
GO:0031175	Neuron projection development	11	697
GO:1903530	Regulation of secretion by cell	11	713
GO:0050767	Regulation of neurogenesis	14	948
GO:0000902	Cell morphogenesis	11	739
GO:0048812	Neuron projection morphogenesis	7	479
GO:0048666	Neuron development	12	855
GO:0043933	Protein-containing complex subunit organizatior	16	1164
GO:0061024	Membrane organization	8	603
GO:0048699	Generation of neurons	21	1660
GO:0051649	Establishment of localization in cell	19	1518
GO:0065003	Protein-containing complex assembly	13	1025
GO:0016192	Vesicle-mediated transport	14	1130
GO:0030182	Neuron differentiation	13	1056
GO:0051129	Negative regulation of cellular component organ	9	733
GO:0030030	Cell projection organization	13	1124
GO:0022402	Cell cycle process	9	784
GO:0007010	Cytoskeleton organization	12	1064
GO:0120036	Plasma membrane bounded cell projection orga	12	1072
GO:0060341	Regulation of cellular localization	12	1083
GO:0051641	Cellular localization	23	2115
GO:0051049	Regulation of transport	20	1862
GO:0046907	Intracellular transport	12	1166
GO:0044087	Regulation of cellular component biogenesis	10	978
GO:0051130	Positive regulation of cellular component organiz	12	1236
GO:0022607	Cellular component assembly	19	1983
GO:0033043	Regulation of organelle organization	12	1258
GO:0051234	Establishment of localization	33	3522
GO:0006810	Transport	31	3382
GO:0033036	Macromolecule localization	20	2198
GO:0044085	Cellular component biogenesis	20	2201
GO:0010941	Regulation of cell death	15	1661
GO:0032879	Regulation of localization	25	2806
GO:0008104	Protein localization	17	1890
GO:0051128	Regulation of cellular component organization	21	2438
GO:0048468	Cell development	15	1730
GO:0034613	Cellular protein localization	12	1392
GO:0006996	Organelle organization	26	3066
GO:0071705	Nitrogen compound transport	13	1534
GO:0071702	Organic substance transport	15	1836
GO:0045595	Regulation of cell differentiation	15	1868
GO:0071840	Cellular component organization or biogenesis	38	4954
GO:0016043	Cellular component organization	37	4769
GO:0051179	Localization	35	4646

GO:0065008	Regulation of biological quality	29	3822
GO:0030154	Cell differentiation	26	3674
GO:0048523	Negative regulation of cellular process	29	4672
GO:0048731	System development	27	4350
GO:0048519	Negative regulation of biological process	30	5108
GO:0048856	Anatomical structure development	29	5258
GO:0048518	Positive regulation of biological process	29	5869
GO:0050794	Regulation of cellular process	44	9541
GO:0050789	Regulation of biological process	45	9973
GO:0009987	Cellular process	60	13330
GO:0065007	Biological regulation	47	10591

hase

				Molecular Fu
strength	false discov	matching pr	matching proteins	#term ID
2.25	***0.016***	***10090.ENSM***	***Grin2b,Camk2a***	GO:0099186
2.15	0.0206	10090.ENSM	Sh3gl2,Dnajc6	GO:0098918
2.15	0.0206	10090.ENSM	Mecp2,Cadps	GO:0019901
1.85	0.0442	10090.ENSM	Cct8,Cct7	GO:0019900
1.82	0.0043	10090.ENSM	Sh3gl2,Dnajc6,Snap	GO:0019904
1.81	0.0492	10090.ENSM	Mecp2,Dlg2	GO:0005524
1.75	0.0064	10090.ENSM	Git1,Camk2a,Dlg2	GO:0035639
1.55	0.0153	10090.ENSM	Git1,Rims1,Dlg2	GO:0032555
1.47	0.0213	10090.ENSM	Pak2,Git1,Camk2a	GO:0000166
1.46	0.0226	10090.ENSM	Grin2b,Rims1,Cam	GO:0044877
1.41	0.0049	10090.ENSM	Fkbp4,Mecp2,Mapt	GO:0036094
1.4	***0.0055***	***10090.ENSM***	***Mecp2,Grin2b,Rim***	GO:0043168
1.37	***0.0342***	***10090.ENSM***	***Vamp3,Cadps,Rim***	GO:0019899
1.32	0.0433	10090.ENSM	Sh3gl2,Dnajc6,Snap	GO:0005515
1.31	0.0088	10090.ENSM	Git1,Rims1,Cttn,Dlg	GO:1901363
1.31	0.0092	10090.ENSM	Grin2b,Rims1,Cam	GO:0043167
1.31	0.0442	10090.ENSM	Sh3gl2,Dnajc6,Nsf	GO:0097159
1.29	0.0486	10090.ENSM	Cttn,Srcin1,Camk2b	GO:0005488
1.18	0.0207	10090.ENSM	Mecp2,Cttn,Srcin1,Camk2b	
1.15	0.0064	10090.ENSM	Sh3gl2,Dnajc6,Cadps,Rims1,Sna	
1.15	0.0065	10090.ENSM	Cct8,Spam1,Cct7,Rims1,Camk2b	
1.13	0.0283	10090.ENSM	Git1,Cttn,Dlg2,Camk2b	
1.1	0.00063	10090.ENSM	Wee1,Map4,Syne4,Arhgap35,Sna	
1.09	0.0107	10090.ENSM	Trap1,Cct8,Cct7,Fkbp4,Dnajc5	
1.08	0.0372	10090.ENSM	Ppp3ca,Cttn,Srcin1,Camk2b	
1.08	0.0381	10090.ENSM	Sh3gl2,Dnajc6,Snap91,Nsf	
1.07	0.0116	10090.ENSM	Git1,Dnajc5,Rims1,Snap91,Camk	
1.04	0.0465	10090.ENSM	Grin2b,Cttn,Srcin1,Camk2b	
1.04	0.0475	10090.ENSM	Cct8,Cct7,Git1,Arhgap35	
1.02	0.0055	10090.ENSM	Nefm,Arhgap35,Snap91,Mapt,Cttn	
0.99	0.0211	10090.ENSM	Pak2,Srpk2,Hk1,Camk2a,Camk2	
0.98	0.00028	10090.ENSM	Sncg,Mecp2,Ppp3ca,Grin2b,Cadp	
0.98	0.0078	10090.ENSM	Mecp2,Grin2b,Rims1,Mapt,Camk	
0.97	0.00031	10090.ENSM	Nefm,Ppp3ca,Arhgap35,Snap91,N	
0.97	0.00081	10090.ENSM	Sncg,Mecp2,Git1,Rims1,Mapt,Ctt	
0.96	0.0263	10090.ENSM	Mecp2,Ppp3ca,Cttn,Srcin1,Camk	
0.94	0.0117	10090.ENSM	Vamp3,Git1,Nsf,Camk2a,Dlg2,Cla	
0.92	0.0133	10090.ENSM	Sncg,Git1,Cadps,Rims1,Snap91,(	
0.92	0.0133	10090.ENSM	Git1,Cadps,Rims1,Nsf,Camk2a,C	
0.92	0.036	10090.ENSM	Fkbp4,Mecp2,Map4,Ppp3ca,Grin	
0.91	3.33E-05	10090.ENSM	Nefm,Mecp2,Ppp3ca,Arhgap35,R	
0.9	0.0419	10090.ENSM	Fkbp4,Mecp2,Mapt,Cttn,Clasp2	
0.89	0.018	10090.ENSM	Mecp2,Grin2b,Snap91,Cttn,Srcin	
0.89	0.0442	10090.ENSM	Sh3gl2,Dnajc6,Ppp3ca,Snap91,N	
0.89	0.0442	10090.ENSM	Pak2,Mecp2,Plec,Mapt,Cttn	
0.89	0.0444	10090.ENSM	Mecp2,Rims1,Snap91,Mapt,Cttn	
0.87	0.00047	10090.ENSM	Pak2,Sncg,Mecp2,Git1,Plec,Rims	
0.85	8.51E-05	10090.ENSM	Nefm,Fkbp4,Mecp2,Ppp3ca,Arhg	
0.83	0.00072	10090.ENSM	Sncg,Mecp2,Git1,Ppp3ca,Grin2b,	
0.83	0.0119	10090.ENSM	Pak2,Fkbp4,Mecp2,Arhgap35,Ma	

0.83	0.0122	10090.ENSM	Mecp2,Arhgap35,Rims1,Snap91,I
0.82	0.0135	10090.ENSM	Sncg,Mecp2,Grin2b,Dnajc5,Srpk2
0.81	0.00046	10090.ENSM	Sh3gl2,Git1,Dnajc6,Ppp3ca,Cadp
0.8	3.78E-05	10090.ENSM	Nefm,Fkbp4,Mecp2,Map4,Ppp3ca
0.8	0.0079	10090.ENSM	Wee1,Mecp2,Map4,Smc4,Ppp3ca
0.8	0.0165	10090.ENSM	Sncg,Vamp3,Mecp2,Cadps,Rims
0.79	0.0087	10090.ENSM	Mecp2,Spag9,Arhgap35,Rims1,S
0.79	0.0087	10090.ENSM	Map4,Spag9,Rims1,Snap91,Pdzd
0.78	0.00014	10090.ENSM	Nefm,Fkbp4,Mecp2,Spag9,Ppp3c
0.77	0.0241	10090.ENSM	Vamp3,Git1,Grin2b,Nsf,Camk2a,I
0.76	0.00098	10090.ENSM	Sh3gl2,Vamp3,Fkbp4,Cadps,SrpI
0.76	0.0115	10090.ENSM	Sh3gl2,Wee1,Arhgap35,Snap91,M
0.76	0.0265	10090.ENSM	Fkbp4,Mecp2,Rims1,Snap91,Map
0.75	0.0011	10090.ENSM	Pak2,Sh3gl2,Wee1,Mecp2,Map4,
0.74	0.0013	10090.ENSM	Sncg,Vamp3,Git1,Ppp3ca,Grin2b
0.72	0.0002	10090.ENSM	Nefm,Fkbp4,Mecp2,Spag9,Ppp3c
0.72	0.0018	10090.ENSM	Il7r,Sh3gl2,Vamp3,Wee1,Arhgap3
0.72	0.0396	10090.ENSM	Sh3gl2,Wee1,Arhgap35,Snap91,M
0.7	0.0012	10090.ENSM	Pak2,Sh3gl2,Wee1,Mecp2,Map4,
0.69	7.65E-05	10090.ENSM	Nefm,Cct8,Sh3gl2,Vamp3,Fkbp4,
0.67	0.0314	10090.ENSM	Slc25a5,Sh3gl2,Vamp3,Spam1,Ee
0.65	4.56E-06	10090.ENSM	Nefm,Pak2,Sh3gl2,Fkbp4,Wee1,M
0.65	2.75E-05	10090.ENSM	Nefm,Atp5b,Sh3gl2,Vamp3,Uqcrc
0.65	0.0013	10090.ENSM	Cct8,Sh3gl2,Vamp3,Fkbp4,Grin2I
0.64	0.00081	10090.ENSM	Atp5b,Sh3gl2,Vamp3,Spag9,Dnajc
0.64	0.0018	10090.ENSM	Pak2,Sh3gl2,Wee1,Mecp2,Map4,
0.64	0.0244	10090.ENSM	Slc25a5,Pak2,Fkbp4,Mecp2,Map
0.61	0.003	10090.ENSM	Pak2,Sh3gl2,Wee1,Mecp2,Map4,
0.61	0.0352	10090.ENSM	Wee1,Mecp2,Map4,Smc4,Ppp3ca
0.6	0.0072	10090.ENSM	Nefm,Wee1,Mecp2,Map4,Arhgap
0.6	0.0077	10090.ENSM	Pak2,Sh3gl2,Wee1,Mecp2,Map4,
0.6	0.0081	10090.ENSM	Sncg,Cct8,Cct7,Mecp2,Git1,Dnaj
0.59	9.45E-06	10090.ENSM	Nefm,Atp5b,Sh3gl2,Vamp3,Uqcrc
0.58	7.65E-05	10090.ENSM	Slc25a5,Sncg,Sh3gl2,Vamp3,Mec
0.56	0.0133	10090.ENSM	Nefm,Atp5b,Vamp3,Uqcrc2,Relch
0.56	0.0385	10090.ENSM	Pak2,Fkbp4,Mecp2,Map4,Arhgap
0.54	0.02	10090.ENSM	Cct8,Sh3gl2,Cct7,Mecp2,Ppp3ca
0.53	0.00059	10090.ENSM	Nefm,Pak2,Cct8,Sh3gl2,Vamp3,F
0.53	0.0216	10090.ENSM	Slc25a5,Pak2,Cct8,Cct7,Fkbp4,M
0.52	2.29E-07	10090.ENSM	Slc25a5,Nefm,Sncg,Atp5b,Cct8,A
0.51	5.21E-07	10090.ENSM	Slc25a5,Nefm,Sncg,Atp5b,Cct8,A
0.51	0.00059	10090.ENSM	Sncg,Vamp3,Fkbp4,Uqcrc2,Mecp
0.51	0.00059	10090.ENSM	Nefm,Pak2,Cct8,Sh3gl2,Vamp3,F
0.51	0.0081	10090.ENSM	Il7r,Trap1,Slc25a5,Pak2,Sncg,Me
0.5	4.90E-05	10090.ENSM	Slc25a5,Sncg,Atp5b,Cct8,Sh3gl2,
0.5	0.003	10090.ENSM	Sncg,Vamp3,Fkbp4,Uqcrc2,Mecp
0.49	0.00063	10090.ENSM	Slc25a5,Nefm,Pak2,Cct8,Sh3gl2,
0.49	0.0115	10090.ENSM	Pak2,Sh3gl2,Vamp3,Wee1,Mecp2
0.49	0.0424	10090.ENSM	Vamp3,Uqcrc2,Git1,Ppp3ca,Grin2
0.48	5.86E-05	10090.ENSM	Tep1,Slc25a5,Nefm,Vamp3,Uqcrc
0.48	0.0317	10090.ENSM	Slc25a5,Sncg,Vamp3,Uqcrc2,Me
0.46	0.0184	10090.ENSM	Slc25a5,Sncg,Vamp3,Uqcrc2,Me
0.46	0.0207	10090.ENSM	Il7r,Nefm,Fkbp4,Mecp2,Spag9,Pp
0.44	2.79E-07	10090.ENSM	Il7r,Tep1,Slc25a5,Nefm,Pak2,Snc
0.44	3.52E-07	10090.ENSM	Il7r,Tep1,Slc25a5,Nefm,Pak2,Snc
0.43	2.88E-06	10090.ENSM	Slc25a5,Nefm,Sncg,Atp5b,Cct8,A

0.43	7.16E-05	10090.ENSM	Il7r,Tep1,Slc25a5,Nefm,Sncg,Atp
0.4	0.00081	10090.ENSM	Il7r,Nefm,Pak2,Sh3gl2,Vamp3,Fk
0.34	0.0018	10090.ENSM	Il7r,Trap1,Slc25a5,Pak2,Sncg,Atp
0.34	0.0039	10090.ENSM	Il7r,Nefm,Pak2,Atp5b,Sh3gl2,Fkb
0.32	0.003	10090.ENSM	Il7r,Trap1,Slc25a5,Pak2,Sncg,Atp
0.29	0.0112	10090.ENSM	Il7r,Nefm,Pak2,Atp5b,Sh3gl2,Vam
0.24	0.0459	10090.ENSM	Il7r,Slc25a5,Pak2,Atp5b,Cct8,Sh3
0.21	0.0024	10090.ENSM	Il7r,Trap1,Slc25a5,Nefm,Pak2,Sn
0.21	0.0029	10090.ENSM	Il7r,Trap1,Slc25a5,Nefm,Pak2,Sn
0.2	2.29E-07	10090.ENSM	Il7r,Trap1,Tep1,Slc25a5,Nefm,Pa
0.2	0.002	10090.ENSM	Il7r,Trap1,Tep1,Slc25a5,Nefm,Pa

unction				
term description	observed ge	background	strength	false discov
Structural constituent of postsynapse	3	22	1.69	0.0075
Structural constituent of synapse	4	31	1.66	0.00056
Protein kinase binding	12	707	0.78	0.00013
Kinase binding	13	792	0.77	0.00013
Protein domain specific binding	11	778	0.7	0.0018
ATP binding	18	1393	0.66	5.58E-05
Purine ribonucleoside triphosphate bindin	19	1704	0.6	8.48E-05
Purine ribonucleotide binding	19	1773	0.58	0.00013
Nucleotide binding	20	2021	0.55	0.00013
Protein-containing complex binding	13	1411	0.52	0.0204
Small molecule binding	22	2406	0.51	0.00013
Anion binding	23	2678	0.48	0.00013
Enzyme binding	19	2277	0.47	0.0018
Protein binding	42	6764	0.34	7.27E-06
Heterocyclic compound binding	26	4771	0.29	0.0376
Ion binding	29	5439	0.28	0.0204
Organic cyclic compound binding	26	4858	0.28	0.0486
Binding	51	11199	0.21	0.00013

p91
)

ap91,Dlg2,Clasp2

:2a

n,Clasp2
:b
ps,Rims1,Snap91,Dlg2,Dlgap2
2a,Camk2b
Mapt,Cttn,Srcin1,Camk2b,Clasp2
:n,Dlg2,Camk2b
2b
asp2
Camk2a
Clasp2
2b
:ims1,Snap91,Pdzd8,Mapt,Cttn,Srcin1,Camk2b,Clasp2

1,Camk2b
sf

s1,Mapt,Cttn,Dlg2,Camk2b
ap35,Rims1,Snap91,Mapt,Cttn,Srcin1,Camk2b,Clasp2
,Rims1,Mapt,Camk2a,Camk2b,Dlgap2
apt,Cttn,Clasp2

Mapt,Cttn,Camk2b
2,Mapt,Set
s,Dnajc5,Rims1,Snap91,Nsf,Camk2a,Clasp2
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		Subcellular Compartments		
matching pr	**matching p**	**#term ID**	**term description**	**observed ge**
10090.ENSM	Git1,Dlg2,Ca	GOCC:0005	Calcium- and calmodulin-dependent prote	2
10090.ENSM	Git1,Rims1,D	GOCC:0005	Chaperonin-containing t-complex	2
10090.ENSM	Trap1,Pak2,	GOCC:0099	Presynaptic cytoskeleton	2
10090.ENSM	Trap1,Pak2,	GOCC:0099	Postsynaptic cytoskeleton	2
10090.ENSM	Mecp2,Dnajc	GOCC:0044	Axonal growth cone	3
10090.ENSM	Trap1,Tep1,	GOCC:0099	Cell cortex region	3
10090.ENSM	Trap1,Tep1,	***GOCC:0014***	***Postsynaptic density***	***12***
10090.ENSM	Trap1,Tep1,	GOCC:0098	Neuron to neuron synapse	13
10090.ENSM	Trap1,Tep1,	GOCC:0030	Transport vesicle membrane	5
10090.ENSM	Nefm,Uqcrc2	GOCC:0030	Synaptic vesicle membrane	4
10090.ENSM	Trap1,Tep1,	**GOCC:0034**	**Nuclear periphery**	**4**
10090.ENSM	Trap1,Tep1,	GOCC:0098	Glutamatergic synapse	8
10090.ENSM	Trap1,Tep1,	GOCC:0008	Synaptic vesicle	6
10090.ENSM	Trap1,Tep1,	GOCC:0044	Neuron spine	5
10090.ENSM	Trap1,Tep1,	GOCC:0098	Postsynapse	16
10090.ENSM	Trap1,Tep1,	GOCC:0099	Cytoplasmic region	6
10090.ENSM	Trap1,Tep1,	GOCC:0016	Nuclear speck	4
10090.ENSM	Trap1,Tep1,	GOCC:0043	Dendritic spine	4
		GOCC:0098	Presynapse	11
		GOCC:0030	Cytoplasmic vesicle membrane	7
		GOCC:0045	Synapse	22
		GOCC:0150	Distal axon	7
		GOCC:0030	Dendrite	10
		GOCC:0030	Axon	11
		GOCC:0005	Spindle	5
		GOCC:0043	Neuronal cell body	7
		GOCC:0098	Mitochondrial protein complex	5
		GOCC:0044	Cell body	9
		GOCC:0099	Supramolecular fiber	10
		GOCC:0099	Polymeric cytoskeletal fiber	6
		GOCC:0036	Somatodendritic compartment	12
		GOCC:0030	Cell junction	24
		GOCC:0043	Neuron projection	17
		GOCC:0099	Secretory vesicle	8
		GOCC:0015	Microtubule cytoskeleton	12
		GOCC:0005	Endosome	8
		GOCC:0098	Whole membrane	14
		GOCC:0005	Cytosol	23
		GOCC:0005	Cytoskeleton	18
		GOCC:0120	Plasma membrane bounded cell projectio	21
		GOCC:0098	Plasma membrane region	11
		GOCC:0043	Intracellular non-membrane-bounded org	29
		GOCC:0098	Bounding membrane of organelle	10
		GOCC:0031	Vesicle	13
		GOCC:0031	Cytoplasmic vesicle	12
		GOCC:0031	Organelle membrane	15
		GOCC:0012	Endomembrane system	18
		GOCC:0005	Cytoplasm	46
		GOCC:0043	Intracellular organelle	53
		GOCC:0043	Organelle	54

GOCC:0043	Membrane-bounded organelle	42
GOCC:0005	Intracellular	56
GOCC:0043	Intracellular membrane-bounded organell	33
GOCC:0016	Membrane	25
GOCC:0032	Protein-containing complex	24
GOCC:0110	Cellular anatomical entity	58

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c6,Papd4,Ppp3ca,Basp1,Bod1l,Prr11,Grin2b,Cadps,Dnajc5,Actg2,Arhgap35,Srpk2,Rims1,Snap

					Cellular Con
background	strength	false discov	matching pr	matching p	#term ID
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9	1.9	0.0159	10090.ENSM	Cct8,Cct7	GO:0005832
12	1.77	0.0241	10090.ENSM	Nefm,Rims1	GO:0099569
17	1.62	0.0421	10090.ENSM	Nefm,Cttn	GO:0099571
42	1.4	0.0108	10090.ENSM	Fkbp4,Mapt,	GO:0044295
53	1.3	0.0192	10090.ENSM	Wee1,Rims1	GO:0098984
288	***1.17***	***7.98E-09***	***10090.ENSM***	***Nefm,Map4,***	GO:0014069
320	1.16	1.88E-09	10090.ENSM	Nefm,Sh3gl2	GO:0098685
129	1.14	0.0022	10090.ENSM	Sh3gl2,Vamp	GO:0030672
102	1.14	0.0095	10090.ENSM	Sh3gl2,Vamp	GO:0034399
112	**1.1**	**0.0123**	**10090.ENSM**	**Tep1,Basp1**	GO:0044309
244	1.07	4.77E-05	10090.ENSM	Mecp2,Git1,(	GO:0008021
185	1.06	0.0011	10090.ENSM	Sh3gl2,Vamp	GO:0098978
171	1.02	0.0061	10090.ENSM	Ppp3ca,Eea	GO:0098794
563	1	1.11E-09	10090.ENSM	Nefm,Map4,(	GO:0043197
212	1	0.0021	10090.ENSM	Wee1,Map4,	GO:0043209
166	0.93	0.043	10090.ENSM	Basp1,Srpk2	GO:0099568
166	0.93	0.043	10090.ENSM	Ppp3ca,Grin	GO:0098793
487	0.9	1.26E-05	10090.ENSM	Nefm,Sncg,S	GO:0030427
321	0.89	0.0022	10090.ENSM	Sh3gl2,Vamp	GO:0043679
1032	0.88	2.70E-11	10090.ENSM	Nefm,Sncg,S	GO:0150034
337	0.87	0.0027	10090.ENSM	Sncg,Fkbp4,	GO:0005819
495	0.86	0.00011	10090.ENSM	Sh3gl2,Ppp3	GO:0030424
554	0.85	4.23E-05	10090.ENSM	Nefm,Sncg,F	GO:0005874
263	0.83	0.0319	10090.ENSM	Slc25a5,Map	GO:0005759
377	0.82	0.0049	10090.ENSM	Nefm,Sncg,(	GO:0044297
270	0.82	0.0352	10090.ENSM	Slc25a5,Mrp	GO:0045202
493	0.81	0.00073	10090.ENSM	Nefm,Sncg,(	GO:0099512
564	0.8	0.00032	10090.ENSM	Nefm,Cct8,(	GO:0045211
346	0.79	0.0169	10090.ENSM	Nefm,Cct8,(	GO:0043025
711	0.78	5.94E-05	10090.ENSM	Nefm,Sncg,S	GO:0030425
1453	0.77	1.85E-10	10090.ENSM	Nefm,Pak2,S	GO:0099513
1054	0.76	4.98E-07	10090.ENSM	Nefm,Sncg,S	GO:0036477
501	0.75	0.0045	10090.ENSM	Sh3gl2,Vamp	GO:0099503
855	0.7	0.00032	10090.ENSM	Slc25a5,Cct	GO:0043005
566	0.7	0.0084	10090.ENSM	Atp6v0d2,Sh	GO:0097060
1027	0.69	7.32E-05	10090.ENSM	Slc25a5,Atp6	GO:0030054
1784	0.66	3.64E-08	10090.ENSM	Pak2,Cct8,S	GO:0015630
1397	0.66	3.91E-06	10090.ENSM	Slc25a5,Nefı	GO:0098805
1774	0.62	1.01E-06	10090.ENSM	Nefm,Sncg,S	GO:0005815
1006	0.59	0.0052	10090.ENSM	Atp6v0d2,Va	GO:0042995
2950	0.54	3.64E-08	10090.ENSM	Tep1,Slc25a	GO:0120025
1019	0.54	0.0195	10090.ENSM	Atp6v0d2,Sh	GO:0005856
1396	0.52	0.0055	10090.ENSM	Atp6v0d2,Sh	GO:0048471
1298	0.52	0.0099	10090.ENSM	Atp6v0d2,Sh	GO:0098590
1749	0.48	0.0044	10090.ENSM	Trap1,Slc25a	GO:0005829
2420	0.42	0.0045	10090.ENSM	Atp6v0d2,Sh	GO:0043232
6579	0.4	2.99E-10	10090.ENSM	Trap1,Tep1,	GO:0005739
8073	0.37	6.58E-12	10090.ENSM	Trap1,Tep1,	GO:0098588
8565	0.35	6.58E-12	10090.ENSM	Trap1,Tep1,	GO:0031982

7176	0.32	1.81E-06	10090.ENSM	Trap1,Tep1,	GO:0031090
9943	0.3	4.60E-11	10090.ENSM	Trap1,Tep1,	GO:0032991
6320	0.27	0.0025	10090.ENSM	Trap1,Tep1,	GO:0012505
4741	0.27	0.0226	10090.ENSM	Il7r,Trap1,Slc	GO:0043229
4654	0.26	0.0405	10090.ENSM	Il7r,Tep1,Slc	GO:0005737
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					GO:0016020
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›2

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nponent				
term description	observed ge	background	strength	false discov
Calcium- and calmodulin-dependent pr	2	5	2.15	0.0061
Chaperonin-containing t-complex	2	9	1.9	0.013
Presynaptic cytoskeleton	2	10	1.85	0.0151
Postsynaptic cytoskeleton	2	17	1.62	0.0311
Axonal growth cone	3	42	1.4	0.0097
Neuron to neuron synapse	16	446	1.11	6.53E-11
Postsynaptic density	15	414	1.11	2.80E-10
Schaffer collateral - CA1 synapse	4	113	1.1	0.0113
Synaptic vesicle membrane	4	129	1.04	0.0156
Nuclear periphery	4	133	1.03	0.0163
Neuron spine	6	216	0.99	0.0017
Synaptic vesicle	6	244	0.94	0.003
Glutamatergic synapse	12	501	0.93	1.37E-06
Postsynapse	18	761	0.92	5.27E-10
Dendritic spine	5	212	0.92	0.012
Myelin sheath	5	212	0.92	0.012
Cytoplasmic region	6	270	0.9	0.0049
Presynapse	14	636	0.89	2.47E-07
Site of polarized growth	5	232	0.88	0.0156
Axon terminus	4	191	0.87	0.0496
Distal axon	8	399	0.85	0.00082
Spindle	7	352	0.85	0.0029
Axon	14	791	0.8	2.84E-06
Microtubule	7	397	0.8	0.0053
Mitochondrial matrix	6	340	0.8	0.013
Cell body	14	836	0.77	5.33E-06
Synapse	24	1492	0.76	2.80E-10
Supramolecular fiber	14	861	0.76	7.30E-06
Postsynaptic membrane	5	322	0.74	0.0497
Neuronal cell body	11	743	0.72	0.00037
Dendrite	11	753	0.72	0.0004
Polymeric cytoskeletal fiber	9	631	0.71	0.003
Somatodendritic compartment	15	1080	0.69	1.57E-05
Secretory vesicle	8	592	0.68	0.0096
Neuron projection	21	1583	0.67	1.20E-07
Synaptic membrane	6	464	0.66	0.0467
Cell junction	26	2050	0.65	2.07E-09
Microtubule cytoskeleton	14	1190	0.62	0.00026
Whole membrane	15	1415	0.58	0.00037
Microtubule organizing center	8	753	0.58	0.0305
Cell projection	26	2472	0.57	8.99E-08
Plasma membrane bounded cell projec	25	2387	0.57	2.15E-07
Cytoskeleton	21	2060	0.56	7.30E-06
Perinuclear region of cytoplasm	8	775	0.56	0.035
Plasma membrane region	12	1310	0.51	0.0096
Cytosol	29	3573	0.46	1.57E-06
Intracellular non-membrane-bounded c	32	4035	0.45	3.31E-07
Mitochondrion	14	1776	0.45	0.012
Bounding membrane of organelle	13	1636	0.45	0.0156
Vesicle	14	2007	0.39	0.0295

Organelle membrane	19	2973	0.36	0.012
Protein-containing complex	27	4895	0.29	0.0058
Endomembrane system	21	3859	0.29	0.0345
Intracellular organelle	59	11084	0.28	1.15E-11
Cytoplasm	55	10283	0.28	8.23E-10
Cell periphery	25	4668	0.28	0.0151
Intracellular organelle lumen	23	4279	0.28	0.0237
Organelle	60	11550	0.27	1.15E-11
Plasma membrane	24	4531	0.27	0.0217
Membrane-bounded organelle	53	10370	0.26	5.03E-08
Membrane	39	7623	0.26	0.00028
Intracellular membrane-bounded orga	46	9507	0.24	4.31E-05
Cellular anatomical entity	62	15632	0.15	7.43E-08

p91,Pdzd8,Hk1,Mapt,Nsf,Cttn,Set,Camk2a,Dlg2,Srcin1,Camk2b,Hnrnpm,Dlgap2,Ablim2,Clas
Ablim2,Clasp2

		Reactome	
matching pr	matching p	#term ID	term description
10090.ENSM	Camk2a,Car	MMU-43806	Unblocking of NMDA receptors, glutamate binding and a
10090.ENSM	Cct8,Cct7	MMU-33715	HSF1-dependent transactivation
10090.ENSM	Nefm,Rims1	MMU-39971	Trafficking of AMPA receptors
10090.ENSM	Nefm,Cttn	MMU-67943	Protein-protein interactions at synapses
10090.ENSM	Fkbp4,Mapt,	MMU-88568	Clathrin-mediated endocytosis
10090.ENSM	Nefm,Pak2,S	MMU-88568	Cargo recognition for clathrin-mediated endocytosis
10090.ENSM	Nefm,Pak2,N	MMU-11231	Neurotransmitter receptors and postsynaptic signal tra
10090.ENSM	Sh3gl2,Ppp3	MMU-11231	Transmission across Chemical Synapses
10090.ENSM	Sh3gl2,Vamp	MMU-11231	Neuronal System
10090.ENSM	Tep1,Basp1,Mapt,Hnrnpm		
10090.ENSM	Ppp3ca,Eea1,Grin2b,Cttn,Camk2a,Dlgap2		

10090.ENSM	Sh3gl2,Vamp	KEGG Pathway	
10090.ENSM	Pak2,Sh3gl2	#term ID	term description
10090.ENSM	Nefm,Pak2,N	mmu04720	Long-term potentiation
10090.ENSM	Ppp3ca,Grin	mmu05031	Amphetamine addiction
10090.ENSM	Slc25a5,Nefm	mmu04728	Dopaminergic synapse
10090.ENSM	Map4,Rims1	mmu05012	Parkinson disease
10090.ENSM	Nefm,Sncg,S	mmu05152	Tuberculosis
10090.ENSM	Fkbp4,Basp1	mmu05010	Alzheimer disease
10090.ENSM	Sncg,Git1,G	mmu05020	Prion disease

10090.ENSM	Sncg,Fkbp4,Git1,Basp1,Grin2b,Snap91,Mapt,Clasp2
10090.ENSM	Slc25a5,Sncg,Map4,Bod1l,Cttn,Camk2b,Clasp2
10090.ENSM	Nefm,Sncg,Fkbp4,Map4,Git1,Basp1,Eea1,Grin2b,Snap91,Mapt,Camk2a,Dlg2,Srci
10090.ENSM	Cct8,Cct7,Fkbp4,Map4,Bod1l,Mapt,Clasp2
10090.ENSM	Trap1,Slc25a5,Mrps23,Atp5b,Uqcrc2,Acsm5
10090.ENSM	Nefm,Sncg,Cct8,Sh3gl2,Cct7,Fkbp4,Grin2b,Actg2,Snap91,Mapt,Camk2a,Dlg2,Src
10090.ENSM	Nefm,Pak2,Sncg,Sh3gl2,Vamp3,Mecp2,Map4,Git1,Dnajc6,Ppp3ca,Grin2b,Cadps,F
10090.ENSM	Nefm,Cct8,Cct7,Fkbp4,Map4,Ppp3ca,Bod1l,Grin2b,Actg2,Plec,Mapt,Cttn,Ablim2,C
10090.ENSM	Grin2b,Snap91,Cttn,Camk2a,Dlg2
10090.ENSM	Nefm,Sncg,Sh3gl2,Fkbp4,Grin2b,Snap91,Mapt,Camk2a,Dlg2,Srcin1,Camk2b
10090.ENSM	Sh3gl2,Ppp3ca,Grin2b,Mapt,Nsf,Cttn,Camk2a,Dlg2,Srcin1,Camk2b,Dlgap2
10090.ENSM	Nefm,Cct8,Cct7,Fkbp4,Map4,Bod1l,Mapt,Cttn,Clasp2
10090.ENSM	Nefm,Sncg,Sh3gl2,Fkbp4,Ppp3ca,Grin2b,Snap91,Mapt,Nsf,Cttn,Camk2a,Dlg2,Src
10090.ENSM	Sh3gl2,Vamp3,Spam1,Grin2b,Cadps,Dnajc5,Snap91,Dlg2
10090.ENSM	Nefm,Sncg,Sh3gl2,Vamp3,Fkbp4,Map4,Git1,Ppp3ca,Basp1,Eea1,Grin2b,Snap91,N
10090.ENSM	Grin2b,Rims1,Snap91,Cttn,Camk2a,Dlg2
10090.ENSM	Nefm,Pak2,Sncg,Sh3gl2,Vamp3,Mecp2,Map4,Git1,Dnajc6,Ppp3ca,Basp1,Grin2b,C
10090.ENSM	Slc25a5,Sncg,Cct8,Cct7,Fkbp4,Mecp2,Map4,Spag9,Bod1l,Arhgap35,Mapt,Cttn,Ca
10090.ENSM	Slc25a5,Atp5b,Atp6v0d2,Sh3gl2,Vamp3,Spam1,Spag9,Syne4,Eea1,Cadps,Dnajc5,
10090.ENSM	Sncg,Cct8,Mecp2,Spag9,Bod1l,Arhgap35,Camk2b,Clasp2
10090.ENSM	Nefm,Sncg,Cct8,Sh3gl2,Vamp3,Fkbp4,Map4,Git1,Ppp3ca,Basp1,Eea1,Grin2b,Act
10090.ENSM	Nefm,Sncg,Cct8,Sh3gl2,Vamp3,Fkbp4,Map4,Git1,Ppp3ca,Basp1,Eea1,Grin2b,Act
10090.ENSM	Slc25a5,Nefm,Sncg,Cct8,Cct7,Fkbp4,Mecp2,Map4,Spag9,Bod1l,Grin2b,Actg2,Arh
10090.ENSM	Pak2,Sncg,Sh3gl2,Vamp3,Fkbp4,Spag9,Plec,Set
10090.ENSM	Atp6v0d2,Vamp3,Grin2b,Plec,Rims1,Snap91,Hk1,Mapt,Cttn,Camk2a,Dlg2,Clasp2
10090.ENSM	Pak2,Cmtr1,Cct8,Sh3gl2,Vamp3,Cct7,Fkbp4,Mecp2,Map4,Git1,Spag9,Smc4,Papd
10090.ENSM	Tep1,Slc25a5,Nefm,Sncg,Mrps23,Atp5b,Cct8,Cct7,Fkbp4,Wee1,Mecp2,Map4,Spa
10090.ENSM	Trap1,Slc25a5,Mrps23,Atp5b,Cct7,Fkbp4,Uqcrc2,Mecp2,Git1,Ppp3ca,Acsm5,Pdz
10090.ENSM	Atp6v0d2,Sh3gl2,Vamp3,Spag9,Syne4,Eea1,Cadps,Rtn3,Dnajc5,Snap91,Hk1,Dlg2
10090.ENSM	Atp6v0d2,Sh3gl2,Vamp3,Spam1,Git1,Relch,Dnajc6,Eea1,Grin2b,Cadps,Dnajc5,Rir

10090.ENSM	Trap1,Slc25a5,Mrps23,Atp5b,Atp6v0d2,Sh3gl2,Vamp3,Uqcrc2,Spag9,Syne4,Eea1
10090.ENSM	Tep1,Slc25a5,Mrps23,Atp5b,Cct8,Atp6v0d2,Vamp3,Cct7,Fkbp4,Uqcrc2,Mecp2,Sr
10090.ENSM	Mrps23,Atp6v0d2,Sh3gl2,Vamp3,Spam1,Git1,Relch,Syne4,Eea1,Grin2b,Cadps,Rt
10090.ENSM	Trap1,Tep1,Slc25a5,Nefm,Pak2,Sncg,Mrps23,Cmtr1,Atp5b,Cct8,Atp6v0d2,Sh3gl2
10090.ENSM	Trap1,Tep1,Slc25a5,Nefm,Pak2,Sncg,Mrps23,Cmtr1,Atp5b,Cct8,Atp6v0d2,Sh3gl2
10090.ENSM	Il7r,Sncg,Atp5b,Atp6v0d2,Vamp3,Spam1,Map4,Ppp3ca,Basp1,Eea1,Grin2b,Dnajc5
10090.ENSM	Trap1,Tep1,Slc25a5,Sncg,Mrps23,Cmtr1,Atp5b,Cct8,Fkbp4,Uqcrc2,Wee1,Mecp2,
10090.ENSM	Trap1,Tep1,Slc25a5,Nefm,Pak2,Sncg,Mrps23,Cmtr1,Atp5b,Cct8,Atp6v0d2,Sh3gl2
10090.ENSM	Il7r,Sncg,Atp5b,Atp6v0d2,Vamp3,Spam1,Map4,Ppp3ca,Basp1,Eea1,Grin2b,Dnajc5
10090.ENSM	Trap1,Tep1,Slc25a5,Pak2,Sncg,Mrps23,Cmtr1,Atp5b,Cct8,Atp6v0d2,Sh3gl2,Vamp
10090.ENSM	Il7r,Trap1,Slc25a5,Pak2,Sncg,Mrps23,Atp5b,Atp6v0d2,Sh3gl2,Vamp3,Spam1,Uqc
10090.ENSM	Trap1,Tep1,Slc25a5,Pak2,Sncg,Mrps23,Cmtr1,Atp5b,Cct8,Atp6v0d2,Vamp3,Cct7,
10090.ENSM	Il7r,Trap1,Tep1,Slc25a5,Nefm,Pak2,Sncg,Mrps23,Cmtr1,Atp5b,Cct8,Atp6v0d2,Sh3

ɜp2,Ddx46

observed ge	background	strength	false discov	matching pr	matching proteins in you
4	21	1.83	0.00078	10090.ENSM	Grin2b,Camk2a,Dlg2,Cam
3	24	1.65	0.0135	10090.ENSM	Fkbp4,Camk2a,Camk2b
3	31	1.54	0.0213	10090.ENSM	Nsf,Camk2a,Camk2b
4	65	1.34	0.0114	10090.ENSM	Grin2b,Rtn3,Dlg2,Dlgap2
6	143	1.17	0.0015	10090.ENSM	Il7r,Sh3gl2,Vamp3,Dnajc6,
4	102	1.14	0.0331	10090.ENSM	Il7r,Sh3gl2,Vamp3,Snap91
5	144	1.09	0.0135	10090.ENSM	Grin2b,Nsf,Camk2a,Dlg2,(
7	210	1.07	0.0013	10090.ENSM	Grin2b,Dnajc5,Rims1,Nsf,(
9	336	0.98	0.00078	10090.ENSM	Grin2b,Rtn3,Dnajc5,Rims1

observed ge	background	strength	false discov	matching pr	matching proteins in you
4	63	1.35	0.0062	10090.ENSM	Ppp3ca,Grin2b,Camk2a,C
4	63	1.35	0.0062	10090.ENSM	Ppp3ca,Grin2b,Camk2a,C
4	127	1.05	0.0278	10090.ENSM	Ppp3ca,Grin2b,Camk2a,C
7	239	1.02	0.0019	10090.ENSM	Trap1,Slc25a5,Atp5b,Uqcr
5	170	1.02	0.0088	10090.ENSM	Atp6v0d2,Ppp3ca,Eea1,Ca
7	359	0.84	0.0062	10090.ENSM	Slc25a5,Atp5b,Uqcrc2,Ppp
5	264	0.83	0.0448	10090.ENSM	Slc25a5,Atp5b,Uqcrc2,Ppp

n1,Clasp2

in1,Camk2b
Rtn3,Dnajc5,Rims1,Snap91,Mapt,Nsf,Cttn,Camk2a,Dlg2,Srcin1,Camk2b,Dlgap2
lasp2

in1,Camk2b,Dlgap2

Mapt,Nsf,Cttn,Camk2a,Dlg2,Srcin1,Camk2b,Dlgap2,Clasp2

Cadps,Rtn3,Dnajc5,Plec,Rims1,Snap91,Mapt,Nsf,Cttn,Camk2a,Dlg2,Srcin1,Camk2b,Dlgap2
mk2b,Clasp2
,Snap91,Hk1,Mapt,Dlg2

g2,Arhgap35,Rims1,Snap91,Hk1,Mapt,Nsf,Cttn,Camk2a,Dlg2,Srcin1,Camk2b,Dlgap2,Clasp2
g2,Arhgap35,Snap91,Hk1,Mapt,Nsf,Cttn,Camk2a,Dlg2,Srcin1,Camk2b,Dlgap2,Clasp2
gap35,Plec,Rims1,Mapt,Cttn,Srcin1,Camk2b,Ablim2,Clasp2

l4,Ppp3ca,Eea1,Dnajc5,Arhgap35,Plec,Las1l,Srpk2,Snap91,Hk1,Mapt,Nsf,Cttn,Set,Camk2a,Ca
g9,Smc4,Ppp3ca,Basp1,Bod1l,Grin2b,Actg2,Arhgap35,Plec,Las1l,Srpk2,Rims1,Mapt,Cttn,Set,
d8,Hk1,Camk2a
2,Camk2b
ms1,Snap91,Dlg2

,Cadps,Rtn3,Dnajc5,Snap91,Pdzd8,Hk1,Dlg2,Camk2b
nc4,Ppp3ca,Basp1,Syne4,Bod1l,Eea1,Grin2b,Las1l,Snap91,Hk1,Mapt,Cttn,Set,Camk2a,Camk
n3,Dnajc5,Snap91,Pdzd8,Nsf,Cttn,Set,Dlg2,Camk2b,Clasp2
,Vamp3,Spam1,Cct7,Fkbp4,Uqcrc2,Wee1,Mecp2,Map4,Git1,Relch,Spag9,Dnajc6,Smc4,Papd
,Vamp3,Spam1,Cct7,Fkbp4,Uqcrc2,Wee1,Mecp2,Map4,Git1,Relch,Spag9,Dnajc6,Smc4,Papd
5,Actg2,Arhgap35,Plec,Rims1,Snap91,Hk1,Mapt,Nsf,Cttn,Camk2a,Dlg2,Dlgap2,Clasp2
,Smc4,Ppp3ca,Basp1,Bod1l,Acsm5,Las1l,Srpk2,Mapt,Set,Hnrnpm,Ddx46
,Vamp3,Spam1,Cct7,Fkbp4,Uqcrc2,Wee1,Mecp2,Map4,Git1,Relch,Spag9,Dnajc6,Smc4,Papd
5,Arhgap35,Plec,Rims1,Snap91,Hk1,Mapt,Nsf,Cttn,Camk2a,Dlg2,Dlgap2,Clasp2
o3,Spam1,Cct7,Fkbp4,Uqcrc2,Wee1,Mecp2,Git1,Relch,Spag9,Dnajc6,Smc4,Papd4,Ppp3ca,Ba
rc2,Map4,Spag9,Ppp3ca,Basp1,Syne4,Eea1,Grin2b,Tmem62,Cadps,Rtn3,Dnajc5,Ugt3a2,Arh
,Fkbp4,Uqcrc2,Wee1,Mecp2,Git1,Relch,Spag9,Dnajc6,Smc4,Papd4,Ppp3ca,Basp1,Syne4,Boc
3gl2,Vamp3,Spam1,Cct7,Fkbp4,Uqcrc2,Wee1,Mecp2,Map4,Git1,Relch,Spag9,Dnajc6,Smc4,P

ur network (labels)
k2b

Snap91,Cttn

Camk2b
Camk2a,Dlg2,Camk2b
,Nsf,Camk2a,Dlg2,Camk2b,Dlgap2

ur network (labels)
amk2b
amk2b
amk2b
c2,Mapt,Camk2a,Camk2b
amk2a,Camk2b
3ca,Grin2b,Rtn3,Mapt
3ca,Grin2b

amk2b,Clasp2
,Srcin1,Camk2b,Ablim2,Clasp2,Ddx46

:2b,Hnrnpm

4,Ppp3ca,Basp1,Syne4,Bod1l,Prr11,Eea1,Grin2b,Acsm5,Cadps,Rtn3,Dnajc5,Ugt3a2,Actg2,Arh
4,Ppp3ca,Basp1,Prr11,Eea1,Grin2b,Acsm5,Cadps,Rtn3,Dnajc5,Actg2,Arhgap35,Plec,Las1l,Srp

4,Ppp3ca,Basp1,Syne4,Bod1l,Prr11,Eea1,Grin2b,Acsm5,Cadps,Rtn3,Dnajc5,Ugt3a2,Actg2,Arh

asp1,Syne4,Bod1l,Prr11,Eea1,Grin2b,Acsm5,Cadps,Rtn3,Dnajc5,Ugt3a2,Arhgap35,Las1l,Srpk2
gap35,Plec,Rims1,Snap91,Pdzd8,Hk1,Mapt,Nsf,Cttn,Camk2a,Dlg2,Camk2b,Dlgap2,Clasp2,Dd
d1l,Prr11,Grin2b,Acsm5,Rtn3,Ugt3a2,Arhgap35,Las1l,Srpk2,Pdzd8,Hk1,Mapt,Nsf,Cttn,Set,Cam
apd4,Ppp3ca,Basp1,Syne4,Bod1l,Prr11,Eea1,Grin2b,Acsm5,Tmem62,Cadps,Rtn3,Dnajc5,Ugt3

gap35,Plec,Las1l,Srpk2,Rims1,Snap91,Pdzd8,Hk1,Mapt,Nsf,Cttn,Set,Camk2a,Dlg2,Srcin1,Ca
k2,Rims1,Snap91,Pdzd8,Hk1,Mapt,Nsf,Cttn,Set,Camk2a,Dlg2,Srcin1,Camk2b,Hnrnpm,Ablim2

gap35,Plec,Las1l,Srpk2,Rims1,Snap91,Pdzd8,Hk1,Mapt,Nsf,Cttn,Set,Camk2a,Dlg2,Srcin1,Ca

