

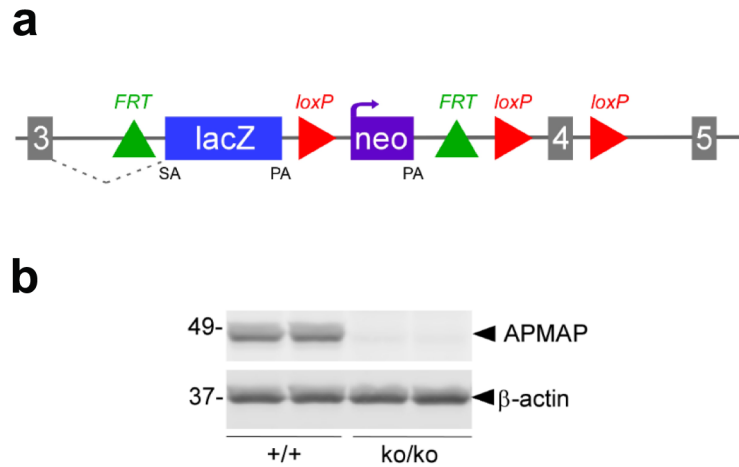
# **The APMAP interactome reveals new modulators of APP processing and beta-amyloid production that are altered in Alzheimer's disease**

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## **SUPPLEMENTARY FIGURES**



**Fig.S1** Generation of the APMAP-KO mouse line. **a** Schematic representation of the knockout-first construct (KOMP Repository; [www.komp.org](http://www.komp.org)) used for the generation of the APMAP full knockout mouse line. **b** The deleted APMAP protein expression was confirmed by Western blot analysis of whole brain extracts from 3-month-old APMAP-KO mice (ko/ko; n=2) and WT mice (+/+; n=2).  $\beta$ -Actin served as a protein loading control.

**a**

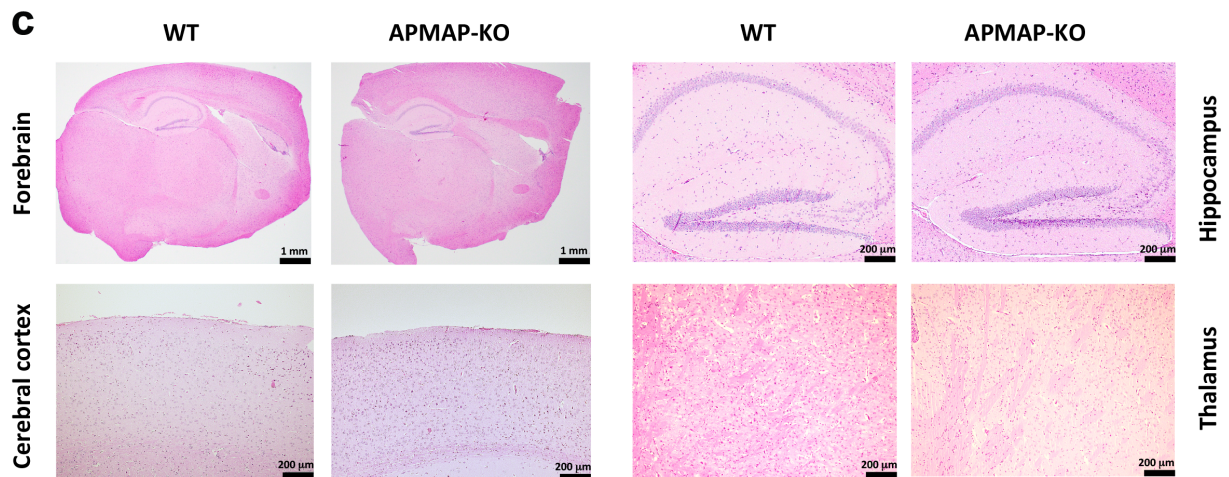
Skin
Mammalian gland
Heart
Tongue
Sternum / Bone marrow
Thymus
Trachea
Oesophagus
Thyroid
Salivary gland
Mandibular Lymphnodes
Lung
Stomach
Small Intestine
Large Intestine
Liver
Kidney right and left
Urinary bladder
Spleen
Pancreas
White adipose tissue
Spine (cervical, thoracic, lumbar)
Knee (joint, bones, muscles)
Head (multiple cross sections)
Brain (1 hemisphere)