,Rims1,Snap91,Pdzd8,Hk1,Mapt,Nsf,Cttn,Set,Camk2a,Dlg2,Camk2b,Hnrnpm,Clasp2,Ddx46
46
k2a,Dlg2,Camk2b,Hnrnpm,Clasp2,Ddx46
a2,Actg2,Arhgap35,Plec,Las1l,Srpk2,Rims1,Snap91,Pdzd8,Hk1,Mapt,Nsf,Cttn,Set,Camk2a,D

mk2b,Hnrnpm,Ablim2,Clasp2,Ddx46
2,Clasp2

mk2b,Hnrnpm,Dlgap2,Ablim2,Clasp2,Ddx46

lg2,Srcin1,Camk2b,Hnrnpm,Dlgap2,Ablim2,Clasp2,Ddx46

Table 18 **Total peptides list for AAV.RAM-MiniTurbo**

n=8, pep = 219, pro = 78, non-overlapping = 51

rAAV	Sample	Biotin	Protein Accession
RAM-MiniTid-Tau	8	d3-6	ACO13_MOUSE
RAM-MiniTid-Tau	3	d3-6	ADT3_MOUSE
RAM-MiniTid-Tau	7	d3-6	AFF1_MOUSE
RAM-MiniTid-Tau	8	d3-6	ALS_MOUSE
RAM-MiniTid-Tau	8	d3-6	ALS_MOUSE
RAM-MiniTid-Tau	3	d3-6	ANK3_MOUSE
RAM-MiniTid-Tau	6	d3-6	AP2M1_MOUSE
RAM-MiniTid-Tau	3	d3-6	ASPM_MOUSE
RAM-MiniTid-Tau	6	d3-6	AT2B1_MOUSE
RAM-MiniTid-Tau	8	d3-6	COR2B_MOUSE
RAM-MiniTid-Tau	8	d3-6	DCTN1_MOUSE
RAM-MiniTid-Tau	6	d3-6	DDX56_MOUSE
RAM-MiniTid-Tau	5	d3-6	DMXL2_MOUSE
RAM-MiniTid-Tau	6	d3-6	EXOC3_MOUSE
RAM-MiniTid-Tau	7	d3-6	F161A_MOUSE
RAM-MiniTid-Tau	1	d3-6	F16B1_MOUSE
RAM-MiniTid-Tau	1	d3-6	F16B1_MOUSE
RAM-MiniTid-Tau	3	d3-6	FSIP2_MOUSE
RAM-MiniTid-Tau	6	d3-6	FUND2_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNAI1_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI1_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI1_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI1_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI1_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI1_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNAI2_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI2_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI2_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI2_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAI2_MOUSE
RAM-MiniTid-Tau	4	d3-6	GNAO_MOUSE
RAM-MiniTid-Tau	4	d3-6	GNAO_MOUSE
RAM-MiniTid-Tau	4	d3-6	GNAO_MOUSE
RAM-MiniTid-Tau	6	d3-6	GNAO_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNAO_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNAO_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAO_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAS_MOUSE
RAM-MiniTid-Tau	4	d3-6	GNAS1_MOUSE
RAM-MiniTid-Tau	6	d3-6	GNAS1_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNAS1_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNAS1_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNAS1_MOUSE
RAM-MiniTid-Tau	8	d3-6	GNAS1_MOUSE

RAM-MiniTid-Tau	6	d3-6	GNAT1_MOUSE
RAM-MiniTid-Tau	6	d3-6	GNAT1_MOUSE
RAM-MiniTid-Tau	6	d3-6	GNAT1_MOUSE
RAM-MiniTid-Tau	4	d3-6	GNAT2_MOUSE
RAM-MiniTid-Tau	4	d3-6	GNAT2_MOUSE
RAM-MiniTid-Tau	4	d3-6	GNAT2_MOUSE
RAM-MiniTid-Tau	7	d3-6	GNL1_MOUSE
RAM-MiniTid-Tau	3	d3-6	H10_MOUSE
RAM-MiniTid-Tau	3	d3-6	H12_MOUSE
RAM-MiniTid-Tau	4	d3-6	H14_MOUSE
RAM-MiniTid-Tau	1	d3-6	HIBCH_MOUSE
RAM-MiniTid-Tau	1	d3-6	HIBCH_MOUSE
RAM-MiniTid-Tau	8	d3-6	HNRPQ_MOUSE
RAM-MiniTid-Tau	6	d3-6	HNRPU_MOUSE
RAM-MiniTid-Tau	6	d3-6	HNRPU_MOUSE
RAM-MiniTid-Tau	8	d3-6	HNRPU_MOUSE
RAM-MiniTid-Tau	3	d3-6	HXK1_MOUSE
RAM-MiniTid-Tau	4	d3-6	HXK1_MOUSE
RAM-MiniTid-Tau	4	d3-6	HXK1_MOUSE
RAM-MiniTid-Tau	1	d3-6	ICAM1_MOUSE
RAM-MiniTid-Tau	1	d3-6	ICAM1_MOUSE
RAM-MiniTid-Tau	3	d3-6	JPH2_MOUSE
RAM-MiniTid-Tau	8	d3-6	KALRN_MOUSE
RAM-MiniTid-Tau	5	d3-6	KC1G1_MOUSE
RAM-MiniTid-Tau	5	d3-6	KC1G1_MOUSE
RAM-MiniTid-Tau	5	d3-6	KC1G1_MOUSE
RAM-MiniTid-Tau	5	d3-6	KC1G1_MOUSE
RAM-MiniTid-Tau	5	d3-6	KC1G1_MOUSE
RAM-MiniTid-Tau	5	d3-6	KC1G3_MOUSE
RAM-MiniTid-Tau	5	d3-6	KC1G3_MOUSE
RAM-MiniTid-Tau	5	d3-6	KCC2D_MOUSE
RAM-MiniTid-Tau	5	d3-6	KCC2D_MOUSE
RAM-MiniTid-Tau	5	d3-6	KCC2D_MOUSE
RAM-MiniTid-Tau	5	d3-6	KCC2D_MOUSE
RAM-MiniTid-Tau	5	d3-6	KCC2D_MOUSE
RAM-MiniTid-Tau	8	d3-6	KCC2D_MOUSE
RAM-MiniTid-Tau	8	d3-6	KIF5C_MOUSE
RAM-MiniTid-Tau	8	d3-6	KIF5C_MOUSE
RAM-MiniTid-Tau	3	d3-6	KIME_MOUSE
RAM-MiniTid-Tau	4	d3-6	KINH_MOUSE
RAM-MiniTid-Tau	6	d3-6	KINH_MOUSE
RAM-MiniTid-Tau	8	d3-6	KS6A4_MOUSE
RAM-MiniTid-Tau	7	d3-6	LIN7C_MOUSE
RAM-MiniTid-Tau	8	d3-6	LX12E_MOUSE
RAM-MiniTid-Tau	3	d3-6	LYAM1_MOUSE
RAM-MiniTid-Tau	3	d3-6	LYAM1_MOUSE
RAM-MiniTid-Tau	5	d3-6	MAP1B_MOUSE
RAM-MiniTid-Tau	7	d3-6	MAP4_MOUSE

RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	1	d3-6	MAP6_MOUSE
RAM-MiniTid-Tau	5	d3-6	MARK4_MOUSE
RAM-MiniTid-Tau	5	d3-6	MARK4_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	MCCA_MOUSE
RAM-MiniTid-Tau	6	d3-6	MDHC_MOUSE
RAM-MiniTid-Tau	1	d3-6	MTAP2_MOUSE
RAM-MiniTid-Tau	1	d3-6	MTAP2_MOUSE
RAM-MiniTid-Tau	1	d3-6	MTAP2_MOUSE
RAM-MiniTid-Tau	1	d3-6	MTAP2_MOUSE
RAM-MiniTid-Tau	1	d3-6	MTAP2_MOUSE
RAM-MiniTid-Tau	1	d3-6	MTAP2_MOUSE
RAM-MiniTid-Tau	3	d3-6	MX1_MOUSE
RAM-MiniTid-Tau	4	d3-6	NCOR1_MOUSE
RAM-MiniTid-Tau	3	d3-6	PACS1_MOUSE
RAM-MiniTid-Tau	2	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	2	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	3	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	3	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	3	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	5	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	6	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	7	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	7	d3-6	PCCA_MOUSE
RAM-MiniTid-Tau	6	d3-6	PDE6A_MOUSE

RAM-MiniTid-Tau	3	d3-6	PHF8_MOUSE
RAM-MiniTid-Tau	6	d3-6	POTEF_MOUSE
RAM-MiniTid-Tau	8	d3-6	POTEF_MOUSE
RAM-MiniTid-Tau	6	d3-6	PP2BA_MOUSE
RAM-MiniTid-Tau	6	d3-6	PP2BA_MOUSE
RAM-MiniTid-Tau	6	d3-6	PP2BA_MOUSE
RAM-MiniTid-Tau	6	d3-6	PP2BA_MOUSE
RAM-MiniTid-Tau	8	d3-6	PUS7_MOUSE
RAM-MiniTid-Tau	8	d3-6	PUS7_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	2	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	3	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	5	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	5	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	6	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	6	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	7	d3-6	PYC_MOUSE
RAM-MiniTid-Tau	4	d3-6	RFIP2_MOUSE
RAM-MiniTid-Tau	3	d3-6	RL4_MOUSE
RAM-MiniTid-Tau	3	d3-6	RL4_MOUSE
RAM-MiniTid-Tau	4	d3-6	RL4_MOUSE
RAM-MiniTid-Tau	3	d3-6	SMS1_MOUSE
RAM-MiniTid-Tau	3	d3-6	SMS1_MOUSE
RAM-MiniTid-Tau	6	d3-6	STIP1_MOUSE
RAM-MiniTid-Tau	8	d3-6	STK40_MOUSE
RAM-MiniTid-Tau	6	d3-6	SYNJ1_MOUSE
RAM-MiniTid-Tau	6	d3-6	SYNJ1_MOUSE
RAM-MiniTid-Tau	6	d3-6	SYNJ1_MOUSE
RAM-MiniTid-Tau	6	d3-6	SYNJ1_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUA_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE

RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	SYUB_MOUSE
RAM-MiniTid-Tau	1	d3-6	TAU_MOUSE
RAM-MiniTid-Tau	1	d3-6	TAU_MOUSE
RAM-MiniTid-Tau	3	d3-6	THOC5_MOUSE
RAM-MiniTid-Tau	3	d3-6	THOC5_MOUSE
RAM-MiniTid-Tau	8	d3-6	TPM1_MOUSE
RAM-MiniTid-Tau	8	d3-6	TPM3_MOUSE
RAM-MiniTid-Tau	3	d3-6	TRPM7_MOUSE
RAM-MiniTid-Tau	3	d3-6	TRPM7_MOUSE
RAM-MiniTid-Tau	5	d3-6	TTLL4_MOUSE
RAM-MiniTid-Tau	5	d3-6	TTLL4_MOUSE
RAM-MiniTid-Tau	3	d3-6	WNK2_MOUSE
RAM-MiniTid-Tau	6	d3-6	ZEB1_MOUSE

›ID-tau in the retrieval-reconsolidation (RRc) spatial memory phase

Protein Description	Peptide Scor	ptide Sequer	Peptide Mod	Position of
Acyl-coenzyme A thioesterase 13 Gene: A	37.57	FKVPGFDR\	Biotin (K)	0.010000000
ADP/ATP translocase 3Gene: SLC25A6	37.83	KYKQIFLGG	Biotin (K)	0.000000000
AF4/FMR2 family member 1Gene: AFF1	39.25	KALSGPEPA	Biotin (K)	0.000000000
Insulin-like growth factor-binding protein co	46.43	GLGNLHEL\	Biotin (K)	0.000000000
Insulin-like growth factor-binding protein co	46.43	GLGNLHEL\	Biotin (K)	0.000000000
Ankyrin-3Gene: ANK3	46.31	GASLSITTKI	Biotin (K)	0.000000000
AP-2 complex subunit mu Gene: AP2M1	38.28	QVICMKGK/	Biotin (K)	0.000000000
Abnormal spindle-like microcephaly-associ	37.83	KIKKAALI	Biotin (K)	0.00010000.(
Plasma membrane calcium-transporting AT	38.27	LLGLLLDLKI	Biotin (K)	0.000000001
Coronin-2B Gene: Coro2b	37.03	RLKEELAQ	Biotin (K)	0.00100000.(
Dynactin subunit 1 Gene: Dctn1	59.11	GADAAAKT\$	Biotin (K)	0.000000000
Probable ATP-dependent RNA helicase DI	40.28	HRGKKPKP/	Biotin (K)	0.000000000
DmX-like protein 2 Gene: Dmxl2	37.18	QETTVK	Biotin (K)	0.000001.0
Exocyst complex component 3 Gene: Exo(	39.48	EQNLQVAA(	Biotin (K)	0.000000000
Protein FAM161A Gene: Fam161a	38.35	KPKQFKARI	Biotin (K)	0.001000000
Protein FAM160B1 OS=Homo sapiens OX=	39.61	SPKALEK	Biotin (K)	0.0010000.0
Protein FAM160B1 OS=Homo sapiens OX=	39.61	SPKALEK	Biotin (K)	0.0010000.0
Fibrous sheath-interacting protein 2Gene: I	37.26	TLEINRGTM	Biotin (K)	0.000000000
FUN14 domain-containing protein 2 Gene:	38.01	SKAEEVVSF	Biotin (K)	0.000000000
Guanine nucleotide-binding protein G(i) sub	38.38	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	38.38	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(i) sub	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(o) su	37.44	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(o) su	37.44	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(o) su	37.44	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(o) su	44.43	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(o) su	38.38	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(o) su	38.38	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(o) su	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(s) su	37.78	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(s) su	37.44	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(s) su	44.43	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(s) su	38.38	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(s) su	38.38	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(s) su	38.38	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(s) su	37.78	KSTIVK	Biotin (K)	0.000001.0

Guanine nucleotide-binding protein G(t) sul	44.43	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(t) sul	44.43	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(t) sul	44.43	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(t) sul	37.44	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(t) sul	37.44	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein G(t) sul	37.44	KSTIVK	Biotin (K)	0.000001.0
Guanine nucleotide-binding protein-like 1 G	41.06	KKPFSVKQK	Biotin (K)	0.010000000
Histone H1.0 Gene: H1f0	37.97	KKKPAATPK	Biotin (K)	0.001000000
Histone H1.2Gene: HIST1H1C	66.97	KAAKSAAKA	Biotin (K)	0.000000010
Histone H1.4 Gene: HIST1H1E	44.99	AVKPKAAKP	Biotin (K)	0.000010000
3-hydroxyisobutyryl-CoA hydrolase, mitocl	47.92	QLKKWEQD	Biotin (K)	0.001000000
3-hydroxyisobutyryl-CoA hydrolase, mitocl	47.92	QLKKWEQD	Biotin (K)	0.001000000
Heterogeneous nuclear ribonucleoprotein C	37.43	KERKAQR	Biotin (K)	0.0001000.0
Heterogeneous nuclear ribonucleoprotein U	42.19	QKAGDKKR	Biotin (K)	0.00000100.(
Heterogeneous nuclear ribonucleoprotein U	38	QKAGDKKR	Biotin (K)	0.00000100.(
Heterogeneous nuclear ribonucleoprotein U	41.3	QKAGDKKR	Biotin (K)	0.00000100.(
Hexokinase-1 Gene: HK1	38.03	KTHPQYSR	Biotin (K)	0.10000000.(
Hexokinase-1 Gene: HK1	37.38	KTHPQYSR	Biotin (K)	0.10000000.(
Hexokinase-1Gene: HK1	37.38	KTHPQYSR	Biotin (K)	0.10000000.(
Intercellular adhesion molecule 1 OS=Rattu	45.76	LQKAQEEAL	Biotin (K)	0.000000000
Intercellular adhesion molecule 1 OS=Rattu	45.76	LQKAQEEAL	Biotin (K)	0.000000000
Junctophilin-2Gene: JPH2	37.3	KAGAKKK	Biotin (K)	0.0000010.0
KalirinGene: KALRN	39.2	KQKKVR	Biotin (K)	0.000100.0
Casein kinase I isoform gamma-1 Gene: C	37.46	DVKPENFLI(	Biotin (K)	0.001000000
Casein kinase I isoform gamma-1 Gene: C	37.46	DVKPENFLI(	Biotin (K)	0.001000000
Casein kinase I isoform gamma-1 Gene: C	37.46	DVKPENFLI(	Biotin (K)	0.001000000
Casein kinase I isoform gamma-1Gene: CS	37.46	DVKPENFLI(	Biotin (K)	0.001000000
Casein kinase I isoform gamma-1 Gene: C	37.46	DVKPENFLI(	Biotin (K)	0.001000000
Casein kinase I isoform gamma-3 Gene: C	37.46	DVKPENFLI(	Biotin (K)	0.001000000
Casein kinase I isoform gamma-3 Gene: C	37.46	DVKPENFLI(	Biotin (K)	0.001000000
Calcium/calmodulin-dependent protein kina	37.15	INKMLTINPA	Biotin (K)	0.001000000
Calcium/calmodulin-dependent protein kina	37.15	INKMLTINPA	Biotin (K)	0.001000000
Calcium/calmodulin-dependent protein kina	37.15	INKMLTINPA	Biotin (K)	0.001000000
Calcium/calmodulin-dependent protein kina	37.15	INKMLTINPA	Biotin (K)	0.001000000
Calcium/calmodulin-dependent protein kina	37.15	INKMLTINPA	Biotin (K)	0.001000000
Calcium/calmodulin-dependent protein kina	45.66	INKMLTINPA	Biotin (K)	0.001000000
Kinesin heavy chain isoform 5C Gene: Kif5	41.34	ELPKLEKR	Biotin (K)	0.00010000.(
Kinesin heavy chain isoform 5C Gene: Kif5	37.12	ELPKLEKR	Biotin (K)	0.00010000.(
Mevalonate kinase Gene: Mvk	46.88	LTKFPEIVAF	Biotin (K)	0.001000000
Kinesin-1 heavy chain Gene: Kif5b	37.83	ELPKLEKR	Biotin (K)	0.00010000.(
Kinesin-1 heavy chain Gene: Kif5b	39.97	ELPKLEKR	Biotin (K)	0.00010000.(
Ribosomal protein S6 kinase alpha-4Gene:	38.03	LGIIYRDLK	Biotin (K)	0.000000001
Protein lin-7 homolog C Gene: Lin7c	37.72	AVELLKA	Biotin (K)	0.0000010.0
Arachidonate 12-lipoxygenase, epidermal-t	37.34	TIYLPEGTAI	Biotin (K)	0.000000000
L-selectinGene: SELL	38.03	CRDNYTDL\	Biotin (K)	0.000000000
L-selectin OS=Pan troglodytes Gene: SELL	38.03	CRDNYTDL\	Biotin (K)	0.000000000
Microtubule-associated protein 1BGene: M	37.08	TPPKEVK	Biotin (K)	0.0001000.0
Microtubule-associated protein 4Gene: MA	40.17	KDMESPTKL	4 Biotin (K); 2	0.103000010

Microtubule-associated protein 6 OS=Mus	96.1	DQGAVLLGI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	96.1	DQGAVLLGI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	58.64	DQGAVLLGI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	58.64	DQGAVLLGI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	51.1	NQDPIIPVPI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	51.1	NQDPIIPVPI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	41.63	NQDPIIPVPI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	41.63	NQDPIIPVPI	Biotin (K)	0.000000000
Microtubule-associated protein 6 OS=Mus	40.7	PIIPVPLKGC	Biotin (K)	0.000000010
Microtubule-associated protein 6 OS=Mus	40.7	PIIPVPLKGC	Biotin (K)	0.000000010
MAP/microtubule affinity-regulating kinase 4	37.38	KEARAKFR	Biotin (K)	0.00000100.0
MAP/microtubule affinity-regulating kinase 4	37.38	KEARAKFR	Biotin (K)	0.00000100.0
Methylcrotonoyl-CoA carboxylase subunit a	66.99	IAMKMEHTII	Biotin (K)	0.000100000
Methylcrotonoyl-CoA carboxylase subunit a	66.99	IAMKMEHTII	Biotin (K)	0.000100000
Methylcrotonoyl-CoA carboxylase subunit a	66.99	IAMKMEHTII	Biotin (K)	0.000100000
Methylcrotonoyl-CoA carboxylase subunit a	66.99	IAMKMEHTII	Biotin (K)	0.000100000
Methylcrotonoyl-CoA carboxylase subunit a	66.99	IAMKMEHTII	Biotin (K)	0.000100000
Methylcrotonoyl-CoA carboxylase subunit a	66.99	IAMKMEHTII	Biotin (K)	0.000100000
Methylcrotonoyl-CoA carboxylase subunit a	40.05	KMEHTIK	Biotin (K)	0.1000000.0
Methylcrotonoyl-CoA carboxylase subunit a	40.05	KMEHTIK	Biotin (K)	0.1000000.0
Methylcrotonoyl-CoA carboxylase subunit a	40.05	KMEHTIK	Biotin (K)	0.1000000.0
Methylcrotonoyl-CoA carboxylase subunit a	40.05	KMEHTIK	Biotin (K)	0.1000000.0
Methylcrotonoyl-CoA carboxylase subunit a	40.05	KMEHTIK	Biotin (K)	0.1000000.0
Methylcrotonoyl-CoA carboxylase subunit a	40.05	KMEHTIK	Biotin (K)	0.1000000.0
Malate dehydrogenase, cytoplasmic Gene:	37.36	GAALEKYAK	Biotin (K)	0.000001000
Microtubule-associated protein 2 OS=Mus	48.95	KLILKPAIK	Biotin (K)	0.000010000
Microtubule-associated protein 2 OS=Mus	48.95	KLILKPAIK	Biotin (K)	0.000010000
Microtubule-associated protein 2 OS=Mus	37.89	KLILKPAIK	2 Biotin (K)	0.100010000
Microtubule-associated protein 2 OS=Mus	37.89	KLILKPAIK	2 Biotin (K)	0.100010000
Microtubule-associated protein 2 OS=Mus	47.68	LILKPAIK	Biotin (K)	0.00010000.0
Microtubule-associated protein 2 OS=Mus	47.68	LILKPAIK	Biotin (K)	0.00010000.0
Interferon-induced GTP-binding protein Mx	46.42	VLKLKRLVK	Biotin (K)	0.000000001
Nuclear receptor corepressor 1 Gene: Ncc	39.91	DKGPPPKSI	Biotin (K)	0.000000100
Phosphofurin acidic cluster sorting protein	37.73	KQKFVALLK	Biotin (K)	0.000000001
Propionyl-CoA carboxylase alpha chain, mi	93.6	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	93.6	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	93.6	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	74.98	KMQNSMTA	Biotin (K); O›	0.130000000
Propionyl-CoA carboxylase alpha chain, mi	56.76	KMQNSMTA	Biotin (K); O›	0.130000000
Propionyl-CoA carboxylase alpha chain, mi	56.76	KMQNSMTA	Biotin (K); O›	0.130000000
Propionyl-CoA carboxylase alpha chain, mi	70.43	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	55.93	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	55.93	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	54.58	AMKMQNSM	Biotin (K)	0.001000000
Propionyl-CoA carboxylase alpha chain, mi	92.72	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	46.02	KMQNSMTA	Biotin (K)	0.100000000
Propionyl-CoA carboxylase alpha chain, mi	44.87	AMKMQNSM	Biotin (K)	0.001000000
Rod cGMP-specific 3~,5~-cyclic phosphod	37.72	KILKTR	Biotin (K)	0.000100.0

Histone lysine demethylase PHF8Gene: PH	37.3	KAQKKK	Biotin (K)	0.000010.0
POTE ankyrin domain family member FGe	38.73	KQDKQKR	Biotin (K)	0.0001000.0
POTE ankyrin domain family member FGe	37.72	KQDKQKR	Biotin (K)	0.0001000.0
Serine/threonine-protein phosphatase 2B c	40.88	NDGKPRVD	2 Biotin (K)	0.000100000
Serine/threonine-protein phosphatase 2B c	40.88	NDGKPRVD	2 Biotin (K)	0.000100000
Serine/threonine-protein phosphatase 2B c	40.88	NDGKPRVD	2 Biotin (K)	0.000100000
Serine/threonine-protein phosphatase 2B c	40.88	NDGKPRVD	2 Biotin (K)	0.000100000
Pseudouridylate synthase 7 homolog Gene	38.74	PRSGAEKG	Biotin (K)	0.000000000
Pseudouridylate synthase 7 homolog Gene	38.74	PRSGAEKG	Biotin (K)	0.000000000
Pyruvate carboxylase, mitochondrial OS=M	76.7	KMETVVTSF	Biotin (K); O›	0.100000000
Pyruvate carboxylase, mitochondrial OS=R	76.7	KMETVVTSF	Biotin (K); O›	0.100000000
Pyruvate carboxylase, mitochondrial OS=M	65.02	GQPLCVLSA	Biotin (K); Ca	0.000020000
Pyruvate carboxylase, mitochondrial OS=R	65.02	GQPLCVLSA	Biotin (K); Ca	0.000020000
Pyruvate carboxylase, mitochondrial OS=R	57.63	GQPLCVLSA	Biotin (K); Ca	0.000020000
Pyruvate carboxylase, mitochondrial OS=R	52.71	GQPLCVLSA	Biotin (K); Ca	0.000020000
Pyruvate carboxylase, mitochondrial OS=M	48.08	GQPLCVLSA	Biotin (K); Ca	0.000020000
Pyruvate carboxylase, mitochondrial OS=R	48.08	GQPLCVLSA	Biotin (K); Ca	0.000020000
Pyruvate carboxylase, mitochondrial OS=M	45.51	KMETVVTSF	Biotin (K); O›	0.130000000
Pyruvate carboxylase, mitochondrial OS=R	45.51	KMETVVTSF	Biotin (K); O›	0.130000000
Pyruvate carboxylase, mitochondrial Gene	61.38	GQPLCVLSA	Biotin (K); Ca	0.000020000
Pyruvate carboxylase, mitochondrial Gene	76.57	KMETVVTSF	Biotin (K)	0.100000000
Pyruvate carboxylase, mitochondrial Gene	76.57	KMETVVTSF	Biotin (K)	0.100000000
Pyruvate carboxylase, mitochondrial Gene	56.75	KMETVVTSF	Biotin (K)	0.100000000
Pyruvate carboxylase, mitochondrial Gene	48.66	SAMKMETV	Biotin (K)	0.000100000
Pyruvate carboxylase, mitochondrial Gene	74.73	KMETVVTSF	Biotin (K)	0.100000000
Rab11 family-interacting protein 2 Gene: Ra	39.98	KPKGK	Biotin (K)	0.00100.0
60S ribosomal protein L4 (Fragment) Gene	40.45	QKKPLVGK	Biotin (K)	0.00100000.0
60S ribosomal protein L4 (Fragment) Gene	40.27	KKQKKPLVG	Biotin (K)	0.000010000
60S ribosomal protein L4 Gene: Rpl4	37.37	KAWNDIK	Biotin (K)	0.0000001.0
Phosphatidylcholine:ceramide cholinephosp	39.11	MILVGLWLF	Biotin (K)	0.000000000
Phosphatidylcholine:ceramide cholinephosp	39.11	MILVGLWLF	Biotin (K)	0.000000000
Stress-induced-phosphoprotein 1 Gene: ST	38.37	QALREKEL	Biotin (K)	0.00000100.0
Serine/threonine-protein kinase 40 Gene: S	42.33	DLKLGNMVI	Biotin (K)	0.001000000
Synaptojanin-1 Gene: Synj1	38.9	TIEPK	Biotin (K)	0.00001.0
Synaptojanin-1 (Fragment) Gene: SYNJ1	38.9	TLEPK	Biotin (K)	0.00001.0
Synaptojanin-1 Gene: Synj1	37.13	TLEPK	Biotin (K)	0.00001.0
Synaptojanin-1 Gene: Synj1	37.13	TIEPK	Biotin (K)	0.00001.0
Alpha-synuclein OS=Mus musculus OX=10	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Alpha-synuclein OS=Rattus norvegicus OX	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Alpha-synuclein OS=Mus musculus OX=10	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Alpha-synuclein OS=Rattus norvegicus OX	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Alpha-synuclein OS=Mus musculus OX=10	51.39	EGVLYVGSK	Biotin (K)	0.000000000
Alpha-synuclein OS=Rattus norvegicus OX	51.39	EGVLYVGSK	Biotin (K)	0.000000000
Alpha-synuclein OS=Mus musculus OX=10	51.39	EGVLYVGSK	Biotin (K)	0.000000000
Alpha-synuclein OS=Rattus norvegicus OX	51.39	EGVLYVGSK	Biotin (K)	0.000000000
Beta-synuclein OS=Mus musculus OX=100	76.21	TKQGVTEA	Biotin (K)	0.000000000
Beta-synuclein OS=Bos taurus OX=9913 G	76.21	TKQGVTEA	Biotin (K)	0.000000000
Beta-synuclein OS=Rattus norvegicus OX=	76.21	TKQGVTEA	Biotin (K)	0.000000000

Beta-synuclein OS=Mus musculus OX=10(	76.21	TKQGVTEA/	Biotin (K)	0.000000000
Beta-synuclein OS=Bos taurus OX=9913 G	76.21	TKQGVTEA/	Biotin (K)	0.000000000
Beta-synuclein OS=Rattus norvegicus OX=	76.21	TKQGVTEA/	Biotin (K)	0.000000000
Beta-synuclein OS=Mus musculus OX=10(	72.8	QGVTEAAEI	Biotin (K)	0.000000001
Beta-synuclein OS=Bos taurus OX=9913 G	72.8	QGVTEAAEI	Biotin (K)	0.000000001
Beta-synuclein OS=Rattus norvegicus OX=	72.8	QGVTEAAEI	Biotin (K)	0.000000001
Beta-synuclein OS=Mus musculus OX=10(	72.8	QGVTEAAEI	Biotin (K)	0.000000001
Beta-synuclein OS=Bos taurus OX=9913 G	72.8	QGVTEAAEI	Biotin (K)	0.000000001
Beta-synuclein OS=Rattus norvegicus OX=	72.8	QGVTEAAEI	Biotin (K)	0.000000001
Beta-synuclein OS=Bos taurus OX=9913 G	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Beta-synuclein OS=Rattus norvegicus OX=	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Beta-synuclein OS=Bos taurus OX=9913 G	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Beta-synuclein OS=Rattus norvegicus OX=	64.82	TKEGVLYVG	Biotin (K)	0.000000000
Beta-synuclein OS=Bos taurus OX=9913 G	51.39	EGVLYVGSI	Biotin (K)	0.000000000
Beta-synuclein OS=Rattus norvegicus OX=	51.39	EGVLYVGSI	Biotin (K)	0.000000000
Beta-synuclein OS=Bos taurus OX=9913 G	51.39	EGVLYVGSI	Biotin (K)	0.000000000
Beta-synuclein OS=Rattus norvegicus OX=	51.39	EGVLYVGSI	Biotin (K)	0.000000000
Beta-synuclein OS=Mus musculus OX=10(	48.5	EGVLYVGSI	Biotin (K)	0.000000001
Beta-synuclein OS=Mus musculus OX=10(	48.5	EGVLYVGSI	Biotin (K)	0.000000001
Microtubule-associated protein tau OS=Go	67.33	IPAKTPPAPI	Biotin (K)	0.000100000
Microtubule-associated protein tau OS=Hyl	45.31	VTSKCGSL(	Biotin (K); Ca	0.000120000
THO complex subunit 5 homolog Gene: TH	39.35	KPKVIR	Biotin (K)	0.001000.0
THO complex subunit 5 homolog Gene: Th	37.35	KPKVIR	Biotin (K)	0.001000.0
Tropomyosin alpha-1 chainGene: TPM1	41.92	DRKYEEVAI	Biotin (K)	0.001000000
Tropomyosin alpha-3 chain Gene: Tpm3	41.92	DRKYEEVAI	Biotin (K)	0.001000000
Transient receptor potential cation channel	39.03	KLPITRK	Biotin (K)	0.1000000.0
Transient receptor potential cation channel	39.03	KLPITRK	Biotin (K)	0.1000000.0
Tubulin polyglutamylase TTLL4 Gene: Ttll4	44.98	QKWIVKP	Biotin (K)	0.0000010.0
Tubulin polyglutamylase TTLL4 Gene: TTL	44.98	QKWIVKP	Biotin (K)	0.0000010.0
Serine/threonine-protein kinase WNK2 Ger	37.35	KPKVLR	Biotin (K)	0.001000.0
Zinc finger E-box-binding homeobox 1 Gen	41.61	SVQEEPLNL	Biotin (K)	0.000000000

peptide modification	RMT-RRc
000.0	ACO13_MOUSE
001.0	ADT3_MOUSE
1.0	AFF1_MOUSE
00001.0	ALS_MOUSE
00001.0	ANK3_MOUSE
1.0	AP2M1_MOUSE
1.0	ASPM_MOUSE
)	AT2B1_MOUSE
0.0	COR2B_MOUSE
)	DCTN1_MOUSE
100.0	DDX56_MOUSE
01.0	DMXL2_MOUSE
	EXOC3_MOUSE
000001.0	F161A_MOUSE
00.0	F16B1_MOUSE
	FSIP2_MOUSE
	FUND2_MOUSE
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00100000000.0	GNAI2_MOUSE
	GNAO_MOUSE
	GNAS_MOUSE
	GNAS1_MOUSE
	GNAT1_MOUSE
	GNAT2_MOUSE
	GNL1_MOUSE
	H10_MOUSE
	H12_MOUSE
	H14_MOUSE
	HIBCH_MOUSE
	HNRPQ_MOUSE
	HNRPU_MOUSE
	HXK1_MOUSE
	ICAM1_MOUSE
	JPH2_MOUSE
	KALRN_MOUSE
	KC1G1_MOUSE
	KC1G3_MOUSE
	KCC2D_MOUSE
	KIF5C_MOUSE
	KIME_MOUSE
	KINH_MOUSE
	KS6A4_MOUSE
	LIN7C_MOUSE
	LX12E_MOUSE

LYAM1_MOUSE
MAP1B_MOUSE
MAP4_MOUSE
MAP6_MOUSE
MARK4_MOUSE
MCCA_MOUSE
0.0 MDHC_MOUSE
0.0 MTAP2_MOUSE
00.0 MX1_MOUSE
000000.0 NCOR1_MOUSE
0.0 PACS1_MOUSE
0.0 PCCA_MOUSE
PDE6A_MOUSE aver
) PHF8_MOUSE avg. local clu
) POTEF_MOUSE expected
) PP2BA_MOUSE PPI er
) PUS7_MOUSE
) PYC_MOUSE
) RFIP2_MOUSE
001000.0 RL4_MOUSE
001000.0 SMS1_MOUSE
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Final list after background is subtracted

RMT-RRc	51	STRING gene names and description
ACO13_MOUSE	Acot13	Acot13 - Acyl-coenzyme A thioesterase 13; Acyl-CoA thioesterases
ALS_MOUSE	Igfals	Igfals - Insulin-like growth factor-binding protein complex acid lab
ANK3_MOUSE	Ank3	Ank3 - Ankyrin 3, epithelial; Ankyrin-3; Membrane-cytoskeleton lin
AP2M1_MOUSE	Ap2m1	Ap2m1 - AP-2 complex subunit mu; Component of the adaptor pro
ASPM_MOUSE	Aspm	Aspm - Abnormal spindle-like microcephaly-associated protein ho
AT2B1_MOUSE	Atp2b1	Atp2b1 - Plasma membrane calcium-transporting ATPase 1; This r
DCTN1_MOUSE	Dctn1	Dctn1 - Dynactin subunit 1; Plays a key role in dynein-mediated ret
DDX56_MOUSE	Ddx56	Ddx56 - Probable ATP-dependent RNA helicase DDX56; May play a
DMXL2_MOUSE	Dmxl2	Dmxl2 - DmX-like protein 2; May serve as a scaffold protein for M
EXOC3_MOUSE	Exoc3	Exoc3 - Exocyst complex component 3; Component of the exocyst c
F161A_MOUSE	Fam161a	Fam161a - Family with sequence similarity 161, member a; Protei
F16B1_MOUSE	Fam160b1	Fam160b1 - Protein FAM160B1; Family with sequence similarity 1
FUND2_MOUSE	Fundc2	Fundc2 - FUN14 domain-containing protein 2; FUN14 domain cont
GNAS1_MOUSE	Gnas	Gnas - Guanine nucleotide-binding protein G(s) subunit alpha isof
GNAT1_MOUSE	Gnat1	Gnat1 - Guanine nucleotide-binding protein G(t) subunit alpha-1; G
GNAT2_MOUSE	Gnat2	Gnat2 - Guanine nucleotide-binding protein G(t) subunit alpha-2; G
GNL1_MOUSE	Gnl1	Gnl1 - Guanine nucleotide-binding protein-like 1; Possible regulato
H12_MOUSE	Hist1h1c	Hist1h1c - H1.2 linker histone, cluster member; Histone H1.2; Histo
H14_MOUSE	Hist1h1e	Hist1h1e - H1.4 linker histone, cluster member; Histone H1.4; Histo
HIBCH_MOUSE	Hibch	Hibch - 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial; Hydrolyz
HNRPQ_MOUSE	Syncrip	Syncrip - Synaptotagmin binding, cytoplasmic rna interacting prote
HNRPU_MOUSE	Hnrnpu	Hnrnpu - Heterogeneous nuclear ribonucleoprotein U; DNA- and RI
KALRN_MOUSE	Kalrn	Kalrn - Kalirin; Promotes the exchange of GDP by GTP. Activates sp
KC1G1_MOUSE	Csnk1g1	Csnk1g1 - Casein kinase I isoform gamma-1; Serine/threonine-pro
KC1G3_MOUSE	Csnk1g3	Csnk1g3 - Casein kinase I isoform gamma-3; Serine/threonine-pro
KIME_MOUSE	Mvk	Mvk - Mevalonate kinase; May be a regulatory site in cholesterol b
KS6A4_MOUSE	Rps6ka4	Rps6ka4 - Ribosomal protein s6 kinase, polypeptide 4; Ribosomal p
LIN7C_MOUSE	Lin7c	Lin7c - Protein lin-7 homolog C; Plays a role in establishing and ma
LX12E_MOUSE	Alox12e	Alox12e - Arachidonate 12-lipoxygenase, epidermal-type; Non-her
MAP1B_MOUSE	Map1b	Map1b - Microtubule-associated protein 1B; Phosphorylated MAP1
MARK4_MOUSE	Mark4	Mark4 - MAP/microtubule affinity-regulating kinase 4; Serine/thre
MDHC_MOUSE	Mdh1	Mdh1 - Malate dehydrogenase, cytoplasmic; Malate dehydrogenas
NCOR1_MOUSE	Ncor1	Ncor1 - Nuclear receptor co-repressor 1; Mediates transcriptional
PACS1_MOUSE	Pacs1	Pacs1 - Phosphofurin acidic cluster sorting protein 1; Coat protein f
PDE6A_MOUSE	Pde6a	Pde6a - Rod cgmp-specific 3',5'-cyclic phosphodiesterase subunit a
PHF8_MOUSE	Phf8	Phf8 - [histone h3]-dimethyl-l-lysine9 demethylase; Histone lysine
PP2BA_MOUSE	Ppp3ca	Ppp3ca - Serine/threonine-protein phosphatase 2B catalytic subun
PUS7_MOUSE	Pus7	Pus7 - Pseudouridylate synthase 7 homolog (S. cerevisiae) [a.k.a. P
RFIP2_MOUSE	Rab11fip2	Rab11fip2 - RAB11 family interacting protein 2 (class I); Rab11 fa
SMS1_MOUSE	Sgms1	Sgms1 - Phosphatidylcholine:ceramide cholinephosphotransferase
STIP1_MOUSE	Stip1	Stip1 - Stress-induced-phosphoprotein 1; Acts as a co-chaperone f
STK40_MOUSE	Stk40	Stk40 - Serine/threonine-protein kinase 40; May be a negative reg
SYNJ1_MOUSE	Synj1	Synj1 - Synaptojanin 1; Phosphatase that acts on various phosphoi
TAU_MOUSE	Mapt	Mapt - Microtubule-associated protein tau; Promotes microtubule

THOC5_MOUSE	Thoc5	Thoc5 - THO complex subunit 5 homolog; Acts as component of th
TPM1_MOUSE	Tpm1	Tpm1 - Tropomyosin alpha-1 chain; Binds to actin filaments in mu
TPM3_MOUSE	Tpm3	Tpm3 - Tropomyosin alpha-3 chain; Tropomyosin 3, gamma; Belor
TRPM7_MOUSE	Trpm7	Trpm7 - Transient receptor potential cation channel, subfamily m,
TTLL4_MOUSE	Ttll4	Ttll4 - Tubulin polyglutamylase TTLL4; Glutamylase which preferer
WNK2_MOUSE	Wnk2	Wnk2 - Wnk lysine deficient protein kinase 2; Serine/threonine-pro
ZEB1_MOUSE	Zeb1	Zeb1 - Zinc finger E-box-binding homeobox 1; Acts as a transcripti

Network properties

number of nodes:	51
number of edges:	33
·age node degree:	1.29
stering coefficient:	0.395
number of edges:	18
ıriched p-value:	0.00104

are a group of enzymes that catalyze the hydrolysis of acyl-CoAs to the free fatty acid and cc
ile subunit; May have an important role in regulating the access of circulating IGFs to the tiss
ker. May participate in the maintenance/targeting of ion channels and cell adhesion molecule
tein complex 2 (AP-2). Adaptor protein complexes function in protein transport via transport
molog; Involved in mitotic spindle regulation and coordination of mitotic processes. The funct
nagnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the transport of
rograde transport of vesicles and organelles along microtubules by recruiting and tethering d
role in later stages of the processing of the pre-ribosomal particles leading to mature 60S ril
ADD and RAB3GA on synaptic vesicles of neuronal and endocrine homeostatic processes (By s
complex involved in the docking of exocytic vesicles with fusion sites on the plasma membrar
in FAM161A; Involved in ciliogenesis [a.k.a. Fam161a-001, Fam161a-002, XP_006514892, F16
.60, member B1 [a.k.a. Kiaa1600, ENSMUSG00000033478, NP_663480.3, F16B1_MOUSE]
taining 2; Belongs to the FUN14 family [a.k.a. Hcbp6, OTTMUSG00000020855, ENSMUST000
orms XLas; Guanine nucleotide-binding proteins (G proteins) function as transducers in nume
Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers ir
Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers ir
ory or functional link with the histocompatibility cluster [a.k.a. Gna-rs1, Mmr1, NP_032162.2,
one H1 protein binds to linker DNA between nucleosomes forming the macromolecular structu
one H1 protein binds to linker DNA between nucleosomes forming the macromolecular struct
es 3-hydroxyisobutyryl-CoA (HIBYL-CoA), a saline catabolite. Has high activity toward isobutyr
ein; Heterogeneous nuclear ribonucleoprotein Q; Heterogeneous nuclear ribonucleoprotein (hr
NA-binding protein involved in several cellular processes such as nuclear chromatin organizati
pecific Rho GTPase family members, thereby inducing various signaling mechanisms that regu
tein kinase. Casein kinases are operationally defined by their preferential utilization of acidic
tein kinase. Casein kinases are operationally defined by their preferential utilization of acidic
biosynthetic pathway; Belongs to the GHMP kinase family. Mevalonate kinase subfamily [a.k.a
protein S6 kinase alpha-4; Serine/threonine-protein kinase that is required for the mitogen or
aintaining the asymmetric distribution of channels and receptors at the plasma membrane of
ne iron-containing dioxygenase that probably catalyzes the stereo-specific peroxidation of fre
LB may play a role in the cytoskeletal changes that accompany neurite extension. Possibly MA
eonine-protein kinase (By similarity). Phosphorylates the microtubule-associated protein MAP
se 1, NAD (soluble) [a.k.a. Mor2, ENSMUST00000146146, Q80Y13, MDHC_MOUSE]
repression by certain nuclear receptors. Part of a complex which promotes histone deacetylat
that is involved in the localization of trans-Golgi network (TGN) membrane proteins that cont
alpha; This protein participates in processes of transmission and amplification of the visual si
demethylase PHF8; Histone lysine demethylase with selectivity for the di- and monomethyl s
it alpha isoform; Calcium-dependent, calmodulin-stimulated protein phosphatase. Many of tl
PUS7, ENSMUST00000151449, NM_178403, PUS7_MOUSE]
mily-interacting protein 2; A Rab11 effector binding preferentially phosphatidylinositol 3,4,5-t
1; Sphingomyelin synthases synthesize the sphingolipid, sphingomyelin, through transfer of t
or HSP90AA1. Mediates the association of the molecular chaperones HSPA8/HSC70 and HSP9
ulator of NF-kappa-B and p53- mediated gene transcription [a.k.a. Lyk4, Stk40-201, XP_0065C
nositides, including phosphatidylinositol 4-phosphate, phosphatidylinositol (4,5)- bisphosphat
assembly and stability, and might be involved in the establishment and maintenance of neur

e THO subcomplex of the TREX complex which is thought to couple mRNA transcription, proc
ıscle and non-muscle cells. Plays a central role, in association with the troponin complex, in th
ıgs to the tropomyosin family [a.k.a. hTM30nm, ENSMUST00000118566, ENSMUSP00000114
member 7; Transient receptor potential cation channel subfamily M member 7; Essential ior
ıtially modifies beta-tubulin and non-tubulin proteins, such as NAP1L1, NAP1L4 and CGAS/MI
ɔtein kinase WNK2; Serine/threonine kinase which plays an important role in the regulation o
onal repressor. Binds to E-box sequences in the immunoglobulin heavy chain enhancer as wel

benzyme A (CoASH), providing the potential to regulate intracellular levels of acyl-CoAs, free f
ues [a.k.a. Als, Albs, ENSMUST00000050714, ALS_MOUSE]
es at the nodes of Ranvier and axonal initial segments (By similarity). In skeletal muscle, requ
vesicles in different membrane traffic pathways. Adaptor protein complexes are vesicle coat
ion in regulating microtubule dynamics at spindle poles including spindle orientation, astral r
calcium. Involved in bone homeostasis. Has a role in osteoclastogenesis where it regulates RA
ynein to microtubules. Binds to both dynein and microtubules providing a link between specif
bosomal subunits. Has intrinsic ATPase activity (By similarity); Belongs to the DEAD box helica
similarity). Plays a role in the brain as a key controller of neuronal and endocrine homeostatic
ne [a.k.a. Sec6l1, ENSMUSP00000039416, Q6KAR6, EXOC3_MOUSE]
51A_MOUSE]

00033541, FUND2_MOUSE]
rous signaling pathways controlled by G protein-coupled receptors (GPCRs). Signaling involve
n various transmembrane signaling systems. Transducin is an amplifier and one of the transdu
n various transmembrane signaling systems. Transducin is an amplifier and one of the transdu
GNL1_MOUSE]
ure known as the chromatin fiber. Histones H1 are necessary for the condensation of nucleoso
ure known as the chromatin fiber. Histones H1 are necessary for the condensation of nucleoso
yl-CoA. Could be an isobutyryl-CoA dehydrogenase that functions in valine catabolism. Also h
nRNP) implicated in mRNA processing mechanisms. Component of the CRD- mediated compl
ion, telomere-length regulation, transcription, mRNA alternative splicing and stability, Xist-m
ulate neuronal shape, growth, and plasticity, through their effects on the actin cytoskeleton. I
proteins such as caseins as substrates. It can phosphorylate a large number of proteins. Parti
proteins such as caseins as substrates. It can phosphorylate a large number of proteins. Parti
a. XM_006530185, AF137598, ENSMUST00000043760, KIME_MOUSE]
stress-induced phosphorylation of the transcription factors CREB1 and ATF1 and for the regu
polarized cells. Forms membrane-associated multiprotein complexes that may regulate deli
e and esterified polyunsaturated fatty acids generating a spectrum of bioactive lipid mediato
AP1B binds to at least two tubulin subunits in the polymer, and this bridging of subunits might
T (By similarity). Also phosphorylates the microtubule-associated proteins MAP2 and MAP4 (

tion and the formation of repressive chromatin structures which may impede the access of ba
tain acidic cluster sorting motifs. Controls the endosome-to-Golgi trafficking of furin and mar
gnal [a.k.a. Pde6a-001, phosphodiesterase 6A, cGMP-specific, rod, alpha, EDL09778.1, PDE6A
states that plays a key role cell cycle progression, rDNA transcription and brain development.
ne substrates contain a PxIxIT motif. This subunit may have a role in the calmodulin activation

trisphosphate (PtdInsP3) and phosphatidic acid (PA) and acting in the regulation of the transp
the phosphatidyl head group, phosphatidylcholine, on to the primary hydroxyl of ceramide. Th
0 [a.k.a. ENSMUST00000025918, MGI:109130, IEF SSP 3521, STIP1_MOUSE]
03505, STK40_MOUSE]
e and phosphatidylinositol (3,4,5)-trisphosphate (By similarity). Has a role in clathrin-mediate
onal polarity. The C-terminus binds axonal microtubules while the N- terminus binds neural p

essing and nuclear export, and which specifically associates with spliced mRNA and not with
ne calcium dependent regulation of vertebrate striated muscle contraction. Smooth muscle co
229, TPM3_MOUSE]
n channel and serine/threonine-protein kinase. Divalent cation channel permeable to calcium
321D1. Involved in the side-chain initiation step of the polyglutamylation reaction rather than
f electrolyte homeostasis, cell signaling, survival, and proliferation. Acts as an activator and i
l as in the regulatory regions of many other tissue-specific genes. Represses E-cadherin prom

fatty acids and CoASH. Has acyl-CoA thioesterase activity towards medium (C12) and long-cha

uired for costamere localization of DMD and betaDAG1. Regulates KCNA1 channel activity in f
components and appear to be involved in cargo selection and vesicle formation. AP-2 is involv
microtubule density and poleward microtubule flux seem to depend on its association with th
ANKL-induced calcium oscillation, a key step in the differentiation process. Also promotes sur
ic cargos, microtubules and dynein. Essential for targeting dynein to microtubule plus ends, re
ase family. DDX56/DBP9 subfamily [a.k.a. D11Ertd619e, Noh61, ENSMUST00000155874, DDX5
processes [a.k.a. Kiaa0856, OTTMUST00000074936, XM_006511085, DMXL2_MOUSE]

s the activation of adenylyl cyclases, resulting in increased levels of the signaling molecule cA
ucers of a visual impulse that performs the coupling between rhodopsin and cGMP-phosphod
ucers of a visual impulse that performs the coupling between rhodopsin and cGMP-phosphod

ome chains into higher-order structured fibers. Acts also as a regulator of individual gene trar
ome chains into higher-order structured fibers. Acts also as a regulator of individual gene trar
ydrolyzes 3-hydroxypropanoyl-CoA (By similarity); Belongs to the enoyl-CoA hydratase/isomer
ex that promotes MYC mRNA stability. Isoform 1 and isoform 2 are associated in vitro with p
ediated transcriptional silencing and mitotic cell progression. Plays a role in the regulation of
nduces lamellipodia independent of its GEF activity (By similarity); Belongs to the protein kin
cipates in Wnt signaling. Phosphorylates CLSPN (By similarity). Regulates fast synaptic transr
cipates in Wnt signaling (By similarity). Regulates fast synaptic transmission mediated by glu

lation of the transcription factor RELA, and that contributes to gene activation by histone pho
very and recycling of proteins to the correct membrane domains. The tripartite complex comp
rs. May preferentially convert arachidonic acid to (12S)-hydroperoxyeicosatetraenoic acid/(12
t be involved in nucleating microtubule polymerization and in stabilizing microtubules. Acts as
By similarity). Involved in regulation of the microtubule network, causing reorganization of m

asal transcription factors. Participates in the transcriptional repressor activity produced by BCl
nose-6-phosphate receptor by connecting the acidic-cluster-containing cytoplasmic domain o
_MOUSE]
Demethylates mono- and dimethylated histone H3 'Lys-9' residue (H3K9Me1 and H3K9Me2),
n of calcineurin. Dephosphorylates DNM1L and HSPB1 (By similarity). Dephosphorylates SSH1;

ort of vesicles from the endosomal recycling compartment (ERC) to the plasma membrane. In
e reaction is bidirectional depending on the respective levels of the sphingolipid and ceramide

ed endocytosis (By similarity). Hydrolyzes PIP2 bound to actin regulatory proteins resulting in t
plasma membrane components, suggesting that tau functions as a linker protein between bot

unspliced pre-mRNA. TREX is recruited to spliced mRNAs by a transcription-independent mec
ontraction is regulated by interaction with caldesmon. In non-muscle cells is implicated in sta

and magnesium. Has a central role in magnesium ion homeostasis and in the regulation of a
in the elongation step. Involved in formation of short side-chains. Mediates initiation of poly
nhibitor of sodium-coupled chloride cotransporters and potassium-coupled chloride cotranspo
noter and induces an epithelial- mesenchymal transition (EMT) by recruiting SMARCA4/BRG1

ıin (C18) fatty acyl-CoA substrates. Can also hydrolyze 3- hydroxyphenylacetyl-CoA (in vitro). M

unction of dietary Mg(2+) levels, and thereby contributes to the regulation of renal Mg(2+) re
ved in clathrin-dependent endocytosis in which cargo proteins are incorporated into vesicles s
e katanin complex formed by KATNA1 and KATNB1. Enhances the microtubule lattice severing
vival of mature osteoclasts, probably by preventing toxic accumulation of intracellular calciun
ecruiting dynein to membranous cargos and enhancing dynein processivity (the ability to move
56_MOUSE]

AMP. GNAS functions downstream of several GPCRs, including beta-adrenergic receptors. XLa
iesterase [a.k.a. Gnat-1, Ird2, transducin, GNAT1_MOUSE]
iesterase [a.k.a. 14686, OTTMUSG00000007183, ENSMUSG00000009108, GNAT2_MOUSE]

ıscription through chromatin remodeling, nucleosome spacing and DNA methylation (By simil
ıscription through chromatin remodeling, nucleosome spacing and DNA methylation [a.k.a. H
ase family [a.k.a. NP_666220, AC110177, HIBCH_MOUSE]
re-mRNA, splicing intermediates and mature mRNA protein complexes. Isoform 1 binds to ap
interphase large-scale gene-rich chromatin organization through chromatin-associated RNAs
ase superfamily. CAMK Ser/Thr protein kinase family [a.k.a. A2CG52, UPI0000D672E7, ENSMU
ıission mediated by glutamate [a.k.a. 9130020E21Rik, Q8BTH8, Csnk1g1-005, KC1G1_MOUSE
ıtamate [a.k.a. XP_006526300, Mm.411061, casein kinase 1, gamma 3, KC1G3_MOUSE]

ısphorylation and functions in the regulation of inflammatory genes. Phosphorylates CREB1 an
ɔosed of LIN7 (LIN7A, LIN7B or LIN7C), CASK and APBA1 may have the potential to couple syn
!S)-HPETE; Belongs to the lipoxygenase family [a.k.a. Alox12-ps2, Aloxe, Alox12e-002, LX12E_
s a positive cofactor in DAPK1-mediated autophagic vesicle formation and membrane blebbin
icrotubules into bundles (By similarity). Required for the initiation of axoneme extension duri

L6. Recruited by ZBTB7A to the androgen response elements/ARE on target genes, negatively
ıf these molecules with the adapter-protein complex-1 (AP-1) of endosomal clathrin- coated r

dimethylated H3 'Lys-27' (H3K27Me2) and monomethylated histone H4 'Lys-20' residue (H4K2
Belongs to the PPP phosphatase family. PP-2B subfamily [a.k.a. Calna, 19055, EC 3.1.3.16, PF

ıvolved in insulin granule exocytosis. Also involved in receptor-mediated endocytosis and mer
e. Golgi apparatus SMS1 directly and specifically recognizes the choline head group on the sul

he rearrangement of actin filaments downstream of tyrosine kinase and ASH/GRB2 (By simil
ch. Axonal polarity is predetermined by tau localization (in the neuronal cell) in the domain of

chanism, binds to mRNA upstream of the exon-junction complex (EJC) and is recruited in a sp
bilizing cytoskeleton actin filaments [a.k.a. Tpm-1, Tpma, OTTMUST00000048455, TPM1_MC

noxic neuronal cell death. Involved in TNF- induced necroptosis downstream of MLKL by medi
glutamylation of nucleosome assembly proteins NAP1L1 and NAP1L4. Also acts as a monoglu
orters respectively. Activates SLC12A2, SCNN1A, SCNN1B, SCNN1D and SGK1 and inhibits SLC
. Represses BCL6 transcription in the presence of the corepressor CTBP1 (By similarity). Positi

May play a role in controlling adaptive thermogenesis [a.k.a. Them2, EDL32477.1, 0610006O17

eabsorption [a.k.a. Ank3-006, ENSMUSP00000138356, AAH21657.1, ANK3_MOUSE]
urrounded by clathrin (clathrin- coated vesicles, CCVs) which are destined for fusion with the
g activity of KATNA1 by recruiting the katanin complex to microtubules. Can block microtubule
n [a.k.a. AK170163, uc007gxf.2, F630024D21, AT2B1_MOUSE]
e along a microtubule for a long distance without falling off the track). Can also act as a brak

s isoforms interact with the same set of receptors as Gnas isoforms [a.k.a. Gnas1, Q3UI70, E

larity) [a.k.a. H1f2, CAA72970.1, 50708, H12_MOUSE]
1f4, mmu:50709, uc007puj.3, H14_MOUSE]

poB mRNA AU-rich sequences (By similarity). Isoform 1 is part of the APOB mRNA editosome
s (caRNAs) in a transcription-dependent manner, and thereby maintains genomic stability (By
USP00000116188, KALRN_MOUSE]
E]

nd ATF1 in response to mitogenic or stress stimuli such as UV-C irradiation, epidermal growth
aptic vesicle exocytosis to cell adhesion in brain. Ensures the proper localization of GRIN2B (s
MOUSE]
ng (By similarity). Facilitates tyrosination of alpha-tubulin in neuronal microtubules. Required
ng cilium assembly (By similarity). Regulates the centrosomal location of ODF2 and phospho

regulates androgen receptor signaling and androgen-induced cell proliferation (By similarity)
membrane pits (By similarity) [a.k.a. PACS1, NM_153129, F830023A05, PACS1_MOUSE]

20Me1). Acts as a transcription activator as H3K9Me1, H3K9Me2, H3K27Me2 and H4K20Me1 a
P2BA_MOUSE]

mbrane trafficking of recycling endosomes, probably originating from clathrin-coated vesicles
bstrate, requiring two fatty chains on the choline-P donor molecule in order to be recognized

larity) [a.k.a. mKIAA0910, UPI0001889C62, Synj1-201, SYNJ1_MOUSE]
the cell body defined by the centrosome. The short isoforms allow plasticity of the cytoskele

licing- and cap-dependent manner to a region near the 5' end of the mRNA where it function
)USE]

ating calcium influx. The kinase activity is essential for the channel function. May be involved
ıtamylase: generates monoglutamylation of CGAS/MB21D1, leading to impair the nucleotidyl
12A5. Negatively regulates the EGF-induced activation of the ERK/MAPK-pathway and the do
ively regulates neuronal differentiation. Represses RCOR1 transcription activation during neu

7Rik, ACO13_MOUSE]

early endosome. The clathrin lattice serves as a mechanical scaffold but [...] [a.k.a. Clapm1, C
e minus-end growth and reversely this function can be enhanced by the katanin [...] [a.k.a. Cal

e to slow the dynein motor during motility along the microtubule. C [...] [a.k.a. XM_00650548

ENSMUSP00000104712, GNAS1_MOUSE]

e complex and may modulate the postranscriptional C to U RNA-editing of the APOB mRNA th
y similarity). Required for the localization of the long non-coding Xist RN [...] [a.k.a. Hnrpu, NM

n factor (EGF) and anisomycin. Plays an essential role in the control of RE [...] [a.k.a. Msk2, Q
ubunit 2B of the NMDA receptor) to neuronal postsynaptic density and may funct [...] [a.k.a. I

for synaptic maturation [a.k.a. Mtap1b, Mtap5, P14873, MAP1B_MOUSE]
rylates ODF2 in vitro (By similarity). Plays a role in cell cycle progressi [...] [a.k.a. Kiaa1860, M

). Mediates the NR1D1-dependent repression and circadian regulation of TSH [...] [a.k.a. Ncor

are epigenetic repressive marks. Involved in cell cycle progression by being required to c [...] [

. Required in a complex with MYO5B and RAB11 for the transport of NPC1L1 to [...] [a.k.a. Nr
efficiently as a substrate. Major form in macrophages. Required for cell [...] [a.k.a. Tmem23,

ton whereas the longer isoforms may preferentially play a role in its stabil [...] [a.k.a. Tau, Mt

s in mRNA export to the cytoplasm via the TAP/NFX1 pathway. THOC5 in conjunction with AL

in a fundamental process that adjusts plasma membrane divalent cation fluxes a [...] [a.k.a. transferase activity of CGAS/MB21D1; Belongs to the tubulin--tyrosine ligase family [a.k.a. Ki wnstream cell cycle progression. Affects MAPK3/MAPK1 activity by modulating th [...] [a.k.a. rogenesis. Represses transcription by binding to the E box (5'-CANNTG-3'). P [...] [a.k.a. Zfx1a

)TTMUSP00000031780, AF001914, AP2M1_MOUSE]
mbp1, Sha1, ASPM, ASPM_MOUSE]

7, XM_006505493, uc009cna.2, DCTN1_MOUSE]

rough eith [...] [a.k.a. Nsap1, Hnrpq, Nsap1l, HNRPQ_MOUSE]
M_016805.2, hnRNP_U, HNRPU_MOUSE]

9Z2B9, NP_064308.2, KS6A4_MOUSE]
Mals3, Veli3, MALS-3, LIN7C_MOUSE]

IAP/microtubule affinity-regulating kinase 4, AY151083, MARK4_MOUSE]

1-006, ENSMUST00000161281, ENSMUST00000159315, NCOR1_MOUSE]

a.k.a. Kiaa1111, ENSMUST00000112662, XM_006528877.3, PHF8_MOUSE]

ip11, Rab11-FIP2, CCDS38033.1, RFIP2_MOUSE]
CCDS29750.1, ENSMUSP00000117336, SMS1_MOUSE]

tapt, ENSMUSP00000102600, TAU_MOUSE]

Y [...] [a.k.a. Kiaa0983, Fmip, ENSMUST00000144371, THOC5_MOUSE]

Ltrpc7, Chak, 1IA9, TRPM7_MOUSE]
aa0173, ENSMUSP00000037406, ENSMUSP00000116733, TTLL4_MOUSE]
Kiaa1760, XM_006516977, NP_001277240.1, WNK2_MOUSE]
, Zfhx1a, Tcf8, ZEB1_MOUSE]

Table 19 **Total peptides list for three control rAAVs in the retrieval-recc**

n = 8, pep = 440, pro = 83

rAAV	Sample	Biotin	Protein Accessio	Protein Des	Peptide Scor
SYN-MiniTid-Tau	6	d3-6	1433F_MOUSE	14-3-3 protei	38.57
SYN-MiniTid-Tau	6	d3-6	1433F_MOUSE	14-3-3 protei	38.57
SYN-MiniTid-Tau	6	d3-6	1433F_MOUSE	14-3-3 protei	37.57
SYN-MiniTid-Tau	6	d3-6	1433F_MOUSE	14-3-3 protei	37.57
SYN-MiniTid-Tau	5	d3-6	ACBP_MOUSE	Acyl-CoA-bir	38.23
SYN-MiniTid-Tau	5	d3-6	ACBP_MOUSE	Acyl-CoA-bir	38.23
RAM-MiniTid	1	d3-6	AFF2_MOUSE	AF4/FMR2 fa	44.37
RAM-MiniTid	1	d3-6	AFF2_MOUSE	AF4/FMR2 fa	44.37
SYN-MiniTid-Tau	4	d3-6	ARHG2_MOUSE	Rho guanine	50.77
SYN-MiniTid-Tau	4	d3-6	ARHG2_MOUSE	Rho guanine	50.77
SYN-MiniTid-Tau	4	d3-6	ARHG2_MOUSE	Rho guanine	50.77
SYN-MiniTid-Tau	4	d3-6	ARHG2_MOUSE	Rho guanine	50.77
SYN-MiniTid-Tau	5	d3-6	ASGL1_MOUSE	Isoaspartyl p	37.99
SYN-MiniTid-Tau	8	d3-6	AT2B4_MOUSE	Plasma mem	37.73
SYN-MiniTid	2	d3-6	BASP1_MOUSE	Brain acid so	68.69
SYN-MiniTid	2	d3-6	BASP1_MOUSE	Brain acid so	68.69
SYN-MiniTid-Tau	4	d3-6	BIN1_MOUSE	Myc box-dep	44.44
SYN-MiniTid-Tau	4	d3-6	BIN1_MOUSE	Myc box-dep	44.44
SYN-MiniTid-Tau	4	d3-6	BIN1_MOUSE	Myc box-dep	44.44
SYN-MiniTid-Tau	4	d3-6	BIN1_MOUSE	Myc box-dep	44.44
SYN-MiniTid-Tau	7	d3-6	BSN_MOUSE	Protein bass	40.08
SYN-MiniTid-Tau	6	d3-6	CAMP1_MOUSE	Calmodulin-r	37.29
SYN-MiniTid-Tau	6	d3-6	CCDC7_MOUSE	Coiled-coil do	40.21
SYN-MiniTid	2	d3-6	CH60_MOUSE	60 kDa heat	60.97
SYN-MiniTid	2	d3-6	CH60_MOUSE	60 kDa heat	60.97
SYN-MiniTid	2	d3-6	CH60_MOUSE	60 kDa heat	60.97
SYN-MiniTid	2	d3-6	CH60_MOUSE	60 kDa heat	60.97
SYN-MiniTid-Tau	6	d3-6	CISY_MOUSE	Citrate synth	37.91
SYN-MiniTid-Tau	4	d3-6	CLAP2_MOUSE	CLIP-associa	81.98
SYN-MiniTid-Tau	4	d3-6	CLAP2_MOUSE	CLIP-associa	81.98
SYN-MiniTid-Tau	6	d3-6	CLH2_MOUSE	Clathrin heav	38.6
SYN-MiniTid-Tau	8	d3-6	CMAH_MOUSE	Cytidine mon	40.04
SYN-MiniTid-Tau	6	d3-6	COR1A_MOUSE	Coronin-1A C	39.76
SYN-MiniTid-Tau	7	d3-6	COR2B_MOUSE	Coronin-2B C	38.49
SYN-MiniTid-Tau	7	d3-6	DYH8_MOUSE	Dynein heavy	38.17
SYN-MiniTid-Tau	7	d3-6	DYH8_MOUSE	Dynein heavy	38.17
SYN-MiniTid	2	d3-6	ESRP2_MOUSE	Epithelial spli	42.72
SYN-MiniTid	2	d3-6	ESRP2_MOUSE	Epithelial spli	42.72
SYN-MiniTid-Tau	5	d3-6	FSIP2_MOUSE	Fibrous shea	40.35
SYN-MiniTid-Tau	6	d3-6	G3P_MOUSE	Glyceraldehy	38.09
SYN-MiniTid	2	d3-6	GLSK_MOUSE	Glutaminase	53.5
SYN-MiniTid	2	d3-6	GLSK_MOUSE	Glutaminase	53.5
SYN-MiniTid-Tau	5	d3-6	GNAI1_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	5	d3-6	GNAI1_MOUSE	Guanine nuc	38.23

SYN-MiniTid-Tau	5	d3-6	GNAI1_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	5	d3-6	GNAI1_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	5	d3-6	GNAI1_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	5	d3-6	GNAI2_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	5	d3-6	GNAI2_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	5	d3-6	GNAL_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	5	d3-6	GNAO_MOUSE	Guanine nuc	38.23
SYN-MiniTid-Tau	7	d3-6	GNAO_MOUSE	Guanine nuc	41.2
SYN-MiniTid-Tau	7	d3-6	GNAO_MOUSE	Guanine nuc	41.2
SYN-MiniTid-Tau	7	d3-6	GNAO_MOUSE	Guanine nuc	41.2
SYN-MiniTid-Tau	5	d3-6	GRM8_MOUSE	Metabotropic	37.11
SYN-MiniTid-Tau	5	d3-6	GRM8_MOUSE	Metabotropic	37.11
SYN-MiniTid-Tau	5	d3-6	GRM8_MOUSE	Metabotropic	37.11
SYN-MiniTid-Tau	8	d3-6	H10_MOUSE	Histone H1.0	38.16
SYN-MiniTid-Tau	8	d3-6	H10_MOUSE	Histone H1.0	38.16
SYN-MiniTid-Tau	8	d3-6	H13_MOUSE	Histone H1.3	38.21
SYN-MiniTid-Tau	4	d3-6	HBA_MOUSE	Hemoglobin s	38.29
SYN-MiniTid-Tau	4	d3-6	HBA_MOUSE	Hemoglobin s	38.29
SYN-MiniTid-Tau	7	d3-6	HEXD_MOUSE	Hexosaminid	41.31
SYN-MiniTid-Tau	8	d3-6	HFE_MOUSE	Hereditary he	38.81
SYN-MiniTid-Tau	8	d3-6	HS74L_MOUSE	Heat shock 7	38.26
SYN-MiniTid-Tau	7	d3-6	HSDL1_MOUSE	Inactive hydr	38.51
SYN-MiniTid-Tau	6	d3-6	HXK1_MOUSE	Hexokinase-	38.54
SYN-MiniTid-Tau	6	d3-6	HXK1_MOUSE	Hexokinase-	38.54
SYN-MiniTid-Tau	6	d3-6	HXK1_MOUSE	Hexokinase-	38.54
SYN-MiniTid-Tau	7	d3-6	HXK1_MOUSE	Hexokinase-	42.06
SYN-MiniTid	2	d3-6	ICAM1_MOUSE	Intercellular a	50.28
SYN-MiniTid	2	d3-6	ICAM1_MOUSE	Intercellular a	50.28
SYN-MiniTid-Tau	4	d3-6	ICAM1_MOUSE	Intercellular a	58.48
SYN-MiniTid-Tau	4	d3-6	ICAM1_MOUSE	Intercellular a	58.48
SYN-MiniTid-Tau	8	d3-6	KCC2D_MOUSE	Calcium/calm	40.45
SYN-MiniTid-Tau	6	d3-6	KIF5C_MOUSE	Kinesin heav	37.92
SYN-MiniTid-Tau	7	d3-6	KINH_MOUSE	Kinesin-1 hea	38.62
SYN-MiniTid-Tau	8	d3-6	KINH_MOUSE	Kinesin-1 hea	41.29
SYN-MiniTid-Tau	7	d3-6	LYAM1_MOUSE	L-selectinGe	39.09
SYN-MiniTid-Tau	7	d3-6	LYAM1_MOUSE	L-selectin OS	39.09
SYN-MiniTid-Tau	6	d3-6	MACF1_MOUSE	Microtubule-a	37.03
SYN-MiniTid-Tau	8	d3-6	MAP4_MOUSE	Microtubule-a	41.83
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	102.69
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	102.69
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	73.52
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	73.52
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	69.54
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	69.54
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	37.72
SYN-MiniTid-Tau	4	d3-6	MAP6_MOUSE	Microtubule-a	37.72
RAM-MiniTid	1	d3-6	MCCA_MOUSE	Methylcroton	43.85
RAM-MiniTid	1	d3-6	MCCA_MOUSE	Methylcroton	43.85

SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	65.88
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	65.88
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	65.88
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	65.88
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	65.88
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	44.13
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	44.13
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	44.13
SYN-MiniTid	2	d3-6	MCCA_MOUSE	Methylcroton	44.13
SYN-MiniTid-Tau	4	d3-6	MCCA_MOUSE	Methylcroton	43.8
SYN-MiniTid-Tau	4	d3-6	MCCA_MOUSE	Methylcroton	43.8
SYN-MiniTid-Tau	4	d3-6	MCCA_MOUSE	Methylcroton	43.8
SYN-MiniTid-Tau	4	d3-6	MCCA_MOUSE	Methylcroton	43.8
SYN-MiniTid-Tau	4	d3-6	MCCA_MOUSE	Methylcroton	43.8
SYN-MiniTid-Tau	4	d3-6	MCCA_MOUSE	Methylcroton	43.8
SYN-MiniTid-Tau	6	d3-6	MCF2_MOUSE	Proto-oncoge	37.17
SYN-MiniTid-Tau	4	d3-6	MINK1_MOUSE	Misshapen-lil	57.5
SYN-MiniTid-Tau	4	d3-6	MINK1_MOUSE	Misshapen-lil	57.5
SYN-MiniTid-Tau	4	d3-6	MINK1_MOUSE	Misshapen-lil	57.5
SYN-MiniTid-Tau	4	d3-6	MINK1_MOUSE	Misshapen-lil	57.5
RAM-MiniTid	1	d3-6	MRO2A_MOUSE	Maestro heat	43.49
RAM-MiniTid	1	d3-6	MRO2A_MOUSE	Maestro heat	43.49
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	62.8
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	62.8
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	58.07
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	58.07
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	54.66
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	54.66
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	52.52
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	52.52
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	38.77
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	38.77
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	45.82
SYN-MiniTid-Tau	4	d3-6	MTAP2_MOUSE	Microtubule-a	45.82
SYN-MiniTid-Tau	7	d3-6	MTAP2_MOUSE	Microtubule-a	37.27
RAM-MiniTid	1	d3-6	MY18A_MOUSE	Unconventio	40.06
RAM-MiniTid	1	d3-6	MY18A_MOUSE	Unconventio	40.06
SYN-MiniTid-Tau	8	d3-6	NBEL2_MOUSE	Neurobeachi	39.87
RAM-MiniTid	1	d3-6	NDUB6_MOUSE	NADH dehyc	107.25
RAM-MiniTid	1	d3-6	NDUB6_MOUSE	NADH dehyc	107.25
SYN-MiniTid-Tau	3	d3-6	NDUB6_MOUSE	NADH dehyc	96.1
SYN-MiniTid-Tau	3	d3-6	NDUB6_MOUSE	NADH dehyc	96.1
SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23
SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23
SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23
SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23
SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23
SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23

SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23
SYN-MiniTid-Tau	4	d3-6	NEUG_MOUSE	Neurogranin	60.23
SYN-MiniTid-Tau	5	d3-6	NFM_MOUSE	Neurofilamer	38.74
RAM-MiniTid	1	d3-6	NHRF3_MOUSE	Na(+)/H(+) e	37.11
RAM-MiniTid	1	d3-6	NHRF3_MOUSE	Na(+)/H(+) e	37.11
SYN-MiniTid-Tau	8	d3-6	NU4M_MOUSE	NADH-ubiqui	37.55
RAM-MiniTid	1	d3-6	PCCA_MOUSE	Propionyl-Co	93.36
RAM-MiniTid	1	d3-6	PCCA_MOUSE	Propionyl-Co	54.25
RAM-MiniTid	1	d3-6	PCCA_MOUSE	Propionyl-Co	48.84
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	93.52
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	93.52
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	93.52
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	93.52
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	93.52
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	93.52
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	93.52
SYN-MiniTid-Tau	3	d3-6	PCCA_MOUSE	Propionyl-Co	73.01
SYN-MiniTid-Tau	8	d3-6	PCCA_MOUSE	Propionyl-Co	55.46
SYN-MiniTid-Tau	5	d3-6	PDIA3_MOUSE	Protein disulf	37.11
SYN-MiniTid-Tau	5	d3-6	PDIA3_MOUSE	Protein disulf	37.11
SYN-MiniTid-Tau	5	d3-6	PDIA3_MOUSE	Protein disulf	37.11
SYN-MiniTid-Tau	8	d3-6	PRAM_MOUSE	PML-RARA-r	38.12
SYN-MiniTid-Tau	8	d3-6	PRG4_MOUSE	Proteoglycar	37.61
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	112.65
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	87.32
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	73.4
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	73.4
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	69.05
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	69.05
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	67.99
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	62.92
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	62.92
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	61.09
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	61.09
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	60.32
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	60.32
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	60.03
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	53.94
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	53.94
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	53.08
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	53.08
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	49.93
RAM-MiniTid	1	d3-6	PYC_MOUSE	Pyruvate car	44.7
SYN-MiniTid	2	d3-6	PYC_MOUSE	Pyruvate car	55.04
SYN-MiniTid	2	d3-6	PYC_MOUSE	Pyruvate car	55.04
SYN-MiniTid	2	d3-6	PYC_MOUSE	Pyruvate car	54.92
SYN-MiniTid	2	d3-6	PYC_MOUSE	Pyruvate car	54.92
SYN-MiniTid	2	d3-6	PYC_MOUSE	Pyruvate car	54.92

SYN-MiniTid	2	d3-6	PYC_MOUSE	Pyruvate car	43.67
SYN-MiniTid	2	d3-6	PYC_MOUSE	Pyruvate car	43.67
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	115.3
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	115.3
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	115.3
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	115.3
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	79.32
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	79.32
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	79.32
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	79.32
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	69.05
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	69.05
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	69.05
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	69.05
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	66.54
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	66.54
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	66.54
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	66.54
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	64.97
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	64.97
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	64.97
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	64.97
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.72
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.72
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.72
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.72
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.34
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.34
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.34
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.34
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.29
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.29
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.29
SYN-MiniTid-Tau	3	d3-6	PYC_MOUSE	Pyruvate car	60.29
SYN-MiniTid-Tau	4	d3-6	PYC_MOUSE	Pyruvate car	44.3
SYN-MiniTid-Tau	4	d3-6	PYC_MOUSE	Pyruvate car	44.3
SYN-MiniTid-Tau	5	d3-6	PYC_MOUSE	Pyruvate car	87.29
SYN-MiniTid-Tau	5	d3-6	PYC_MOUSE	Pyruvate car	82.42
SYN-MiniTid-Tau	5	d3-6	PYC_MOUSE	Pyruvate car	51.94
SYN-MiniTid-Tau	7	d3-6	PYC_MOUSE	Pyruvate car	82.11
SYN-MiniTid-Tau	7	d3-6	PYC_MOUSE	Pyruvate car	76.95
SYN-MiniTid-Tau	8	d3-6	RBP2_MOUSE	E3 SUMO-pr	38.21
SYN-MiniTid-Tau	7	d3-6	RL13_MOUSE	60S ribosom	39.24
SYN-MiniTid-Tau	7	d3-6	RL13_MOUSE	60S ribosom	38.24
SYN-MiniTid-Tau	7	d3-6	RL13_MOUSE	60S ribosom	38.24
SYN-MiniTid-Tau	6	d3-6	RL21_MOUSE	60S ribosom	39.78
SYN-MiniTid-Tau	5	d3-6	RL4_MOUSE	60S ribosom	37.11
SYN-MiniTid-Tau	8	d3-6	RRNAD_MOUSE	Protein RRN	38.41

SYN-MiniTid-Tau	4	d3-6	SHAN2_MOUSE	SH3 and mul	60.36
SYN-MiniTid-Tau	4	d3-6	SHAN2_MOUSE	SH3 and mul	60.36
SYN-MiniTid-Tau	4	d3-6	SHAN2_MOUSE	SH3 and mul	60.36
SYN-MiniTid-Tau	4	d3-6	SHAN2_MOUSE	SH3 and mul	60.36
SYN-MiniTid-Tau	4	d3-6	SHAN2_MOUSE	SH3 and mul	60.36
SYN-MiniTid-Tau	4	d3-6	SHAN2_MOUSE	SH3 and mul	60.36
SYN-MiniTid-Tau	5	d3-6	SLIK4_MOUSE	SLIT and NT	37.97
SYN-MiniTid-Tau	3	d3-6	SMCA2_MOUSE	Probable glol	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA2_MOUSE	Probable glol	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA2_MOUSE	Probable glol	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA2_MOUSE	Probable glol	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	3	d3-6	SMCA4_MOUSE	Transcriptior	41.31
SYN-MiniTid-Tau	8	d3-6	SYNE1_MOUSE	Nesprin-1 Ge	37.18
SYN-MiniTid-Tau	4	d3-6	SYNRG_MOUSE	Synergin gar	75.92
SYN-MiniTid-Tau	4	d3-6	SYNRG_MOUSE	Synergin gar	75.92
SYN-MiniTid-Tau	7	d3-6	SYT6_MOUSE	Synaptotagm	42.82
SYN-MiniTid-Tau	7	d3-6	SYT6_MOUSE	Synaptotagm	37.97
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	81.24
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	81.24
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	81.24
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	81.24
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	69.5
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	69.5
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	69.5
SYN-MiniTid-Tau	4	d3-6	SYUA_MOUSE	Alpha-synucl	69.5
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	87.43
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	87.43
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	81.24
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	81.24
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	81.24
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	81.24
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	69.5
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	69.5
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	69.5
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	69.5
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	69.5
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	46.22
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	46.22
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	46.22
SYN-MiniTid-Tau	4	d3-6	SYUB_MOUSE	Beta-synucle	46.22
SYN-MiniTid-Tau	4	d3-6	TAU_MOUSE	Microtubule-a	55.7

SYN-MiniTid-Tau	6	d3-6	TBX4_MOUSE	T-box transc	37.44
SYN-MiniTid-Tau	5	d3-6	TF3C1_MOUSE	General trans	37.84
SYN-MiniTid-Tau	7	d3-6	TTC16_MOUSE	Tetratricopep	41.75
SYN-MiniTid-Tau	7	d3-6	TTLL1_MOUSE	Probable tubu	43.33
SYN-MiniTid-Tau	6	d3-6	UN45B_MOUSE	Protein unc-4	37.25
SYN-MiniTid-Tau	6	d3-6	WDR87_MOUSE	WD repeat-c	38.24
SYN-MiniTid-Tau	5	d3-6	ZC3H6_MOUSE	Zinc finger C	40.85

ɔnsolidation (RRc) spatial memory phase

ɒtide Sequer	Peptide Mod	Position of peptide modification	Unique Proteins
LAEVASGEK	Biotin (K)	0.0000000001.0	1433F_MOUSE
LAEVASGEK	Biotin (K)	0.0000000001.0	ACBP_MOUSE
LAEVASGEK	Biotin (K)	0.0000000001.0	AFF2_MOUSE
LAEVASGEK	Biotin (K)	0.0000000001.0	ARHG2_MOUSE
AAEEVKR	Biotin (K)	0.0000010.0	ASGL1_MOUSE
AAEEVKR	Biotin (K)	0.0000010.0	AT2B4_MOUSE
QITSTKPKR	Biotin (K)	0.000000010.0	BASP1_MOUSE
QITSTKPKR	Biotin (K)	0.000000010.0	BIN1_MOUSE
AAVASVTPE	Biotin (K)	0.00000000010000000000.0	BSN_MOUSE
AAVASVTPE	Biotin (K)	0.00000000010000000000.0	CAMP1_MOUSE
AAVASVTPE	Biotin (K)	0.00000000010000000000.0	CCDC7_MOUSE
AAVASVTPE	Biotin (K)	0.00000000010000000000.0	CH60_MOUSE
KTPHCFLTC	Biotin (K)	0.00000000000001.0	CISY_MOUSE
GEIKSFRSK	Biotin (K)	0.000000001.0	CLAP2_MOUSE
AGTEEEGTC	Biotin (K)	0.000000000100000000000000.0	CLH2_MOUSE
AGTEEEGTC	Biotin (K)	0.000000000100000000000000.0	CMAH_MOUSE
IAKPVSLLEK	Biotin (K)	0.0010000000.0	COR1A_MOUSE
IAKPVSLLEK	Biotin (K)	0.0010000000.0	COR2B_MOUSE
IAKPVSLLEK	Biotin (K)	0.0010000000.0	DYH8_MOUSE
IAKPVSLLEK	Biotin (K)	0.0010000000.0	ESRP2_MOUSE
KAKSGVKR	Biotin (K)	0.00000010.0	FSIP2_MOUSE
GKPKSKPKK	Biotin (K)	0.0001000000000.0	G3P_MOUSE
KLLKSEGKT	Biotin (K)	0.00010000000.0	GLSK_MOUSE
VKDGKTLNI	Biotin (K)	0.000010000000000000.0	GNAI1_MOUSE
VKDGKTLNI	Biotin (K)	0.000010000000000000.0	GNAI2_MOUSE
VKDGKTLNI	Biotin (K)	0.000010000000000000.0	GNAL_MOUSE
VKDGKTLNI	Biotin (K)	0.000010000000000000.0	GNAO_MOUSE
LLTAAARLF	Biotin (K)	0.000000000001.0	GRM8_MOUSE
AGGDAADG	Biotin (K)	0.00000000000000010000000000000.0	H10_MOUSE
AGGDAADG	Biotin (K)	0.00000000000000010000000000000.0	H13_MOUSE
LAKTSR	Biotin (K)	0.001000.0	HBA_MOUSE
YILYKSKSRI	Biotin (K)	0.00000010000.0	HEXD_MOUSE
LEEEMRK	Biotin (K)	0.0000001.0	HFE_MOUSE
RLKEELAQ	Biotin (K)	0.00100000.0	HS74L_MOUSE
KGKGELLLK	Biotin (K)	0.001000000.0	HSDL1_MOUSE
KGKGELLLK	Biotin (K)	0.001000000.0	HXK1_MOUSE
SSQLFSKPE	Biotin (K)	0.000000000001.0	ICAM1_MOUSE
SSQLFSKPE	Biotin (K)	0.000000000001.0	KCC2D_MOUSE
VGIVQTKSIF	Biotin (K)	0.0000001000.0	KIF5C_MOUSE
GALQNIIPAS	Biotin (K)	0.0000000000000010.0	KINH_MOUSE
FKKCVQSNI	2 Biotin (K)	0.01100000000000000.0	LYAM1_MOUSE
FKKCVQSNI	2 Biotin (K)	0.01100000000000000.0	MACF1_MOUSE
KSTIVK	Biotin (K)	0.000001.0	MAP4_MOUSE
KSTIVK	Biotin (K)	0.000001.0	MAP6_MOUSE

KSTIVK	Biotin (K)	0.000001.0	MCCA_MOUSE
KSTIVK	Biotin (K)	0.000001.0	MCF2_MOUSE
KSTIVK	Biotin (K)	0.000001.0	MINK1_MOUSE
KSTIVK	Biotin (K)	0.000001.0	MRO2A_MOUSE
KSTIVK	Biotin (K)	0.000001.0	MTAP2_MOUSE
KSTIVK	Biotin (K)	0.000001.0	MY18A_MOUSE
KSTIVK	Biotin (K)	0.000001.0	NBEL2_MOUSE
KSTIVK	Biotin (K)	0.000001.0	NDUB6_MOUSE
KSTIVK	Biotin (K)	0.000001.0	NEUG_MOUSE
KSTIVK	Biotin (K)	0.000001.0	NFM_MOUSE
KSVTAPKFI	Biotin (K)	0.000000100.0	NHRF3_MOUSE
KSVTAPKFI	Biotin (K)	0.000000100.0	NU4M_MOUSE
KSVTAPKFI	Biotin (K)	0.000000100.0	PCCA_MOUSE
KKAAKPKK	Biotin (K)	0.00000001.0	PDIA3_MOUSE
KKAAKPKK	Biotin (K)	0.00000001.0	PRAM_MOUSE
KVSKSPKK	Biotin (K)	0.00000001.0	PRG4_MOUSE
VNFKLLGHC	Biotin (K); Ca	0.0000000020000000000000000000001000000000(	PYC_MOUSE
VNFKLLGHC	Biotin (K); Ca	0.0000000020000000000000000000001000000000(	RBP2_MOUSE
LLVEKYRK	Biotin (K)	0.00000001.0	RL13_MOUSE
QLKQVLELC	Biotin (K)	0.0010000000.0	RL21_MOUSE
KKIQLVMK	Biotin (K)	0.00000001.0	RL4_MOUSE
SGREIYLPIF	Biotin (K)	0.00000000000001.0	RRNAD_MOUSE
KTHPQYSR	Biotin (K)	0.10000000.0	SHAN2_MOUSE
KTHPQYSR	Biotin (K)	0.10000000.0	SLIK4_MOUSE
KTHPQYSR	Biotin (K)	0.10000000.0	SMCA2_MOUSE
KTHPQYSR	Biotin (K)	0.10000000.0	SMCA4_MOUSE
LQKAQEEAL	Biotin (K)	0.000000000001000.0	SYNE1_MOUSE
LQKAQEEAL	Biotin (K)	0.000000000001000.0	SYNRG_MOUSE
LQKAQEEAL	Biotin (K)	0.000000000001000.0	SYT6_MOUSE
LQKAQEEAL	Biotin (K)	0.000000000001000.0	SYUA_MOUSE
INKMLTINPA	Biotin (K)	0.001000000000.0	SYUB_MOUSE
ELPKLEKR	Biotin (K)	0.00010000.0	TAU_MOUSE
ELPKLEKR	Biotin (K)	0.00010000.0	TBX4_MOUSE
ELPKLEKR	Biotin (K)	0.00010000.0	TF3C1_MOUSE
CRDNYTDL\	Biotin (K)	0.00000000000001.0	TTC16_MOUSE
CRDNYTDL\	Biotin (K)	0.00000000000001.0	TTLL1_MOUSE
HKPHIDK	Biotin (K)	0.0000001.0	UN45B_MOUSE
KPTSTKPSS	Biotin (K)	0.000001000000000000000000000.0	WDR87_MOUSE
DQGAVLLG	Biotin (K)	0.0000000000100000000000.0	ZC3H6_MOUSE
DQGAVLLG	Biotin (K)	0.0000000000100000000000.0	
GHDSVFVAI	Biotin (K)	0.0000000000100000000000.0	
GHDSVFVAI	Biotin (K)	0.0000000000100000000000.0	
DQGAVLLG	Biotin (K)	0.0000000000100000000000.0	
DQGAVLLG	Biotin (K)	0.0000000000100000000000.0	
PIIPVPLKGC	Biotin (K)	0.0000000100000000000.0	
PIIPVPLKGC	Biotin (K)	0.0000000100000000000.0	
KMEHTIK	Biotin (K)	0.1000000.0	
KMEHTIK	Biotin (K)	0.1000000.0	

IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
LKELLKYSK	Biotin (K)	0.000000001.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
KDTEAGIAG	Biotin (K)	0.000000000001.0
KDTEAGIAG	Biotin (K)	0.000000000001.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
TPGTPKSGI	Biotin (K)	0.000001000000000.0
TPGTPKSGI	Biotin (K)	0.000001000000000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
EASPPTSAD	Biotin (K)	0.000000000100.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
LILKPAIK	Biotin (K)	0.00010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
LSAEPPAPK	Biotin (K)	0.000000000001.0
SIILLGSSGS	Biotin (K)	0.000000000001.0
SIILLGSSGS	Biotin (K)	0.000000000001.0
LWSEKLFEG	Biotin (K)	0.0000100000000000.0
IVSSKPRIFP	Biotin (K)	0.000010000000000000000000000.0
IVSSKPRIFP	Biotin (K)	0.000010000000000000000000000.0
IVSSKPRIFP	Biotin (K)	0.000010000000000000000000000.0
IVSSKPRIFP	Biotin (K)	0.000010000000000000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0

KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KPKDVPDKH	2 Biotin (K)	0.0010000100.0
KAVKKQVDI	Biotin (K)	0.0001000000.0
KAVKKQVDI	Biotin (K)	0.0001000000.0
IMASQNHLN	Biotin (K)	0.0000000000000001.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K); Ox	0.1000030000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KKLNPKK	Biotin (K)	0.0100000.0
KKLNPKK	Biotin (K)	0.0100000.0
KKLNPKK	Biotin (K)	0.0100000.0
PPRKFSQPI	Biotin (K)	0.0000000000000010.0
KTTLKPQKF	Biotin (K)	0.000000000000000000001.0
GQPLCVLSA	Biotin (K); Ca	0.000020000010000000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000010000000300000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000010000000300000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
SAMKMETV	Biotin (K)	0.000100000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000300000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0

GQPLCVLS/	Biotin (K); Ca	0.000020000010000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.0000200000100000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.0000200000100000000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.1000000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
LYKNGSLR	Biotin (K)	0.00100000.0
KKEKAR	Biotin (K)	0.000100.0
KKEKAR	Biotin (K)	0.000100.0
KKEKAR	Biotin (K)	0.000100.0
KGKILAKR	Biotin (K)	0.00100000.0
KKPAVGKK	Biotin (K)	0.01000000.0
VKPKKQHEI	Biotin (K)	0.0100000000.0

IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
CLLVFVLRR	Biotin (K)	0.0000000000000001.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
IKDDAEVER	Biotin (K)	0.010000000.0
QLWEGQAA	Biotin (K)	0.000000000100000.0
GISTDKPSE	Biotin (K)	0.00000000000000000000100000.0
GISTDKPSE	Biotin (K)	0.00000000000000000000100000.0
AEVKKSFKE	2 Biotin (K)	0.0001100000000.0
AEVKKSFKE	2 Biotin (K)	0.0001100000000.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
IPAKTPPAPI	Biotin (K)	0.0001000000.0

QLVSFQKLK	Biotin (K)	0.00000000100.0
RSKCLQPR	Biotin (K)	0.00100000.0
KPKLTPSKV	Biotin (K)	0.0000000100000.0
AGKVKWVTK	2 Biotin (K)	0.0010100000000.0
QITSHLLDM	Biotin (K)	0.00000000000001.0
SELTKDEKK	Biotin (K)	0.000000001.0
GLPKKIKR	Biotin (K)	0.00001000.0

Table 20 **GO for tau interactome from retrieval-reconsolidation (RRc) spatial me**

Biological Process			
#term ID	**term description**	**observed g**	**backgroun**
GO:0007	**G protein-coupled receptor signaling p**	**2***	**5**
	***included Gnas in Fig 3.4D for presentation purposes (see ad**		
GO:0070	***CRD-mediated mRNA stabilization***	***2***	***5***
GO:0060	Negative regulation of gene silencing	4	30
GO:0031	Positive regulation of microtubule polym	3	31
GO:0010	Positive regulation of sodium ion transp	3	41
GO:0090	Positive regulation of canonical wnt sign	4	98
GO:0031	Protein-containing complex localization	6	195
GO:1902	Regulation of chromatin organization	6	209
GO:0070	Regulation of microtubule cytoskeleton	5	202
GO:0010	Negative regulation of organelle organi	7	388
GO:1903	Regulation of cellular protein localizatio	9	576
GO:0010	Positive regulation of organelle organiz	9	606
GO:0000	Microtubule cytoskeleton organization	7	484
GO:0051	Positive regulation of cellular componer	13	1236
GO:0007	Cytoskeleton organization	11	1064
GO:0050	Nervous system process	11	1066
GO:0032	Regulation of protein localization	10	978
GO:0060	Regulation of cellular localization	11	1083
GO:0048	Chemical homeostasis	11	1124
GO:0033	Regulation of organelle organization	12	1258
GO:0003	System process	15	1578
GO:0007	Nervous system development	17	2358
GO:0051	Cellular localization	15	2115
GO:0022	Cellular component assembly	14	1983
GO:0044	Cellular component biogenesis	15	2201
GO:0051	Regulation of cellular component organ	16	2438
GO:0006	Organelle organization	19	3066
GO:0065	Regulation of biological quality	23	3822
GO:0048	System development	23	4350
GO:0048	Positive regulation of biological process	30	5869
GO:0048	Positive regulation of cellular process	27	5407
GO:0071	Cellular component organization or bio	24	4954
GO:0009	Cellular process	50	13330
GO:0065	Biological regulation	40	10591
GO:0050	Regulation of biological process	37	9973
GO:0050	Regulation of cellular process	36	9541

emory phase

				Molecular Fu
strength	**false disco**	**matching p**	**matching p**	**#term ID**
2.24	**0.0425**	**10090.ENS**	**Gnat1,Gna**	**GO:003168**
jacent Mol Function GO table)				GO:000801
2.24	***0.0425***	***10090.ENS***	***Hnrnpu,Sy***	GO:001563
1.76	0.0071	10090.ENS	Hist1h1c,Pp	GO:000467
1.62	0.0354	10090.ENS	Map1b,Map	GO:001630
1.5	0.0477	10090.ENS	Gnas,Wnk2	GO:000809
1.25	0.0402	10090.ENS	Csnk1g1,As	GO:001677
1.12	0.0124	10090.ENS	Ap2m1,Exo	GO:003563
1.09	0.0127	10090.ENS	Rps6ka4,H	GO:001990
1.03	0.0425	10090.ENS	Hnrnpu,Ma	GO:003255
0.89	0.0223	10090.ENS	Hist1h1c,H	GO:000552
0.83	0.0124	10090.ENS	Ap2m1,Thc	GO:000016
0.81	0.0127	10090.ENS	Rps6ka4,H	GO:004487
0.8	0.0443	10090.ENS	Ttll4,Aspm,	GO:009736
0.66	0.0092	10090.ENS	Ddx56,Ap2	GO:004316
0.65	0.0223	10090.ENS	Ttll4,Aspm,	GO:190136
0.65	0.0223	10090.ENS	Gnat1,Pde6	GO:009715
0.65	0.0375	10090.ENS	Ap2m1,Thc	GO:000382
0.64	0.0223	10090.ENS	Ap2m1,Thc	GO:000551
0.63	0.0262	10090.ENS	Atp2b1,Pde	GO:004316
0.62	0.0223	10090.ENS	Rps6ka4,H	GO:000548
0.61	0.0071	10090.ENS	Gnat1,Atp2b1,Pde6a,Pp	
0.49	0.0134	10090.ENS	Ddx56,Gnat1,Atp2b1,Ze	
0.49	0.0341	10090.ENS	Ap2m1,Pacs1,Lin7c,Exo	
0.48	0.0433	10090.ENS	Acot13,Ap2m1,Hist1h1c	
0.47	0.0411	10090.ENS	Ddx56,Acot13,Ap2m1,H	
0.45	0.0375	10090.ENS	Ddx56,Ap2m1,Rps6ka4	
0.43	0.0223	10090.ENS	Ap2m1,Rps6ka4,Fundc	
0.42	0.0092	10090.ENS	Acot13,Ap2m1,Atp2b1,P	
0.36	0.0224	10090.ENS	Ddx56,Gnat1,Atp2b1,Ze	
0.34	0.0071	10090.ENS	Ddx56,Ap2m1,Atp2b1,Z	
0.33	0.0134	10090.ENS	Ddx56,Ap2m1,Zeb1,Rp	
0.32	0.0411	10090.ENS	Ddx56,Acot13,Ap2m1,R	
0.21	3.28E-06	10090.ENS	Ddx56,Acot13,Ap2m1,G	
0.21	0.0125	10090.ENS	Ddx56,Acot13,Ap2m1,G	
0.21	0.0375	10090.ENS	Ddx56,Acot13,Ap2m1,G	
0.21	0.0375	10090.ENS	Ddx56,Ap2m1,Gnat1,At	

unction				
term description	observed g	backgroun	strength	false disco
G-protein beta/gamma-subunit complex b	**3**	**25**	**1.71**	**0.0047**
Microtubule binding	5	247	0.94	0.0327
Tubulin binding	7	352	0.93	0.0026
Protein serine/threonine kinase activity	8	432	0.9	0.0012
Kinase activity	10	714	0.78	0.00096
Cytoskeletal protein binding	13	947	0.77	6.66E-05
Phosphotransferase activity, alcohol group	9	659	0.77	0.0027
Purine ribonucleoside triphosphate binding	18	1704	0.66	3.83E-05
Protein domain specific binding	8	778	0.65	0.0452
Purine ribonucleotide binding	18	1773	0.64	4.68E-05
ATP binding	14	1393	0.64	0.00054
Nucleotide binding	19	2021	0.61	4.68E-05
Protein-containing complex binding	13	1411	0.6	0.0023
Carbohydrate derivative binding	19	2089	0.59	4.68E-05
Anion binding	20	2678	0.51	0.00026
Heterocyclic compound binding	27	4771	0.39	0.00027
Organic cyclic compound binding	27	4858	0.38	0.00036
Catalytic activity	27	5224	0.35	0.0011
Protein binding	31	6764	0.3	0.0014
Ion binding	25	5439	0.3	0.0179
Binding	46	11199	0.25	7.47E-06

)p3ca,Gnat2,Gnas,Ank3,Stk40,Mapt,Trpm7,Tpm1,Dctn1,Kalrn,Synj1,Tpm3
eb1,Ppp3ca,Gnat2,Aspm,Igfals,Map1b,Ncor1,Mark4,Ank3,Mapt,Dctn1,Kalrn,Synj1,Phf8
oc3,Thoc5,Hnrnpu,Ppp3ca,Aspm,Rab11fip2,Map1b,Ank3,Mapt,Dctn1,Kalrn,Synj1
c,Hist1h1e,Aspm,Fam161a,Map1b,Ncor1,Ank3,Mapt,Trpm7,Tpm1,Dctn1,Synj1
list1h1c,Hist1h1e,Aspm,Fam161a,Map1b,Ncor1,Ank3,Mapt,Trpm7,Tpm1,Dctn1,Synj1
,Hist1h1c,Hnrnpu,Ppp3ca,Hist1h1e,Map1b,Ncor1,Mark4,Mapt,Tpm1,Dctn1,Kalrn,Synj1,Phf
2,Ttll4,Hist1h1c,Hnrnpu,Hist1h1e,Aspm,Fam161a,Map1b,Ncor1,Mark4,Ank3,Mapt,Trpm7,Tp
Pde6a,Lin7c,Hnrnpu,Ppp3ca,Gnat2,Aspm,Rab11fip2,Syncrip,Map1b,Ncor1,Gnas,Wnk2,Ank
eb1,Pde6a,Thoc5,Hnrnpu,Ppp3ca,Gnat2,Aspm,Igfals,Map1b,Ncor1,Gnas,Mark4,Ank3,Stk40
Zeb1,Rps6ka4,Csnk1g1,Thoc5,Hist1h1c,Hnrnpu,Ppp3ca,Hist1h1e,Aspm,Rab11fip2,Fam161
s6ka4,Csnk1g1,Thoc5,Hist1h1c,Hnrnpu,Ppp3ca,Hist1h1e,Aspm,Rab11fip2,Fam161a,Map1
Rps6ka4,Fundc2,Ttll4,Hist1h1c,Hnrnpu,Hist1h1e,Aspm,Igfals,Fam161a,Map1b,Ncor1,Mark4
Gnat1,Alox12e,Atp2b1,Zeb1,Pde6a,Pacs1,Rps6ka4,Stip1,Lin7c,Fundc2,Csnk1g1,Mvk,Ttll4,E
Gnat1,Atp2b1,Zeb1,Pde6a,Pacs1,Rps6ka4,Lin7c,Csnk1g1,Mvk,Thoc5,Hist1h1c,Hnrnpu,Ppp
Gnat1,Atp2b1,Zeb1,Pde6a,Rps6ka4,Csnk1g1,Mvk,Thoc5,Hist1h1c,Hnrnpu,Ppp3ca,Gnat2,Hi
p2b1,Zeb1,Pde6a,Rps6ka4,Csnk1g1,Mvk,Thoc5,Hist1h1c,Hnrnpu,Ppp3ca,Gnat2,Hist1h1e,

		Subcellular Compartments		
matching p	matching p	#term ID	term description	observed g
10090.ENS	Gnat1,Gna	GOCC:00	CRD-mediated mRNA stability complex	2
10090.ENS	Fam161a,M	GOCC:00	Clathrin coat of coated pit	2
10090.ENS	Ttll4,Fam16	GOCC:00	Varicosity	2
10090.ENS	Rps6ka4,C	GOCC:00	Heterotrimeric g-protein complex	3
10090.ENS	Rps6ka4,C	GOCC:00	9+0 non-motile cilium	6
10090.ENS	Lin7c,Ttll4,I	GOCC:00	Photoreceptor outer segment	4
10090.ENS	Rps6ka4,C	GOCC:00	Photoreceptor inner segment	3
10090.ENS	Ddx56,Gna	GOCC:00	Main axon	4
10090.ENS	Ap2m1,Atp	GOCC:00	Photoreceptor cell cilium	5
10090.ENS	Ddx56,Gna	GOCC:00	Mitotic spindle	5
10090.ENS	Ddx56,Atp2	GOCC:00	Cytoplasmic side of plasma membrane	5
10090.ENS	Ddx56,Gna	GOCC:00	Microtubule	6
10090.ENS	Gnat1,Hist1	GOCC:00	Polymeric cytoskeletal fiber	8
10090.ENS	Ddx56,Gna	GOCC:00	Supramolecular fiber	9
10090.ENS	Ddx56,Gna	GOCC:00	Cilium	8
10090.ENS	Ddx56,Gna	GOCC:00	Neuron projection	15
10090.ENS	Ddx56,Gna	GOCC:00	Cell body	7
10090.ENS	Ddx56,Aco	GOCC:00	Presynapse	6
10090.ENS	Ap2m1,Gna	GOCC:00	Somatodendritic compartment	8
10090.ENS	Ddx56,Gna	GOCC:00	Synapse	11
10090.ENS	Ddx56,Ap2	GOCC:00	Microtubule cytoskeleton	9
		GOCC:00	Plasma membrane region	10
		GOCC:00	Cytoskeleton	13
		GOCC:01	Plasma membrane bounded cell projec	16
		GOCC:00	Cytosol	13
		GOCC:00	Intracellular non-membrane-bounded o	18
8		GOCC:00	Cytoplasm	33
pm1,Dctn1,Tpm3,Phf8		GOCC:00	Protein-containing complex	21
3,Mapt,Trpm7,Tpm1,Dc		GOCC:00	Organelle	38
,Mapt,Tpm1,Dctn1,Kalrn		GOCC:00	Intracellular	43
la,Syncrip,Map1b,Ncor1		GOCC:00	Intracellular organelle	34
lb,Ncor1,Csnk1g3,Gnas		GOCC:01	Cellular anatomical entity	44

,Ank3,Mapt,Trpm7,Tpm1,Dctn1,Kalrn,Synj1,Tpm3,Phf8

Exoc3,Thoc5,Hibch,Hist1h1c,Hnrnpu,Ppp3ca,Gnat2,Hist1h1e,Aspm,Rab11fip2,Igfals,F

3ca,Gnat2,Hist1h1e,Aspm,Rab11fip2,Fam161a,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,

ist1h1e,Aspm,Rab11fip2,Fam161a,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,Mark4,Wnk2,

,Aspm,Rab11fip2,Fam161a,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,Mark4,Wnk2,Ank3,S

					Cellular C
backgroun	strength	false disco	matching p	matching p	#term ID
6	*2.16*	*0.0103*	*10090.ENS*	*Hnrnpu,Syn*	GO:0070
12	***1.86***	***0.0266***	***10090.ENS***	***Ap2m1,Sy***	GO:0043
16	1.73	0.0433	10090.ENS	Map1b,Trp	GO:0030
28	1.67	0.0045	10090.ENS	Gnat1,Gnat	GO:0005
117	1.35	0.00019	10090.ENS	Gnat1,Pde6	GO:0044
79	1.34	0.0043	10090.ENS	Gnat1,Pde6	GO:0001
59	1.34	0.0239	10090.ENS	Gnat1,Gnat	GO:0097
81	1.33	0.0044	10090.ENS	Map1b,Ank	GO:0072
108	1.3	0.0011	10090.ENS	Gnat1,Pde6	GO:0009
124	1.24	0.0017	10090.ENS	Hnrnpu,Asp	GO:0001
142	1.18	0.0025	10090.ENS	Gnat1,Atp2	GO:0097
204	1.1	0.0013	10090.ENS	Hnrnpu,Asp	GO:0036
346	1	0.0005	10090.ENS	Zeb1,Hnrnp	GO:0000
564	0.84	0.0011	10090.ENS	Zeb1,Hnrnp	GO:0030
553	0.8	0.0043	10090.ENS	Gnat1,Pde6	GO:0005
1054	0.79	1.86E-05	10090.ENS	Gnat1,Atp2	GO:0005
493	0.79	0.0103	10090.ENS	Gnat1,Atp2	GO:0099
487	**0.73**	**0.0498**	**10090.ENS**	**Atp2b1,Ex**	GO:0031
711	0.69	0.0142	10090.ENS	Gnat1,Atp2	GO:0099
1032	0.66	0.0025	10090.ENS	Atp2b1,Lin	GO:0098
855	0.66	0.0103	10090.ENS	Ttll4,Hnrnp	GO:0005
1006	0.63	0.0071	10090.ENS	Ap2m1,Atp	GO:0098
1397	0.6	0.0018	10090.ENS	Zeb1,Ttll4,H	GO:0098
1774	0.59	0.0005	10090.ENS	Gnat1,Atp2	GO:0036
1784	0.5	0.0108	10090.ENS	Zeb1,Rps6	GO:0043
2950	0.42	0.0053	10090.ENS	Ddx56,Zeb	GO:0043
6579	0.34	0.00019	10090.ENS	Acot13,Ap2	GO:0098
4654	0.29	0.0498	10090.ENS	Ap2m1,Gna	GO:0030
8565	0.28	0.00019	10090.ENS	Ddx56,Aco	GO:0098
9943	0.27	1.86E-05	10090.ENS	Ddx56,Aco	GO:0015
8073	0.26	0.0018	10090.ENS	Ddx56,Aco	GO:0120
12108	0.2	0.0005	10090.ENS	Ddx56,Aco	GO:0045
					GO:0005
am161a,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,Mark4,Gnl1,V					GO:0005
Mark4,Wnk2,Ank3,Stk40,Mapt,Trpm7,Tpm1,Dctn1,Kalrn,Syn					GO:0071
,Ank3,Stk40,Mapt,Trpm7,Tpm1,Dctn1,Kalrn,Synj1,Pus7,Sgm					GO:0005
tk40,Mapt,Trpm7,Tpm1,Dctn1,Kalrn,Synj1,Pus7,Sgms1,Phf8					GO:0043
					GO:0032
					GO:0043
					GO:0005
					GO:0005
					GO:0043
					GO:0043

GO:0043
GO:0110

omponent					
term description	**observed g**	**backgroun**	**strength**	**false disco**	**matching p**
CRD-mediated mRNA stability	2	6	2.16	0.0088	10090.ENS
Varicosity	2	16	1.73	0.0294	10090.ENS
Clathrin coat of coated pit	2	19	1.66	0.0383	10090.ENS
Heterotrimeric g-protein compl	3	33	1.59	0.0058	10090.ENS
Main axon	4	81	1.33	0.0038	10090.ENS
Photoreceptor inner segment	3	65	1.3	0.0227	10090.ENS
9+0 non-motile cilium	5	122	1.25	0.0013	10090.ENS
Mitotic spindle	5	123	1.24	0.0013	10090.ENS
Cytoplasmic side of plasma me	6	163	1.2	0.0007	10090.ENS
Photoreceptor outer segment	3	84	1.19	0.0383	10090.ENS
Photoreceptor cell cilium	4	114	1.18	0.0093	10090.ENS
Ciliary basal body	4	152	1.06	0.0207	10090.ENS
Spindle pole	4	162	1.03	0.0238	10090.ENS
Midbody	4	179	0.99	0.0309	10090.ENS
Microtubule	7	397	0.88	0.0035	10090.ENS
Spindle	6	352	0.87	0.0095	10090.ENS
Polymeric cytoskeletal fiber	9	631	0.79	0.0015	10090.ENS
Cell leading edge	6	438	0.77	0.0227	10090.ENS
Supramolecular fiber	11	861	0.74	0.00086	10090.ENS
Presynapse	8	636	0.74	0.0071	10090.ENS
Cilium	8	646	0.73	0.0076	10090.ENS
Plasma membrane protein cor	6	503	0.71	0.0383	10090.ENS
Glutamatergic synapse	6	501	0.71	0.0383	10090.ENS
Somatodendritic compartment	12	1080	0.68	0.0009	10090.ENS
Neuron projection	17	1583	0.67	6.18E-05	10090.ENS
Neuronal cell body	8	743	0.67	0.0149	10090.ENS
Postsynapse	8	761	0.66	0.017	10090.ENS
Axon	8	791	0.64	0.0207	10090.ENS
Plasma membrane region	11	1310	0.56	0.0095	10090.ENS
Microtubule cytoskeleton	10	1190	0.56	0.017	10090.ENS
Plasma membrane bounded c	19	2387	0.54	0.00031	10090.ENS
Synapse	12	1492	0.54	0.0078	10090.ENS
Cytoskeleton	14	2060	0.47	0.0096	10090.ENS
Cytosol	20	3573	0.38	0.0055	10090.ENS
Cell periphery	24	4668	0.35	0.0035	10090.ENS
Plasma membrane	22	4531	0.32	0.0115	10090.ENS
Intracellular non-membrane-bo	19	4035	0.31	0.0383	10090.ENS
Protein-containing complex	22	4895	0.29	0.0269	10090.ENS
Organelle	45	11550	0.23	6.18E-05	10090.ENS
Cytoplasm	40	10283	0.23	0.00086	10090.ENS
Intracellular	47	12596	0.21	6.18E-05	10090.ENS
Intracellular organelle	41	11084	0.2	0.0012	10090.ENS
Membrane-bounded organelle	36	10370	0.18	0.0238	10090.ENS

Intracellular membrane-bound	33	9507	0.18	0.05	10090.ENS
Cellular anatomical entity	49	15632	0.13	0.0009	10090.ENS

	KEGG Pathway					
matching p	#term ID	term descr	observed g	backgroun	strength	false disco
Hnrnpu,Syn	mmu04744	Phototransc	3	25	1.71	0.0121
Map1b,Trpm7						
Ap2m1,Synj1						
Gnat1,Gnat2,Gnas						
Map1b,Ank3,Mapt,Trpm7						
Gnat1,Gnat2,Fam161a						
Gnat1,Ttll4,Gnat2,Fam161a,Map1b						
Hnrnpu,Aspm,Fam161a,Ncor1,Dctn1						
Gnat1,Atp2b1,Ppp3ca,Gnat2,Gnas,Mapt						
Gnat1,Gnat2,Map1b						
Gnat1,Gnat2,Fam161a,Map1b						
Ttll4,Fam161a,Mark4,Dctn1						
Hnrnpu,Aspm,Fam161a,Dctn1						
Exoc3,Hnrnpu,Aspm,Mark4						
Ttll4,Hnrnpu,Aspm,Fam161a,Map1b,Mapt,Dctn1						
Acot13,Hnrnpu,Aspm,Fam161a,Ncor1,Dctn1						
Ttll4,Hnrnpu,Aspm,Fam161a,Map1b,Mapt,Tpm1,Dctn1,Tpm3						
Atp2b1,Gnas,Mapt,Trpm7,Tpm1,Dctn1						
Ttll4,Hnrnpu,Ppp3ca,Aspm,Fam161a,Map1b,Ank3,Mapt,Tpm1,Dctn1,Tpm3						
Ap2m1,Atp2b1,Lin7c,Exoc3,Trpm7,Kalrn,Synj1,Dmxl2						
Gnat1,Ttll4,Gnat2,Fam161a,Map1b,Mark4,Mapt,Dctn1						
Ap2m1,Gnat1,Lin7c,Gnat2,Gnas,Synj1						
Ap2m1,Atp2b1,Lin7c,Ppp3ca,Kalrn,Synj1						
Gnat1,Atp2b1,Hnrnpu,Ppp3ca,Map1b,Gnas,Mark4,Ank3,Mapt,Trpm7,Dctn1,Kalrn						
Gnat1,Atp2b1,Exoc3,Hnrnpu,Ppp3ca,Gnat2,Fam161a,Map1b,Gnas,Mark4,Ank3,Ma						
Gnat1,Atp2b1,Map1b,Gnas,Mapt,Trpm7,Dctn1,Kalrn						
Ap2m1,Lin7c,Ppp3ca,Map1b,Ank3,Mapt,Kalrn,Synj1						
Exoc3,Map1b,Ank3,Mapt,Trpm7,Dctn1,Synj1,Tpm3						
Ap2m1,Gnat1,Atp2b1,Lin7c,Exoc3,Aspm,Gnas,Ank3,Mapt,Tpm1,Synj1						
Acot13,Ttll4,Hnrnpu,Aspm,Fam161a,Map1b,Ncor1,Mark4,Mapt,Dctn1						
Gnat1,Atp2b1,Ttll4,Exoc3,Hnrnpu,Ppp3ca,Gnat2,Fam161a,Map1b,Gnas,Mark4,Ank						
Ap2m1,Atp2b1,Lin7c,Exoc3,Ppp3ca,Map1b,Ank3,Mapt,Trpm7,Kalrn,Synj1,Dmxl2						
Acot13,Ttll4,Hnrnpu,Aspm,Fam161a,Map1b,Ncor1,Mark4,Ank3,Mapt,Tpm1,Dctn1,K						
Acot13,Alox12e,Zeb1,Rps6ka4,Stip1,Csnk1g1,Mvk,Ppp3ca,Map1b,Ncor1,Gnas,Mar						
Ap2m1,Gnat1,Alox12e,Atp2b1,Pde6a,Lin7c,Csnk1g1,Exoc3,Ppp3ca,Gnat2,Aspm,R						
Ap2m1,Gnat1,Alox12e,Atp2b1,Pde6a,Lin7c,Csnk1g1,Exoc3,Ppp3ca,Gnat2,Aspm,R						
Ddx56,Acot13,Ttll4,Hist1h1c,Hnrnpu,Ppp3ca,Hist1h1e,Aspm,Fam161a,Map1b,Ncor						
Ap2m1,Gnat1,Stip1,Lin7c,Exoc3,Thoc5,Hist1h1c,Hnrnpu,Ppp3ca,Gnat2,Hist1h1e,Ig						
Ddx56,Acot13,Ap2m1,Gnat1,Atp2b1,Zeb1,Pacs1,Rps6ka4,Stip1,Lin7c,Fundc2,Csnk						
Acot13,Ap2m1,Gnat1,Alox12e,Zeb1,Pacs1,Rps6ka4,Stip1,Lin7c,Fundc2,Csnk1g1,M						
Ddx56,Acot13,Ap2m1,Gnat1,Alox12e,Atp2b1,Zeb1,Pacs1,Rps6ka4,Stip1,Lin7c,Fun						
Ddx56,Acot13,Ap2m1,Atp2b1,Zeb1,Pacs1,Rps6ka4,Stip1,Fundc2,Csnk1g1,Mvk,Ttll						
Ddx56,Acot13,Ap2m1,Atp2b1,Zeb1,Pacs1,Rps6ka4,Stip1,Fundc2,Csnk1g1,Mvk,Exo						

Ddx56,Acot13,Ap2m1,Atp2b1,Zeb1,Pacs1,Rps6ka4,Stip1,Fundc2,Csnk1g1,Mvk,Exo
Ddx56,Acot13,Ap2m1,Gnat1,Alox12e,Atp2b1,Zeb1,Pde6a,Pacs1,Rps6ka4,Stip1,Lin

matching p	**matching proteins in your network (labels)**
10090.ENS	Gnat1,Pde6a,Gnat2

pt,Trpm7,Dctn1,Kalrn,Synj1,Tpm3

3,Mapt,Trpm7,Tpm1,Dctn1,Kalrn,Synj1,Tpm3

alrn,Tpm3
rk4,Wnk2,Stk40,Mapt,Mdh1,Tpm1,Dctn1,Kalrn,Tpm3
ab11fip2,Map1b,Csnk1g3,Gnas,Wnk2,Ank3,Mapt,Trpm7,Tpm1,Dctn1,Synj1,Tpm3,S
ab11fip2,Map1b,Csnk1g3,Gnas,Wnk2,Ank3,Mapt,Trpm7,Tpm1,Synj1,Sgms1
1,Mark4,Ank3,Mapt,Tpm1,Dctn1,Kalrn,Tpm3,Phf8
fals,Syncrip,Map1b,Ncor1,Gnas,Mark4,Mapt,Tpm1,Dctn1,Synj1,Dmxl2
k1g1,Mvk,Ttll4,Exoc3,Thoc5,Hibch,Hist1h1c,Hnrnpu,Ppp3ca,Gnat2,Hist1h1e,Aspm,R
Mvk,Ttll4,Exoc3,Thoc5,Hibch,Hnrnpu,Ppp3ca,Aspm,Rab11fip2,Fam161a,Syncrip,Ma
dc2,Csnk1g1,Mvk,Ttll4,Exoc3,Thoc5,Hibch,Hist1h1c,Hnrnpu,Ppp3ca,Gnat2,Hist1h1
4,Exoc3,Thoc5,Hibch,Hist1h1c,Hnrnpu,Ppp3ca,Hist1h1e,Aspm,Rab11fip2,Fam161a
oc3,Thoc5,Hibch,Hist1h1c,Hnrnpu,Ppp3ca,Hist1h1e,Aspm,Rab11fip2,Syncrip,Ncor1

ɔc3,Thoc5,Hibch,Hist1h1c,Hnrnpu,Ppp3ca,Hist1h1e,Aspm,Rab11fip2,Syncrip,Ncor1
ı7c,Fundc2,Csnk1g1,Mvk,Ttll4,Exoc3,Thoc5,Hibch,Hist1h1c,Hnrnpu,Ppp3ca,Gnat2,H

gms1

ab11fip2,Fam161a,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,Mark4,Ank3,Stk40,Mapt,T
1b,Ncor1,Csnk1g3,Gnas,Mark4,Wnk2,Ank3,Stk40,Mapt,Trpm7,Mdh1,Tpm1,Dctn1,K
,Aspm,Rab11fip2,Fam161a,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,Mark4,Wnk2,Ank
,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,Mark4,Ank3,Stk40,Mapt,Trpm7,Mdh1,Tpm1,D
,Csnk1g3,Gnas,Ank3,Stk40,Mapt,Trpm7,Mdh1,Dctn1,Kalrn,Synj1,Dmxl2,Pus7,Sgms

,Csnk1g3,Gnas,Ank3,Stk40,Mapt,Mdh1,Dctn1,Kalrn,Pus7,Sgms1,Phf8
Hist1h1e,Aspm,Rab11fip2,Igfals,Fam161a,Syncrip,Map1b,Ncor1,Csnk1g3,Gnas,Mar

rpm7,Mdh1,Tpm1,Dctn1,Kalrn,Synj1,Dmxl2,Pus7,Tpm3,Sgms1,Phf8
Kalrn,Synj1,Dmxl2,Tpm3,Sgms1
3,Stk40,Mapt,Trpm7,Mdh1,Tpm1,Dctn1,Kalrn,Synj1,Dmxl2,Pus7,Tpm3,Sgms1,Phf8
ctn1,Kalrn,Dmxl2,Pus7,Tpm3,Sgms1,Phf8
1,Phf8

k4,Wnk2,Ank3,Stk40,Mapt,Trpm7,Mdh1,Tpm1,Dctn1,Kalrn,Synj1,Dmxl2,Pus7,Tpm3,

Sgms1,Phf8

Table 21 **Total peptides list for AAV.RAM-MiniTurboID-tau in the encodi**

n = 12, pep = 526, pro = 75, non-overlapping = 34

rAAV	Sample	Biotin	Protein Accessio	Protein Descr	Peptide Scor
RAM-MiniTid-Tau	1	d1-6	AAK1_MOUSE	AP2-associate	55.86
RAM-MiniTid-Tau	1	d1-6	AAK1_MOUSE	AP2-associate	55.86
RAM-MiniTid-Tau	7	d1-6	AAK1_MOUSE	AP2-associate	59.53
RAM-MiniTid-Tau	8	d1-6	AAK1_MOUSE	AP2-associate	69.17
RAM-MiniTid-Tau	4	d1-6	ABLM2_MOUSE	Actin-binding L	65.44
RAM-MiniTid-Tau	4	d1-6	ABLM2_MOUSE	Actin-binding L	65.44
RAM-MiniTid-Tau	8	d1-6	ADT1_MOUSE	ADP/ATP trans	53.43
RAM-MiniTid-Tau	6	d1-6	ALBU_MOUSE	Albumin OS=C	51.06
RAM-MiniTid-Tau	6	d1-6	ALBU_MOUSE	Albumin OS=C	50.55
RAM-MiniTid-Tau	6	d1-6	ALBU_MOUSE	Albumin OS=F	49.39
RAM-MiniTid-Tau	6	d1-6	ALBU_MOUSE	Albumin OS=F	48.99
RAM-MiniTid-Tau	1	d1-6	ANR35_MOUSE	Ankyrin repeat	40.09
RAM-MiniTid-Tau	1	d1-6	ANR35_MOUSE	Ankyrin repeat	40.09
RAM-MiniTid-Tau	2	d1-6	ANR35_MOUSE	Ankyrin repeat	40.25
RAM-MiniTid-Tau	2	d1-6	ANR35_MOUSE	Ankyrin repeat	40.25
RAM-MiniTid-Tau	5	d1-6	BBS12_MOUSE	Bardet-Biedl sy	24.09
RAM-MiniTid-Tau	8	d1-6	CAMP3_MOUSE	Calmodulin-reg	59.57
RAM-MiniTid-Tau	8	d1-6	CAMP3_MOUSE	Calmodulin-reg	59.57
RAM-MiniTid-Tau	8	d1-6	CAPS1_MOUSE	Calcium-depen	49.89
RAM-MiniTid-Tau	4	d1-6	CAPS1_MOUSE	Calcium-depen	40.63
RAM-MiniTid-Tau	4	d1-6	CCL3_MOUSE	C-C motif chem	22.22
RAM-MiniTid-Tau	7	d1-6	CEND_MOUSE	Cell cycle exit a	71.66
RAM-MiniTid-Tau	7	d1-6	CEND_MOUSE	Cell cycle exit a	71.66
RAM-MiniTid-Tau	8	d1-6	CEND_MOUSE	Cell cycle exit a	64.95
RAM-MiniTid-Tau	10	d1-6	CEND_MOUSE	Cell cycle exit a	51.3
RAM-MiniTid-Tau	8	d1-6	CH10_MOUSE	10 kDa heat sh	51.61
RAM-MiniTid-Tau	8	d1-6	CH10_MOUSE	10 kDa heat sh	51.61
RAM-MiniTid-Tau	1	d1-6	CLAP2_MOUSE	CLIP-associati	77.73
RAM-MiniTid-Tau	1	d1-6	CLAP2_MOUSE	CLIP-associati	77.73
RAM-MiniTid-Tau	10	d1-6	CLAP2_MOUSE	CLIP-associati	72.57
RAM-MiniTid-Tau	7	d1-6	CPLX1_MOUSE	Complexin-1, G	72.59
RAM-MiniTid-Tau	7	d1-6	CPLX1_MOUSE	Complexin-1, G	72.59
RAM-MiniTid-Tau	8	d1-6	CPLX1_MOUSE	Complexin-1, G	51.92
RAM-MiniTid-Tau	8	d1-6	CPLX1_MOUSE	Complexin-1 G	51.92
RAM-MiniTid-Tau	8	d1-6	CPLX1_MOUSE	Complexin-1, G	51.92
RAM-MiniTid-Tau	8	d1-6	CPLX1_MOUSE	Complexin-1, G	51.92
RAM-MiniTid-Tau	7	d1-6	CPLX2_MOUSE	Complexin-2 G	72.59
RAM-MiniTid-Tau	7	d1-6	CPLX2_MOUSE	Complexin-2, G	72.59
RAM-MiniTid-Tau	7	d1-6	CPLX2_MOUSE	Complexin-2, G	72.59
RAM-MiniTid-Tau	7	d1-6	CPLX2_MOUSE	Complexin-2, G	72.59
RAM-MiniTid-Tau	10	d1-6	CPLX2_MOUSE	Complexin-2 G	55.79
RAM-MiniTid-Tau	10	d1-6	CPLX2_MOUSE	Complexin-2, G	55.79
RAM-MiniTid-Tau	10	d1-6	CPLX2_MOUSE	Complexin-2, G	55.79
RAM-MiniTid-Tau	10	d1-6	CPLX2_MOUSE	Complexin-2, G	55.79
RAM-MiniTid-Tau	8	d1-6	DCLK1_MOUSE	Serine/threonin	60.33
RAM-MiniTid-Tau	8	d1-6	DCLK1_MOUSE	Serine/threonin	60.33
RAM-MiniTid-Tau	8	d1-6	DCLK1_MOUSE	Serine/threonin	60.33
RAM-MiniTid-Tau	2	d1-6	DCTN1_MOUSE	Dynactin subur	62.14
RAM-MiniTid-Tau	4	d1-6	DDX31_MOUSE	Probable ATP-(	31.96
RAM-MiniTid-Tau	6	d1-6	DGKI_MOUSE	Diacylglycerol I	34.28
RAM-MiniTid-Tau	6	d1-6	DGKI_MOUSE	Diacylglycerol I	34.28

RAM-MiniTid-Tau	12	d1-6	DMXL2_MOUSE	DmX-like prote	20.01
RAM-MiniTid-Tau	4	d1-6	DPF1_MOUSE	Zinc finger prot	36.8
RAM-MiniTid-Tau	7	d1-6	DPYL2_MOUSE	Dihydropyrimid	45
RAM-MiniTid-Tau	7	d1-6	DPYL2_MOUSE	Dihydropyrimid	45
RAM-MiniTid-Tau	8	d1-6	DPYL2_MOUSE	Dihydropyrimid	53.45
RAM-MiniTid-Tau	8	d1-6	DPYL2_MOUSE	Dihydropyrimid	53.45
RAM-MiniTid-Tau	10	d1-6	DPYL2_MOUSE	Dihydropyrimid	53.3
RAM-MiniTid-Tau	10	d1-6	DPYL2_MOUSE	Dihydropyrimid	53.3
RAM-MiniTid-Tau	4	d1-6	EDIL3_MOUSE	EGF-like repea	29.47
RAM-MiniTid-Tau	1	d1-6	F16B1_MOUSE	Protein FAM16	39.37
RAM-MiniTid-Tau	1	d1-6	F16B1_MOUSE	Protein FAM16	39.37
RAM-MiniTid-Tau	11	d1-6	GLP2R_MOUSE	Glucagon-like p	44.54
RAM-MiniTid-Tau	2	d1-6	GNAT1_MOUSE	Guanine nucleo	53.32
RAM-MiniTid-Tau	1	d1-6	ICAM1_MOUSE	Intercellular adl	44.88
RAM-MiniTid-Tau	1	d1-6	ICAM1_MOUSE	Intercellular adl	44.88
RAM-MiniTid-Tau	5	d1-6	ILRL2_MOUSE	Interleukin-1 re	26.33
RAM-MiniTid-Tau	3	d1-6	KALRN_MOUSE	KalirinGene: KA	42.34
RAM-MiniTid-Tau	3	d1-6	KC1G3_MOUSE	Casein kinase	45.12
RAM-MiniTid-Tau	4	d1-6	LDHA_MOUSE	L-lactate dehyc	20.29
RAM-MiniTid-Tau	4	d1-6	LDHA_MOUSE	L-lactate dehyc	20.29
RAM-MiniTid-Tau	4	d1-6	LDHA_MOUSE	L-lactate dehyc	20.29
RAM-MiniTid-Tau	4	d1-6	LDHA_MOUSE	L-lactate dehyc	20.29
RAM-MiniTid-Tau	4	d1-6	LDHA_MOUSE	L-lactate dehyc	20.29
RAM-MiniTid-Tau	4	d1-6	LDHA_MOUSE	L-lactate dehyc	20.29
RAM-MiniTid-Tau	7	d1-6	LNEBL_MOUSE	LIM zinc-bindin	77.86
RAM-MiniTid-Tau	8	d1-6	LNEBL_MOUSE	LIM zinc-bindin	79.83
RAM-MiniTid-Tau	10	d1-6	LNEBL_MOUSE	LIM zinc-bindin	59.92
RAM-MiniTid-Tau	2	d1-6	MAP1A_MOUSE	Microtubule-as	45.48
RAM-MiniTid-Tau	2	d1-6	MAP1A_MOUSE	Microtubule-as	45.48
RAM-MiniTid-Tau	7	d1-6	MAP1A_MOUSE	Microtubule-as	47.43
RAM-MiniTid-Tau	7	d1-6	MAP1A_MOUSE	Microtubule-as	40.47
RAM-MiniTid-Tau	7	d1-6	MAP1A_MOUSE	Microtubule-as	49.45
RAM-MiniTid-Tau	7	d1-6	MAP1A_MOUSE	Microtubule-as	52.88
RAM-MiniTid-Tau	7	d1-6	MAP1A_MOUSE	Microtubule-as	75.23
RAM-MiniTid-Tau	8	d1-6	MAP1A_MOUSE	Microtubule-as	53.31
RAM-MiniTid-Tau	8	d1-6	MAP1A_MOUSE	Microtubule-as	64.64
RAM-MiniTid-Tau	8	d1-6	MAP1A_MOUSE	Microtubule-as	46.28
RAM-MiniTid-Tau	10	d1-6	MAP1A_MOUSE	Microtubule-as	74.4
RAM-MiniTid-Tau	7	d1-6	MAP1B_MOUSE	Microtubule-as	86.44
RAM-MiniTid-Tau	8	d1-6	MAP1B_MOUSE	Microtubule-as	50.96
RAM-MiniTid-Tau	8	d1-6	MAP1B_MOUSE	Microtubule-as	84.58
RAM-MiniTid-Tau	7	d1-6	MAP4_MOUSE	Microtubule-as	54.21
RAM-MiniTid-Tau	8	d1-6	MAP4_MOUSE	Microtubule-as	57.6
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	48.21
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	34.67
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	110.85
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	64.57
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	50.74
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	76.58
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	48.21
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	34.67
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	110.85
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	64.57
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	50.74
RAM-MiniTid-Tau	1	d1-6	MAP6_MOUSE	Microtubule-as	76.58
RAM-MiniTid-Tau	2	d1-6	MAP6_MOUSE	Microtubule-as	37.9

RAM-MiniTid-Tau	2	d1-6	MAP6_MOUSE	Microtubule-as	66.24
RAM-MiniTid-Tau	2	d1-6	MAP6_MOUSE	Microtubule-as	42.89
RAM-MiniTid-Tau	2	d1-6	MAP6_MOUSE	Microtubule-as	37.9
RAM-MiniTid-Tau	2	d1-6	MAP6_MOUSE	Microtubule-as	66.24
RAM-MiniTid-Tau	2	d1-6	MAP6_MOUSE	Microtubule-as	42.89
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	46.3
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	63.37
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	50.46
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	83.17
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	46.3
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	63.37
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	50.46
RAM-MiniTid-Tau	3	d1-6	MAP6_MOUSE	Microtubule-as	83.17
RAM-MiniTid-Tau	4	d1-6	MAP6_MOUSE	Microtubule-as	43.68
RAM-MiniTid-Tau	4	d1-6	MAP6_MOUSE	Microtubule-as	24.99
RAM-MiniTid-Tau	5	d1-6	MAP6_MOUSE	Microtubule-as	49.04
RAM-MiniTid-Tau	7	d1-6	MAP6_MOUSE	Microtubule-as	48.72
RAM-MiniTid-Tau	7	d1-6	MAP6_MOUSE	Microtubule-as	51.1
RAM-MiniTid-Tau	7	d1-6	MAP6_MOUSE	Microtubule-as	49.4
RAM-MiniTid-Tau	7	d1-6	MAP6_MOUSE	Microtubule-as	41.13
RAM-MiniTid-Tau	7	d1-6	MAP6_MOUSE	Microtubule-as	47.21
RAM-MiniTid-Tau	7	d1-6	MAP6_MOUSE	Microtubule-as	52.78
RAM-MiniTid-Tau	7	d1-6	MAP6_MOUSE	Microtubule-as	39.6
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	52.89
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	51.64
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	53.75
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	70.59
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	100.01
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	79.78
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	43.61
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	49.2
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	62.62
RAM-MiniTid-Tau	8	d1-6	MAP6_MOUSE	Microtubule-as	64.19
RAM-MiniTid-Tau	9	d1-6	MAP6_MOUSE	Microtubule-as	66.16
RAM-MiniTid-Tau	9	d1-6	MAP6_MOUSE	Microtubule-as	46.45
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	56.73
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	64.38
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	90.37
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	71.06
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	58.53
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	73.32
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	55.47
RAM-MiniTid-Tau	10	d1-6	MAP6_MOUSE	Microtubule-as	52.82
RAM-MiniTid-Tau	11	d1-6	MAP6_MOUSE	Microtubule-as	89.47
RAM-MiniTid-Tau	11	d1-6	MAP6_MOUSE	Microtubule-as	57.01
RAM-MiniTid-Tau	11	d1-6	MAP6_MOUSE	Microtubule-as	40.77
RAM-MiniTid-Tau	11	d1-6	MAP6_MOUSE	Microtubule-as	43.19
RAM-MiniTid-Tau	12	d1-6	MAP6_MOUSE	Microtubule-as	65.85
RAM-MiniTid-Tau	12	d1-6	MAP6_MOUSE	Microtubule-as	26.64
RAM-MiniTid-Tau	12	d1-6	MAP6_MOUSE	Microtubule-as	23.05
RAM-MiniTid-Tau	1	d1-6	MCCA_MOUSE	Methylcrotonoy	68.35
RAM-MiniTid-Tau	1	d1-6	MCCA_MOUSE	Methylcrotonoy	43.94
RAM-MiniTid-Tau	1	d1-6	MCCA_MOUSE	Methylcrotonoy	68.35
RAM-MiniTid-Tau	1	d1-6	MCCA_MOUSE	Methylcrotonoy	43.94
RAM-MiniTid-Tau	1	d1-6	MCCA_MOUSE	Methylcrotonoy	68.35
RAM-MiniTid-Tau	2	d1-6	MCCA_MOUSE	Methylcrotonoy	42.3

RAM-MiniTid-Tau	2	d1-6	MCCA_MOUSE	Methylcrotonoy	59.37
RAM-MiniTid-Tau	2	d1-6	MCCA_MOUSE	Methylcrotonoy	59.37
RAM-MiniTid-Tau	3	d1-6	MCCA_MOUSE	Methylcrotonoy	42.21
RAM-MiniTid-Tau	3	d1-6	MCCA_MOUSE	Methylcrotonoy	42.21
RAM-MiniTid-Tau	3	d1-6	MCCA_MOUSE	Methylcrotonoy	55.91
RAM-MiniTid-Tau	3	d1-6	MCCA_MOUSE	Methylcrotonoy	51.63
RAM-MiniTid-Tau	11	d1-6	MCCA_MOUSE	Methylcrotonoy	52.52
RAM-MiniTid-Tau	11	d1-6	MCCA_MOUSE	Methylcrotonoy	52.52
RAM-MiniTid-Tau	1	d1-6	MINK1_MOUSE	Misshapen-like	54.7
RAM-MiniTid-Tau	1	d1-6	MINK1_MOUSE	Misshapen-like	54.7
RAM-MiniTid-Tau	1	d1-6	MINK1_MOUSE	Misshapen-like	54.7
RAM-MiniTid-Tau	1	d1-6	MINK1_MOUSE	Misshapen-like	54.7
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	34.88
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	37.28
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	52.12
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	22.99
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	24.03
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	42.82
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	34.88
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	37.28
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	52.12
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	22.99
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	24.03
RAM-MiniTid-Tau	1	d1-6	MTAP2_MOUSE	Microtubule-as	42.82
RAM-MiniTid-Tau	2	d1-6	MTAP2_MOUSE	Microtubule-as	28.88
RAM-MiniTid-Tau	2	d1-6	MTAP2_MOUSE	Microtubule-as	54.38
RAM-MiniTid-Tau	2	d1-6	MTAP2_MOUSE	Microtubule-as	28.88
RAM-MiniTid-Tau	2	d1-6	MTAP2_MOUSE	Microtubule-as	54.38
RAM-MiniTid-Tau	3	d1-6	MTAP2_MOUSE	Microtubule-as	36.38
RAM-MiniTid-Tau	3	d1-6	MTAP2_MOUSE	Microtubule-as	36.38
RAM-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-as	49.53
RAM-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-as	49.53
RAM-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-as	21.1
RAM-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-as	21.1
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	35.93
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	35.93
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	35.16
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	35.16
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	33.67
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	31.4
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	26.38
RAM-MiniTid-Tau	5	d1-6	MTAP2_MOUSE	Microtubule-as	26.38
RAM-MiniTid-Tau	6	d1-6	MTAP2_MOUSE	Microtubule-as	50.82
RAM-MiniTid-Tau	6	d1-6	MTAP2_MOUSE	Microtubule-as	27.39
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	32.69
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	45.86
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	62.66
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	60.38
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	55.25
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	50.41
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	112.77
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	58.89
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	55.81
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	42.63
RAM-MiniTid-Tau	7	d1-6	MTAP2_MOUSE	Microtubule-as	45.11
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	35.84

RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	38.32
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	24.35
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	72.17
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	42.84
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	119.32
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	70.09
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	52.83
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	81.75
RAM-MiniTid-Tau	8	d1-6	MTAP2_MOUSE	Microtubule-as	81.22
RAM-MiniTid-Tau	9	d1-6	MTAP2_MOUSE	Microtubule-as	29.38
RAM-MiniTid-Tau	9	d1-6	MTAP2_MOUSE	Microtubule-as	45.9
RAM-MiniTid-Tau	9	d1-6	MTAP2_MOUSE	Microtubule-as	70.4
RAM-MiniTid-Tau	9	d1-6	MTAP2_MOUSE	Microtubule-as	49.25
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	36.64
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	22.55
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	58.42
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	46.39
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	44.11
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	52.63
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	49.35
RAM-MiniTid-Tau	10	d1-6	MTAP2_MOUSE	Microtubule-as	53.5
RAM-MiniTid-Tau	12	d1-6	MTAP2_MOUSE	Microtubule-as	56.08
RAM-MiniTid-Tau	12	d1-6	MTAP2_MOUSE	Microtubule-as	56.08
RAM-MiniTid-Tau	12	d1-6	MTAP2_MOUSE	Microtubule-as	21.36
RAM-MiniTid-Tau	12	d1-6	MTAP2_MOUSE	Microtubule-as	21.36
RAM-MiniTid-Tau	12	d1-6	MTAP2_MOUSE	Microtubule-as	20.76
RAM-MiniTid-Tau	12	d1-6	MTAP2_MOUSE	Microtubule-as	20.76
RAM-MiniTid-Tau	5	d1-6	MTG16_MOUSE	Protein CBFA2	24.93
RAM-MiniTid-Tau	3	d1-6	MYCPP_MOUSE	C-myc promote	40.24
RAM-MiniTid-Tau	3	d1-6	MYCPP_MOUSE	C-myc promote	40.24
RAM-MiniTid-Tau	8	d1-6	NEUG_MOUSE	Neurogranin G	76.87
RAM-MiniTid-Tau	8	d1-6	NEUG_MOUSE	Neurogranin G	76.87
RAM-MiniTid-Tau	8	d1-6	NEUG_MOUSE	Neurogranin, G	76.87
RAM-MiniTid-Tau	8	d1-6	NEUG_MOUSE	Neurogranin, G	76.87
RAM-MiniTid-Tau	7	d1-6	NFH_MOUSE	Neurofilament h	52.16
RAM-MiniTid-Tau	7	d1-6	NFH_MOUSE	Neurofilament h	44.54
RAM-MiniTid-Tau	1	d1-6	NFM_MOUSE	Neurofilament m	49.17
RAM-MiniTid-Tau	1	d1-6	NFM_MOUSE	Neurofilament m	49.17
RAM-MiniTid-Tau	1	d1-6	NFM_MOUSE	Neurofilament m	49.17
RAM-MiniTid-Tau	1	d1-6	NFM_MOUSE	Neurofilament m	49.17
RAM-MiniTid-Tau	1	d1-6	NFM_MOUSE	Neurofilament m	49.17
RAM-MiniTid-Tau	1	d1-6	NFM_MOUSE	Neurofilament m	49.17
RAM-MiniTid-Tau	7	d1-6	NFM_MOUSE	Neurofilament m	46.78
RAM-MiniTid-Tau	8	d1-6	NFM_MOUSE	Neurofilament m	47.49
RAM-MiniTid-Tau	8	d1-6	NFM_MOUSE	Neurofilament m	47.49
RAM-MiniTid-Tau	10	d1-6	NFM_MOUSE	Neurofilament m	47.54
RAM-MiniTid-Tau	5	d1-6	NR1I3_MOUSE	Nuclear recept	20.02
RAM-MiniTid-Tau	1	d1-6	PCCA_MOUSE	Propionyl-CoA	75.88
RAM-MiniTid-Tau	1	d1-6	PCCA_MOUSE	Propionyl-CoA	75.88
RAM-MiniTid-Tau	1	d1-6	PCCA_MOUSE	Propionyl-CoA	75.88
RAM-MiniTid-Tau	2	d1-6	PCCA_MOUSE	Propionyl-CoA	74.05
RAM-MiniTid-Tau	2	d1-6	PCCA_MOUSE	Propionyl-CoA	74.81
RAM-MiniTid-Tau	2	d1-6	PCCA_MOUSE	Propionyl-CoA	74.81
RAM-MiniTid-Tau	3	d1-6	PCCA_MOUSE	Propionyl-CoA	51.14
RAM-MiniTid-Tau	3	d1-6	PCCA_MOUSE	Propionyl-CoA	51.14
RAM-MiniTid-Tau	5	d1-6	PCCA_MOUSE	Propionyl-CoA	39.44

RAM-MiniTid-Tau	5	d1-6	PCCA_MOUSE	Propionyl-CoA	39.44
RAM-MiniTid-Tau	5	d1-6	PCCA_MOUSE	Propionyl-CoA	39.44
RAM-MiniTid-Tau	6	d1-6	PCCA_MOUSE	Propionyl-CoA	74.84
RAM-MiniTid-Tau	6	d1-6	PCCA_MOUSE	Propionyl-CoA	74.84
RAM-MiniTid-Tau	8	d1-6	PCCA_MOUSE	Propionyl-CoA	56.07
RAM-MiniTid-Tau	9	d1-6	PCCA_MOUSE	Propionyl-CoA	67.96
RAM-MiniTid-Tau	9	d1-6	PCCA_MOUSE	Propionyl-CoA	39.44
RAM-MiniTid-Tau	9	d1-6	PCCA_MOUSE	Propionyl-CoA	49.81
RAM-MiniTid-Tau	10	d1-6	PCCA_MOUSE	Propionyl-CoA	76.88
RAM-MiniTid-Tau	10	d1-6	PCCA_MOUSE	Propionyl-CoA	46.33
RAM-MiniTid-Tau	10	d1-6	PCCA_MOUSE	Propionyl-CoA	76.88
RAM-MiniTid-Tau	10	d1-6	PCCA_MOUSE	Propionyl-CoA	46.33
RAM-MiniTid-Tau	11	d1-6	PCCA_MOUSE	Propionyl-CoA	63.83
RAM-MiniTid-Tau	12	d1-6	PCCA_MOUSE	Propionyl-CoA	93.47
RAM-MiniTid-Tau	12	d1-6	PCCA_MOUSE	Propionyl-CoA	53.06
RAM-MiniTid-Tau	12	d1-6	PCCA_MOUSE	Propionyl-CoA	53.06
RAM-MiniTid-Tau	1	d1-6	PLAP_MOUSE	Phospholipase	65.67
RAM-MiniTid-Tau	1	d1-6	PLAP_MOUSE	Phospholipase	65.67
RAM-MiniTid-Tau	1	d1-6	PLAP_MOUSE	Phospholipase	65.67
RAM-MiniTid-Tau	1	d1-6	PLAP_MOUSE	Phospholipase	65.67
RAM-MiniTid-Tau	7	d1-6	PLAP_MOUSE	Phospholipase	66.24
RAM-MiniTid-Tau	7	d1-6	PLAP_MOUSE	Phospholipase	66.24
RAM-MiniTid-Tau	8	d1-6	PLAP_MOUSE	Phospholipase	50.3
RAM-MiniTid-Tau	8	d1-6	PLAP_MOUSE	Phospholipase	46.97
RAM-MiniTid-Tau	8	d1-6	PLAP_MOUSE	Phospholipase	50.3
RAM-MiniTid-Tau	8	d1-6	PLAP_MOUSE	Phospholipase	46.97
RAM-MiniTid-Tau	8	d1-6	PLEC_MOUSE	Plectin (Fragm	46.79
RAM-MiniTid-Tau	8	d1-6	PLEC_MOUSE	Plectin, Gene:	46.79
RAM-MiniTid-Tau	8	d1-6	PLEC_MOUSE	Plectin, Gene:	46.79
RAM-MiniTid-Tau	8	d1-6	PP2BA_MOUSE	Serine/threonin	42.11
RAM-MiniTid-Tau	7	d1-6	PP2BA_MOUSE	Serine/threonin	43.77
RAM-MiniTid-Tau	8	d1-6	PPID_MOUSE	Peptidyl-prolyl	43.17
RAM-MiniTid-Tau	8	d1-6	PPID_MOUSE	Peptidyl-prolyl	43.17
RAM-MiniTid-Tau	8	d1-6	PPID_MOUSE	Peptidyl-prolyl	43.17
RAM-MiniTid-Tau	1	d1-6	PYC_MOUSE	Pyruvate carbo	46.12
RAM-MiniTid-Tau	1	d1-6	PYC_MOUSE	Pyruvate carbo	45.7
RAM-MiniTid-Tau	1	d1-6	PYC_MOUSE	Pyruvate carbo	47.53
RAM-MiniTid-Tau	2	d1-6	PYC_MOUSE	Pyruvate carbo	43.56
RAM-MiniTid-Tau	2	d1-6	PYC_MOUSE	Pyruvate carbo	83.53
RAM-MiniTid-Tau	3	d1-6	PYC_MOUSE	Pyruvate carbo	56.74
RAM-MiniTid-Tau	3	d1-6	PYC_MOUSE	Pyruvate carbo	44.63
RAM-MiniTid-Tau	3	d1-6	PYC_MOUSE	Pyruvate carbo	58.51
RAM-MiniTid-Tau	3	d1-6	PYC_MOUSE	Pyruvate carbo	54.25
RAM-MiniTid-Tau	7	d1-6	PYC_MOUSE	Pyruvate carbo	54.13
RAM-MiniTid-Tau	7	d1-6	PYC_MOUSE	Pyruvate carbo	79.33
RAM-MiniTid-Tau	7	d1-6	PYC_MOUSE	Pyruvate carbo	66.5
RAM-MiniTid-Tau	7	d1-6	PYC_MOUSE	Pyruvate carbo	81.14
RAM-MiniTid-Tau	8	d1-6	PYC_MOUSE	Pyruvate carbo	58.6
RAM-MiniTid-Tau	8	d1-6	PYC_MOUSE	Pyruvate carbo	64.63
RAM-MiniTid-Tau	8	d1-6	PYC_MOUSE	Pyruvate carbo	64.98
RAM-MiniTid-Tau	8	d1-6	PYC_MOUSE	Pyruvate carbo	45.42
RAM-MiniTid-Tau	9	d1-6	PYC_MOUSE	Pyruvate carbo	80.13
RAM-MiniTid-Tau	9	d1-6	PYC_MOUSE	Pyruvate carbo	48.75
RAM-MiniTid-Tau	10	d1-6	PYC_MOUSE	Pyruvate carbo	81.69
RAM-MiniTid-Tau	10	d1-6	PYC_MOUSE	Pyruvate carbo	83.4
RAM-MiniTid-Tau	10	d1-6	PYC_MOUSE	Pyruvate carbo	57.23

RAM-MiniTid-Tau	10	d1-6	PYC_MOUSE	Pyruvate carbc	56.09
RAM-MiniTid-Tau	11	d1-6	PYC_MOUSE	Pyruvate carbc	58.78
RAM-MiniTid-Tau	11	d1-6	PYC_MOUSE	Pyruvate carbc	93.58
RAM-MiniTid-Tau	11	d1-6	PYC_MOUSE	Pyruvate carbc	71.51
RAM-MiniTid-Tau	11	d1-6	PYC_MOUSE	Pyruvate carbc	51.18
RAM-MiniTid-Tau	12	d1-6	PYC_MOUSE	Pyruvate carbc	75.57
RAM-MiniTid-Tau	12	d1-6	PYC_MOUSE	Pyruvate carbc	75.57
RAM-MiniTid-Tau	12	d1-6	PYC_MOUSE	Pyruvate carbc	25.2
RAM-MiniTid-Tau	12	d1-6	PYC_MOUSE	Pyruvate carbc	25.2
RAM-MiniTid-Tau	12	d1-6	QCR2_MOUSE	Cytochrome b-	21.57
RAM-MiniTid-Tau	5	d1-6	RT23_MOUSE	28S ribosomal	24.32
RAM-MiniTid-Tau	5	d1-6	RT23_MOUSE	28S ribosomal	20.49
RAM-MiniTid-Tau	7	d1-6	RT31_MOUSE	28S ribosomal	49.75
RAM-MiniTid-Tau	7	d1-6	RT31_MOUSE	28S ribosomal	49.75
RAM-MiniTid-Tau	10	d1-6	RT31_MOUSE	28S ribosomal	56.3
RAM-MiniTid-Tau	10	d1-6	RT31_MOUSE	28S ribosomal	56.3
RAM-MiniTid-Tau	8	d1-6	RTN3_MOUSE	Reticulon-3, Ge	51.98
RAM-MiniTid-Tau	7	d1-6	SH3G2_MOUSE	Endophilin-A1,	45.79
RAM-MiniTid-Tau	7	d1-6	SH3G2_MOUSE	Endophilin-A1,	45.79
RAM-MiniTid-Tau	7	d1-6	SH3G2_MOUSE	Endophilin-A1,	45.79
RAM-MiniTid-Tau	8	d1-6	SH3G2_MOUSE	Endophilin-A1,	42.14
RAM-MiniTid-Tau	8	d1-6	SH3G2_MOUSE	Endophilin-A1,	42.14
RAM-MiniTid-Tau	8	d1-6	SH3G2_MOUSE	Endophilin-A1,	42.14
RAM-MiniTid-Tau	8	d1-6	SHAN2_MOUSE	SH3 and multip	50.82
RAM-MiniTid-Tau	8	d1-6	SHAN2_MOUSE	SH3 and multip	50.82
RAM-MiniTid-Tau	8	d1-6	SHAN2_MOUSE	SH3 and multip	50.82
RAM-MiniTid-Tau	1	d1-6	SPTN1_MOUSE	Spectrin alpha	40.68
RAM-MiniTid-Tau	1	d1-6	SPTN1_MOUSE	Spectrin alpha	40.68
RAM-MiniTid-Tau	7	d1-6	SPTN1_MOUSE	Spectrin alpha	40.82
RAM-MiniTid-Tau	7	d1-6	SPTN1_MOUSE	Spectrin alpha	60.42
RAM-MiniTid-Tau	8	d1-6	SPTN1_MOUSE	Spectrin alpha	56.65
RAM-MiniTid-Tau	7	d1-6	SRC8_MOUSE	Src substrate c	52.82
RAM-MiniTid-Tau	7	d1-6	SRC8_MOUSE	Src substrate c	52.82
RAM-MiniTid-Tau	8	d1-6	SRC8_MOUSE	Src substrate c	57.7
RAM-MiniTid-Tau	8	d1-6	SRC8_MOUSE	Src substrate c	68.51
RAM-MiniTid-Tau	8	d1-6	SRC8_MOUSE	Src substrate c	57.7
RAM-MiniTid-Tau	8	d1-6	SRC8_MOUSE	Src substrate c	68.51
RAM-MiniTid-Tau	8	d1-6	SRCN1_MOUSE	SRC kinase sig	63.52
RAM-MiniTid-Tau	8	d1-6	SRCN1_MOUSE	SRC kinase sig	63.52
RAM-MiniTid-Tau	9	d1-6	SRPK2_MOUSE	SRSF protein k	43.28
RAM-MiniTid-Tau	5	d1-6	SYNRG_MOUSE	Synergin gamn	33.44
RAM-MiniTid-Tau	5	d1-6	SYNRG_MOUSE	Synergin gamn	33.44
RAM-MiniTid-Tau	7	d1-6	SYNRG_MOUSE	Synergin gamn	60.98
RAM-MiniTid-Tau	8	d1-6	SYNRG_MOUSE	Synergin gamn	67.88
RAM-MiniTid-Tau	1	d1-6	SYUA_MOUSE	Alpha-synuclei	73.57
RAM-MiniTid-Tau	1	d1-6	SYUA_MOUSE	Alpha-synuclei	73.57
RAM-MiniTid-Tau	1	d1-6	SYUA_MOUSE	Alpha-synuclei	73.57
RAM-MiniTid-Tau	1	d1-6	SYUA_MOUSE	Alpha-synuclei	73.57
RAM-MiniTid-Tau	2	d1-6	SYUA_MOUSE	Alpha-synuclei	40.68
RAM-MiniTid-Tau	2	d1-6	SYUA_MOUSE	Alpha-synuclei	40.68
RAM-MiniTid-Tau	2	d1-6	SYUA_MOUSE	Alpha-synuclei	40.68
RAM-MiniTid-Tau	2	d1-6	SYUA_MOUSE	Alpha-synuclei	40.68
RAM-MiniTid-Tau	4	d1-6	SYUA_MOUSE	Alpha-synuclei	23.89
RAM-MiniTid-Tau	4	d1-6	SYUA_MOUSE	Alpha-synuclei	23.89
RAM-MiniTid-Tau	4	d1-6	SYUA_MOUSE	Alpha-synuclei	23.89
RAM-MiniTid-Tau	5	d1-6	SYUA_MOUSE	Alpha-synuclei	73.17

RAM-MiniTid-Tau	5	d1-6	SYUA_MOUSE	Alpha-synuclei	73.17
RAM-MiniTid-Tau	5	d1-6	SYUA_MOUSE	Alpha-synuclei	73.17
RAM-MiniTid-Tau	5	d1-6	SYUA_MOUSE	Alpha-synuclei	73.17
RAM-MiniTid-Tau	5	d1-6	SYUA_MOUSE	Alpha-synuclei	73.17
RAM-MiniTid-Tau	5	d1-6	SYUA_MOUSE	Alpha-synuclei	73.17
RAM-MiniTid-Tau	7	d1-6	SYUA_MOUSE	Alpha-synuclei	67.02
RAM-MiniTid-Tau	7	d1-6	SYUA_MOUSE	Alpha-synuclei	63.64
RAM-MiniTid-Tau	7	d1-6	SYUA_MOUSE	Alpha-synuclei	67.02
RAM-MiniTid-Tau	7	d1-6	SYUA_MOUSE	Alpha-synuclei	63.64
RAM-MiniTid-Tau	8	d1-6	SYUA_MOUSE	Alpha-synuclei	67.67
RAM-MiniTid-Tau	8	d1-6	SYUA_MOUSE	Alpha-synuclei	76.86
RAM-MiniTid-Tau	8	d1-6	SYUA_MOUSE	Alpha-synuclei	73.46
RAM-MiniTid-Tau	8	d1-6	SYUA_MOUSE	Alpha-synuclei	67.67
RAM-MiniTid-Tau	8	d1-6	SYUA_MOUSE	Alpha-synuclei	76.86
RAM-MiniTid-Tau	8	d1-6	SYUA_MOUSE	Alpha-synuclei	73.46
RAM-MiniTid-Tau	9	d1-6	SYUA_MOUSE	Alpha-synuclei	53.82
RAM-MiniTid-Tau	9	d1-6	SYUA_MOUSE	Alpha-synuclei	53.82
RAM-MiniTid-Tau	10	d1-6	SYUA_MOUSE	Alpha-synuclei	64.24
RAM-MiniTid-Tau	10	d1-6	SYUA_MOUSE	Alpha-synuclei	82.55
RAM-MiniTid-Tau	10	d1-6	SYUA_MOUSE	Alpha-synuclei	64.24
RAM-MiniTid-Tau	10	d1-6	SYUA_MOUSE	Alpha-synuclei	82.55
RAM-MiniTid-Tau	11	d1-6	SYUA_MOUSE	Alpha-synuclei	57.23
RAM-MiniTid-Tau	11	d1-6	SYUA_MOUSE	Alpha-synuclei	57.23
RAM-MiniTid-Tau	12	d1-6	SYUA_MOUSE	Alpha-synuclei	24.17
RAM-MiniTid-Tau	12	d1-6	SYUA_MOUSE	Alpha-synuclei	24.17
RAM-MiniTid-Tau	12	d1-6	SYUA_MOUSE	Alpha-synuclei	24.17
RAM-MiniTid-Tau	12	d1-6	SYUA_MOUSE	Alpha-synuclei	24.17
RAM-MiniTid-Tau	1	d1-6	SYUB_MOUSE	Beta-synuclein	45.6
RAM-MiniTid-Tau	1	d1-6	SYUB_MOUSE	Beta-synuclein	73.57
RAM-MiniTid-Tau	1	d1-6	SYUB_MOUSE	Beta-synuclein	81.4
RAM-MiniTid-Tau	1	d1-6	SYUB_MOUSE	Beta-synuclein	45.6
RAM-MiniTid-Tau	1	d1-6	SYUB_MOUSE	Beta-synuclein	73.57
RAM-MiniTid-Tau	1	d1-6	SYUB_MOUSE	Beta-synuclein	81.4
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	55.81
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	55.81
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	40.68
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	55.81
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	40.68
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	55.81
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	55.81
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	40.68
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	55.81
RAM-MiniTid-Tau	2	d1-6	SYUB_MOUSE	Beta-synuclein	40.68
RAM-MiniTid-Tau	3	d1-6	SYUB_MOUSE	Beta-synuclein	61.03
RAM-MiniTid-Tau	3	d1-6	SYUB_MOUSE	Beta-synuclein	61.03
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	75.86
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	75.86
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	75.86
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	45.43
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	26.31
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	26.31
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	26.31
RAM-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synuclein	23.89
RAM-MiniTid-Tau	5	d1-6	SYUB_MOUSE	Beta-synuclein	73.17
RAM-MiniTid-Tau	5	d1-6	SYUB_MOUSE	Beta-synuclein	73.17
RAM-MiniTid-Tau	6	d1-6	SYUB_MOUSE	Beta-synuclein	72.99

RAM-MiniTid-Tau	6	d1-6	SYUB_MOUSE	Beta-synuclein	48.2
RAM-MiniTid-Tau	7	d1-6	SYUB_MOUSE	Beta-synuclein	48.43
RAM-MiniTid-Tau	7	d1-6	SYUB_MOUSE	Beta-synuclein	48.52
RAM-MiniTid-Tau	7	d1-6	SYUB_MOUSE	Beta-synuclein	64.88
RAM-MiniTid-Tau	7	d1-6	SYUB_MOUSE	Beta-synuclein	42.21
RAM-MiniTid-Tau	7	d1-6	SYUB_MOUSE	Beta-synuclein	76.15
RAM-MiniTid-Tau	7	d1-6	SYUB_MOUSE	Beta-synuclein	113.82
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	52.68
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	53.54
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	76.83
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	76.86
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	50.06
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	78.26
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	63.59
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	78.52
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	120.24
RAM-MiniTid-Tau	8	d1-6	SYUB_MOUSE	Beta-synuclein	104.68
RAM-MiniTid-Tau	9	d1-6	SYUB_MOUSE	Beta-synuclein	55.08
RAM-MiniTid-Tau	9	d1-6	SYUB_MOUSE	Beta-synuclein	61.98
RAM-MiniTid-Tau	9	d1-6	SYUB_MOUSE	Beta-synuclein	46
RAM-MiniTid-Tau	10	d1-6	SYUB_MOUSE	Beta-synuclein	54.68
RAM-MiniTid-Tau	10	d1-6	SYUB_MOUSE	Beta-synuclein	63.17
RAM-MiniTid-Tau	10	d1-6	SYUB_MOUSE	Beta-synuclein	82.55
RAM-MiniTid-Tau	10	d1-6	SYUB_MOUSE	Beta-synuclein	81.08
RAM-MiniTid-Tau	10	d1-6	SYUB_MOUSE	Beta-synuclein	51.13
RAM-MiniTid-Tau	10	d1-6	SYUB_MOUSE	Beta-synuclein	75.86
RAM-MiniTid-Tau	10	d1-6	SYUB_MOUSE	Beta-synuclein	80.62
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	46.73
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	24
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	46.73
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	46.73
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	46.73
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	24.17
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	24.17
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	24
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	24
RAM-MiniTid-Tau	12	d1-6	SYUB_MOUSE	Beta-synuclein	24
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	45.59
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03

RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	3	d1-6	SYUG_MOUSE	Gamma-synuc	61.03
RAM-MiniTid-Tau	4	d1-6	SYUG_MOUSE	Gamma-synuc	75.86
RAM-MiniTid-Tau	4	d1-6	SYUG_MOUSE	Gamma-synuc	75.86
RAM-MiniTid-Tau	4	d1-6	SYUG_MOUSE	Gamma-synuc	26.31
RAM-MiniTid-Tau	4	d1-6	SYUG_MOUSE	Gamma-synuc	26.31
RAM-MiniTid-Tau	1	d1-6	TAU_MOUSE	Microtubule-as	43.97
RAM-MiniTid-Tau	5	d1-6	TEP1_MOUSE	Telomerase pr	21.55
RAM-MiniTid-Tau	1	d1-6	TF3C1_MOUSE	General transc	42.96
RAM-MiniTid-Tau	1	d1-6	TF3C1_MOUSE	General transc	42.96
RAM-MiniTid-Tau	1	d1-6	TF3C1_MOUSE	General transc	42.96
RAM-MiniTid-Tau	1	d1-6	TF3C1_MOUSE	General transc	42.96
RAM-MiniTid-Tau	4	d1-6	TIGAR_MOUSE	Fructose-2,6-b	20
RAM-MiniTid-Tau	4	d1-6	TIM44_MOUSE	Mitochondrial ir	47.94
RAM-MiniTid-Tau	5	d1-6	TIM44_MOUSE	Mitochondrial ir	55.85
RAM-MiniTid-Tau	5	d1-6	TIM44_MOUSE	Mitochondrial ir	55.85
RAM-MiniTid-Tau	4	d1-6	TITIN_MOUSE	Titin OS=Homc	44.24
RAM-MiniTid-Tau	4	d1-6	TITIN_MOUSE	Titin OS=Mus r	44.24
RAM-MiniTid-Tau	4	d1-6	TITIN_MOUSE	Titin OS=Homc	44.24
RAM-MiniTid-Tau	5	d1-6	TNR21_MOUSE	Tumor necrosi	47.16
RAM-MiniTid-Tau	7	d1-6	TPM3_MOUSE	Tropomyosin a	41.92
RAM-MiniTid-Tau	11	d1-6	TRI29_MOUSE	Tripartite motif-	44.54
RAM-MiniTid-Tau	2	d1-6	VAMP3_MOUSE	Vesicle-associa	51.14
RAM-MiniTid-Tau	2	d1-6	VAMP3_MOUSE	Vesicle-associa	52.11
RAM-MiniTid-Tau	3	d1-6	WRN_MOUSE	Werner syndro	37.25
RAM-MiniTid-Tau	3	d1-6	WRN_MOUSE	Werner syndro	37.25
RAM-MiniTid-Tau	3	d1-6	WRN_MOUSE	Werner syndro	37.25
RAM-MiniTid-Tau	3	d1-6	WRN_MOUSE	Werner syndro	37.25

ıg-consolidation-retrieval-reconsolidation (ECRRc) spatial memory phases [in pı

ptide Sequer	Peptide Mod	Position of peptide modification
VAEDEFDPI	Biotin (K)	0.000000000000000100000000.0
VAEDEFDPI	Biotin (K)	0.000000000000000100000000.0
VAEDEFDPI	Biotin (K)	0.000000000000000100000000.0
VAEDEFDPI	Biotin (K)	0.000000000000000100000000.0
TTWLLLKGI	Biotin (K)	0.0000001000000.0
TTWLLLKGI	Biotin (K)	0.0000001000000.0
LAADVGKG:	Biotin (K)	0.000000100000.0
RHPYFYAPE	Biotin (K)	0.000000000000000000000000000000000000001.0
RHPYFYAPE	Biotin (K); Ca	0.000000000000000000000000000000000020001.0
RHPYFYAPE	Biotin (K); Ca	0.000000000000000000010000002000.0
RHPYFYAPE	Biotin (K); Ca	0.000000000000000000010000002000.0
LASRKSARF	Biotin (K)	0.00000000001.0
LASRKSARF	Biotin (K)	0.00000000001.0
LASRKSARF	Biotin (K)	0.00000000001.0
LASRKSARF	Biotin (K)	0.00000000001.0
NSRIAILLKT	Biotin (K)	0.0000000010000.0
LGKSAFLQ\	Biotin (K)	0.001000000000.0
LGKSAFLQ\	Biotin (K)	0.001000000000.0
LNAKGGNVI	Biotin (K)	0.00010000000000000000000.0
LNAKGGNVI	Biotin (K)	0.00010000000000000000000.0
CSQPGVIFL	Biotin (K)	0.00000000001.0
GKSASSPKF	Biotin (K)	0.010000000000.0
GKSASSPKF	Biotin (K)	0.010000000000.0
GKSASSPKF	Biotin (K)	0.010000000000.0
GKSASSPKF	Biotin (K)	0.010000000000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
AGGDAADG	Biotin (K)	0.000000000000000100000000000000.0
AGGDAADG	Biotin (K)	0.000000000000000100000000000000.0
AGGDAADG	Biotin (K)	0.000000000000000100000000000000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
SGKSPSPSF	Biotin (K)	0.0010000000000000.0
SGKSPSPSF	Biotin (K)	0.0010000000000000.0
SGKSPSPSF	Biotin (K)	0.0010000000000000.0
GADAAAKT:	Biotin (K)	0.000000000100.0
RRSEISSVL/	Biotin (K)	0.00000000001.0
RPFVIKPISS	Biotin (K)	0.000001000000000000000000.0
RPFVIKPISS	Biotin (K)	0.000001000000000000000000.0

EYSSKAHST	Biotin (K)	0.00000000000000000000000100.0
GIGGLRKR	Biotin (K)	0.00000010.0
GLYDGPVC	Biotin (K)	0.000000020000001000000000.0
GLYDGPVC	Biotin (K)	0.000000020000001000000000.0
TSPAKQQAI	Biotin (K)	0.000010000000.0
TSPAKQQAI	Biotin (K)	0.000010000000.0
GLYDGPVC	Biotin (K)	0.000000020000001000000000.0
GLYDGPVC	Biotin (K)	0.000000020000001000000000.0
KRSVAVWLI	Biotin (K)	0.10000000000.0
SPKALEK	Biotin (K)	0.0010000.0
SPKALEK	Biotin (K)	0.0010000.0
KETTQK	Biotin (K)	0.000001.0
KSTIVK	Biotin (K)	0.000001.0
LQKAQEEAI	Biotin (K)	0.000000000001000.0
LQKAQEEAI	Biotin (K)	0.000000000001000.0
IAVNLTVLK	Biotin (K)	0.000000001.0
KQKKVR	Biotin (K)	0.000100.0
DVKPENFLI	Biotin (K)	0.00100000000.0
GAVGMACA	Biotin (K)	0.00000000000001.0
GAVGMACA	Biotin (K)	0.00000000000001.0
GAVGMACA	Biotin (K)	0.00000000000001.0
GAVGMACA	Biotin (K)	0.00000000000001.0
GAVGMACA	Biotin (K)	0.00000000000001.0
GAVGMACA	Biotin (K)	0.00000000000001.0
STQVVSDA/	Biotin (K)	0.000000000100000000000.0
STQVVSDA/	Biotin (K)	0.000000000100000000000.0
STQVVSDA/	Biotin (K)	0.000000000100000000000.0
DFQEPLPQI	Biotin (K)	0.000000001000000.0
DFQEPLPQI	Biotin (K)	0.000000001000000.0
DKVLVLEDR	Biotin (K)	0.010000000.0
SSFLEDKST	Biotin (K)	0.000000100000.0
DTAVELGKC	Biotin (K)	0.0000000100000.0
TQGQKSSF	Biotin (K)	0.000010000000.0
DFQEPLPQI	Biotin (K)	0.000000001000000.0
SSFLEDKST	Biotin (K)	0.000000100000.0
DFQEPLPQI	Biotin (K)	0.000000001000000.0
GKDLYLEDC	Biotin (K)	0.0100000000000000.0
DFQEPLPQI	Biotin (K)	0.000000001000000.0
ITKTPQAST	Biotin (K)	0.00100000000000000.0
SAKTATAGF	Biotin (K)	0.0010000000000.0
ITKTPQAST	Biotin (K)	0.00100000000000000.0
CGSKDNIK	Biotin (K)	0.20010000.0
CGSKDNIK	Biotin (K)	0.20010000.0
YLKGHDSVF	Biotin (K)	0.00100000000000.0
PIIPVPLKGC	Biotin (K)	0.0000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
GHDSVFVAI	Biotin (K)	0.000000000100000000000.0
YLKGHDSVF	Biotin (K)	0.00100000000000.0
PIIPVPLKGC	Biotin (K)	0.0000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
GHDSVFVAI	Biotin (K)	0.000000000100000000000.0
PIIPVPLKGC	Biotin (K)	0.0000000100000000000.0

DQGAVLLG	Biotin (K)	0.00000000001000000000.0
NQDPIIPVPL	Biotin (K)	0.00000000001000000000.0
PIIPVPLKGC	Biotin (K)	0.0000001000000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
NQDPIIPVPL	Biotin (K)	0.00000000001000000000.0
PIIPVPLKGC	Biotin (K)	0.0000001000000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
PIIPVPLKGC	Biotin (K)	0.0000001000000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
PIIPVPLKGC	Biotin (K)	0.0000001000000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
YLKGHDSVF	Biotin (K)	0.00100000000000.0
YLKGHDSVF	Biotin (K)	0.00100000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
NQSPVVPAS	Biotin (K)	0.00000000001000000000.0
GHDSVFVAI	Biotin (K)	0.00000000001000000000.0
NQDPIIPVPL	Biotin (K)	0.00000000001000000000.0
YLKGHDSVF	Biotin (K)	0.00100000000000.0
YLKGHDSVF	Biotin (K)	0.00100000000000.0
PIIPVPLKGC	Biotin (K)	0.0000001000000000000.0
NQGLAGPE	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
NQSPVVPAS	Biotin (K)	0.00000000001000000000.0
GHDSVFVAI	Biotin (K)	0.00000000001000000000.0
NQDPIIPVPL	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
GQSPTAPG	2 Biotin (K)	0.00000000001000000000100000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
NQDPIIPVPL	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
DQGAVLLG	Biotin (K)	0.00000000001000000000.0
NQDPIIPVPL	Biotin (K)	0.00000000001000000000.0
NQDPIIPVPL	Biotin (K)	0.00000000001000000000.0
GQSPTAPG	Biotin (K)	0.00000000000000000000100000000000.0
RGDHPWIPI	Biotin (K)	0.000000010000000000000000000.0
YLKGHDSVF	Biotin (K)	0.00100000000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
KMEHTIK	Biotin (K)	0.1000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
KMEHTIK	Biotin (K)	0.1000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
KMEHTIK	Biotin (K)	0.1000000.0

IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
AGDALMVM	Biotin (K); Ox	0.000003000001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
KLILKPAIK	2 Biotin (K)	0.100010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
TPGTPKSGI	Biotin (K)	0.000001000000000.0
KLILKPAIK	2 Biotin (K)	0.100010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
TPGTPKSGI	Biotin (K)	0.000001000000000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
LILKPAIK	Biotin (K)	0.00010000.0
LILKPAIK	Biotin (K)	0.00010000.0
LILKPAIK	Biotin (K)	0.00010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
ELITTKDTSI	Biotin (K)	0.000001000000.0
TPGTPKSGI	Biotin (K)	0.000001000000000.0
LRDDKTGVI	Biotin (K)	0.0000100000000000000.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
LEGAGSATI	Biotin (K)	0.0000000000000000000100000.0
NKLEGAGS/	Biotin (K)	0.000000000000000000000100000.0
VSDFGQMA	Biotin (K)	0.000000300000000100000.0
LILKPAIK	Biotin (K)	0.00010000.0

KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
TLGKVTSEF	Biotin (K)	0.000100000000000.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
LEGAGSATI	Biotin (K)	0.0000000000000000000100000.0
GLSSVPEVA	Biotin (K)	0.000000000000000100000000000.0
NKLEGAGS/	Biotin (K)	0.00000000000000000000100000.0
YTVPLPSPV	Biotin (K)	0.0000000000000000000000000000001000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
TPGTPKSGI	Biotin (K)	0.000001000000000.0
LRDDKTGVI	Biotin (K)	0.000100000000000000.0
VSDFGQMA	Biotin (K)	0.00000000000000000100000.0
LEGAGSATI	Biotin (K)	0.0000000000000000000100000.0
NKLEGAGS/	Biotin (K)	0.00000000000000000000100000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	2 Biotin (K)	0.100010000.0
KLILKPAIK	2 Biotin (K)	0.100010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KEKAAAMPI	Biotin (K)	0.0010000000.0
QRLLLGLTS	Biotin (K)	0.0000000000001.0
QRLLLGLTS	Biotin (K)	0.0000000000001.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
IGFGPSPFS	Biotin (K)	0.00000000000000001000000000.0
VKSEEMIK	Biotin (K)	0.01000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YAKLMGLLA	Biotin (K)	0.001000000000.0
KMQNSMTA	Biotin (K); O>	0.1300000000.0
KMQNSMTA	Biotin (K); O>	0.1300000000.0
KMQNSMTA	Biotin (K); O>	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K); O>	0.1300000000.0
KMQNSMTA	Biotin (K); O>	0.1300000000.0
KMQNSMTA	Biotin (K); O>	0.1000030000.0
KMQNSMTA	Biotin (K); O>	0.1000030000.0
KMQNSMTA	Biotin (K)	0.1000000000.0

KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000030000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
ASFAEKTAC	Biotin (K)	0.000001000000.0
ASFAEKTAC	Biotin (K)	0.000001000000.0
ASFAEKTAC	Biotin (K)	0.000001000000.0
NDGKPRVD	Biotin (K)	0.00010000001.0
NDGKPRVD	Biotin (K)	0.00010000001.0
DKEKAVYAK	Biotin (K)	0.000100000.0
DKEKAVYAK	Biotin (K)	0.000100000.0
DKEKAVYAK	Biotin (K)	0.000100000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000010000000300000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000310000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
MKMETVVTS	Biotin (K)	0.0100000000000000.0
GQPLCVLSA	Biotin (K)	0.000020000010000000000000.0
GQPLCVLSA	Biotin (K)	0.000020000310000000000000.0
KMETVVTSF	Biotin (K)	0.100000000300000.0
KMETVVTSF	Biotin (K)	0.130000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLSA	Biotin (K)	0.000020000013000000000000.0

KMETVVTSF	Biotin (K)	0.100000000300000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000300000.0
KMETVVTSF	Biotin (K)	0.130000000000000.0
SAMKMETV	Biotin (K)	0.000100000000000000.0
SAMKMETV	Biotin (K)	0.000100000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLSA	Biotin (K); Ca	0.000020000013000000000000000.0
TSSLTTKGA	Biotin (K)	0.0000000000001000.0
EAGKALLAE	Biotin (K)	0.00010000000000.0
EAGKALLAE	Biotin (K)	0.00010000000000.0
QTTKSELLR	Biotin (K)	0.000100000.0
QTTKSELLR	Biotin (K)	0.000100000.0
QTTKSELLR	Biotin (K)	0.000100000.0
QTTKSELLR	Biotin (K)	0.000100000.0
IADFKNTLP	Biotin (K)	0.000010000000000000000000000.0
QGKIPDEEL	Biotin (K)	0.0010000000.0
QGKIPDEEL	Biotin (K)	0.0010000000.0
QGKIPDEEL	Biotin (K)	0.0010000000.0
QGKIPDEEL	Biotin (K)	0.0010000000.0
QGKIPDEEL	Biotin (K)	0.0010000000.0
QGKIPDEEL	Biotin (K)	0.0010000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
TASPWKSAF	Biotin (K)	0.000001000.0
TASPWKSAF	Biotin (K)	0.000001000.0
TASPWKSAF	Biotin (K)	0.000001000.0
DEADSKTAS	Biotin (K)	0.000001000000.0
TASPWKSAF	Biotin (K)	0.000001000.0
VDKSAVGFI	Biotin (K)	0.0010000000000.0
VDKSAVGFI	Biotin (K)	0.0010000000000.0
VDKSAVGFI	Biotin (K)	0.0010000000000.0
TVPIEAVTSK	Biotin (K)	0.000000000100000.0
VDKSAVGFI	Biotin (K)	0.0010000000000.0
TVPIEAVTSK	Biotin (K)	0.000000000100000.0
AALTQYSAK	Biotin (K)	0.0000000010000.0
AALTQYSAK	Biotin (K)	0.0000000010000.0
AKTRAAD	Biotin (K)	0.0100000.0
ASTDKYAVF	Biotin (K)	0.0000100000.0
ASTDKYAVF	Biotin (K)	0.0000100000.0
GISTDKPSE	Biotin (K)	0.000000000000000000000100000.0
GISTDKPSE	Biotin (K)	0.000000000000000000000100000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0

TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
QGVAEAAG	Biotin (K)	0.00000000100.0
QGVAEAAG	Biotin (K)	0.00000000100.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
QGVAEAAG	Biotin (K)	0.00000000001.0
QGVAEAAG	Biotin (K)	0.00000000001.0
EGVLYVGSK	Biotin (K)	0.00000000001.0
EGVLYVGSK	Biotin (K)	0.00000000001.0
EGVLYVGSK	Biotin (K)	0.00000000001.0
EGVLYVGSK	Biotin (K)	0.00000000001.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0

TKQGVTEA/	Biotin (K)	0.0000000000001.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKQGVTEA/	Biotin (K)	0.01000000000.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKQGVTEA/	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000001.0
GLSMAKEG'	Biotin (K)	0.000001000000000.0
EGVLYVGSK	Biotin (K)	0.00000000100000000000000.0
EGVLYVGSK	Biotin (K)	0.00000000100000000000000.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.01000000000.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKQGVTEA/	Biotin (K)	0.0000000000001.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
EGVLYVGSK	Biotin (K)	0.00000000100000000000000.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
QGVTEAAEI	Biotin (K)	0.00000000001.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
QGVTEAAEI	Biotin (K)	0.00000000001.0
QGVTEAAEI	Biotin (K)	0.00000000001.0
QGVTEAAEI	Biotin (K)	0.00000000001.0
EGVLYVGSK	Biotin (K)	0.00000000001.0
EGVLYVGSK	Biotin (K)	0.00000000001.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
VGAVEKTKC	2 Biotin (K)	0.00000100000000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0

QGVTEAAEI	Biotin (K)	0.00000000100.0
QGVTEAAEI	Biotin (K)	0.00000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
TKQGVTEA/	Biotin (K)	0.0000000000100.0
KIETHKLTFI	Biotin (K)	0.0000010000.0
HVNSKCLF\	Biotin (K)	0.00001000000000.0
RSKCLQPR	Biotin (K)	0.00100000.0
RSKCLQPR	Biotin (K)	0.00100000.0
RSKCLQPR	Biotin (K)	0.00100000.0
RSKCLQPR	Biotin (K)	0.00100000.0
VVRHGETRI	Biotin (K)	0.0000000000001.0
LGKTAAFK	Biotin (K)	0.00100000.0
LGKTAAFK	Biotin (K)	0.00100000.0
LGKTAAFK	Biotin (K)	0.00100000.0
EEQLLSTGI	2 Biotin (K)	0.000000000101000000000000000.0
EEQLLSTGI	2 Biotin (K)	0.000000000101000000000000000.0
SSKTVTSLS	Biotin (K)	0.00000000001.0
QDPSAIMEK	Biotin (K)	0.000000000000010.0
DRKYEEVAI	Biotin (K)	0.001000000.0
KETTQK	Biotin (K)	0.000001.0
VNVDKVLEI	Biotin (K)	0.000010000.0
VNVDKVLEI	Biotin (K)	0.000010000.0
KFGIGLPILI	Biotin (K)	0.100000000000.0
KFGIGIPILI	Biotin (K)	0.100000000000.0
KFGIGLPILI	Biotin (K)	0.100000000000.0
KFGIGIPILI	Biotin (K)	0.100000000000.0

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Unique proteins	75
AAK1_MOUSE	
ABLM2_MOUSE	
ADT1_MOUSE	
ALBU_MOUSE	
ANR35_MOUSE	
BBS12_MOUSE	
CAMP3_MOUSE	
CAPS1_MOUSE	
CCL3_MOUSE	
CEND_MOUSE	
CH10_MOUSE	
CLAP2_MOUSE	
CPLX1_MOUSE	
CPLX2_MOUSE	
DCLK1_MOUSE	
DCTN1_MOUSE	
DDX31_MOUSE	
DGKI_MOUSE	
DMXL2_MOUSE	
DPF1_MOUSE	
DPYL2_MOUSE	
EDIL3_MOUSE	
F16B1_MOUSE	
GLP2R_MOUSE	
GNAT1_MOUSE	
ICAM1_MOUSE	
ILRL2_MOUSE	
KALRN_MOUSE	
KC1G3_MOUSE	
LDHA_MOUSE	
LNEBL_MOUSE	
MAP1A_MOUSE	
MAP1B_MOUSE	
MAP4_MOUSE	
MAP6_MOUSE	
MCCA_MOUSE	
MINK1_MOUSE	
MTAP2_MOUSE	
MTG16_MOUSE	
MYCPP_MOUSE	
NEUG_MOUSE	
NFH_MOUSE	
NFM_MOUSE	
NR1I3_MOUSE	
PCCA_MOUSE	
PLAP_MOUSE	
PLEC_MOUSE	
PP2BA_MOUSE	
PPID_MOUSE	
PYC_MOUSE	
QCR2_MOUSE	

Final list after background is subtracted

RMT-ECRRc	34	STRING ge
ABLM2_MOUSE	Ablim2	Ablim2 - Actir
BBS12_MOUSE	Bbs12	Bbs12 - Bard
CAMP3_MOUSE	Camsap3	Camsap3 - C
CAPS1_MOUSE	Cadps	Cadps - Calc
CCL3_MOUSE	Ccl3	Ccl3 - C-C m
DCTN1_MOUSE	Dctn1	Dctn1 - Dyna
DDX31_MOUSE	Ddx31	Ddx31 - Prob
DPF1_MOUSE	Dpf1	Dpf1 - D4, zir
F16B1_MOUSE	Fam160b1	Fam160b1 - I
GLP2R_MOUSE	Glp2r	Glp2r - Gluca
GNAT1_MOUSE	Gnat1	Gnat1 - Guar
ILRL2_MOUSE	Il1rl2	Il1rl2 - Interle
KALRN_MOUSE	Kalrn	Kalrn - Kalirin
KC1G3_MOUSE	Csnk1g3	Csnk1g3 - Ca
LDHA_MOUSE	Ldha	Ldha - L-lacta
MAP4_MOUSE	Map4	Map4 - Micro
MTG16_MOUSE	Cbfa2t3	Cbfa2t3 - CB
NFH_MOUSE	Nefh	Nefh - Neuro
NR1I3_MOUSE	Nr1i3	Nr1i3 - Nucle
PP2BA_MOUSE	Ppp3ca	Ppp3ca - Ser
PPID_MOUSE	Ppid	Ppid - Peptidy
QCR2_MOUSE	Uqcrc2	Uqcrc2 - Cyt
RT23_MOUSE	Mrps23	Mrps23 - Mito
SH3G2_MOUSE	Sh3gl2	Sh3gl2 - SH3
SRCN1_MOUSE	Srcin1	Srcin1 - Src k
SRPK2_MOUSE	Srpk2	Srpk2 - SRSI
TAU_MOUSE	Mapt	Mapt - Microt
TF3C1_MOUSE	Gtf3c1	Gtf3c1 - Gen
TIGAR_MOUSE	Tigar	Tigar - Fructo
TNR21_MOUSE	Tnfrsf21	Tnfrsf21 - Tu
TPM3_MOUSE	Tpm3	Tpm3 - Tropo
TRI29_MOUSE	Trim29	Trim29 - Trip
VAMP3_MOUSE	Vamp3	Vamp3 - Ves
WRN_MOUSE	Wrn	Wrn - Werner

Network Properties

number of nodes:	34
number of edges:	12
average node degree:	0.706
avg. local clustering coefficient:	0.475
expected number of edges:	7
PPI enrichment p-value:	0.0507

RT23_MOUSE
RT31_MOUSE
RTN3_MOUSE
SH3G2_MOUSE
SHAN2_MOUSE
SPTN1_MOUSE
SRC8_MOUSE
SRCN1_MOUSE
SRPK2_MOUSE
SYNRG_MOUSE
SYUA_MOUSE
SYUB_MOUSE
SYUG_MOUSE
TAU_MOUSE
TEP1_MOUSE
TF3C1_MOUSE
TIGAR_MOUSE
TIM44_MOUSE
TITIN_MOUSE
TNR21_MOUSE
TPM3_MOUSE
TRI29_MOUSE
VAMP3_MOUSE
WRN_MOUSE

ne names and description

n-binding LIM protein 2; May act as scaffold protein. May stimulate ABRA activity and ABRA-de
let-Biedl syndrome 12 protein homolog; Probable molecular chaperone. Assists the folding of pr
Calmodulin-regulated spectrin-associated protein 3; Key microtubule-organizing protein that spe
ium-dependent secretion activator 1; Calcium-binding protein involved in exocytosis of vesicles
otif chemokine 3; Monokine with inflammatory, pyrogenic and chemokinetic properties. Has a p
actin subunit 1; Plays a key role in dynein-mediated retrograde transport of vesicles and organe
bable ATP-dependent RNA helicase DDX31; Probable ATP-dependent RNA helicase (By simila
nc and double PHD fingers family 1; Zinc finger protein neuro-d4; May have an important role in
Protein FAM160B1; Family with sequence similarity 160, member B1 [a.k.a. Kiaa1600, ENSMU
agon-like peptide 2 receptor; This is a receptor for glucagon-like peptide 2. The activity of this re
nine nucleotide-binding protein G(t) subunit alpha-1; Guanine nucleotide-binding proteins (G pro
ukin-1 receptor-like 2; Receptor for interleukin-36 (IL36A, IL36B and IL36G). After binding to int
; Promotes the exchange of GDP by GTP. Activates specific Rho GTPase family members, th
asein kinase I isoform gamma-3; Serine/threonine-protein kinase. Casein kinases are operation
ate dehydrogenase a chain; Lactate dehydrogenase A; Belongs to the LDH/MDH superfamily.
otubule-associated protein 4; Non-neuronal microtubule-associated protein. Promotes microtubu
FA2/RUNX1 translocation partner 3; Protein CBFA2T3; Transcriptional corepressor which faci
filament, heavy polypeptide; Neurofilament heavy polypeptide; Neurofilaments usually contain t
ear receptor subfamily 1, group i, member 3; Nuclear receptor subfamily 1 group I member 3; B
rine/threonine-protein phosphatase 2B catalytic subunit alpha isoform; Calcium-dependent, caln
yl-prolyl cis-trans isomerase D; PPIases accelerate the folding of proteins. It catalyzes the cis-
ochrome b-c1 complex subunit 2, mitochondrial; This is a component of the ubiquinol-cytochro
ochondrial ribosomal protein S23; Belongs to the mitochondrion-specific ribosomal protein mS2
-domain GRB2-like 2; Endophilin-A1; Implicated in synaptic vesicle endocytosis. May recruit ot
kinase signaling inhibitor 1; Acts as a negative regulator of SRC by activating CSK which inhibits
F protein kinase 2; Serine/arginine-rich protein-specific kinase which specifically phosphorylate
tubule-associated protein tau; Promotes microtubule assembly and stability, and might be involv
neral transcription factor 3C polypeptide 1; Required for RNA polymerase III-mediated transcript
ose-2,6-bisphosphatase TIGAR; Fructose-bisphosphatase hydrolyzing fructose-2,6- bisphosp
mor necrosis factor receptor superfamily member 21; Promotes apoptosis, possibly via a path
omyosin alpha-3 chain; Tropomyosin 3, gamma; Belongs to the tropomyosin family [a.k.a. hTM
artite motif-containing protein 29; Plays a crucial role in the regulation of macrophage activation
icle-associated membrane protein 3; SNARE involved in vesicular transport from the late endos
r syndrome ATP-dependent helicase homolog; Multifunctional enzyme that has both magnesiur

pendent SRF transcriptional activity [a.k.a. ENSMUST00000114206, CCDS51477.1, NP_0011
oteins upon ATP hydrolysis. As part of the BBS/CCT complex may play a role in the assembly
cifically binds the minus-end of non-centrosomal microtubules and regulates their dynamics an
s filled with neurotransmitters and neuropeptides. Probably acts upstream of fusion in the bioge
otent chemotactic activity for eosinophils. Binding to a high-affinity receptor activates calcium r
elles along microtubules by recruiting and tethering dynein to microtubules. Binds to both dyneir
rity). Plays a role in ribosome biogenesis and TP53/p53 regulation through its interaction with N
developing neurons by participating in regulation of cell survival, possibly as a neurospecific tr
SG00000033478, NP_663480.3, F16B1_MOUSE]
eceptor is mediated by G proteins which activate adenylyl cyclase (By similarity) [a.k.a. Q5IXF
oteins) are involved as modulators or transducers in various transmembrane signaling systems
terleukin-36 associates with the coreceptor IL1RAP to form the interleukin-36 receptor complex
ereby inducing various signaling mechanisms that regulate neuronal shape, growth, and plastic
nally defined by their preferential utilization of acidic proteins such as caseins as substrates. It c
LDH family [a.k.a. Ldh-1, Ldh1, Ldhm, LDHA_MOUSE]
ule assembly [a.k.a. Mtap4, XP_006512018.1, XM_006511956.1, MAP4_MOUSE]
litates transcriptional repression via its association with DNA-binding transcription factors and r
hree intermediate filament proteins: L, M, and H which are involved in the maintenance of neuro
inds and transactivates the retinoic acid response elements that control expression of the retin
nodulin-stimulated protein phosphatase. Many of the substrates contain a PxIxIT motif. This su
trans isomerization of proline imidic peptide bonds in oligopeptides. Proposed to act as a co-ch
me c reductase complex (complex III or cytochrome b-c1 complex), which is part of the mitoch
3 family [a.k.a. Mrps23-004, OTTMUSP00000001431, CCDS25227.1, RT23_MOUSE]
her proteins to membranes with high curvature. Required for BDNF-dependent dendrite outgro
s SRC activity and downstream signaling, leading to impaired cell spreading and migration. Reg
s its substrates at serine residues located in regions rich in arginine/serine dipeptides, known a
ved in the establishment and maintenance of neuronal polarity. The C-terminus binds axonal mi
tion. Component of TFIIIC that initiates transcription complex assembly on tRNA and is require
hate as well as fructose-1,6-bisphosphate (By similarity). Acts as a negative regulator of glyco
way that involves the activation of NF-kappa-B. Can also promote apoptosis mediated by BAX
30nm, ENSMUST00000118566, ENSMUSP00000114229, TPM3_MOUSE]
in response to viral or bacterial infections within the respiratory tract. Mechanistically, TRIM29
somes to the trans-Golgi network [a.k.a. Syb3, D130027G05Rik, AK169087, VAMP3_MOUSE]
n and ATP- dependent DNA-helicase activity and 3'->5' exonuclease activity towards double-s

71170.1, ABLM2_MOUSE]
of BBSome, a complex involved in ciliogenesis regulating transports vesicles to the cilia. Involv
ıd organization. Specifically recognizes growing microtubule minus-ends and autonomously dec
nesis or maintenance of mature secretory vesicles. Regulates catecholamine loading of DCVs
elease in neutrophils; Belongs to the intercrine beta (chemokine CC) family [a.k.a. Mip1a, Scya
ı and microtubules providing a link between specific cargos, microtubules and dynein. Essentia
IPM1 (By similarity); Belongs to the DEAD box helicase family. DDX31/DBP7 subfamily [a.k.a. A
anscription factor. Belongs to the neuron-specific chromatin remodeling complex (nBAF compl

8, GLP-2R, GLP2R_MOUSE]
s. Transducin is an amplifier and one of the transducers of a visual impulse that performs the c
x which mediates interleukin-36-dependent activation of NF-kappa-B, MAPK and other pathway
city, through their effects on the actin cytoskeleton. Induces lamellipodia independent of its GEF
can phosphorylate a large number of proteins. Participates in Wnt signaling (By similarity). Regu

ecruitment of other corepressors and histone-modifying enzymes. Can repress the expressio
ɔnal caliber. NF-H has an important function in mature axons that is not subserved by the two s
oic acid receptor beta 2 and alcohol dehydrogenase 3 genes. Transactivates both the phenoba
bunit may have a role in the calmodulin activation of calcineurin. Dephosphorylates DNM1L an
aperone in HSP90 complexes such as in unligated steroid receptors heterocomplexes. Differe
ıondrial respiratory chain. The core protein 2 is required for the assembly of the complex (By s

ɔwth. Cooperates with SH3GL2 to mediate BDNF-NTRK2 early endocytic trafficking and signali
ɹulates dendritic spine morphology. Involved in calcium-dependent exocytosis. May play a role
as RS domains and is involved in the phosphorylation of SR splicing factors and the regulation
icrotubules while the N- terminus binds neural plasma membrane components, suggesting that
d for transcription of 5S rRNA and other stable nuclear and cytoplasmic RNAs. Binds to the bo
lysis by lowering intracellular levels of fructose-2,6-bisphosphate in a p53/TP53- dependent ma
and by the release of cytochrome c from the mitochondria into the cytoplasm. Plays a role in n

interacts with IKBKG/NEMO in the lysosome where it induces its 'Lys-48' ubiquitination and su

tranded DNA with a 5'-overhang. Has no nuclease activity towards single-stranded DNA or blu

ved in adipogenic differentiation (By similarity) [a.k.a. Gm1805, XP_011247984.1, LOC386537,
corates and stabilizes microtubule lattice formed by microtubule minus-end polymerization. Acts
. May specifically mediate the Ca(2+)-dependent exocytosis of large dense-core vesicles (DC
a3, AAI11444.1, CCL3_MOUSE]
l for targeting dynein to microtubule plus ends, recruiting dynein to membranous cargos and er
A3KMM3, ENSMUST00000152685, mmu:227674, DDX31_MOUSE]
ex). During neural development a switch from a stem/progenitor to a post-mitotic chromatin rer

oupling between rhodopsin and cGMP-phosphodiesterase [a.k.a. Gnat-1, Ird2, transducin, GN
ys. The IL-36 signaling system is thought to be present in epithelial barriers and to take part in l
F activity (By similarity); Belongs to the protein kinase superfamily. CAMK Ser/Thr protein kinas
ulates fast synaptic transmission mediated by glutamate [a.k.a. XP_006526300, Mm.411061, c

n of MMP7 in a ZBTB33-dependent manner. Reduces the protein levels and stability of the tran
smaller NF proteins [a.k.a. Kiaa0845, Nfh, ENSMUST00000093369, NFH_MOUSE]
arbital responsive element module of the human CYP2B6 gene and the CYP3A4 xenobiotic resp
d HSPB1 (By similarity). Dephosphorylates SSH1; Belongs to the PPP phosphatase family. PP-
nt co-chaperones seem to compete for association with HSP90 thus establishing distinct HSP9
similarity); Belongs to the peptidase M16 family. UQCRC2/QCR2 subfamily [a.k.a. Q8BK11, EN

ing from early endosomes [a.k.a. Sh3d2a, Een1, A830014P03, SH3G2_MOUSE]
in neurotransmitter release or synapse maintenance (By similarity) [a.k.a. P140, UPI000059D0
of splicing. Promotes neuronal apoptosis by up-regulating cyclin-D1 (CCND1) expression. This
tau functions as a linker protein between both. Axonal polarity is predetermined by tau localiza
x B promoter element (By similarity); Belongs to the TFIIIC subunit 1 family [a.k.a. AAH04708.1
anner, resulting in the pentose phosphate pathway (PPP) activation and NADPH production. Co
neuronal apoptosis, including apoptosis in response to amyloid peptides derived from APP, and

ubsequent degradation. In turn, the expression of type I interferons and the production of proinfl

unt-ended double- stranded DNA. Binds preferentially to DNA substrates containing alternate se

BBS12_MOUSE]
s on free microtubule minus-ends that are not capped by microtubule-nucleating proteins or oth
Vs) and other dense-core vesicles by acting as a PtdIns(4,5)P2-binding protein that acts at pre

nhancing dynein processivity (the ability to move along a microtubule for a long distance withou

nodeling mechanism occurs as neurons exit the cell cycle and become committed to their adul

AT1_MOUSE]
ocal inflammatory response; it is similar to the IL-1 system. Seems to be involved in skin inflam
e family [a.k.a. A2CG52, UPI0000D672E7, ENSMUSP00000116188, KALRN_MOUSE]
asein kinase 1, gamma 3, KC1G3_MOUSE]

scriptinal regulator HIF1A; interacts with EGLN1 and promotes the HIF1A prolyl hydroxylation-

ponse element (By similarity) [a.k.a. Car, O35627, Constitutive androstane receptor, NR1I3_M
-2B subfamily [a.k.a. Calna, 19055, EC 3.1.3.16, PP2BA_MOUSE]
0-co-chaperone-receptor complexes with the potential to exert tissue-specific receptor activity
SMUST00000148958, OTTMUST00000062908, QCR2_MOUSE]

CDF, XP_006533843.1, SRCN1_MOUSE]
s is done by the phosphorylation of SRSF2, leading to the suppression of p53/TP53 phosphoryl
tion (in the neuronal cell) in the domain of the cell body defined by the centrosome. The short is
, ENSMUSP00000056719, BAE25245.1, TF3C1_MOUSE]
ontributes to the generation of reduced glutathione to cause a decrease in intracellular reactive
is required for both normal cell body death and axonal pruning. Trophic-factor deprivation trigg

ammatory cytokines are inhibited. Additionally, induces the 'Lys-48' ubiquitination of STING1 in

econdary structures, such as replication forks and Holliday junctions. May play an important ro

ıer factors and protects microtubule minus-ends from depolymerization. In addition, it also redu
efusion step following ATP-dependent priming and participates in DCVs-membrane fusion. How

t falling off the track). Can also act as a brake to slow the dynein motor during motility along the

t state. The transition from proliferating neural stem/progenitor cells to post-mitotic neurons req

matory response by induction of the IL-23/IL-17/IL- 22 pathway [a.k.a. XM_006495611, XM_00

dependent ubiquitination and proteasomal degradation pathway. Contributes to inhibition of glyc

OUSE]

control. May have a preference for estrogen receptor complexes and is not found in glucocor

ation thereby relieving the repressive effect of p53/TP53 on cyclin-D1 (CCND1) expression. Pl
soforms allow plasticity of the cytoskeleton whereas the longer isoforms may preferentially play

oxygen species (ROS) content, correlating with its ability to protect cells from oxidative or met
ers the cleavage of surface APP by beta-secretase to release sAPP-beta which is further clea

a similar way, leading to its degradation [a.k.a. Q9CSC9, TRI29_MOUSE, XP_006510679.1]

le in the dissociation of joint DNA molecules that can arise as products of homologous recombi

ıces the velocity of microtubule [...] [a.k.a. Kiaa1543, NM_001163749, 5M50, CAMP3_MOUSE]
ever, it may also participate in [...] [a.k.a. Kiaa1121, Caps1, Caps, CAPS1_MOUSE]

microtubule. C [...] [a.k.a. XM_006505487, XM_006505493, uc009cna.2, DCTN1_MOUSE]

uires a switch in [...] [a.k.a. Neud4, Baf45b, OTTMUST00000061549, DPF1_MOUSE]

)6495608, uc007atx.1, ILRL2_MOUSE]

colysis and stimulation of mitoch [...] [a.k.a. Mtgr2, Cbfa2t3h, OTTMUSG00000027605, MTG16

ticoid receptor complexe [...] [a.k.a. BC011499, ENSMUSG00000027804, OTTMUST0000007

hosphorylates ACIN1, and [...] [a.k.a. 7120479J06, Srpk2-201, XP_006535727.1, SRPK2_MOU
a role in its stabil [...] [a.k.a. Tau, Mtapt, ENSMUSP00000102600, TAU_MOUSE]

abolic stress-induced ce [...] [a.k.a. 9630033F20Rik, ENSMUST00000039913, 3.1.3.46, TIGAR
ved to release an N-terminal frag [...] [a.k.a. Dr6, Q91W77, Q543Y9, TNR21_MOUSE]

ination, at stalled replication forks [...] [a.k.a. Werner syndrome homolog (human), NP_0011162

_MOUSE]

2905, PPID_MOUSE]

JSE]

R_MOUSE]

294.1, Q9Z242, WRN_MOUSE]

Table 22 **Total peptides list for three control rAAVs in the encoding-cons**

n = 18, pep = 757, pro = 148

rAAV	Sample	Biotin	Protein Accession	Protein Des	Peptide Scor
SYN-MiniTid	6	d1-6	AAK1_MOUSE	AP2-associa	82.58
SYN-MiniTid	6	d1-6	AAK1_MOUSE	AP2-associa	82.58
RAM-MiniTid	15	d1-6	ABI1_MOUSE	Abl interactor	63.59
RAM-MiniTid	15	d1-6	ABI1_MOUSE	Abl interactor	63.59
RAM-MiniTid	15	d1-6	ABI1_MOUSE	Abl interactor	63.59
SYN-MiniTid-Tau	17	d1-6	ADA2B_MOUSE	Alpha-2B adr	46.37
RAM-MiniTid	12	d1-6	ADDA_MOUSE	Alpha-adduci	45.92
RAM-MiniTid	12	d1-6	ADDA_MOUSE	Alpha-adduci	39.37
RAM-MiniTid	15	d1-6	ADDB_MOUSE	Beta-adducir	72.22
RAM-MiniTid	12	d1-6	ADDG_MOUSE	Gamma-add	50.91
RAM-MiniTid	15	d1-6	ADT1_MOUSE	ADP/ATP tra	63.91
RAM-MiniTid	15	d1-6	ADT1_MOUSE	ADP/ATP tra	56.83
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	49.81
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	49.81
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	49.81
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	49.81
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	43.17
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	43.17
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	43.17
RAM-MiniTid	15	d1-6	ADT2_MOUSE	ADP/ATP tra	43.17
RAM-MiniTid	15	d1-6	AGFG1_MOUSE	Arf-GAP dom	119.17
RAM-MiniTid	15	d1-6	AGFG1_MOUSE	Arf-GAP dom	119.17
RAM-MiniTid	15	d1-6	AGFG1_MOUSE	Arf-GAP dom	119.17
RAM-MiniTid	12	d1-6	AINX_MOUSE	Alpha-interne	104.16
RAM-MiniTid	12	d1-6	AINX_MOUSE	Alpha-interne	71.05
RAM-MiniTid	15	d1-6	AINX_MOUSE	Alpha-interne	108.79
RAM-MiniTid	10	d1-6	ALBU_MOUSE	Albumin OS=	45.5
SYN-MiniTid	18	d1-6	ALBU_MOUSE	Albumin OS=	66.88
RAM-MiniTid	12	d1-6	ALDOA_MOUSE	Fructose-bis	53.44
RAM-MiniTid	15	d1-6	ANK3_MOUSE	Ankyrin-3, G	52.97
RAM-MiniTid	1	d1-6	ANR35_MOUSE	Ankyrin repe	40.22
RAM-MiniTid	1	d1-6	ANR35_MOUSE	Ankyrin repe	40.22
SYN-MiniTid-Tau	4	d1-6	ANR35_MOUSE	Ankyrin repe	38.03
SYN-MiniTid-Tau	4	d1-6	ANR35_MOUSE	Ankyrin repe	38.03
RAM-MiniTid	12	d1-6	AP180_MOUSE	Clathrin coat	71.5
SYN-MiniTid-Tau	9	d1-6	AP3B1_MOUSE	AP-3 comple	40.97
SYN-MiniTid-Tau	9	d1-6	AP3B1_MOUSE	AP-3 comple	40.97
SYN-MiniTid-Tau	9	d1-6	AP3B1_MOUSE	AP-3 comple	40.97
RAM-MiniTid	12	d1-6	ASAP1_MOUSE	Arf-GAP with	87.6
RAM-MiniTid	15	d1-6	AT1A1_MOUSE	Sodium/potas	93.55
RAM-MiniTid	15	d1-6	AT1A1_MOUSE	Sodium/potas	93.55
RAM-MiniTid	16	d1-6	AT1A1_MOUSE	Sodium/potas	39.2
RAM-MiniTid	16	d1-6	AT1A1_MOUSE	Sodium/potas	39.2
RAM-MiniTid	15	d1-6	ATPB_MOUSE	ATP synthas	59.63
RAM-MiniTid	15	d1-6	ATPB_MOUSE	ATP synthas	50.99
RAM-MiniTid	12	d1-6	AUXI_MOUSE	Putative tyro	52.63
RAM-MiniTid	2	d1-6	B2MG_MOUSE	Beta-2-micro	41.25
RAM-MiniTid	12	d1-6	BAIP2_MOUSE	Brain-specifi	40.66
RAM-MiniTid	12	d1-6	BASP1_MOUSE	Brain acid so	52.17
SYN-MiniTid-Tau	17	d1-6	BASP1_MOUSE	Brain acid so	39.09
RAM-MiniTid	12	d1-6	BIN1_MOUSE	Myc box-dep	67.09
RAM-MiniTid	12	d1-6	BIN1_MOUSE	Myc box-dep	42.34

RAM-MiniTid	15	d1-6	BIN1_MOUSE	Myc box-dep	41.52
RAM-MiniTid	15	d1-6	BIN1_MOUSE	Myc box-dep	41.52
SYN-MiniTid-Tau	9	d1-6	BMP2_MOUSE	Bone morpho	41.04
SYN-MiniTid-Tau	9	d1-6	BMP2_MOUSE	Bone morpho	41.04
RAM-MiniTid	15	d1-6	BRAF_MOUSE	Serine/threor	57.11
RAM-MiniTid	15	d1-6	BRAF_MOUSE	Serine/threor	57.11
RAM-MiniTid	12	d1-6	BSN_MOUSE	Protein bass	71.37
RAM-MiniTid	12	d1-6	BSN_MOUSE	Protein bass	49.76
RAM-MiniTid	12	d1-6	BSN_MOUSE	Protein bass	47.87
RAM-MiniTid	15	d1-6	BSN_MOUSE	Protein bass	48.54
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	8	d1-6	CALR_MOUSE	Calreticulin C	37.08
RAM-MiniTid	12	d1-6	CEND_MOUSE	Cell cycle ex	59.29
RAM-MiniTid	12	d1-6	CEND_MOUSE	Cell cycle ex	41.55
RAM-MiniTid	15	d1-6	CEND_MOUSE	Cell cycle ex	52.72
SYN-MiniTid	6	d1-6	CFTR_MOUSE	Cystic fibrosi	39.45
SYN-MiniTid	6	d1-6	CFTR_MOUSE	Cystic fibrosi	39.45
RAM-MiniTid	13	d1-6	CH10_MOUSE	10 kDa heat	67.98
RAM-MiniTid	13	d1-6	CH10_MOUSE	10 kDa heat	67.98
RAM-MiniTid	13	d1-6	CH10_MOUSE	10 kDa heat	57.18
RAM-MiniTid	13	d1-6	CH10_MOUSE	10 kDa heat	57.18
RAM-MiniTid	15	d1-6	CH10_MOUSE	10 kDa heat	67.33
RAM-MiniTid	15	d1-6	CH10_MOUSE	10 kDa heat	67.33
RAM-MiniTid	15	d1-6	CH10_MOUSE	10 kDa heat	67.33
RAM-MiniTid	15	d1-6	CH10_MOUSE	10 kDa heat	67.33
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	3	d1-6	CH60_MOUSE	60 kDa heat	72.76
RAM-MiniTid	12	d1-6	CHM4B_MOUSE	Charged mul	58.58
SYN-MiniTid-Tau	9	d1-6	CHST9_MOUSE	Carbohydrat	41.04
RAM-MiniTid	15	d1-6	CLAP2_MOUSE	CLIP-associa	56.7
SYN-MiniTid-Tau	9	d1-6	COR1A_MOUSE	Coronin-1A C	41.41
SYN-MiniTid-Tau	17	d1-6	COR1A_MOUSE	Coronin-1A C	41.28
RAM-MiniTid	12	d1-6	CPLX1_MOUSE	Complexin-1	65.67
RAM-MiniTid	13	d1-6	CPLX1_MOUSE	Complexin-1	54.55
RAM-MiniTid	13	d1-6	CPLX1_MOUSE	Complexin-1	54.55
RAM-MiniTid	13	d1-6	CPLX1_MOUSE	Complexin-1	54.55
RAM-MiniTid	13	d1-6	CPLX1_MOUSE	Complexin-1	54.55
RAM-MiniTid	13	d1-6	CPLX2_MOUSE	Complexin-2	54.55
RAM-MiniTid	13	d1-6	CPLX2_MOUSE	Complexin-2	54.55
RAM-MiniTid	13	d1-6	CPLX2_MOUSE	Complexin-2	54.55
RAM-MiniTid	13	d1-6	CPLX2_MOUSE	Complexin-2	54.55
RAM-MiniTid	15	d1-6	CPLX2_MOUSE	Complexin-2	81.26

RAM-MiniTid	15	d1-6	CPLX2_MOUSE	Complexin-2	81.26
RAM-MiniTid	15	d1-6	CPLX2_MOUSE	Complexin-2	81.26
RAM-MiniTid	15	d1-6	CPLX2_MOUSE	Complexin-2	81.26
RAM-MiniTid	12	d1-6	CRIP2_MOUSE	Cysteine-rich	54.8
SYN-MiniTid-Tau	9	d1-6	CYLC2_MOUSE	Cylicin-2 OS	41.04
RAM-MiniTid	15	d1-6	CYLD_MOUSE	Ubiquitin carb	53.98
RAM-MiniTid	15	d1-6	CYLD_MOUSE	Ubiquitin carb	53.98
SYN-MiniTid	18	d1-6	DCLK1_MOUSE	Serine/threor	39.04
SYN-MiniTid-Tau	17	d1-6	DCR1C_MOUSE	Protein artem	42.11
RAM-MiniTid	12	d1-6	DCTN2_MOUSE	Dynactin sub	46.43
SYN-MiniTid-Tau	9	d1-6	DDX46_MOUSE	Probable ATP	41.41
SYN-MiniTid-Tau	9	d1-6	DDX46_MOUSE	Probable ATP	41.41
SYN-MiniTid-Tau	9	d1-6	DDX46_MOUSE	Probable ATP	41.41
SYN-MiniTid-Tau	9	d1-6	DDX46_MOUSE	Probable ATP	41.41
RAM-MiniTid	15	d1-6	DLG2_MOUSE	Disks large h	59.67
RAM-MiniTid	15	d1-6	DLG2_MOUSE	Disks large h	59.67
RAM-MiniTid	10	d1-6	DMXL2_MOUSE	DmX-like pro	41.44
RAM-MiniTid	15	d1-6	DOCK7_MOUSE	Dedicator of	42.34
RAM-MiniTid	15	d1-6	DOCK7_MOUSE	Dedicator of	42.34
RAM-MiniTid	12	d1-6	DPYL2_MOUSE	Dihydropyrim	78.21
RAM-MiniTid	12	d1-6	DPYL2_MOUSE	Dihydropyrim	57.52
RAM-MiniTid	15	d1-6	DPYL2_MOUSE	Dihydropyrim	89.68
RAM-MiniTid	15	d1-6	DPYL2_MOUSE	Dihydropyrim	89.68
RAM-MiniTid	15	d1-6	DPYL2_MOUSE	Dihydropyrim	60.44
RAM-MiniTid	15	d1-6	DPYL2_MOUSE	Dihydropyrim	60.44
RAM-MiniTid	12	d1-6	E41L1_MOUSE	Band 4.1-like	88.23
RAM-MiniTid	12	d1-6	E41L1_MOUSE	Band 4.1-like	50.32
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	117.59
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	117.59
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	117.59
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	107.69
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	107.69
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	107.69
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	46.04
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	46.04
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	46.04
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	45.22
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	45.22
RAM-MiniTid	15	d1-6	E41L1_MOUSE	Band 4.1-like	45.22
RAM-MiniTid	12	d1-6	E41L3_MOUSE	Band 4.1-like	63.66
SYN-MiniTid-Tau	9	d1-6	EDIL3_MOUSE	EGF-like rep	41.04
SYN-MiniTid-Tau	9	d1-6	EDIL3_MOUSE	EGF-like rep	41.04
RAM-MiniTid	15	d1-6	ELFN1_MOUSE	Protein ELFN	76.5
RAM-MiniTid	1	d1-6	ESRP2_MOUSE	Epithelial spli	42.42
RAM-MiniTid	1	d1-6	ESRP2_MOUSE	Epithelial spli	42.42
RAM-MiniTid	15	d1-6	FRS3_MOUSE	Fibroblast gr	40.64
RAM-MiniTid	15	d1-6	FUBP2_MOUSE	Far upstrean	41.72
RAM-MiniTid	15	d1-6	FUBP2_MOUSE	Far upstrean	41.72
RAM-MiniTid	15	d1-6	GBRA1_MOUSE	Gamma-amir	52.59
RAM-MiniTid	15	d1-6	GBRA1_MOUSE	Gamma-amir	52.59
RAM-MiniTid	15	d1-6	GBRA1_MOUSE	Gamma-amir	52.59
RAM-MiniTid	15	d1-6	GBRA1_MOUSE	Gamma-amir	52.59
RAM-MiniTid	15	d1-6	GBRA1_MOUSE	Gamma-amir	52.59
RAM-MiniTid	15	d1-6	GBRA1_MOUSE	Gamma-amir	52.59
RAM-MiniTid	15	d1-6	GGA1_MOUSE	ADP-ribosyla	43.13
RAM-MiniTid	15	d1-6	GGA1_MOUSE	ADP-ribosyla	43.13

RAM-MiniTid	15	d1-6	GIT1_MOUSE	ARF GTPas	50.24
RAM-MiniTid	16	d1-6	GNAI1_MOUSE	Guanine nuc	46.66
RAM-MiniTid	16	d1-6	GNAO_MOUSE	Guanine nuc	46.66
RAM-MiniTid	16	d1-6	GNAT3_MOUSE	Guanine nuc	46.66
RAM-MiniTid	12	d1-6	GRIN1_MOUSE	G protein-re	57.51
RAM-MiniTid	12	d1-6	GRIN1_MOUSE	G protein-re	55.99
RAM-MiniTid	12	d1-6	GRIN1_MOUSE	G protein-re	54.65
RAM-MiniTid	15	d1-6	GRIN1_MOUSE	G protein-re	60.39
RAM-MiniTid	15	d1-6	GRIN1_MOUSE	G protein-re	53.88
RAM-MiniTid	12	d1-6	H2B1A_MOUSE	Histone H2B	43.77
RAM-MiniTid	2	d1-6	ICAM1_MOUSE	Intercellular a	47.2
RAM-MiniTid	2	d1-6	ICAM1_MOUSE	Intercellular a	47.2
RAM-MiniTid	3	d1-6	ICAM1_MOUSE	Intercellular a	52.38
RAM-MiniTid	3	d1-6	ICAM1_MOUSE	Intercellular a	52.38
SYN-MiniTid-Tau	4	d1-6	ICAM1_MOUSE	Intercellular a	51.03
SYN-MiniTid-Tau	4	d1-6	ICAM1_MOUSE	Intercellular a	51.03
SYN-MiniTid	6	d1-6	ICAM1_MOUSE	Intercellular a	49.12
SYN-MiniTid	6	d1-6	ICAM1_MOUSE	Intercellular a	49.12
RAM-MiniTid	12	d1-6	IF4B_MOUSE	Eukaryotic tr	66.43
RAM-MiniTid	12	d1-6	IF4G3_MOUSE	Eukaryotic tr	61.8
RAM-MiniTid	8	d1-6	ITPI1_MOUSE	Protein ITPR	37.98
SYN-MiniTid-Tau	9	d1-6	ITSN2_MOUSE	Intersectin-2	41.04
SYN-MiniTid-Tau	9	d1-6	K1C9_MOUSE	Keratin, type	41.15
SYN-MiniTid-Tau	9	d1-6	K1C9_MOUSE	Keratin, type	41.15
RAM-MiniTid	15	d1-6	KCC2B_MOUSE	Calcium/calm	100.19
RAM-MiniTid	15	d1-6	KCC2B_MOUSE	Calcium/calm	100.19
RAM-MiniTid	12	d1-6	KT3K_MOUSE	Ketosamine-	66.81
RAM-MiniTid	15	d1-6	LAS1L_MOUSE	Ribosomal bi	48.38
RAM-MiniTid	15	d1-6	LAS1L_MOUSE	Ribosomal bi	44.43
RAM-MiniTid	12	d1-6	LASP1_MOUSE	LIM and SH3	88.44
RAM-MiniTid	12	d1-6	LGUL_MOUSE	Lactoylglutatl	47.94
RAM-MiniTid	15	d1-6	LNEBL_MOUSE	LIM zinc-binc	90.04
RAM-MiniTid	15	d1-6	LNEBL_MOUSE	LIM zinc-binc	75.21
RAM-MiniTid	12	d1-6	MAP1A_MOUSE	Microtubule-a	72.99
RAM-MiniTid	13	d1-6	MAP1A_MOUSE	Microtubule-a	77.34
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	77.58
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	66.52
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	61.66
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	61.24
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	60.64
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	55.44
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	53.07
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	42.59
RAM-MiniTid	15	d1-6	MAP1A_MOUSE	Microtubule-a	42.34
RAM-MiniTid	12	d1-6	MAP1B_MOUSE	Microtubule-a	75.87
RAM-MiniTid	12	d1-6	MAP1B_MOUSE	Microtubule-a	56.83
RAM-MiniTid	15	d1-6	MAP1B_MOUSE	Microtubule-a	80.01
SYN-MiniTid-Tau	4	d1-6	MAP6_MOUSE	Microtubule-a	54.2
SYN-MiniTid-Tau	4	d1-6	MAP6_MOUSE	Microtubule-a	54.2
SYN-MiniTid	5	d1-6	MAP6_MOUSE	Microtubule-a	45.23
SYN-MiniTid	5	d1-6	MAP6_MOUSE	Microtubule-a	45.23
RAM-MiniTid	13	d1-6	MAP6_MOUSE	Microtubule-a	103.18
RAM-MiniTid	13	d1-6	MAP6_MOUSE	Microtubule-a	60.29
RAM-MiniTid	13	d1-6	MAP6_MOUSE	Microtubule-a	54.07
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	121.95
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	121.56

RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	73.99
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	72
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	71.97
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	60.23
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	52.05
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	51.76
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	51.4
RAM-MiniTid	15	d1-6	MAP6_MOUSE	Microtubule-a	49.88
RAM-MiniTid	16	d1-6	MAP6_MOUSE	Microtubule-a	44.01
RAM-MiniTid	2	d1-6	MCCA_MOUSE	Methylcroton	63.5
RAM-MiniTid	2	d1-6	MCCA_MOUSE	Methylcroton	63.5
RAM-MiniTid	2	d1-6	MCCA_MOUSE	Methylcroton	63.5
RAM-MiniTid	2	d1-6	MCCA_MOUSE	Methylcroton	63.5
RAM-MiniTid	2	d1-6	MCCA_MOUSE	Methylcroton	63.5
RAM-MiniTid	2	d1-6	MCCA_MOUSE	Methylcroton	63.5
RAM-MiniTid	3	d1-6	MCCA_MOUSE	Methylcroton	66.97
RAM-MiniTid	3	d1-6	MCCA_MOUSE	Methylcroton	66.97
RAM-MiniTid	3	d1-6	MCCA_MOUSE	Methylcroton	66.97
RAM-MiniTid	3	d1-6	MCCA_MOUSE	Methylcroton	66.97
RAM-MiniTid	3	d1-6	MCCA_MOUSE	Methylcroton	66.97
RAM-MiniTid	3	d1-6	MCCA_MOUSE	Methylcroton	66.97
SYN-MiniTid-Tau	4	d1-6	MCCA_MOUSE	Methylcroton	59.83
SYN-MiniTid-Tau	4	d1-6	MCCA_MOUSE	Methylcroton	59.83
SYN-MiniTid-Tau	4	d1-6	MCCA_MOUSE	Methylcroton	59.83
SYN-MiniTid	6	d1-6	MCCA_MOUSE	Methylcroton	63.27
SYN-MiniTid	6	d1-6	MCCA_MOUSE	Methylcroton	63.27
SYN-MiniTid	6	d1-6	MCCA_MOUSE	Methylcroton	63.27
SYN-MiniTid	6	d1-6	MCCA_MOUSE	Methylcroton	63.27
SYN-MiniTid	6	d1-6	MCCA_MOUSE	Methylcroton	63.27
SYN-MiniTid	6	d1-6	MCCA_MOUSE	Methylcroton	63.27
RAM-MiniTid	10	d1-6	MCCA_MOUSE	Methylcroton	42.24
RAM-MiniTid	10	d1-6	MCCA_MOUSE	Methylcroton	42.24
RAM-MiniTid	10	d1-6	MCCA_MOUSE	Methylcroton	42.24
RAM-MiniTid	11	d1-6	MCCA_MOUSE	Methylcroton	53.47
RAM-MiniTid	11	d1-6	MCCA_MOUSE	Methylcroton	53.47
RAM-MiniTid	11	d1-6	MCCA_MOUSE	Methylcroton	53.47
RAM-MiniTid	13	d1-6	MCCA_MOUSE	Methylcroton	60.76
RAM-MiniTid	13	d1-6	MCCA_MOUSE	Methylcroton	60.76
SYN-MiniTid	18	d1-6	MCCA_MOUSE	Methylcroton	50.91
SYN-MiniTid	18	d1-6	MCCA_MOUSE	Methylcroton	46.69
RAM-MiniTid	15	d1-6	MECP2_MOUSE	Methyl-CpG-	40.18
RAM-MiniTid	15	d1-6	MECP2_MOUSE	Methyl-CpG-	40.18
RAM-MiniTid	15	d1-6	MECP2_MOUSE	Methyl-CpG-	40.18
RAM-MiniTid	15	d1-6	MECP2_MOUSE	Methyl-CpG-	40.18
SYN-MiniTid-Tau	7	d1-6	MEIOS_MOUSE	Meiosis initiat	40.27
RAM-MiniTid	16	d1-6	MET_MOUSE	Hepatocyte g	46.79
RAM-MiniTid	16	d1-6	MET_MOUSE	Hepatocyte g	46.79
RAM-MiniTid	16	d1-6	MET_MOUSE	Hepatocyte g	46.79
RAM-MiniTid	16	d1-6	MET_MOUSE	Hepatocyte g	46.04
RAM-MiniTid	16	d1-6	MET_MOUSE	Hepatocyte g	46.04
RAM-MiniTid	16	d1-6	MET_MOUSE	Hepatocyte g	46.04
SYN-MiniTid	6	d1-6	MINK1_MOUSE	Misshapen-lil	56.9
SYN-MiniTid	6	d1-6	MINK1_MOUSE	Misshapen-lil	56.9
SYN-MiniTid	6	d1-6	MINK1_MOUSE	Misshapen-lil	56.9
SYN-MiniTid	6	d1-6	MINK1_MOUSE	Misshapen-lil	56.9
RAM-MiniTid	15	d1-6	MINK1_MOUSE	Misshapen-lil	51.01

RAM-MiniTid	10	d1-6	MRTFB_MOUSE	Myocardin-re	38.25
SYN-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-a	58
SYN-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-a	58
SYN-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-a	44.38
SYN-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-a	44.38
SYN-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-a	41.93
SYN-MiniTid-Tau	4	d1-6	MTAP2_MOUSE	Microtubule-a	41.93
SYN-MiniTid	5	d1-6	MTAP2_MOUSE	Microtubule-a	46.87
SYN-MiniTid	5	d1-6	MTAP2_MOUSE	Microtubule-a	46.87
SYN-MiniTid	6	d1-6	MTAP2_MOUSE	Microtubule-a	56.55
SYN-MiniTid	6	d1-6	MTAP2_MOUSE	Microtubule-a	56.55
RAM-MiniTid	10	d1-6	MTAP2_MOUSE	Microtubule-a	42.73
RAM-MiniTid	10	d1-6	MTAP2_MOUSE	Microtubule-a	39.65
RAM-MiniTid	10	d1-6	MTAP2_MOUSE	Microtubule-a	39.65
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	64.47
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	54.8
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	53.91
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	47.99
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	44.51
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	42.64
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	42.35
RAM-MiniTid	12	d1-6	MTAP2_MOUSE	Microtubule-a	41.87
RAM-MiniTid	13	d1-6	MTAP2_MOUSE	Microtubule-a	48.58
RAM-MiniTid	13	d1-6	MTAP2_MOUSE	Microtubule-a	43.72
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	124.29
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	108.58
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	99.24
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	84.58
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	66.81
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	59.3
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	51.86
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	49.54
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	42.14
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	38.47
RAM-MiniTid	15	d1-6	MTAP2_MOUSE	Microtubule-a	41.97
SYN-MiniTid-Tau	17	d1-6	MTAP2_MOUSE	Microtubule-a	41.62
SYN-MiniTid	18	d1-6	MTAP2_MOUSE	Microtubule-a	40.52
SYN-MiniTid	18	d1-6	NDUAA_MOUSE	NADH dehyc	41.02
RAM-MiniTid	12	d1-6	NECP1_MOUSE	Adaptin ear-b	46.1
RAM-MiniTid	12	d1-6	NEUG_MOUSE	Neurogranin,	84.94
RAM-MiniTid	15	d1-6	NEUG_MOUSE	Neurogranin,	49.74
RAM-MiniTid	15	d1-6	NEUG_MOUSE	Neurogranin,	49.74
RAM-MiniTid	15	d1-6	NEUG_MOUSE	Neurogranin,	49.74
RAM-MiniTid	15	d1-6	NEUG_MOUSE	Neurogranin,	49.74
RAM-MiniTid	12	d1-6	NFM_MOUSE	Neurofilamer	47.27
RAM-MiniTid	12	d1-6	NFM_MOUSE	Neurofilamer	45.78
RAM-MiniTid	12	d1-6	NFM_MOUSE	Neurofilamer	42.54
RAM-MiniTid	13	d1-6	NFM_MOUSE	Neurofilamer	48.37
RAM-MiniTid	13	d1-6	NFM_MOUSE	Neurofilamer	48.37
RAM-MiniTid	15	d1-6	NFM_MOUSE	Neurofilamer	52.89
RAM-MiniTid	15	d1-6	NFM_MOUSE	Neurofilamer	49.4
RAM-MiniTid	15	d1-6	NMDE2_MOUSE	Glutamate re	42.56
RAM-MiniTid	15	d1-6	NMDE2_MOUSE	Glutamate re	42.56
RAM-MiniTid	12	d1-6	NOS1_MOUSE	Nitric oxide s	104.29
RAM-MiniTid	15	d1-6	NOS1_MOUSE	Nitric oxide s	62.93
RAM-MiniTid	15	d1-6	ODP2_MOUSE	Dihydrolipoyl	68.67

RAM-MiniTid	15	d1-6	ODP2_MOUSE	Dihydrolipoyl	47.42
SYN-MiniTid-Tau	9	d1-6	OTU7A_MOUSE	OTU domain	41.04
RAM-MiniTid	12	d1-6	OXR1_MOUSE	Oxidation res	53.92
RAM-MiniTid	1	d1-6	PCCA_MOUSE	Propionyl-Co	88.48
RAM-MiniTid	1	d1-6	PCCA_MOUSE	Propionyl-Co	88.48
RAM-MiniTid	1	d1-6	PCCA_MOUSE	Propionyl-Co	52.54
RAM-MiniTid	1	d1-6	PCCA_MOUSE	Propionyl-Co	52.54
RAM-MiniTid	2	d1-6	PCCA_MOUSE	Propionyl-Co	72.81
RAM-MiniTid	2	d1-6	PCCA_MOUSE	Propionyl-Co	72.81
RAM-MiniTid	3	d1-6	PCCA_MOUSE	Propionyl-Co	70.58
RAM-MiniTid	3	d1-6	PCCA_MOUSE	Propionyl-Co	70.58
RAM-MiniTid	3	d1-6	PCCA_MOUSE	Propionyl-Co	70.58
RAM-MiniTid	3	d1-6	PCCA_MOUSE	Propionyl-Co	70.58
SYN-MiniTid-Tau	4	d1-6	PCCA_MOUSE	Propionyl-Co	44.46
SYN-MiniTid-Tau	4	d1-6	PCCA_MOUSE	Propionyl-Co	44.46
SYN-MiniTid	5	d1-6	PCCA_MOUSE	Propionyl-Co	93.54
SYN-MiniTid	5	d1-6	PCCA_MOUSE	Propionyl-Co	93.54
SYN-MiniTid	6	d1-6	PCCA_MOUSE	Propionyl-Co	88.29
SYN-MiniTid	6	d1-6	PCCA_MOUSE	Propionyl-Co	50.02
SYN-MiniTid	6	d1-6	PCCA_MOUSE	Propionyl-Co	48.21
SYN-MiniTid	6	d1-6	PCCA_MOUSE	Propionyl-Co	48.21
SYN-MiniTid-Tau	7	d1-6	PCCA_MOUSE	Propionyl-Co	79.14
SYN-MiniTid-Tau	7	d1-6	PCCA_MOUSE	Propionyl-Co	79.14
RAM-MiniTid	10	d1-6	PCCA_MOUSE	Propionyl-Co	66.89
RAM-MiniTid	10	d1-6	PCCA_MOUSE	Propionyl-Co	66.89
RAM-MiniTid	10	d1-6	PCCA_MOUSE	Propionyl-Co	66.89
RAM-MiniTid	11	d1-6	PCCA_MOUSE	Propionyl-Co	73.82
RAM-MiniTid	11	d1-6	PCCA_MOUSE	Propionyl-Co	73.82
RAM-MiniTid	11	d1-6	PCCA_MOUSE	Propionyl-Co	68.86
RAM-MiniTid	11	d1-6	PCCA_MOUSE	Propionyl-Co	68.86
RAM-MiniTid	12	d1-6	PCCA_MOUSE	Propionyl-Co	68.59
RAM-MiniTid	12	d1-6	PCCA_MOUSE	Propionyl-Co	52.87
RAM-MiniTid	12	d1-6	PCCA_MOUSE	Propionyl-Co	47.09
RAM-MiniTid	12	d1-6	PCCA_MOUSE	Propionyl-Co	38.74
RAM-MiniTid	13	d1-6	PCCA_MOUSE	Propionyl-Co	72.6
RAM-MiniTid	13	d1-6	PCCA_MOUSE	Propionyl-Co	72.6
RAM-MiniTid	14	d1-6	PCCA_MOUSE	Propionyl-Co	71.65
RAM-MiniTid	14	d1-6	PCCA_MOUSE	Propionyl-Co	71.65
RAM-MiniTid	15	d1-6	PCCA_MOUSE	Propionyl-Co	48.53
RAM-MiniTid	15	d1-6	PCCA_MOUSE	Propionyl-Co	48.53
RAM-MiniTid	15	d1-6	PCCA_MOUSE	Propionyl-Co	44.65
RAM-MiniTid	16	d1-6	PCCA_MOUSE	Propionyl-Co	41.99
SYN-MiniTid	18	d1-6	PCCA_MOUSE	Propionyl-Co	83.89
SYN-MiniTid	18	d1-6	PCCA_MOUSE	Propionyl-Co	83.89
SYN-MiniTid	18	d1-6	PCCA_MOUSE	Propionyl-Co	41.3
SYN-MiniTid	18	d1-6	PCCA_MOUSE	Propionyl-Co	41.3
SYN-MiniTid	18	d1-6	PCCA_MOUSE	Propionyl-Co	41.89
RAM-MiniTid	15	d1-6	PCLO_MOUSE	Protein picco	52.56
RAM-MiniTid	12	d1-6	PFD2_MOUSE	Prefoldin sub	79.91
RAM-MiniTid	12	d1-6	PGAM1_MOUSE	Phosphoglyc	56.2
RAM-MiniTid	15	d1-6	PLAP_MOUSE	Phospholipas	87.67
RAM-MiniTid	15	d1-6	PLAP_MOUSE	Phospholipas	87.67
RAM-MiniTid	15	d1-6	PLAP_MOUSE	Phospholipas	52.65
RAM-MiniTid	15	d1-6	PLAP_MOUSE	Phospholipas	52.65
RAM-MiniTid	12	d1-6	PLEC_MOUSE	Plectin (Frag	63.19
RAM-MiniTid	15	d1-6	PLEC_MOUSE	Plectin, Gene	51.58

RAM-MiniTid	12	d1-6	PP1RB_MOUSE	E3 ubiquitin-p	44.32
RAM-MiniTid	1	d1-6	PYC_MOUSE	Pyruvate car	100.96
RAM-MiniTid	1	d1-6	PYC_MOUSE	Pyruvate car	100.96
RAM-MiniTid	1	d1-6	PYC_MOUSE	Pyruvate car	53.35
RAM-MiniTid	2	d1-6	PYC_MOUSE	Pyruvate car	71.09
RAM-MiniTid	2	d1-6	PYC_MOUSE	Pyruvate car	55.12
RAM-MiniTid	2	d1-6	PYC_MOUSE	Pyruvate car	55.12
RAM-MiniTid	2	d1-6	PYC_MOUSE	Pyruvate car	51.96
RAM-MiniTid	2	d1-6	PYC_MOUSE	Pyruvate car	51.96
RAM-MiniTid	2	d1-6	PYC_MOUSE	Pyruvate car	50.61
RAM-MiniTid	3	d1-6	PYC_MOUSE	Pyruvate car	50.01
RAM-MiniTid	3	d1-6	PYC_MOUSE	Pyruvate car	50.01
RAM-MiniTid	3	d1-6	PYC_MOUSE	Pyruvate car	48.63
RAM-MiniTid	3	d1-6	PYC_MOUSE	Pyruvate car	48.63
SYN-MiniTid-Tau	4	d1-6	PYC_MOUSE	Pyruvate car	97.32
SYN-MiniTid-Tau	4	d1-6	PYC_MOUSE	Pyruvate car	61.2
SYN-MiniTid-Tau	4	d1-6	PYC_MOUSE	Pyruvate car	59.18
SYN-MiniTid-Tau	4	d1-6	PYC_MOUSE	Pyruvate car	57.38
SYN-MiniTid-Tau	4	d1-6	PYC_MOUSE	Pyruvate car	54.42
SYN-MiniTid-Tau	4	d1-6	PYC_MOUSE	Pyruvate car	46.49
SYN-MiniTid-Tau	4	d1-6	PYC_MOUSE	Pyruvate car	45.47
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	58.96
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	58.96
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	48.87
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	48.87
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	44.57
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	44.57
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	43.85
SYN-MiniTid	5	d1-6	PYC_MOUSE	Pyruvate car	43.85
SYN-MiniTid	6	d1-6	PYC_MOUSE	Pyruvate car	70.11
SYN-MiniTid	6	d1-6	PYC_MOUSE	Pyruvate car	63.79
SYN-MiniTid	6	d1-6	PYC_MOUSE	Pyruvate car	51.71
SYN-MiniTid-Tau	9	d1-6	PYC_MOUSE	Pyruvate car	56.5
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	126.27
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	126.27
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	110.76
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	110.76
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	89.15
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	89.15
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	77.1
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	77.1
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	72.41
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	72.41
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	70.04
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	70.04
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	69.22
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	69.22
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	63.57
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	63.57
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	61.01
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	61.01
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	57.97
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	57.97
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	57.52
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	57.52
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	54.9

RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	54.9
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	54.77
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	54.77
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	54.12
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	54.12
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	50.67
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	50.67
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	43.02
RAM-MiniTid	11	d1-6	PYC_MOUSE	Pyruvate car	43.02
RAM-MiniTid	12	d1-6	PYC_MOUSE	Pyruvate car	61.98
RAM-MiniTid	12	d1-6	PYC_MOUSE	Pyruvate car	51.66
RAM-MiniTid	12	d1-6	PYC_MOUSE	Pyruvate car	50.75
RAM-MiniTid	13	d1-6	PYC_MOUSE	Pyruvate car	82.52
RAM-MiniTid	13	d1-6	PYC_MOUSE	Pyruvate car	82.52
RAM-MiniTid	13	d1-6	PYC_MOUSE	Pyruvate car	64.13
RAM-MiniTid	13	d1-6	PYC_MOUSE	Pyruvate car	64.13
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	123.19
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	123.19
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	72.52
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	72.52
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	69.66
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	69.66
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	55.82
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	55.82
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	55.61
RAM-MiniTid	14	d1-6	PYC_MOUSE	Pyruvate car	55.61
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	127.27
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	110.72
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	85.69
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	85.6
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	82.85
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	81.97
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	77.54
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	66.77
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	65.16
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	63.97
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	63.2
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	57.41
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	51.67
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	48.1
RAM-MiniTid	15	d1-6	PYC_MOUSE	Pyruvate car	45.96
RAM-MiniTid	16	d1-6	PYC_MOUSE	Pyruvate car	39.77
SYN-MiniTid	18	d1-6	PYC_MOUSE	Pyruvate car	79.66
SYN-MiniTid	18	d1-6	PYC_MOUSE	Pyruvate car	55.08
SYN-MiniTid	18	d1-6	PYC_MOUSE	Pyruvate car	49.66
SYN-MiniTid	18	d1-6	PYC_MOUSE	Pyruvate car	39.67
RAM-MiniTid	15	d1-6	RAF1_MOUSE	RAF proto-or	57.11
RAM-MiniTid	15	d1-6	RAF1_MOUSE	RAF proto-or	57.11
RAM-MiniTid	15	d1-6	RAF1_MOUSE	RAF proto-or	57.11
RAM-MiniTid	15	d1-6	RAF1_MOUSE	RAF proto-or	57.11
RAM-MiniTid	15	d1-6	RAF1_MOUSE	RAF proto-or	57.11
RAM-MiniTid	15	d1-6	RASL1_MOUSE	RasGAP-act	43.04
SYN-MiniTid-Tau	9	d1-6	RGS22_MOUSE	Regulator of	41.04
RAM-MiniTid	8	d1-6	RL3_MOUSE	60S ribosoma	39.22
RAM-MiniTid	3	d1-6	RS3A_MOUSE	40S ribosoma	52.23
RAM-MiniTid	3	d1-6	RS3A_MOUSE	40S ribosoma	52.23

RAM-MiniTid	3	d1-6	RS3A_MOUSE	40S ribosoma	52.23
RAM-MiniTid	3	d1-6	RS3A_MOUSE	40S ribosoma	52.23
RAM-MiniTid	15	d1-6	RS3A_MOUSE	40S ribosoma	71.2
RAM-MiniTid	15	d1-6	RT31_MOUSE	28S ribosoma	53.59
RAM-MiniTid	15	d1-6	RT31_MOUSE	28S ribosoma	53.59
RAM-MiniTid	15	d1-6	RTN1_MOUSE	Reticulon-1,	83.17
RAM-MiniTid	15	d1-6	RTN3_MOUSE	Reticulon-3,	54.05
RAM-MiniTid	15	d1-6	RTN3_MOUSE	Reticulon-3,	37.35
RAM-MiniTid	15	d1-6	S12A5_MOUSE	Solute carrier	64.35
RAM-MiniTid	15	d1-6	S12A5_MOUSE	Solute carrier	64.35
RAM-MiniTid	15	d1-6	S12A5_MOUSE	Solute carrier	64.35
RAM-MiniTid	15	d1-6	SET_MOUSE	Protein SET,	41.03
RAM-MiniTid	15	d1-6	SET_MOUSE	Protein SET,	41.03
SYN-MiniTid	6	d1-6	SHAN2_MOUSE	SH3 and mul	60.27
SYN-MiniTid	6	d1-6	SHAN2_MOUSE	SH3 and mul	60.27
SYN-MiniTid	6	d1-6	SHAN2_MOUSE	SH3 and mul	60.27
SYN-MiniTid	6	d1-6	SHAN2_MOUSE	SH3 and mul	60.27
SYN-MiniTid	6	d1-6	SHAN2_MOUSE	SH3 and mul	60.27
SYN-MiniTid	6	d1-6	SHAN2_MOUSE	SH3 and mul	60.27
RAM-MiniTid	12	d1-6	SHAN2_MOUSE	SH3 and mul	46.46
RAM-MiniTid	15	d1-6	SHAN2_MOUSE	SH3 and mul	92.55
RAM-MiniTid	15	d1-6	SHAN2_MOUSE	SH3 and mul	92.55
RAM-MiniTid	15	d1-6	SHAN2_MOUSE	SH3 and mul	60.38
RAM-MiniTid	15	d1-6	SHAN2_MOUSE	SH3 and mul	60.38
RAM-MiniTid	15	d1-6	SHAN2_MOUSE	SH3 and mul	54.51
RAM-MiniTid	15	d1-6	SHAN2_MOUSE	SH3 and mul	54.51
SYN-MiniTid	18	d1-6	SHAN2_MOUSE	SH3 and mul	45.29
RAM-MiniTid	16	d1-6	SHOC1_MOUSE	Protein short	50.18
SYN-MiniTid-Tau	7	d1-6	SMC4_MOUSE	Structural ma	41.88
SYN-MiniTid-Tau	7	d1-6	SMC4_MOUSE	Structural ma	41.88
SYN-MiniTid-Tau	7	d1-6	SMC4_MOUSE	Structural ma	41.24
SYN-MiniTid-Tau	7	d1-6	SMC4_MOUSE	Structural ma	41.24
SYN-MiniTid-Tau	7	d1-6	SMC4_MOUSE	Structural ma	41.54
SYN-MiniTid-Tau	7	d1-6	SMC4_MOUSE	Structural ma	41.54
RAM-MiniTid	10	d1-6	SMC4_MOUSE	Structural ma	38.95
RAM-MiniTid	10	d1-6	SMC4_MOUSE	Structural ma	38.95
RAM-MiniTid	10	d1-6	SMC4_MOUSE	Structural ma	41.81
RAM-MiniTid	10	d1-6	SMC4_MOUSE	Structural ma	41.81
RAM-MiniTid	10	d1-6	SMC4_MOUSE	Structural ma	41.81
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
SYN-MiniTid	5	d1-6	SNP25_MOUSE	Synaptosoma	64.87
RAM-MiniTid	12	d1-6	SPAST_MOUSE	Spastin, Gen	43.12
SYN-MiniTid	6	d1-6	SPTN1_MOUSE	Spectrin alph	39.8
SYN-MiniTid	6	d1-6	SPTN1_MOUSE	Spectrin alph	39.8

RAM-MiniTid	12	d1-6	SPTN1_MOUSE	Spectrin alph	52.46
RAM-MiniTid	12	d1-6	SPTN1_MOUSE	Spectrin alph	49.98
RAM-MiniTid	12	d1-6	SRBS1_MOUSE	Sorbin and S	53.51
RAM-MiniTid	12	d1-6	SRC8_MOUSE	Src substrate	47.86
RAM-MiniTid	12	d1-6	SRC8_MOUSE	Src substrate	40.42
RAM-MiniTid	15	d1-6	SRC8_MOUSE	Src substrate	71.92
RAM-MiniTid	15	d1-6	SRC8_MOUSE	Src substrate	71.92
RAM-MiniTid	15	d1-6	SRC8_MOUSE	Src substrate	55.13
RAM-MiniTid	15	d1-6	SRC8_MOUSE	Src substrate	55.13
RAM-MiniTid	15	d1-6	SRRM2_MOUSE	Serine/arginir	46.9
RAM-MiniTid	12	d1-6	STMN1_MOUSE	Stathmin, Ge	103.6
RAM-MiniTid	12	d1-6	STMN1_MOUSE	Stathmin, Ge	46.7
RAM-MiniTid	12	d1-6	STMN1_MOUSE	Stathmin, Ge	42.41
SYN-MiniTid-Tau	7	d1-6	STON1_MOUSE	Stonin-1 OS=	40.2
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid-Tau	4	d1-6	STXB1_MOUSE	Syntaxin-binc	58.1
SYN-MiniTid	6	d1-6	SUGP2_MOUSE	SURP and G	56.21
SYN-MiniTid	6	d1-6	SUGP2_MOUSE	SURP and G	56.21
RAM-MiniTid	15	d1-6	SUGP2_MOUSE	SURP and G	80.7
RAM-MiniTid	15	d1-6	SUGP2_MOUSE	SURP and G	44.93
RAM-MiniTid	15	d1-6	SYGP1_MOUSE	Ras/Rap GT	60.63
RAM-MiniTid	15	d1-6	SYGP1_MOUSE	Ras/Rap GT	60.63
RAM-MiniTid	12	d1-6	SYN1_MOUSE	Synapsin-1, (	49.45
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid-Tau	4	d1-6	SYNC_MOUSE	Asparagine--	51.57
SYN-MiniTid	6	d1-6	SYNC_MOUSE	Asparagine--	44.75
SYN-MiniTid	6	d1-6	SYNC_MOUSE	Asparagine--	44.75
SYN-MiniTid	6	d1-6	SYNC_MOUSE	Asparagine--	44.75
SYN-MiniTid	6	d1-6	SYNC_MOUSE	Asparagine--	44.75
SYN-MiniTid	6	d1-6	SYNC_MOUSE	Asparagine--	44.75
SYN-MiniTid	6	d1-6	SYNC_MOUSE	Asparagine--	44.75
RAM-MiniTid	10	d1-6	SYNE1_MOUSE	Nesprin-1 OS	40.04
RAM-MiniTid	12	d1-6	SYNJ1_MOUSE	Synaptojanin	46.03
RAM-MiniTid	15	d1-6	SYNRG_MOUSE	Synergin gan	100.94
RAM-MiniTid	15	d1-6	SYNRG_MOUSE	Synergin gan	84.06
RAM-MiniTid	15	d1-6	SYNRG_MOUSE	Synergin gan	51.45
SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	54.81
SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	54.81
SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	54.81
SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	54.81
SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	47.72
SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	47.72

SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	47.72
SYN-MiniTid	6	d1-6	SYUA_MOUSE	Alpha-synucl	47.72
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	39.09
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	39.09
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	39.09
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	39.09
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	39.09
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	39.09
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	41.69
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	41.69
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	41.69
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	41.69
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	41.69
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	41.69
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	38.74
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	38.74
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	38.74
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	38.74
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	38.74
RAM-MiniTid	10	d1-6	SYUA_MOUSE	Alpha-synucl	38.74
RAM-MiniTid	13	d1-6	SYUA_MOUSE	Alpha-synucl	72.25
RAM-MiniTid	13	d1-6	SYUA_MOUSE	Alpha-synucl	72.25
RAM-MiniTid	13	d1-6	SYUA_MOUSE	Alpha-synucl	43.61
RAM-MiniTid	13	d1-6	SYUA_MOUSE	Alpha-synucl	43.61
RAM-MiniTid	13	d1-6	SYUA_MOUSE	Alpha-synucl	41.96
RAM-MiniTid	13	d1-6	SYUA_MOUSE	Alpha-synucl	41.96
RAM-MiniTid	15	d1-6	SYUA_MOUSE	Alpha-synucl	73.41
RAM-MiniTid	15	d1-6	SYUA_MOUSE	Alpha-synucl	73.41
RAM-MiniTid	15	d1-6	SYUA_MOUSE	Alpha-synucl	65.5
RAM-MiniTid	15	d1-6	SYUA_MOUSE	Alpha-synucl	65.5
SYN-MiniTid	18	d1-6	SYUA_MOUSE	Alpha-synucl	38.34
SYN-MiniTid	18	d1-6	SYUA_MOUSE	Alpha-synucl	38.34
SYN-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synucle	77.99
SYN-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synucle	77.99
SYN-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synucle	48.89
SYN-MiniTid-Tau	4	d1-6	SYUB_MOUSE	Beta-synucle	48.89
SYN-MiniTid	5	d1-6	SYUB_MOUSE	Beta-synucle	49.73
SYN-MiniTid	5	d1-6	SYUB_MOUSE	Beta-synucle	49.73
SYN-MiniTid	5	d1-6	SYUB_MOUSE	Beta-synucle	45.22
SYN-MiniTid	5	d1-6	SYUB_MOUSE	Beta-synucle	45.22
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.79
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.79
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.79
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.79
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.79
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.79
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.41
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	73.41
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	70.61
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	70.61
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	70.61
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	70.61
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	70.61
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	70.61
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	54.81
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	54.81

SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	54.81
SYN-MiniTid	6	d1-6	SYUB_MOUSE	Beta-synucle	54.81
RAM-MiniTid	10	d1-6	SYUB_MOUSE	Beta-synucle	81.12
RAM-MiniTid	10	d1-6	SYUB_MOUSE	Beta-synucle	81.12
RAM-MiniTid	10	d1-6	SYUB_MOUSE	Beta-synucle	81.12
RAM-MiniTid	10	d1-6	SYUB_MOUSE	Beta-synucle	43.14
RAM-MiniTid	10	d1-6	SYUB_MOUSE	Beta-synucle	41.69
RAM-MiniTid	10	d1-6	SYUB_MOUSE	Beta-synucle	41.69
RAM-MiniTid	11	d1-6	SYUB_MOUSE	Beta-synucle	57.17
RAM-MiniTid	12	d1-6	SYUB_MOUSE	Beta-synucle	78.15
RAM-MiniTid	12	d1-6	SYUB_MOUSE	Beta-synucle	77.82
RAM-MiniTid	12	d1-6	SYUB_MOUSE	Beta-synucle	77.82
RAM-MiniTid	12	d1-6	SYUB_MOUSE	Beta-synucle	46.58
RAM-MiniTid	12	d1-6	SYUB_MOUSE	Beta-synucle	46.58
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	74.73
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	74.73
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	74.73
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	73.56
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	73.56
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	73.56
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	72.25
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	72.25
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	50.72
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	48.81
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	48.81
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	48.81
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	41.96
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	41.96
RAM-MiniTid	13	d1-6	SYUB_MOUSE	Beta-synucle	41.96
RAM-MiniTid	14	d1-6	SYUB_MOUSE	Beta-synucle	85.13
RAM-MiniTid	14	d1-6	SYUB_MOUSE	Beta-synucle	53.96
RAM-MiniTid	15	d1-6	SYUB_MOUSE	Beta-synucle	133.02
RAM-MiniTid	15	d1-6	SYUB_MOUSE	Beta-synucle	85.96
RAM-MiniTid	15	d1-6	SYUB_MOUSE	Beta-synucle	81.1
RAM-MiniTid	15	d1-6	SYUB_MOUSE	Beta-synucle	73.41
RAM-MiniTid	15	d1-6	SYUB_MOUSE	Beta-synucle	61.31
RAM-MiniTid	15	d1-6	SYUB_MOUSE	Beta-synucle	49.48
RAM-MiniTid	15	d1-6	SYUB_MOUSE	Beta-synucle	42.45
SYN-MiniTid-Tau	17	d1-6	SYUB_MOUSE	Beta-synucle	37.82
RAM-MiniTid	10	d1-6	SYUG_MOUSE	Gamma-synu	81.12
RAM-MiniTid	10	d1-6	SYUG_MOUSE	Gamma-synu	81.12
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	4	d1-6	TAU_MOUSE	Microtubule-a	52.9
SYN-MiniTid-Tau	7	d1-6	TAU_MOUSE	Microtubule-a	38.79
SYN-MiniTid-Tau	7	d1-6	TAU_MOUSE	Microtubule-a	38.79
SYN-MiniTid-Tau	7	d1-6	TAU_MOUSE	Microtubule-a	38.79
SYN-MiniTid-Tau	7	d1-6	TAU_MOUSE	Microtubule-a	38.79
SYN-MiniTid-Tau	7	d1-6	TAU_MOUSE	Microtubule-a	38.79
SYN-MiniTid-Tau	17	d1-6	TAU_MOUSE	Microtubule-a	38.17

SYN-MiniTid-Tau	17	d1-6	TAU_MOUSE	Microtubule-a	38.17
RAM-MiniTid	15	d1-6	TB182_MOUSE	182 kDa tank	62.47
RAM-MiniTid	12	d1-6	TBCB_MOUSE	Tubulin-foldir	51.62
RAM-MiniTid	10	d1-6	TCOF_MOUSE	Treacle prote	41.63
RAM-MiniTid	8	d1-6	TEP1_MOUSE	Telomerase p	41.59
RAM-MiniTid	8	d1-6	TEP1_MOUSE	Telomerase p	38.41
SYN-MiniTid-Tau	9	d1-6	TEP1_MOUSE	Telomerase p	41.66
RAM-MiniTid	10	d1-6	TIM44_MOUSE	Mitochondria	49.82
RAM-MiniTid	10	d1-6	TIM44_MOUSE	Mitochondria	49.82
RAM-MiniTid	13	d1-6	TIM44_MOUSE	Mitochondria	49.59
RAM-MiniTid	13	d1-6	TIM44_MOUSE	Mitochondria	49.59
RAM-MiniTid	15	d1-6	TIM44_MOUSE	Mitochondria	55.57
RAM-MiniTid	15	d1-6	TIM44_MOUSE	Mitochondria	55.57
SYN-MiniTid	18	d1-6	TIM44_MOUSE	Mitochondria	58.49
RAM-MiniTid	3	d1-6	TMM17_MOUSE	Transmembr	40.12
RAM-MiniTid	3	d1-6	TMM17_MOUSE	Transmembr	40.12
RAM-MiniTid	15	d1-6	TRAP1_MOUSE	Heat shock p	50.32
RAM-MiniTid	15	d1-6	TRAP1_MOUSE	Heat shock p	50.32
RAM-MiniTid	15	d1-6	TRAP1_MOUSE	Heat shock p	50.32
RAM-MiniTid	12	d1-6	VAMP2_MOUSE	Vesicle-asso	58.46
SYN-MiniTid	5	d1-6	VCIP1_MOUSE	Deubiquitinat	40.62
SYN-MiniTid	5	d1-6	VCIP1_MOUSE	Deubiquitinat	40.62
RAM-MiniTid	15	d1-6	VCIP1_MOUSE	Deubiquitinat	74.05
SYN-MiniTid-Tau	7	d1-6	WEE1_MOUSE	Wee1-like pr	40.43
SYN-MiniTid-Tau	7	d1-6	WEE1_MOUSE	Wee1-like pr	40.43
RAM-MiniTid	12	d1-6	WIPF3_MOUSE	WAS/WASL-i	77.52
SYN-MiniTid-Tau	9	d1-6	WNT2_ECHTE	Protein Wnt-2	41.04
RAM-MiniTid	2	d1-6	ZEB1_MOUSE	Zinc finger E·	41.79
RAM-MiniTid	2	d1-6	ZEB1_MOUSE	Zinc finger E·	41.79
RAM-MiniTid	2	d1-6	ZEB1_MOUSE	Zinc finger E·	41.79
RAM-MiniTid	2	d1-6	ZEB1_MOUSE	Zinc finger E·	41.79
RAM-MiniTid	2	d1-6	ZEB1_MOUSE	Zinc finger E·	41.79
RAM-MiniTid	2	d1-6	ZEB1_MOUSE	Zinc finger E·	41.79

olidation-retrieval-reconsolidation (RRc) spatial memory phases [in progress]

ptide Sequer	Peptide Mod	Position of peptide modification
VAEDEFDPI	Biotin (K)	0.00000000000000100000000.0
VAEDEFDPI	Biotin (K)	0.00000000000000100000000.0
TLEPVKPPT	Biotin (K)	0.00000100000000000000.0
TLEPVKPPT	Biotin (K)	0.00000100000000000000.0
TLEPVKPPT	Biotin (K)	0.00000100000000000000.0
RKPRAKGKI	Biotin (K)	0.0100000000.0
HSFQKQQR	Biotin (K)	0.00001000.0
SLVQGELVT	Biotin (K)	0.00000000000100000.0
ADEVEKSSS	Biotin (K)	0.00000100000000.0
ITWMKAEDS	Biotin (K)	0.00001000000.0
LAADVGKGS	Biotin (K)	0.000000100000.0
LLLQVQHAS	Biotin (K)	0.0000000001000000.0
LAADVGKAC	Biotin (K)	0.000000100000.0
LAADVGKAC	Biotin (K)	0.000000100000.0
LAADVGKAC	Biotin (K)	0.000000100000.0
LAADVGKAC	Biotin (K)	0.000000100000.0
LLLQVQHAS	Biotin (K)	0.0000000001000000.0
LLLQVQHAS	Biotin (K)	0.0000000001000000.0
LLLQVQHAS	Biotin (K)	0.0000000001000000.0
LLLQVQHAS	Biotin (K)	0.0000000001000000.0
AGLQTADK'	Biotin (K)	0.00000001000000000000000000000000000000.0
AGLQTADK'	Biotin (K)	0.00000001000000000000000000000000000000.0
AGLQTADK'	Biotin (K)	0.00000001000000000000000000000000000000.0
TGKSATEES	Biotin (K)	0.001000000000000.0
KTGKSATEE	Biotin (K)	0.1000000000000000.0
ILSSTASKVS	Biotin (K)	0.00000001000000000.0
RHPYFYAPE	Biotin (K)	0.0000000000000000100.0
TCVADESHA	2 Carbamido	0.0200000000200.0
IVAPGKGILA	Biotin (K)	0.00000100000000000000.0
SSLFLASSA	Biotin (K)	0.000000000010000000000000000.0
LASRKSARF	Biotin (K)	0.00000000001.0
LASRKSARF	Biotin (K)	0.00000000001.0
LASRKSARF	Biotin (K)	0.00000000001.0
LASRKSARF	Biotin (K)	0.00000000001.0
KGDLQWNA	Biotin (K)	0.10000000000.0
EKTVIGSVLI	Biotin (K)	0.01000000000.0
EKTVIGSVLI	Biotin (K)	0.01000000000.0
EKTVIGSVLI	Biotin (K)	0.01000000000.0
TANKFEGLS	Biotin (K)	0.00010000000000000.0
MGIVGSDVS	Biotin (K)	0.3000000001000030000000000000000000.0
MGIVGSDVS	Biotin (K)	0.3000000001000030000000000000000000.0
MGIVGSDVS	Biotin (K)	0.0000000001000030000000000000000000.0
MGIVGSDVS	Biotin (K)	0.0000000001000030000000000000000000.0
AQASAAPKA	Biotin (K)	0.000000010000000.0
AAQASAAPK	Biotin (K)	0.0000000010000000.0
GKGSTNLE(	Biotin (K)	0.0100000000.0
SLSGLEAIQ	Biotin (K)	0.0000000000001.0
SQGSKNPQ	Biotin (K)	0.000010000.0
SDAAPAASL	Biotin (K)	0.00000000010000000000.0
QSVAVKE	Biotin (K)	0.0000010.0
GVTAGKIAS	Biotin (K)	0.0000010000000.0
IAKPVSLLEK	Biotin (K)	0.0010000000.0

IAKPVSLLEK	Biotin (K)	0.0010000000.0
IAKPVSLLEK	Biotin (K)	0.0010000000.0
EKQGVSKR	Biotin (K)	0.00000010.0
EKQGVSKR	Biotin (K)	0.00000010.0
VFLPNKQR	Biotin (K)	0.00000100.0
VFLPNKQR	Biotin (K)	0.00000100.0
TGGTASPKI	Biotin (K)	0.00000001000.0
ASPQATKAS	Biotin (K)	0.00000010000000.0
AEHQAASKA	Biotin (K)	0.00000001000000.0
GLAGPTTVF	Biotin (K)	0.00000000000100000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
CGPGTKKVI	Biotin (K)	0.000001000000000.0
GKSASSPKF	Biotin (K)	0.010000000000.0
ATPAADGKA	Biotin (K)	0.00000000000010000.0
GKSASSPKF	Biotin (K)	0.010000000000.0
ACLVVLCLLI	Biotin (K)	0.00000000001.0
ACLVVLCLLI	Biotin (K)	0.00000000001.0
SAAETVTKG	Biotin (K)	0.0000000100000000.0
SAAETVTKG	Biotin (K)	0.0000000100000000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
SAAETVTKG	Biotin (K)	0.0000000100030000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
VKDGKTLNI	Biotin (K)	0.000010000000000000.0
AGKGGPTP	Biotin (K)	0.00100000000000.0
EKKRDQK	Biotin (K)	0.0000001.0
AGGDAADG	Biotin (K)	0.00000000000000010000000000000000.0
LEEEMRK	Biotin (K)	0.0000001.0
LEEEMRK	Biotin (K)	0.0000001.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0

QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
QALGGATK	Biotin (K)	0.000000010000.0
KTSGPPKG	Biotin (K)	0.00000010000.0
EKGAKKDR	Biotin (K)	0.00000100.0
SKNPWYIDE	Biotin (K)	0.0100000000000000.0
SKNPWYIDE	Biotin (K)	0.0100000000000000.0
LYLVMELVK	Biotin (K)	0.000000001.0
KPLGKLKR	Biotin (K)	0.00001000.0
SSKGSSGG	Biotin (K)	0.001000000.0
LEEEMRK	Biotin (K)	0.0000001.0
LEEEMRK	Biotin (K)	0.0000001.0
LEEEMRK	Biotin (K)	0.0000001.0
LEEEMRK	Biotin (K)	0.0000001.0
FNAKPGVID	Biotin (K)	0.000000000010000000000000.0
FNAKPGVID	Biotin (K)	0.000000000010000000000000.0
GVKSRWVL	Biotin (K)	0.0010000000.0
SIIGSKGLDI	Biotin (K)	0.0000010000.0
SIIGSKGLDI	Biotin (K)	0.0000010000.0
TVTPASSAK	Biotin (K)	0.00000000100000.0
TSPAKQQAI	Biotin (K)	0.000010000000.0
GLYDGPVC	Biotin (K)	0.00000002000000100000000.0
GLYDGPVC	Biotin (K)	0.00000002000000100000000.0
GLYDGPVC	Biotin (K)	0.00000002000000100000000.0
GLYDGPVC	Biotin (K)	0.00000002000000100000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
TLKEPNSKL	Biotin (K)	0.000000010000.0
SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
SLSPIIGKDV	Biotin (K)	0.000000010000000000000000000000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
TVKGGFSE	Biotin (K)	0.0010000000.0
TVKGGFSE	Biotin (K)	0.0010000000.0
TVKGGFSE	Biotin (K)	0.0010000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
SGKGAAAM	Biotin (K)	0.00100000000000000000.0
GKEGSSVTI	Biotin (K)	0.010000000000.0
EKQRKDK	Biotin (K)	0.0000001.0
EKQRKDK	Biotin (K)	0.0000001.0
SGAVSAAEI	Biotin (K)	0.000000000000000000001000000000.0
SSQLFSKPE	Biotin (K)	0.000000000001.0
SSQLFSKPE	Biotin (K)	0.000000000001.0
KTAAMSDL	Biotin (K)	0.1000000000.0
KDAFADAV	Biotin (K)	0.1000000000.0
KDAFADAV	Biotin (K)	0.1000000000.0
GDPGLATIA	Biotin (K)	0.00000000010000000.0
GDPGLATIA	Biotin (K)	0.00000000010000000.0
GDPGLATIA	Biotin (K)	0.00000000010000000.0
GDPGLATIA	Biotin (K)	0.00000000010000000.0
GDPGLATIA	Biotin (K)	0.00000000010000000.0
GDPGLATIA	Biotin (K)	0.00000000010000000.0
NVIFEDEEK	Biotin (K)	0.00000000001.0
NVIFEDEEK	Biotin (K)	0.00000000001.0

SMYEPGSAI	Biotin (K)	0.00000000010000000000000.0
KSTIVK	Biotin (K)	0.000001.0
KSTIVK	Biotin (K)	0.000001.0
KSTIVK	Biotin (K)	0.000001.0
TALVSPGKV	Biotin (K)	0.0000000100000000.0
TVPTSSGKT	Biotin (K)	0.0000000100000000.0
KVETISSGK	Biotin (K)	0.100000000.0
AETVSPGEV	Biotin (K)	0.00000000000000000100000000.0
ASLPASEKT	Biotin (K)	0.0000000100000000.0
AVTKYTSSK	Biotin (K)	0.000000001.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
LQKAQEEAL	Biotin (K)	0.000000000001000.0
AASIFGGAK	Biotin (K)	0.0000000010000000.0
VLDPSKFLK	Biotin (K)	0.000001000.0
GAMPYKG	Biotin (K)	0.0000010.0
EKQRKDK	Biotin (K)	0.0000001.0
GSGGSYGG	Biotin (K)	0.00000000000000001.0
GSGGSYGG	Biotin (K)	0.00000000000000001.0
NSSAITSPK(	Biotin (K)	0.00000000100000000000000000000000.0
NSSAITSPK(	Biotin (K)	0.00000000100000000000000000000000.0
EAGTVGKG	Biotin (K)	0.00000010000000.0
TKCSNLPLK	Biotin (K)	0.012000000.0
KTKCSNLPL	Biotin (K)	0.0012000000.0
GKGFSVVAI	Biotin (K)	0.010000000000000.0
KPDDGKMK	Biotin (K)	0.00000100.0
KSTQVVSDA	Biotin (K)	0.000000000001000000000000.0
STQVVSDAA	Biotin (K)	0.00000000001000000000000.0
DTAVELGKC	Biotin (K)	0.0000000100000.0
DFQEPLPQI	Biotin (K)	0.000000001000000.0
EGEGGAGA	Biotin (K)	0.0000000000000000100000000000.0
GKDLYLEDC	Biotin (K)	0.0100000000000000.0
SPWASDFKI	Biotin (K)	0.00000000000000001000000.0
DFQEPLPQI	Biotin (K)	0.000000001000000.0
DTAVELGKC	Biotin (K)	0.0000000100000.0
TQGQKSSF	Biotin (K)	0.000010000000.0
GVEQQDGA	Biotin (K)	0.00000000000100.0
DQILSEKAA	Biotin (K)	0.0000001000000.0
SSFLEDKST	Biotin (K)	0.000000100000.0
ITKTPQAST	Biotin (K)	0.00100000000000000.0
SAKTATAGF	Biotin (K)	0.0010000000000.0
ITKTPQAST	Biotin (K)	0.00100000000000000.0
NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
NQDPIIPVPL	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0
DQGAVLLG	Biotin (K)	0.000000000100000000000.0

RGDHPWIPI	Biotin (K)	0.00000000100000000000000000000.0
NQDPIIPVPl	Biotin (K)	0.0000000000100000000000.0
DQGAVLLG	Biotin (K)	0.0000000000100000000000.0
NQDPIIPVPl	Biotin (K)	0.0000000000100000000000.0
RGDHPWIPI	Biotin (K)	0.00000000100000000000000000000.0
NQSPVVLGI	Biotin (K)	0.0000000000100000000000.0
GHDSVFVAI	Biotin (K)	0.0000000000100000000000.0
DQGAVLLG	Biotin (K)	0.0000000000100000000000.0
DQGAVLLG	Biotin (K)	
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
KMEHTIK	Biotin (K)	0.1000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
IAMKMEHTII	Biotin (K)	0.0001000000.0
KMEHTIK	Biotin (K)	0.1000000.0
EVVKPLLVS	Biotin (K)	0.00010000000000.0
EVVKPLLVS	Biotin (K)	0.00010000000000.0
EVVKPLLVS	Biotin (K)	0.00010000000000.0
EVVKPLLVS	Biotin (K)	0.00010000000000.0
WLLKGKLRI	Biotin (K)	0.000100000.0
QLNLQLPLK	Biotin (K)	0.00000000100.0
QLNLQLPLK	Biotin (K)	0.00000000100.0
QLNLQLPLK	Biotin (K)	0.00000000100.0
QLNLQLPLK	Biotin (K)	0.00000000001.0
QLNLQLPLK	Biotin (K)	0.00000000001.0
QLNLQLPLK	Biotin (K)	0.00000000001.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0
GINPADKPA	Biotin (K)	0.000000100000.0

QKSLKEVLC	Biotin (K)	0.01000000000.0
VSDFGQMA	Biotin (K)	0.0000000000000000100000.0
VSDFGQMA	Biotin (K)	0.0000000000000000100000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
LILKPAIK	Biotin (K)	0.00010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
VSDFGQMA	Biotin (K)	0.0000000000000000100000.0
VSDFGQMA	Biotin (K)	0.0000000000000000100000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
LILKPAIK	Biotin (K)	0.00010000.0
LILKPAIK	Biotin (K)	0.00010000.0
TLGKVTSEF	Biotin (K)	0.000100000000000.0
TLGKVTSEF	Biotin (K)	0.0001000000000000.0
TLGKVTSEF	Biotin (K)	0.000100000000000.0
MFTIDPKVY	Biotin (K)	0.000000100000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
MFTIDPKVY	Biotin (K)	0.0000001000000.0
MFTIDPKVY	Biotin (K)	0.300000100000.0
MFTIDPKVY	Biotin (K)	0.3000001000000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
KLILKPAIK	Biotin (K)	0.000010000.0
TADKNKLEG	Biotin (K)	0.00000000000000000000000000100000.0
VSEGPRPFA	Biotin (K)	0.00000000000000000010000000000000.0
TADKNKLEG	Biotin (K)	0.00000000000000000000000000100000.0
LEGAGSATI	Biotin (K)	0.000000000000000000000100000.0
EASPPTSAD	Biotin (K)	0.000000000100.0
AEPSQLDIK	Biotin (K)	0.00000000100000000000000000.0
LRDDKTGVI	Biotin (K)	0.0000100000000000000.0
NKDDLTLSF	Biotin (K)	0.010000000.0
TPGTPKSGI	Biotin (K)	0.000001000000000.0
KLILKPAIK	Biotin (K)	0.000010000.0
LILKPAIK	Biotin (K)	0.00010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
KLILKPAIK	Biotin (K)	0.000010000.0
YKKTFLPK	2 Biotin (K)	0.01000001.0
KGGASKPR	Biotin (K)	0.10000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
KGPGPGGF	Biotin (K)	0.100000000000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
SVKVSLEKD	Biotin (K)	0.00100000000.0
SVKVSLEKD	Biotin (K)	0.00100000000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
YITKSVTVTC	Biotin (K)	0.00010000000.0
KVEKVTSHA	Biotin (K)	0.000100000000.0
ALVTNKPVV	Biotin (K)	0.0000010000000000000.0
ALVTNKPVV	Biotin (K)	0.0000010000000000000.0
VTQPLGTPT	Biotin (K)	0.0000000001000000.0
VTQPLGTPT	Biotin (K)	0.0000000001000000.0
KLAAEKGID	Biotin (K)	0.00000100000000.0

KDIDSFVPS	Biotin (K)	0.1000000000.0
EKQRKDK	Biotin (K)	0.0000001.0
QAPQASKPI	Biotin (K)	0.000000100000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000030000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1300000000.0
KMQNSMTA	Biotin (K)	0.1000030000.0
KMQNSMTA	Biotin (K)	
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K)	0.1000000000.0
KMQNSMTA	Biotin (K); Ox	0.1300000000.0
AQGLPKGS	Biotin (K)	0.0000010000000000000000.0
VGKSGGSG	Biotin (K)	0.00100000000.0
AETAAKHGI	Biotin (K)	0.0000010000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
SAASKTVNI	Biotin (K)	0.0000100000000.0
LLASGKVAC	Biotin (K)	0.0000010000.0
LLEAAAQSS	Biotin (K)	0.00000000010000000000000000000.0

SSKCCCIYE	Biotin (K); 3 (	0.001222000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000313000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000300000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000010000000300000.0
GQPLCVLS/	Biotin (K); Ca	0.000020000013000000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
MKMETVVT!	Biotin (K)	0.0100000000000000.0
MKMETVVT!	Biotin (K)	0.0100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000300000.0
GQPLCVLS/	Biotin (K)	0.000020000010000000300000.0
GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
GQPLCVLS/	Biotin (K)	0.000020000310000000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000300000.0

KMETVVTSF	Biotin (K)	0.100000000300000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000130000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000130000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003130000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003130000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000300000.0
KMETVVTSF	Biotin (K)	0.130000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003130000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003130000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.00002000001000000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000130000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200000100000000000000.0
SAMKMETV'	Biotin (K)	0.000100000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
GQPLCVLS/	Biotin (K)	0.0000200003100000000300000.0
KMETVVTSF	Biotin (K)	0.100000000300000.0
GQPLCVLS/	Biotin (K)	0.0000200003100000000000000.0
KMETVVTSF	Biotin (K)	
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K); Ox	0.130000000000000.0
KMETVVTSF	Biotin (K)	0.100000000000000.0
KMETVVTSF	Biotin (K); Ox	0.100000000300000.0
VFLPNKQR	Biotin (K)	0.00000100.0
VFLPNKQR	Biotin (K)	0.00000100.0
VFLPNKQR	Biotin (K)	0.00000100.0
VFLPNKQR	Biotin (K)	0.00000100.0
VFLPNKQR	Biotin (K)	0.00000100.0
ISFKGTPTE	Biotin (K)	0.0001000000000.0
EKKGGKER	Biotin (K)	0.00000100.0
KVACIGAWH	Biotin (K)	0.10000000000000.0
ELGKLMELH	Biotin (K)	0.000100000000000000.0
ELGKLMELH	Biotin (K)	0.000100000000000000.0

ELGKLMELH	Biotin (K)	0.00010000000000000.0
ELGKLMELH	Biotin (K)	0.00010000000000000.0
AAGDETGA	Biotin (K)	0.000000001000.0
QTTKSELLR	Biotin (K)	0.000100000.0
QTTKSELLR	Biotin (K)	0.000100000.0
ILADPLDQM	Biotin (K)	0.000000000100000.0
IADFKNTLP	Biotin (K)	0.000010000000000000000000.0
GKDPLVLLD	Biotin (K)	0.0100000000.0
NKGPSPVS	Biotin (K)	0.0100000000000.0
NKGPSPVS	Biotin (K)	0.0100000000000.0
NKGPSPVS	Biotin (K)	0.0100000000000.0
LEDKSASPG	Biotin (K)	0.000100000000.0
LEDKSASPG	Biotin (K)	0.000100000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
GQMPENPY	Biotin (K)	0.00000000000010000.0
SVKPGEGLE	Biotin (K)	0.0000000000000010000000.0
SVKPGEGLE	Biotin (K)	0.0000000000000010000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IASKAVYVPA	Biotin (K)	0.00010000000000.0
IGSSSITK	Biotin (K)	
NITKSVAVN	Biotin (K)	0.00000000001.0
NITKSVAVN	Biotin (K)	0.00000000001.0
NITKSVAVN	Biotin (K)	0.00000000001.0
NITKSVAVN	Biotin (K)	0.00000000001.0
NITKSVAVN	Biotin (K)	0.00000000001.0
NITKSVAVN	Biotin (K)	0.00000000001.0
ITKSVAVNPI	Biotin (K)	0.0000000001.0
ITKSVAVNPI	Biotin (K)	0.0000000001.0
TKSVAVNPK	Biotin (K)	0.000000001.0
TKSVAVNPK	Biotin (K)	0.000000001.0
TKSVAVNPK	Biotin (K)	0.000000001.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
AYKKAWGN	2 Biotin (K)	0.0011000000000000000000.0
TNKPSTPTT	Biotin (K)	0.001000000000.0
TASPWKSAF	Biotin (K)	0.000001000.0
TASPWKSAF	Biotin (K)	0.000001000.0

TASPWKSAI	Biotin (K)	0.000001000.0
EQADYCVSI	Biotin (K)	0.000002000000000100.0
SIYEYQPGK	Biotin (K)	0.00000000100000000.0
GFGGKFGV	Biotin (K)	0.000010000000.0
GFGGKFGV	Biotin (K)	0.000010000300.0
VDKSAVGFI	Biotin (K)	0.0010000000000.0
VDKSAVGFI	Biotin (K)	0.0010000000000.0
NASTFEEVV	Biotin (K)	0.00000000000000000010000000000.0
NASTFEEVV	Biotin (K)	0.00000000000000000010000000000.0
TKPDSSIYPI	Biotin (K)	0.000000000000010000000.0
SKESVPDFF	Biotin (K)	0.01000000000000.0
EAQMAAKLE	Biotin (K)	0.0003001000.0
LTHKMEANI	Biotin (K)	0.000100000000.0
ELMKLPAVS	Biotin (K)	0.0001000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
DINKRREPL	Biotin (K)	0.000100000000000000000000.0
LTDKNVGFC	Biotin (K)	0.0001000000000.0
LTDKNVGFC	Biotin (K)	0.0001000000000.0
LTDKNVGFC	Biotin (K)	0.0001000000000.0
LTDKNVGFC	Biotin (K)	0.0001000000000.0
SEDLSSGVF	Biotin (K)	0.000000000100000000000000000000000000.0
SEDLSSGVF	Biotin (K)	0.000000000100000000000000000000000000.0
QASISGPAP	Biotin (K)	0.0000000000100000000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
KNLMFLVLR	Biotin (K)	0.100000000.0
HIKELEKLLI	Biotin (K)	0.000000100000000.0
IYAGTGALE	Biotin (K)	0.0000000000001.0
GISTDKPSE	Biotin (K)	0.000000000000000000100000.0
ASDKYEALR	Biotin (K)	0.000000000000000000000000000000000100000.0
EEVSPSPLS	Biotin (K)	0.000000000000000000000000100000.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
QGVAEAAG	Biotin (K)	0.00000000100.0
QGVAEAAG	Biotin (K)	0.00000000100.0

QGVAEAAG	Biotin (K)	0.00000000100.0
QGVAEAAG	Biotin (K)	0.00000000100.0
TKQGVAEA	Biotin (K)	0.0000000000001.0
TKQGVAEA	Biotin (K)	0.0000000000001.0
TKQGVAEA	Biotin (K)	0.0000000000001.0
TKQGVAEA	Biotin (K)	0.0000000000001.0
TKQGVAEA	Biotin (K)	0.0000000000001.0
TKQGVAEA	Biotin (K)	0.0000000000001.0
TKEGVLYV	Biotin (K)	0.0000000000100.0
TKEGVLYV	Biotin (K)	0.0000000000100.0
TKEGVLYV	Biotin (K)	0.0000000000100.0
TKEGVLYV	Biotin (K)	0.0000000000100.0
TKEGVLYV	Biotin (K)	0.0000000000100.0
TKEGVLYV	Biotin (K)	0.0000000000100.0
TKQGVAEA	Biotin (K)	0.0000000000100.0
TKQGVAEA	Biotin (K)	0.0000000000100.0
TKQGVAEA	Biotin (K)	0.0000000000100.0
TKQGVAEA	Biotin (K)	0.0000000000100.0
TKQGVAEA	Biotin (K)	0.0000000000100.0
TKQGVAEA	Biotin (K)	0.0000000000100.0
TKEGVLYV	Biotin (K)	0.0000000000001.0
TKEGVLYV	Biotin (K)	0.0000000000001.0
QGVAEAAG	Biotin (K)	0.00000000001.0
QGVAEAAG	Biotin (K)	0.00000000001.0
TKEGVLYV	Biotin (K)	0.01000000000.0
TKEGVLYV	Biotin (K)	0.01000000000.0
TKEGVLYV	Biotin (K)	0.01000000000.0
TKEGVLYV	Biotin (K)	0.01000000000.0
QGVAEAAG	Biotin (K)	0.00000000100.0
QGVAEAAG	Biotin (K)	0.00000000100.0
EGVLYVGS	Biotin (K)	0.00000000001.0
EGVLYVGS	Biotin (K)	0.00000000001.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
EGVLYVGS	Biotin (K)	0.000000001000000000000000.0
EGVLYVGS	Biotin (K)	0.000000001000000000000000.0
QGVTEAAE	Biotin (K)	0.00000000100.0
QGVTEAAE	Biotin (K)	0.00000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
TKQGVTEA	Biotin (K)	0.0000000000100.0
EGVLYVGS	Biotin (K)	0.000000001000000000000000.0
EGVLYVGS	Biotin (K)	0.000000001000000000000000.0
QGVTEAAE	Biotin (K)	0.00000000100.0
QGVTEAAE	Biotin (K)	0.00000000100.0
QGVTEAAE	Biotin (K)	0.00000000100.0
QGVTEAAE	Biotin (K)	0.00000000100.0
QGVTEAAE	Biotin (K)	0.00000000100.0
QGVTEAAE	Biotin (K)	0.00000000100.0
TKEGVLYV	Biotin (K)	0.0000000000001.0
TKEGVLYV	Biotin (K)	0.0000000000001.0

TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
TKEGVLYVG	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000100.0
EGVLYVGSK	Biotin (K)	0.000000001000000000000000.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKQGVTEAA	Biotin (K)	0.01000000000.0
TKQGVTEAA	Biotin (K)	0.01000000000.0
AKEGVVAAA	Biotin (K)	0.01000000000.0
AKEGVVAAA	Biotin (K)	0.01000000000.0
QGVTEAAEK	Biotin (K)	0.00000000100.0
QGVTEAAEK	Biotin (K)	0.00000000100.0
QGVTEAAEK	Biotin (K)	0.00000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
EGVLYVGSK	Biotin (K)	0.000000001000000000000000.0
TKEGVLYVG	Biotin (K)	0.010000000000000000000000000.0
TKEGVLYVG	Biotin (K)	0.00000000001000000000000000.0
EGVLYVGSK	Biotin (K)	0.000000001000000000000000.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
TKEGVLYVG	Biotin (K)	0.01000000000.0
TKQGVTEAA	Biotin (K)	0.01000000000.0
TKQGVTEAA	Biotin (K)	0.0000000000100.0
QGVTEAAEK	Biotin (K)	0.00000000100.0
TKQGVTEAA	Biotin (K)	0.000000000100000000000.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
TKQGVTEAA	Biotin (K)	0.0000000000001.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0
HVPGGGSV	Biotin (K)	0.0000000000001000000.0

HVPGGGSV	Biotin (K)	0.0000000000001000000.0
ATAQQNQE	Biotin (K)	0.00000000001000000000000000.0
SKLGPYNEE	Biotin (K)	0.01000000000.0
ASGKAVAAF	Biotin (K)	0.00010000000.0
HVNSKCLF\	Biotin (K)	0.00001000000000.0
NSKCLFVS\	Biotin (K)	0.001000000000.0
HVNSKCLF\	Biotin (K)	0.00001000000000.0
LGKTAAFK	Biotin (K)	0.00100000.0
LGKTAAFK	Biotin (K)	0.00100000.0
ESLDEVSKS	Biotin (K)	0.0000000100000.0
ESLDEVSKS	Biotin (K)	0.0000000100000.0
ESLDEVSKS	Biotin (K)	0.0000000100000.0
ESLDEVSKS	Biotin (K)	0.0000000100000.0
LGKTAAFK	Biotin (K)	0.00100000.0
KMVNQLAVI	Biotin (K); O×	0.130000000.0
KMVNQLAVI	Biotin (K); O×	0.130000000.0
MQQLAKTQ	Biotin (K)	0.00000100000.0
MQQLAKTQ	Biotin (K)	0.00000100000.0
MQQLAKTQ	Biotin (K)	0.00000100000.0
VNVDKVLEF	Biotin (K)	0.000010000.0
VGDVQGQE	Biotin (K)	0.00000000000000010000000.0
VGDVQGQE	Biotin (K)	0.00000000000000010000000.0
VGDVQGQE	Biotin (K)	0.00000000000000010000000.0
CVKRLDGC	Biotin (K)	0.0000000000001.0
CVKRLDGC	Biotin (K)	0.0000000000001.0
DVSGGKSG	Biotin (K)	0.00000100000000.0
EKKGKDAR	Biotin (K)	0.00001000.0
SVQEEPLNL	Biotin (K)	0.0000000000001.0
SVQEEPLNL	Biotin (K)	0.0000000000001.0
SVQEEPLNL	Biotin (K)	0.0000000000001.0
SVQEEPLNL	Biotin (K)	0.0000000000001.0
SVQEEPLNL	Biotin (K)	0.0000000000001.0
SVQEEPLNL	Biotin (K)	0.0000000000001.0

Unique Protein	148
AAK1_MOUSE	
ABI1_MOUSE	
ADA2B_MOUSE	
ADDA_MOUSE	
ADDB_MOUSE	
ADDG_MOUSE	
ADT1_MOUSE	
ADT2_MOUSE	
AGFG1_MOUSE	
AINX_MOUSE	
ALBU_MOUSE	
ALDOA_MOUSE	
ANK3_MOUSE	
ANR35_MOUSE	
AP180_MOUSE	
AP3B1_MOUSE	
ASAP1_MOUSE	
AT1A1_MOUSE	
ATPB_MOUSE	
AUXI_MOUSE	
B2MG_MOUSE	
BAIP2_MOUSE	
BASP1_MOUSE	
BIN1_MOUSE	
BMP2_MOUSE	
BRAF_MOUSE	
BSN_MOUSE	
CALR_MOUSE	
CEND_MOUSE	
CFTR_MOUSE	
CH10_MOUSE	
CH60_MOUSE	
CHM4B_MOUSE	
CHST9_MOUSE	
CLAP2_MOUSE	
COR1A_MOUSE	
CPLX1_MOUSE	
CPLX2_MOUSE	
CRIP2_MOUSE	
CYLC2_MOUSE	
CYLD_MOUSE	
DCLK1_MOUSE	
DCR1C_MOUSE	
DCTN2_MOUSE	
DDX46_MOUSE	
DLG2_MOUSE	
DMXL2_MOUSE	
DOCK7_MOUSE	
DPYL2_MOUSE	
E41L1_MOUSE	
E41L3_MOUSE	
EDIL3_MOUSE	

ELFN1_MOUSE
ESRP2_MOUSE
FRS3_MOUSE
FUBP2_MOUSE
GBRA1_MOUSE
GGA1_MOUSE
GIT1_MOUSE
GNAI1_MOUSE
GNAO_MOUSE
GNAT3_MOUSE
GRIN1_MOUSE
H2B1A_MOUSE
ICAM1_MOUSE
IF4B_MOUSE
IF4G3_MOUSE
ITPI1_MOUSE
ITSN2_MOUSE
K1C9_MOUSE
KCC2B_MOUSE
KT3K_MOUSE
LAS1L_MOUSE
LASP1_MOUSE
LGUL_MOUSE
LNEBL_MOUSE
MAP1A_MOUSE
MAP1B_MOUSE
MAP6_MOUSE
MCCA_MOUSE
MECP2_MOUSE
MEIOS_MOUSE
MET_MOUSE
MINK1_MOUSE
MRTFB_MOUSE
MTAP2_MOUSE
NDUAA_MOUSE
NECP1_MOUSE
NEUG_MOUSE
NFM_MOUSE
NMDE2_MOUSE
NOS1_MOUSE
ODP2_MOUSE
OTU7A_MOUSE
OXR1_MOUSE
PCCA_MOUSE
PCLO_MOUSE
PFD2_MOUSE
PGAM1_MOUSE
PLAP_MOUSE
PLEC_MOUSE
PP1RB_MOUSE
PYC_MOUSE
RAF1_MOUSE
RASL1_MOUSE
RGS22_MOUSE
RL3_MOUSE
RS3A_MOUSE

RT31_MOUSE
RTN1_MOUSE
RTN3_MOUSE
S12A5_MOUSE
SET_MOUSE
SHAN2_MOUSE
SHOC1_MOUSE
SMC4_MOUSE
SNP25_MOUSE
SPAST_MOUSE
SPTN1_MOUSE
SRBS1_MOUSE
SRC8_MOUSE
SRRM2_MOUSE
STMN1_MOUSE
STON1_MOUSE
STXB1_MOUSE
SUGP2_MOUSE
SYGP1_MOUSE
SYN1_MOUSE
SYNC_MOUSE
SYNE1_MOUSE
SYNJ1_MOUSE
SYNRG_MOUSE
SYUA_MOUSE
SYUB_MOUSE
SYUG_MOUSE
TB182_MOUSE
TBCB_MOUSE
TCOF_MOUSE
TEP1_MOUSE
TIM44_MOUSE
TMM17_MOUSE
TRAP1_MOUSE
VAMP2_MOUSE
VCIP1_MOUSE
WEE1_MOUSE
WIPF3_MOUSE
WNT2_ECHTE
ZEB1_MOUSE

Table 23 **GO for tau interactome [in progress] from encoding-comnsolidation-re**

Biological Process				
#term ID	**term description**	**rved gene c**	**round gene**	**strength**
GO:004866	**Neuron development**	**8**	**855**	**0.78**
GO:012003	Plasma membrane boun	10	1072	0.78
GO:005164	Establishment of localiza	11	1518	0.67
GO:004846	Cell development	12	1730	0.65
GO:002200	Neurogenesis	11	1784	0.6
GO:005164	Cellular localization	13	2115	0.6
GO:000739	Nervous system develop	14	2358	0.59
GO:000699	Organelle organization	16	3066	0.53
GO:004886	Cellular developmental p	17	3731	0.47
GO:003015	Cell differentiation	16	3674	0.45
GO:007184	Cellular component orga	20	4954	0.42
GO:001604	Cellular component orga	19	4769	0.41
GO:005079	Regulation of cellular pro	27	9541	0.26
GO:000998	Cellular process	32	13330	0.19

etrieval-reconsolidation (ECRRc) spatial memory phases

			Subcellular Compartments		
e discovery	teins in your	ins in your	#term ID	term description	rved gene c
0.0441	**10090.ENSM**	**Gnat1,Tnfr**	GOCC:004	Neuron projection	10
0.0441	10090.ENSM	Tnfrsf21,Sh	GOCC:012	Plasma membrane bou	13
0.0441	10090.ENSM	Ccl3,Sh3gl	GOCC:000	Cytosol	12
0.0441	10090.ENSM	Gnat1,Tnfrs	GOCC:003	Somatodendritic comp	8
0.0441	10090.ENSM	Ccl3,Gnat1	GOCC:009	Neuron to neuron syna	6
0.0441	10090.ENSM	Ccl3,Sh3gl	GOCC:004	Synapse	9
0.0441	10090.ENSM	Ccl3,Gnat1	GOCC:000	Cytoplasm	22
0.0441	10090.ENSM	Ccl3,Ppid,V	GOCC:011	Cellular anatomical en	30
0.0441	10090.ENSM	Ccl3,Nr1i3,	GOCC:000	Intracellular	27
0.0441	10090.ENSM	Ccl3,Nr1i3,	GOCC:003	Cell junction	10
0.0441	10090.ENSM	Ccl3,Tnfrsf2	GOCC:009	Neurofibrillary tangle	2
0.0441	10090.ENSM	Ccl3,Tnfrsf2	GOCC:001	Postsynaptic density	5
0.0441	10090.ENSM	Ccl3,Nr1i3,	GOCC:009	Basal dendrite	2
0.0441	10090.ENSM	Ccl3,Nr1i3,	GOCC:000	Cilium	6
			GOCC:004	Organelle	24
			GOCC:000	Cytoskeleton	9
			GOCC:009	Postsynapse	6
			GOCC:009	Supramolecular fiber	6
			GOCC:009	Cytoplasmic region	4

					Cellular Component	
round gene	strength	discovery	eins in your	ins in your	#term ID	term description
1054	0.79	0.0024	10090.ENS	Gnat1,Tnfrs	**GO:004300**	**Neuron projectior**
1774	0.68	0.0024	10090.ENS	Gnat1,Tnfrs	GO:004323	Intracellular non-m
1784	0.64	0.0044	10090.ENS	Ccl3,Nr1i3,	GO:012002	Plasma membrane
711	0.86	0.0044	10090.ENS	Gnat1,Sh3g	GO:000573	Cytoplasm
320	1.08	0.0044	10090.ENS	Sh3gl2,Mar	GO:009741	Neurofibrillary tang
1032	0.75	0.0062	10090.ENS	Sh3gl2,Var	GO:009951	Supramolecular fib
6579	0.34	0.0076	10090.ENS	Ccl3,Nr1i3,	GO:004322	Organelle
12108	0.21	0.0085	10090.ENS	Ccl3,Nr1i3,	GO:009898	Neuron to neuron
9943	0.25	0.0102	10090.ENS	Ccl3,Nr1i3,	GO:000562	Intracellular
1453	0.65	0.0102	10090.ENS	Sh3gl2,Var	GO:004302	Neuronal cell body
6	2.33	0.0116	10090.ENS	Nefh,Mapt	GO:011016	Cellular anatomica
288	1.05	0.0134	10090.ENS	Map4,Nefh	GO:000585	Cytoskeleton
10	2.11	0.0215	10090.ENS	Sh3gl2,Nef	GO:003042	Axon
553	0.85	0.0228	10090.ENS	Gnat1,Map-	GO:003647	Somatodendritic c
8565	0.26	0.0228	10090.ENS	Nr1i3,Gnat	GO:004520	Synapse
1397	0.62	0.0234	10090.ENS	Wrn,Map4,I	GO:009951	Polymeric cytoskel
563	0.84	0.0234	10090.ENS	Map4,Ppp3	GO:000582	Cytosol
564	0.84	0.0234	10090.ENS	Ppp3ca,Ne	GO:000592	Cilium
212	1.09	0.0309	10090.ENS	Map4,Mapt	GO:001406	Postsynaptic dens
					GO:004322	Intracellular organ
					GO:009868	Schaffer collateral
					GO:003005	Cell junction

rved gene c	round gene	strength	e discovery	eins in your	matching proteins in your
13	**1583**	**0.73**	**0.00052**	**10090.ENS**	**Gnat1,Tnfrsf21,Sh3gl2,Va**
19	4035	0.48	0.00071	10090.ENS	Nr1i3,Mrps23,Ppid,Wrn,M
15	2387	0.61	0.00071	10090.ENS	Gnat1,Tnfrsf21,Sh3gl2,Va
29	10283	0.26	0.001	10090.ENS	Ccl3,Nr1i3,Gnat1,Mrps23,
2	4	2.51	0.0083	10090.ENS	Nefh,Mapt
8	861	0.78	0.0086	10090.ENS	Map4,Ppp3ca,Nefh,Mapt,D
29	11550	0.21	0.01	10090.ENS	Nr1i3,Gnat1,Mrps23,Ppid,
6	446	0.94	0.01	10090.ENS	Sh3gl2,Map4,Nefh,Mapt,S
30	12596	0.19	0.0136	10090.ENS	Ccl3,Nr1i3,Gnat1,Mrps23,
7	743	0.79	0.016	10090.ENS	Gnat1,Sh3gl2,Nefh,Mapt,S
33	15632	0.14	0.016	10090.ENS	Ccl3,Nr1i3,Gnat1,Mrps23,
11	2060	0.54	0.0202	10090.ENS	Nr1i3,Wrn,Map4,Nefh,Ma
7	791	0.76	0.0202	10090.ENS	Tnfrsf21,Map4,Nefh,Mapt
8	1080	0.68	0.0202	10090.ENS	Gnat1,Sh3gl2,Ppp3ca,Nefh
9	1492	0.59	0.0284	10090.ENS	Sh3gl2,Vamp3,Map4,Ppp3
6	631	0.79	0.0307	10090.ENS	Map4,Nefh,Mapt,Dctn1,Tp
14	3573	0.4	0.0327	10090.ENS	Ccl3,Nr1i3,Ppid,Sh3gl2,Va
6	646	0.78	0.0327	10090.ENS	Gnat1,Map4,Bbs12,Mapt,I
5	414	0.89	0.0327	10090.ENS	Map4,Nefh,Mapt,Srcin1,Ka
27	11084	0.2	0.0327	10090.ENS	Nr1i3,Mrps23,Ppid,Sh3gl2,
3	113	1.24	0.0454	10090.ENS	Sh3gl2,Ppp3ca,Nefh
10	2050	0.5	0.0461	10090.ENS	Sh3gl2,Vamp3,Map4,Ppp3

network (labels)

mp3,Wrn,Map4,Ppp3ca,Nefh,Mapt,Srcin1,Dctn1,Kalrn,Tpm3

ap4,Ppp3ca,Dpf1,Gtf3c1,Srpk2,Nefh,Mapt,Srcin1,Ddx31,Dctn1,Kalrn,Tpm3,Cbfa2t3,Ablim2,Ca

mp3,Wrn,Map4,Bbs12,Ppp3ca,Nefh,Mapt,Srcin1,Ldha,Dctn1,Kalrn,Tpm3

Tnfrsf21,Ppid,Sh3gl2,Vamp3,Uqcrc2,Wrn,Trim29,Map4,Tigar,Ppp3ca,Dpf1,Cadps,Csnk1g3,Srpl

Dctn1,Tpm3,Ablim2,Camsap3

Sh3gl2,Vamp3,Uqcrc2,Wrn,Trim29,Map4,Tigar,Bbs12,Ppp3ca,Dpf1,Gtf3c1,Cadps,Csnk1g3,Srp

rcin1,Kalrn

Tnfrsf21,Ppid,Sh3gl2,Vamp3,Uqcrc2,Wrn,Trim29,Map4,Tigar,Ppp3ca,Dpf1,Gtf3c1,Cadps,Csnk1

Srcin1,Dctn1,Kalrn

Tnfrsf21,Ppid,Sh3gl2,Vamp3,Uqcrc2,Wrn,Trim29,Map4,Tigar,Bbs12,Ppp3ca,Dpf1,Gtf3c1,Glp2

pt,Srcin1,Dctn1,Kalrn,Tpm3,Ablim2,Camsap3

,Srcin1,Dctn1,Tpm3

n,Mapt,Srcin1,Dctn1,Kalrn

ca,Cadps,Nefh,Mapt,Srcin1,Kalrn

pm3,Camsap3

mp3,Map4,Tigar,Ppp3ca,Srpk2,Mapt,Ldha,Dctn1,Kalrn,Tpm3

Ldha,Dctn1

alrn

,Vamp3,Uqcrc2,Wrn,Trim29,Map4,Tigar,Ppp3ca,Dpf1,Gtf3c1,Cadps,Csnk1g3,Srpk2,Nefh,Mapt

ca,Cadps,Nefh,Mapt,Srcin1,Kalrn,Camsap3

msap3

‹2,Nefh,Mapt,Srcin1,Ldha,Ddx31,Dctn1,Kalrn,Tpm3,Cbfa2t3,Ablim2,Camsap3

k2,Nefh,Mapt,Srcin1,Ldha,Ddx31,Dctn1,Kalrn,Tpm3,Cbfa2t3,Ablim2,Camsap3

lg3,Srpk2,Nefh,Mapt,Srcin1,Ldha,Ddx31,Dctn1,Kalrn,Tpm3,Cbfa2t3,Ablim2,Camsap3

r,Cadps,Csnk1g3,Srpk2,Nefh,Il1rl2,Mapt,Srcin1,Ldha,Ddx31,Dctn1,Kalrn,Tpm3,Cbfa2t3,Ablim2,

:,Srcin1,Ldha,Ddx31,Dctn1,Kalrn,Tpm3,Cbfa2t3,Ablim2,Camsap3

Camsap3

Table 24 **Total peptides list for non-cue (spatial) c**

n = 4, pep = 294, pro = 46

rAAV	Sample	Biotin	Protein Accessio
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid	NCC-2	d1-6	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ALBU_MOUSE
RAM-MiniTid	NCC-1	d1-6	APC_MOUSE
RAM-MiniTid	NCC-1	d1-6	APC_MOUSE
RAM-MiniTid	NCC-1	d1-6	APC_MOUSE

RAM-MiniTid	NCC-2	d1-6	AT1A2_MOUSE
RAM-MiniTid	NCC-2	d1-6	AT1A2_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	CAP2_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	CATD_MOUSE
RAM-MiniTid	NCC-1	d1-6	CH60_MOUSE
RAM-MiniTid	NCC-1	d1-6	CH60_MOUSE
RAM-MiniTid	NCC-1	d1-6	CH60_MOUSE
RAM-MiniTid	NCC-1	d1-6	CLNK_MOUSE
RAM-MiniTid	NCC-1	d1-6	CO4A1_MOUSE
RAM-MiniTid	NCC-1	d1-6	CO4A1_MOUSE
RAM-MiniTid	NCC-1	d1-6	COR1A_MOUSE
RAM-MiniTid	NCC-1	d1-6	COR1A_MOUSE
RAM-MiniTid	NCC-1	d1-6	COR1A_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	COR1A_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	COR1A_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	COR1A_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	COR1A_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	COR1A_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	COR1A_MOUSE
RAM-MiniTid	NCC-1	d1-6	DDX4_MOUSE
RAM-MiniTid	NCC-1	d1-6	DDX4_MOUSE
RAM-MiniTid	NCC-1	d1-6	DDX4_MOUSE
RAM-MiniTid	NCC-1	d1-6	DDX4_MOUSE
RAM-MiniTid	NCC-2	d1-6	E41L1_MOUSE
RAM-MiniTid	NCC-2	d1-6	E41L1_MOUSE
RAM-MiniTid	NCC-2	d1-6	E41L1_MOUSE
RAM-MiniTid	NCC-2	d1-6	E41L1_MOUSE
RAM-MiniTid	NCC-2	d1-6	E41L1_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ECI1_MOUSE
RAM-MiniTid	NCC-1	d1-6	G3PT_MOUSE
RAM-MiniTid	NCC-1	d1-6	GNAI3_MOUSE
RAM-MiniTid	NCC-1	d1-6	GNAI3_MOUSE
RAM-MiniTid	NCC-1	d1-6	GNAI3_MOUSE
RAM-MiniTid	NCC-1	d1-6	GOGA4_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	GSTMU_MOUSE
RAM-MiniTid	NCC-2	d1-6	H90B3_MOUSE
RAM-MiniTid	NCC-2	d1-6	H90B3_MOUSE
RAM-MiniTid	NCC-2	d1-6	H90B3_MOUSE
RAM-MiniTid	NCC-1	d1-6	HELZ_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS904_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS904_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS904_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE

RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90A_MOUSE
RAM-MiniTid	NCC-2	d1-6	HS90B_HORSE
RAM-MiniTid	NCC-2	d1-6	HS90B_HORSE
RAM-MiniTid	NCC-2	d1-6	HS90B_MOU

RAM-MiniTid	NCC-2	d1-6	MTAP2_MOUSE
RAM-MiniTid	NCC-2	d1-6	MTAP2_MOUSE
RAM-MiniTid	NCC-2	d1-6	MTAP2_MOUSE
RAM-MiniTid	NCC-2	d1-6	MTAP2_MOUSE
RAM-MiniTid	NCC-2	d1-6	MTAP2_MOUSE
RAM-MiniTid	NCC-2	d1-6	MTAP2_MOUSE
RAM-MiniTid	NCC-2	d1-6	MTAP2_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH1_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH1_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH1_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH2_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH2_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH2_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH4_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH4_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH4_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH4_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH4_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH8_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH8_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYH8_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYOME_MOUSE
RAM-MiniTid	NCC-1	d1-6	MYSS_MOUSE
RAM-MiniTid	NCC-1	d1-6	NISCH_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	ODP2_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PCCA_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PCCA_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PCCA_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PCCA_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PCCA_MOUSE
RAM-MiniTid	NCC-2	d1-6	PEA15_MOUSE
RAM-MiniTid	NCC-2	d1-6	PEA15_MOUSE
RAM-MiniTid	NCC-2	d1-6	PEA15_MOUSE
RAM-MiniTid	NCC-2	d1-6	PEA15_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE

RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid	NCC-2	d1-6	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	PYC_MOUSE
RAM-MiniTid	NCC-1	d1-6	SCC4_MOUSE
RAM-MiniTid	NCC-1	d1-6	SCC4_MOUSE
RAM-MiniTid	NCC-2	d1-6	STMN1_MOUSE
RAM-MiniTid	NCC-2	d1-6	STMN1_MOUSE
RAM-MiniTid	NCC-1	d1-6	SYN1_MOUSE
RAM-MiniTid	NCC-1	d1-6	SYN1_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE

RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUA_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUB

RAM-MiniTid	NCC-2	d1-6	SYUB_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUB_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUB_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUB_MOUSE
RAM-MiniTid	NCC-2	d1-6	SYUB_MOUSE
RAM-MiniTid	NCC-1	d1-6	TITIN_MOUSE
RAM-MiniTid	NCC-1	d1-6	TITIN_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	TRI41_MOUSE
RAM-MiniTid-tau	NCC-3	d1-4	TRI41_MOUSE
RAM-MiniTid	NCC-1	d1-6	UBP36_MOUSE

controls from combined rAAV grounds and memory phases [in progress]

Protein Description	Peptide Scor	Peptide Sequenc	Peptide Moc
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	66.74	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	66.74	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	45.96	RHPYFYAPELLY	Biotin (K)
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	45.96	RHPYFYAPELLY	Biotin (K)
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	45.61	RHPYFYAPELLY	Biotin (K)
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	45.61	RHPYFYAPELLY	Biotin (K)
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	41.61	RHPYFYAPELLY	Biotin (K)
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	41.61	RHPYFYAPELLY	Biotin (K)
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	44.08	RHPYFYAPELLY	Biotin (K)
Albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV	39.12	KKYLYEIAR	2 Biotin (K)
Albumin OS=Pongo abelii OX=9601 GN=ALB PE=2 SV=2	39.12	KKYLYEIAR	2 Biotin (K)
Albumin OS=Felis catus OX=9685 GN=ALB PE=1 SV=1	39.78	RHPYFYAPELLY	Biotin (K)
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	71.76	CDQFEKLGEYG	Biotin (K); Ca
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	59.65	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	56.55	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	56.48	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	55.29	CDQFEKLGEYG	Biotin (K); Ca
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	54.01	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	53.81	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	50.56	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	50.33	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	49.03	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	47.07	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	45.83	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	44.93	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	42.95	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	40.95	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	40.53	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Canis lupus familiaris OX=9615 GN=ALB PE	40.35	FQNALLVRYTKH	2 Biotin (K)
Albumin (Fragments) OS=Capra hircus OX=9925 GN=Al	46.86	VDEPQNLIKKHC	2 Biotin (K)
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	46.45	YEATLEECCAKD	Biotin (K); Ca
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	42.39	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	39.93	CIAEVEKDAIPEN	Biotin (K); Ca
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	39.82	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	39.29	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	38.46	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Oryctolagus cuniculus OX=9986 GN=ALB F	41.67	EFTALLDKCCSA	2 Biotin (K); C
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	40.72	CIAEVEKDAIPEN	Biotin (K); 2 C
Albumin OS=Canis lupus familiaris OX=9615 GN=ALB PE	37.67	YKSEIAHR	Biotin (K)
Albumin OS=Sus scrofa OX=9823 GN=ALB PE=1 SV=2	37.67	YKSEIAHR	Biotin (K)
Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4	40.59	CIAEVEKDAIPEN	Biotin (K); 2 C
Adenomatous polyposis coli protein OS=Homo sapiens C	40.73	KLSQLPR	Biotin (K)
Adenomatous polyposis coli protein OS=Mus musculus C	40.73	KLSQLPR	Biotin (K)
Adenomatous polyposis coli protein OS=Rattus norvegicu	40.73	KLSQLPR	Biotin (K)

Sodium/potassium-transporting ATPase subunit alpha-2 (	40.01	VMKGAPERILDF	Biotin (K); O›
Sodium/potassium-transporting ATPase subunit alpha-2 (	40.01	VMKGAPERILDF	Biotin (K); O›
Adenylyl cyclase-associated protein 2 OS=Mus musculu:	38.51	PQDDDYREFPIF	Biotin (K)
Cathepsin D OS=Canis lupus familiaris OX=9615 GN=CT	37.05	PCKSALSGLAGI	Biotin (K)
60 kDa heat shock protein, mitochondrial OS=Cricetulus	42.29	KGKGEKAQIEK	Biotin (K)
60 kDa heat shock protein, mitochondrial OS=Cricetulus	39.23	KGKGEKAQIEK	Biotin (K)
60 kDa heat shock protein, mitochondrial OS=Cricetulus	40.58	KGKGEKAQIEK	Biotin (K)
Cytokine-dependent hematopoietic cell linker OS=Homo s	41.87	IKILPARPIK	Biotin (K)
Collagen alpha-1(IV) chain OS=Homo sapiens OX=9606	41.82	KGDFATKGEK	Biotin (K)
Collagen alpha-1(IV) chain OS=Homo sapiens OX=9606	41.7	KGDFATKGEK	Biotin (K)
Coronin-1A OS=Bos taurus OX=9913 GN=CORO1A PE=	41.65	LEEEMRK	Biotin (K)
Coronin-1A OS=Homo sapiens OX=9606 GN=CORO1A	41.65	LEEEMRK	Biotin (K)
Coronin-1A OS=Macaca fascicularis OX=9541 GN=COR	41.65	LEEEMRK	Biotin (K)
Coronin-1A OS=Homo sapiens OX=9606 GN=CORO1A	41.69	LEEEMRK	Biotin (K)
Coronin-1A OS=Bos taurus OX=9913 GN=CORO1A PE=	41.69	LEEEMRK	Biotin (K)
Coronin-1A OS=Macaca fascicularis OX=9541 GN=COR	41.69	LEEEMRK	Biotin (K)
Coronin-1A OS=Homo sapiens OX=9606 GN=CORO1A	40.81	LEEEMRK	Biotin (K)
Coronin-1A OS=Bos taurus OX=9913 GN=CORO1A PE=	40.81	LEEEMRK	Biotin (K)
Coronin-1A OS=Macaca fascicularis OX=9541 GN=COR	40.81	LEEEMRK	Biotin (K)
Probable ATP-dependent RNA helicase DDX4 OS=Maca	38.72	LMDIIGKEKIGLK	Biotin (K)
ATP-dependent RNA helicase DDX4 OS=Mus musculus	38.72	LMDIIGKEKIGLK	Biotin (K)
Probable ATP-dependent RNA helicase DDX4 OS=Sus s	38.72	LMDIIGKEKIGLK	Biotin (K)
Probable ATP-dependent RNA helicase DDX4 OS=Rattu:	38.72	LMDIIGKEKIGLK	Biotin (K)
Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=	83.79	SLSPIIGKDVLTS	Biotin (K)
Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=	83.79	SLSPIIGKDVLTS	Biotin (K)
Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=	54.15	SGKGAAAMIPGI	Biotin (K)
Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=	54.15	SGKGAAAMIPGI	Biotin (K)
Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=	44.52	SGKGAAAMIPGI	Biotin (K); O›
Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus mu	40.59	GVAVMKLR	Biotin (K)
Glyceraldehyde-3-phosphate dehydrogenase, testis-spe	40.52	EAIKAAAKGP	Biotin (K)
Guanine nucleotide-binding protein G(i) subunit alpha OS	41.23	KAAKEVK	Biotin (K)
Guanine nucleotide-binding protein G(i) subunit alpha OS	41.23	KAAKEVK	Biotin (K)
Guanine nucleotide-binding protein G(i) subunit alpha OS	41.23	KAAKEVK	Biotin (K)
Golgin subfamily A member 4 OS=Rattus norvegicus OX	40.94	QDVTLAGLQGC	Biotin (K)
Glutathione S-transferase OS=Mesocricetus auratus OX	40.79	QIFAKMAVW	Biotin (K); O›
Putative heat shock protein HSP 90-beta-3 OS=Homo sa	46.79	IMKAQALR	Biotin (K)
Putative heat shock protein HSP 90-beta-3 OS=Homo sa	46.79	IMKAQALR	Biotin (K)
Putative heat shock protein HSP 90-beta-3 OS=Homo sa	41.74	IMKAQALR	Biotin (K); O›
Probable helicase with zinc finger domain OS=Mus musc	41.34	RPGVVYSNTKFI	Biotin (K)
Putative heat shock protein HSP 90-alpha A4 OS=Homo	46.79	IMKAQALR	Biotin (K)
Putative heat shock protein HSP 90-alpha A4 OS=Homo	46.79	IMKAQALR	Biotin (K)
Putative heat shock protein HSP 90-alpha A4 OS=Homo	41.74	IMKAQALR	Biotin (K); O›
Heat shock protein HSP 90-alpha OS=Mus musculus OX	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-alpha OS=Oryctolagus cunic	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-alpha OS=Rattus norvegicus	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-alpha OS=Mus musculus OX	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-alpha OS=Oryctolagus cunic	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-alpha OS=Rattus norvegicus	46.79	IMKAQALR	Biotin (K)

Heat shock protein HSP 90-alpha OS=Mus musculus OX	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-alpha OS=Oryctolagus cunic	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-alpha OS=Rattus norvegicus	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-beta OS=Equus caballus OX	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Equus caballus OX	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-beta OS=Homo sapiens OX=	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Macaca fascicularis	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Mus musculus OX=	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Pongo abelii OX=96	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Oryctolagus cunicu	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Rattus norvegicus (	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Equus caballus OX	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Homo sapiens OX=	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Macaca fascicularis	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Mus musculus OX=	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Pongo abelii OX=96	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Oryctolagus cunicu	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Rattus norvegicus (	46.79	IMKAQALR	Biotin (K)
Heat shock protein HSP 90-beta OS=Homo sapiens OX=	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-beta OS=Macaca fascicularis	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-beta OS=Mus musculus OX=	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-beta OS=Pongo abelii OX=96	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-beta OS=Oryctolagus cunicu	41.74	IMKAQALR	Biotin (K); Ox
Heat shock protein HSP 90-beta OS=Rattus norvegicus (	41.74	IMKAQALR	Biotin (K); Ox
Keratin, type II cytoskeletal 1b OS=Homo sapiens OX=96	41.64	LQQSKEELAR	Biotin (K)
Katanin-interacting protein OS=Mus musculus OX=10090	37.07	KGNKMDRILSAI	Biotin (K)
L-lactate dehydrogenase B chain OS=Pan troglodytes OX	40.62	ATIPNNK	Biotin (K)
L-lactate dehydrogenase B chain OS=Pan troglodytes OX	40.26	ATIPNNK	Biotin (K)
Microtubule-associated protein 11 OS=Mus musculus OX	42.3	VWKREVEAPEVI	Biotin (K)
Microtubule-associated protein 2 OS=Mus musculus OX=	96.72	NKLEGAGSATIA	Biotin (K); Ox
Microtubule-associated protein 2 OS=Mus musculus OX=	96.72	NKLEGAGSATIA	Biotin (K); Ox
Microtubule-associated protein 2 OS=Rattus norvegicus	63.27	LEGAGSATVAE\	Biotin (K); Ox
Microtubule-associated protein 2 OS=Rattus norvegicus	63.27	LEGAGSATVAE\	Biotin (K); Ox
Microtubule-associated protein 2 OS=Homo sapiens OX=	63.2	IEGVGAATSAEL	Biotin (K); Ox
Microtubule-associated protein 2 OS=Homo sapiens OX=	63.2	IEGVGAATSAEL	Biotin (K); Ox
Microtubule-associated protein 2 OS=Mus musculus OX=	60.6	TADKNKLEGAG	Biotin (K); Ox
Microtubule-associated protein 2 OS=Mus musculus OX=	60.6	TADKNKLEGAG	Biotin (K); Ox
Microtubule-associated protein 2 OS=Homo sapiens OX=	54.23	NKDDLTLSR	Biotin (K)
Microtubule-associated protein 2 OS=Mus musculus OX=	54.23	NKDDLTLSR	Biotin (K)
Microtubule-associated protein 2 OS=Rattus norvegicus	54.23	NKDDLTLSR	Biotin (K)
Microtubule-associated protein 2 OS=Homo sapiens OX=	54.23	NKDDLTLSR	Biotin (K)
Microtubule-associated protein 2 OS=Mus musculus OX=	54.23	NKDDLTLSR	Biotin (K)
Microtubule-associated protein 2 OS=Rattus norvegicus	54.23	NKDDLTLSR	Biotin (K)
Microtubule-associated protein 2 OS=Homo sapiens OX=	39.97	DLHSKNKDDLTI	Biotin (K)
Microtubule-associated protein 2 OS=Mus musculus OX=	39.97	DLHSKNKDDLTI	Biotin (K)
Microtubule-associated protein 2 OS=Rattus norvegicus	39.97	DLHSKNKDDLTI	Biotin (K)
Microtubule-associated protein 2 OS=Mus musculus OX=	39.88	KLILKPAIK	Biotin (K)
Microtubule-associated protein 2 OS=Rattus norvegicus	39.88	KLILKPAIK	Biotin (K)

Microtubule-associated protein 2 OS=Homo sapiens OX=	38.54	MFTIDPKVYGEK	Biotin (K); Ox
Microtubule-associated protein 2 OS=Mus musculus OX=	38.54	MFTIDPKVYGEK	Biotin (K); Ox
Microtubule-associated protein 2 OS=Rattus norvegicus	38.54	MFTIDPKVYGEK	Biotin (K); Ox
Microtubule-associated protein 2 OS=Mus musculus OX=	38.14	LILKPAIK	Biotin (K)
Microtubule-associated protein 2 OS=Rattus norvegicus	38.14	LILKPAIK	Biotin (K)
Microtubule-associated protein 2 OS=Homo sapiens OX=	40.92	GGQVQIVTKK	Biotin (K)
Microtubule-associated protein 2 OS=Mus musculus OX=	40.92	GGQVQIVTKK	Biotin (K)
Myosin-1 OS=Bos taurus OX=9913 GN=MYH1 PE=2 SV=	37.34	LTKAKTK	Biotin (K)
Myosin-1 OS=Equus caballus OX=9796 GN=MYH1 PE=2	37.34	LTKAKTK	Biotin (K)
Myosin-1 OS=Sus scrofa OX=9823 GN=MYH1 PE=2 SV=	37.34	LTKAKTK	Biotin (K)
Myosin-2 OS=Bos taurus OX=9913 GN=MYH2 PE=2 SV=	37.34	LTKAKTK	Biotin (K)
Myosin-2 OS=Equus caballus OX=9796 GN=MYH2 PE=2	37.34	LTKAKTK	Biotin (K)
Myosin-2 OS=Sus scrofa OX=9823 GN=MYH2 PE=2 SV=	37.34	LTKAKTK	Biotin (K)
Myosin-4 OS=Canis lupus familiaris OX=9615 GN=MYH4	37.34	LTKAKTK	Biotin (K)
Myosin-4 OS=Homo sapiens OX=9606 GN=MYH4 PE=2	37.34	LTKAKTK	Biotin (K)
Myosin-4 OS=Mus musculus OX=10090 GN=Myh4 PE=2	37.34	LTKAKTK	Biotin (K)
Myosin-4 OS=Sus scrofa OX=9823 GN=MYH4 PE=2 SV=	37.34	LTKAKTK	Biotin (K)
Myosin-4 OS=Oryctolagus cuniculus OX=9986 GN=MYH	37.34	LTKAKTK	Biotin (K)
Myosin-8 OS=Canis lupus familiaris OX=9615 GN=MYH8	37.34	LTKAKTK	Biotin (K)
Myosin-8 OS=Homo sapiens OX=9606 GN=MYH8 PE=1	37.34	LTKAKTK	Biotin (K)
Myosin-8 OS=Mus musculus OX=10090 GN=Myh8 PE=2	37.34	LTKAKTK	Biotin (K)
Myomegalin OS=Mus musculus OX=10090 GN=Pde4dip	40.5	GAGKASLGP	Biotin (K)
Myosin heavy chain, skeletal muscle (Fragments) OS=O	37.34	LTKAKTK	Biotin (K)
Nischarin OS=Homo sapiens OX=9606 GN=NISCH PE=	43.2	QDLKTVVIAK	Biotin (K)
Dihydrolipoyllysine-residue acetyltransferase component	39.97	ELNKMLEGKGK	Biotin (K)
Propionyl-CoA carboxylase alpha chain, mitochondrial OS	61.47	KMQNSMTAGK	Biotin (K)
Propionyl-CoA carboxylase alpha chain, mitochondrial OS	42.87	KMQNSMTAGK	Biotin (K)
Propionyl-CoA carboxylase alpha chain, mitochondrial OS	42.87	KMQNSMTAGK	Biotin (K)
Propionyl-CoA carboxylase alpha chain, mitochondrial OS	42.87	KMQNSMTAGK	Biotin (K)
Propionyl-CoA carboxylase alpha chain, mitochondrial OS	42.87	KMQNSMTAGK	Biotin (K)
Astrocytic phosphoprotein PEA-15 OS=Mus musculus O	63.42	ISEEEELDTKLTF	Biotin (K)
Astrocytic phosphoprotein PEA-15 OS=Mus musculus O	63.42	ISEEEELDTKLTF	Biotin (K)
Astrocytic phosphoprotein PEA-15 OS=Mus musculus O	40.11	ISEEEELDTKLTF	Biotin (K)
Astrocytic phosphoprotein PEA-15 OS=Mus musculus O	40.11	ISEEEELDTKLTF	Biotin (K)
Pyruvate carboxylase, mitochondrial OS=Mus musculus	68.64	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	68.64	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	68.64	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	68.64	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	67.96	KMETVVTSPME	Biotin (K); 2 C
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	67.96	KMETVVTSPME	Biotin (K); 2 C
Pyruvate carboxylase, mitochondrial OS=Mus musculus	67.96	KMETVVTSPME	Biotin (K); 2 C
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	67.96	KMETVVTSPME	Biotin (K); 2 C
Pyruvate carboxylase, mitochondrial OS=Mus musculus	66.23	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	66.23	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	66.23	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	66.23	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	64.99	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	64.99	GQPLCVLSAMK	Biotin (K); Ca

Pyruvate carboxylase, mitochondrial OS=Mus musculus	64.99	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	64.99	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	46.93	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	46.93	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	46.93	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	46.93	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	37.08	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	37.08	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	46.42	KMETVVTSPME	Biotin (K)
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	46.42	KMETVVTSPME	Biotin (K)
Pyruvate carboxylase, mitochondrial OS=Mus musculus	43.81	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	43.81	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Mus musculus	41.23	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	41.23	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	62.86	KMETVVTSPME	Biotin (K)
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	62.86	KMETVVTSPME	Biotin (K)
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	58.41	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	58.41	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	47.95	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	47.95	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	45.27	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	45.27	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	37.99	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	37.99	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	41.45	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	41.45	GQPLCVLSAMK	Biotin (K); Ca
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	38.75	KMETVVTSPME	Biotin (K)
Pyruvate carboxylase, mitochondrial OS=Rattus norvegic	37.21	GQPLCVLSAMK	Biotin (K); Ca
MAU2 chromatid cohesion factor homolog OS=Homo sap	39.12	LAQLHTLEK	Biotin (K)
MAU2 chromatid cohesion factor homolog OS=Mus musc	39.12	LAQLHTLEK	Biotin (K)
Stathmin OS=Mus musculus OX=10090 GN=Stmn1 PE=	38.77	EAQMAAKLER	Biotin (K); Ox
Stathmin OS=Rattus norvegicus OX=10116 GN=Stmn1 P	38.77	EAQMAAKLER	Biotin (K); Ox
Synapsin-1 OS=Bos taurus OX=9913 GN=SYN1 PE=1 S	41.1	GKKIHGEIDIK	Biotin (K)
Synapsin-1 OS=Mus musculus OX=10090 GN=Syn1 PE	41.1	GKKIHGEIDIK	Biotin (K)
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca	42.24	QGVAEAAGKTK	Biotin (K)
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=S	42.24	QGVAEAAGKTK	Biotin (K)
Alpha-synuclein OS=Saguinus labiatus OX=78454 GN=S	42.24	QGVAEAAGKTK	Biotin (K)
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca	42.24	QGVAEAAGKTK	Biotin (K)
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=S	42.24	QGVAEAAGKTK	Biotin (K)
Alpha-synuclein OS=Saguinus labiatus OX=78454 GN=S	42.24	QGVAEAAGKTK	Biotin (K)
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca	46.27	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=S	46.27	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Saguinus labiatus OX=78454 GN=S	46.27	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca	40.17	TKEGVLYVGSK	Biotin (K)
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=S	40.17	TKEGVLYVGSK	Biotin (K)
Alpha-synuclein OS=Saguinus labiatus OX=78454 GN=S	40.17	TKEGVLYVGSK	Biotin (K)
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca	41.08	TKQGVAEAAGK	Biotin (K)
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=S	41.08	TKQGVAEAAGK	Biotin (K)

Alpha-synuclein OS=Saguinus labiatus OX=78454 GN=S	41.08	TKQGVAEAAGK	Biotin (K)
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca	38.9	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=S	38.9	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Saguinus labiatus OX=78454 GN=S	38.9	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca	40.81	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=S	40.81	EGVLYVGSKTK	Biotin (K)
Alpha-synuclein OS=Saguinus labiatus OX=78454 GN=S	40.81	EGVLYVGSKTK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	153.2	TKEQASHLGGA	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	153.2	TKEQASHLGGA	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	153.2	TKEQASHLGGA	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	153.2	TKEQASHLGGA	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	153.2	TKEQASHLGGA	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	153.2	TKEQASHLGGA	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	67.01	EGVLYVGSKTS(	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	67.01	EGVLYVGSKTS(	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	52.39	QGVTEAAEKTK	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	52.39	QGVTEAAEKTK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	52.39	QGVTEAAEKTK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	52.39	QGVTEAAEKTK	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	52.39	QGVTEAAEKTK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	52.39	QGVTEAAEKTK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	45.76	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	45.76	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	45.76	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	45.76	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	45.76	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	45.76	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	37.42	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	37.42	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	37.42	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	37.42	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	37.42	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	37.42	GLSMAKEGVVA	Biotin (K); O›
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	46.27	EGVLYVGSKTK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	46.27	EGVLYVGSKTK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	41.42	TKQGVTEAAEK	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	41.42	TKQGVTEAAEK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	41.42	TKQGVTEAAEK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	40.17	TKEGVLYVGSK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	40.17	TKEGVLYVGSK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	38.12	GLSMAKEGVVA	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	38.12	GLSMAKEGVVA	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	38.12	GLSMAKEGVVA	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	41.11	TKQGVTEAAEK	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	41.11	TKQGVTEAAEK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	41.11	TKQGVTEAAEK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	39.15	EQASHLGGAVF	Biotin (K)
Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb	39.15	EQASHLGGAVF	Biotin (K)

Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	39.15	EQASHLGGAVF	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	38.9	EGVLYVGSKTK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	38.9	EGVLYVGSKTK	Biotin (K)
Beta-synuclein OS=Bos taurus OX=9913 GN=SNCB PE=	40.81	EGVLYVGSKTK	Biotin (K)
Beta-synuclein OS=Rattus norvegicus OX=10116 GN=S	40.81	EGVLYVGSKTK	Biotin (K)
Titin OS=Homo sapiens OX=9606 GN=TTN PE=1 SV=4	37.33	KKAPPPPK	2 Biotin (K)
Titin OS=Mus musculus OX=10090 GN=Ttn PE=1 SV=1	37.33	KPKAPPPK	2 Biotin (K)
E3 ubiquitin-protein ligase TRIM41 OS=Homo sapiens O	37.31	VVPLEEVVQEYK	Biotin (K)
E3 ubiquitin-protein ligase TRIM41 OS=Mus musculus O	37.31	VVPLEEVVQEYK	Biotin (K)
Ubiquitin carboxyl-terminal hydrolase 36 OS=Mus muscu	38.4	SRVKCSVCK	Biotin (K)

Position of peptide modification	Unique Protein
0.2000001000000000000000000020.0	ALBU_MOUSE
0.2000001000000000000000000020.0	APC_MOUSE
0.00000000000000000100.0	AT1A2_MOUSE
0.00000000000000000100.0	CAP2_MOUSE
0.00000000000000000100.0	CATD_MOUSE
0.00000000000000000100.0	CH60_MOUSE
0.00000000000000000100.0	CLNK_MOUSE
0.00000000000000000100.0	CO4A1_MOUSE
0.00000000000000000100.0	COR1A_MOUSE
0.110000000.0	DDX4_MOUSE
0.110000000.0	E41L1_MOUSE
0.00000000000000000100.0	ECI1_MOUSE
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0.2000001000000000000000000020.0	GOGA4_MOUSE
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0.2000001000000000000000000020.0	HELZ_MOUSE
0.2000001000000000000000000020.0	HS904_MOUSE
0.2000001000000000000000000020.0	HS90A_MOUSE
0.2000001000000000000000000020.0	HS90B_HORSE
0.2000001000000000000000000020.0	HS90B_MOUSE
0.2000001000000000000000000020.0	K2C1B_MOUSE
0.2000001000000000000000000020.0	KATIP_MOUSE
0.2000001000000000000000000020.0	LDHB_MOUSE
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Table 25 **STRING Protein ontology-based overview of candidate ta**
The top result (based on Strength algorithm) from each selected protein

MiniTid-POI	***Biologicall Process***
Ap2m1	Postsynaptic receptor endocytosis
Csnk1g1	Beta-catenin destruction complex disassembly
Csnk1g3	Positive regulation of protein insertion into mitochondrial mem
Cttn	Regulation of actin cytoskeleton organization
Vamp3	Vesicle fusion
Pak2	Negative regulation of perk-mediated unfolded protein response
Ppp3ca	calcineurin-NFAT signaling cascade
Sh3gl2	Synaptic vesicle uncoating
Set	Regulation of cell cycle process
Camk2a	NMDA selective glutamate receptor signaling pathway
Lin7c	Protein localization to basolateral plasma membrane
Mecp2	Regulation of histone h3-k9 trimethylation

*The Reactome pathway top result was used if KEGG result did not appear

au proteins of interest

ontology domain according to STRING is shown in this table

Molecular Function	***Subcellular localisation***
Clathrin binding	Clathrin-coated pit
Beta-catenin binding	Wnt signalosome
Protein domain specific binding	Cytosol
Protein-containing complex binding	Actin cytoskeleton
SNAP receptor activity	SNARE complex
MAP kinase activity	Storage vacuole
Ca2+-dep protein S/T phosphatase a	Calcineurin complex
D2 dopamine receptor binding	Postsynaptic endocytic zone membr
Nuclear export signal receptor activity	Nucleus
Glutamate-gated calcium ion channel activity	Calcium- and calmodulin-dependent
PDZ domain binding	Presynaptic membrane
Krueppel-associated box domain binding	Set3 complex

KEGG* Pathway
Endocrine, other factor-reg Ca2+ reabsorption
Basal cell carcinoma
Cell cycle
Adherens junction
SNARE interactions in vesicular transport
VEGF signaling pathway
Long-term potentiation
Endocrine, other factor-reg Ca2+ reabsorption
Condensation of Prophase Chromosomes
Long-term potentiation
Dopamine Neurotransmitter Release Cycle
Amphetamine addiction

Table 26 **Properties of the hybrid network.**

Expanded engram (ECRRc) list

	Node	Edges	Cumulative edges	Edge contribution (%)	Expected edge contribution (%)
1	Creb1	17	17	5.90	3.85
2	**Mecp2**	**17**	34	5.90	3.85
3	Crebbp	16	50	5.56	3.85
4	Ctnnb1	16	66	5.56	3.85
5	Gsk3b	15	81	5.21	3.85
6	Hdac1	15	96	5.21	3.85
7	Hdac2	15	111	5.21	3.85
8	**Camk2a**	**13**	124	4.51	3.85
9	*Camk2b***	13	137	4.51	3.85
10	Dlg4	12	149	4.17	3.85
11	Dnmt1	12	161	4.17	3.85
12	Sin3a	12	173	4.17	3.85
13	Grin1	11	184	3.82	3.85
14	*Grin2b***	11	195	3.82	3.85
15	**Mapt (tau)**	**11**	206	3.82	3.85
16	**Ppp3ca**	**11**	217	3.82	3.85
17	Yy1	11	228	3.82	3.85
18	Rbbp7	10	238	3.47	3.85
19	Atrx	8	246	2.78	3.85
20	Sap30	8	254	2.78	3.85
21	Sin3b	8	262	2.78	3.85
22	**Lin7c**	**7**	269	2.43	3.85
23	Nfatc1	6	275	2.08	3.85
24	Ppp3r1	6	281	2.08	3.85
25	Crtc2	4	285	1.39	3.85
26	**Sh3gl2**	**3**	288	1.04	3.85
		288*			

Fin
Av
Avg. local c
PPI

**Includes 3 new manually confirmed PPIs*

**Protein was exclusive to tau interactome RMT-EC but introduced automatically by STF

al number of nodes: 26
Number of edges: 141
erage node degree: **10.8**
lustering coefficient: 0.686
enrichment p-value: < 1.0e-16

RING

Table 26 **Network analysis: Expanded (hybrid) engram network compared to unbias**
Proteins were randomly selected from a list of entire human proteome available in UniProt.

		Interactor controls		
	Experimental	1A	2A	3A
	MeCP2	AIP	ILKAP	IMPACT
	Sh3gl2	HPS3	MOCS2	COPS7A
	Lin7c	NDFIP1	ARHGEF3	KCNMA1
	Camk2a	ZNF330	PLTP	VPS37A
	Ppp3ca	SMC4	NVL	RASL11A
	MAPT	**MAPT**	**MAPT**	**MAPT**
Final number of nodes:	26	26	26	26
Number of edges:	141	95	67	94
Average node degree:	**10.8**	7.31	5.15	7.23
Avg. local clustering coefficient:	0.686	0.796	0.721	0.702
PPI enrichment p-value:	< 1.0e-16	0.00051	4.96E-05	1.08E-11
	↓	↓	↓	↓
	Tau controls			
	-Tau + 1 rando	1B	2B	3B
	MeCP2	AIP	ILKAP	IMPACT
	Sh3gl2	HPS3	MOCS2	COPS7A
	Lin7c	NDFIP1	ARHGEF3	KCNMA1
	Camk2a	ZNF330	PLTP	VPS37A
	Ppp3ca	SMC4	NVL	RASL11A
	TFG	***EXT2***	***WBP2***	***NUP88***
Final number of nodes:	26	26	26	26
Number of edges:	118	82	60	120
Average node degree:	**9.08**	6.31	4.62	9.23
Avg. local clustering coefficient:	0.706	0.794	0.83	0.775
PPI enrichment p-value:	< 1.0e-16	1.48E-05	7.98E-07	< 1.0e-16

MeCP2
Sh3gl2
Lin7c
Camk2a
Ppp3ca
MAPT

Cellular Component

#term ID	**term descrip**	**observed ger**
GO:0098978	Glutamatergic	5
GO:0045202	Synapse	6
GO:0098794	Postsynapse	5
GO:0098685	Schaffer collat	3
GO:0098984	Neuron to neu	4
GO:0030425	Dendrite	4
GO:0099523	Presynaptic cy	2
GO:0014069	Postsynaptic (	3
GO:0098793	Presynapse	3

KEGG Pathways

#term ID	**term descrip**	**observed ger**
mmu04020	Calcium signa	2
mmu04114	Oocyte meios	2
mmu04310	Wnt signaling	2
mmu04360	Axon guidanc	2
mmu04720	Long-term po	2
mmu04728	Dopaminergic	2
mmu04921	Oxytocin sign	2

mmu04922	Glucagon sigr	2
mmu05031	Amphetamine	2
mmu05152	Tuberculosis	2

Subcellular Localisation

#term ID	term descrip	observed ger
GOCC:00452	Synapse	6
GOCC:00304	Dendrite	4
GOCC:00058	Cytosol	5
GOCC:00995	Presynaptic cy	2
GOCC:00989	Neuron to neu	3
GOCC:00986	Schaffer collat	2

ed networks

Tau + 5 random protein starting nodes						
4A	5A	6A	7A	8A	9A	10A
TPST2	GPS2	RCN3	PTGR2	RDH14	ITCH	APOL2
AP1S1	HERC1	NAIF1	USP48	AGAP1	MUS81	SPRY3
MACROH2A	APBB2	KLF7	CCNL2	ZNF410	AP1S3	PTGIS
RNMT	HTATSF1	UBA5	FAM120B	HCFC1R1	TGM7	HDAC2
CHD3	PPP1R11	SEPTIN6	TXNDC12	PARD3	BBS2	HERPUD1
MAPT	**MAPT**	**MAPT**	**MAPT**	**MAPT**	**MAPT**	**MAPT**
26	26	26	26	26	26	26
120	77	88	88	88	88	88
9.23	5.92	6.77	6.77	6.77	6.77	6.77
0.784	0.724	0.572	0.572	0.572	0.572	0.572
3.33E-16	1.65E-07	2.06E-06	2.06E-06	2.06E-06	2.06E-06	2.06E-06
↓	↓	↓	↓	↓	↓	↓
4B	5B	6B	7B	8B	9B	10B
TPST2	GPS2	RCN3	PTGR2	RDH14	ITCH	APOL2
AP1S1	HERC1	NAIF1	USP48	AGAP1	MUS81	SPRY3
MACROH2A	APBB2	KLF7	CCNL2	ZNF410	AP1S3	PTGIS
RNMT	HTATSF1	UBA5	FAM120B	HCFC1R1	TGM7	HDAC2
CHD3	PPP1R11	SEPTIN6	TXNDC12	PARD3	BBS2	HERPUD1
RAB18	***MLH3***	***ABC***	***RBM7***	***EIF1AY***	***ZNF18***	***PKIG***
26	26	26	26	26	26	26
123	104	123	114	105	114	141
9.46	8	9.46	8.77	8.08	8.77	10.8
0.784	0.865	0.861	0.823	0.627	0.823	0.68
< 1.0e-16	< 1.0e-16	< 1.0e-16	< 1.0e-16	< 1.0e-16	< 1.0e-16	< 1.0e-16

background	strength	false discove	matching pro	matching proteins in your network (labe
501	1.56	6.22E-05	10090.ENSM	Lin7c,Sh3gl2,Mecp2,Ppp3ca,Camk2a
1492	1.17	8.25E-05	10090.ENSM	Lin7c,Sh3gl2,Mecp2,Ppp3ca,Mapt,Camk2
761	1.38	0.00016	10090.ENSM	Lin7c,Mecp2,Ppp3ca,Mapt,Camk2a
113	1.99	0.00084	10090.ENSM	Sh3gl2,Ppp3ca,Camk2a
446	1.52	0.00084	10090.ENSM	Lin7c,Sh3gl2,Mapt,Camk2a
753	1.29	0.0047	10090.ENSM	Sh3gl2,Ppp3ca,Mapt,Camk2a
24	2.49	0.0047	10090.ENSM	Sh3gl2,Camk2a
414	1.43	0.0182	10090.ENSM	Lin7c,Mapt,Camk2a
636	1.24	0.048	10090.ENSM	Lin7c,Sh3gl2,Camk2a

background	strength	false discove	matching pro	matching proteins in your network (labe
193	1.58	0.0423	10090.ENSM	Ppp3ca,Camk2a
115	1.81	0.0423	10090.ENSM	Ppp3ca,Camk2a
157	1.67	0.0423	10090.ENSM	Ppp3ca,Camk2a
176	1.62	0.0423	10090.ENSM	Ppp3ca,Camk2a
63	2.07	0.0423	10090.ENSM	Ppp3ca,Camk2a
127	1.76	0.0423	10090.ENSM	Ppp3ca,Camk2a
145	1.7	0.0423	10090.ENSM	Ppp3ca,Camk2a

99	1.87	0.0423	10090.ENSM	Ppp3ca,Camk2a
63	2.07	0.0423	10090.ENSM	Ppp3ca,Camk2a
170	1.64	0.0423	10090.ENSM	Ppp3ca,Camk2a

background	strength	false discove	matching pro	matching proteins in your network (labe
1032	1.33	2.32E-05	10090.ENSM	Lin7c,Sh3gl2,Mecp2,Ppp3ca,Mapt,Camk2
495	1.47	0.0027	10090.ENSM	Sh3gl2,Ppp3ca,Mapt,Camk2a
1784	1.01	0.0071	10090.ENSM	Sh3gl2,Mecp2,Ppp3ca,Mapt,Camk2a
24	2.49	0.0071	10090.ENSM	Sh3gl2,Camk2a
320	1.54	0.0145	10090.ENSM	Sh3gl2,Mapt,Camk2a
82	1.95	0.0419	10090.ENSM	Sh3gl2,Camk2a

Tau, expansions		6 random
MAPT	**MAPT**	PFKFB3 SP6 PABPN1 HPS6 BICD2 GBF1
21	31	26
88	144	60
8.38	9.29	4.62
0.708	0.662	0.793
4.60E-07	5.05E-13	3.12E-08

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