<b>Female genital tract:</b>
Uterus
Ovary right and left
Vagina

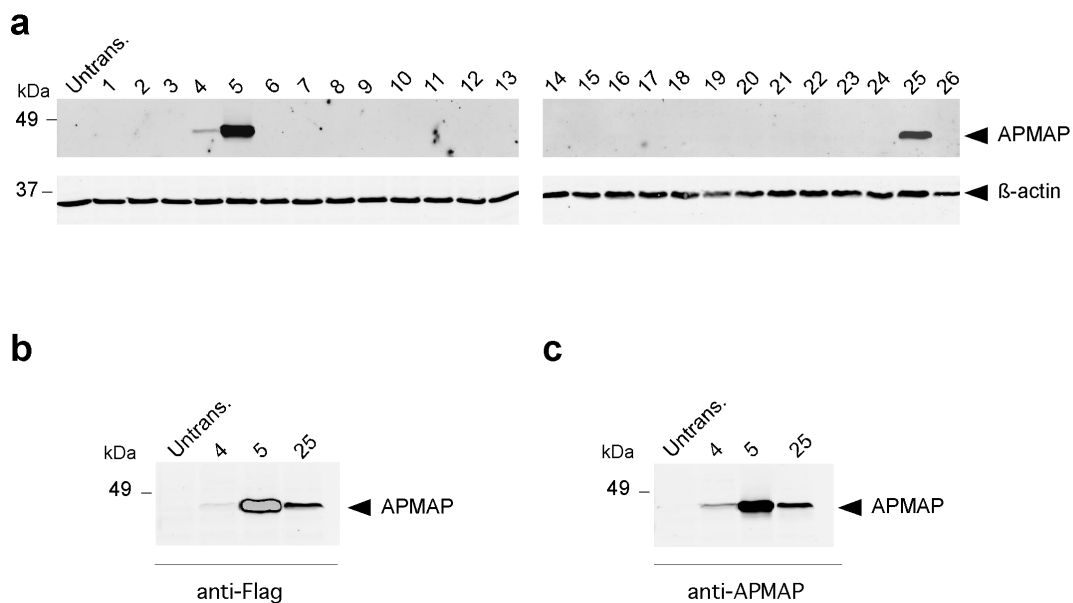
<b>Male genital tract:</b>
Testis right and left
Seminal vesicle
Prostate
Preputial glands

**b**

	chow diet		high fat diet		significance
	n per group	grade / score	n per group	grade / score	
<b>Lung</b>					
leucocytic infiltrates	ko-4, wt-8	ko 1.8, wt 3.7	ko-3, wt-1	ko 3, wt 2.5	inflammatory change
<b>Kidney</b>					
leucocytic infiltrates, perivascular	ko-8, wt-10	ko 3.8, wt 4.1	ko-4, wt-3	ko 3.7, wt 2.8	background lesion
tubular lipidosis	ko-3, wt-3	ko 1.2, wt 1.2	ko-5, wt-2	ko-1.8, wt 1.2	incidental finding
tubular basophilia	ko-1, wt-2				background lesion
tubular proteinaceous casts	wt-2		wt-1		background lesion
basement membrane thickening	wt-1				background lesion
glomerular sklerosis	wt-1		ko-1		background lesion
mesangial cell proliferation	wt-1		wt-2		background lesion
<b>Liver</b>					
leucocytic infiltrates	ko-3, wt-7	ko 1.1, wt 2.5	ko-5, wt-2	ko 4.8, wt 1.2	inflammatory change
hepatic lipidosis	ko-0, wt-0		ko-5, wt-5	ko 8, wt 8	diet related related to inflammation
extramedullary hematopoiesis	ko-2, wt-1		wt-2		
<b>Stomach</b>					
leucocytic infiltrates	ko-4, wt-4	ko 1.3, wt 1	ko-1, wt-0	ko 1.2	inflammatory change
<b>Oesophagus</b>					
bacteria intracorneal			ko-1, wt-1		incidental finding
<b>Spleen</b>					
activated lymph follicles	ko-0, wt-1		ko-2, wt-2		background lesion
hemosiderosis	ko-6, wt-3	ko 2.7, wt 1.7	ko-1, wt-0	ko 1.2	background lesion related to inflammation
extramedullary hematopoiesis	ko-1, wt-1		ko-1, wt-0		
<b>Salivary gland</b>					
leucocytic infiltrates	ko-7, wt-8	ko 4, wt 4.2	ko-3, wt-1	ko 3.6, wt 1	background lesion
<b>Lymph nodes (mandibular, mediastinal, mesenteric)</b>					
activated lymph follicles			ko-2, wt-3		background lesion
sinus histiocytosis	ko-4, wt-7	ko 2.5, wt 3.7	ko-5, wt-12	ko 5.3, wt 1.9	background lesion
<b>Pancreas</b>					
leucocytic infiltrates	ko-3, wt-6	ko 1.7, wt 3.3	ko-0, wt-0		inflammatory change
<b>Testis</b>					
leucocytic infiltrates	ko-1, wt-2	ko-1, wt-1.17	ko-0, wt-1	wt 1	background lesion
<b>Seminal Vesicles</b>					
histiocytes intraluminal			ko-1		incidental finding
<b>Preputial glands</b>					
leucocytic infiltrates	ko-2, wt-2	ko 2.3, wt 1.5	ko-3, wt-2	ko 2.8, wt 1.6	background lesion
fibrosis	ko-0, wt-1				background lesion
cystic dilation	ko-1, wt-3		wt-3		background lesion
<b>Skin</b>					
leucocytic infiltrates w/wo bacteria			ko-4, wt-3	ko-3.6, wt 2.6	inflammatory change
<b>Gingiva</b>					
leucocytic infiltrates			ko-1	ko 0.8	incidental finding
<b>Muscle</b>					
leucocytic infiltrates			ko-1		incidental finding
muscle fiber regeneration			ko-1		incidental finding
<b>Urinary bladder</b>					
leucocytic infiltrates	wt-1				background lesion



**Fig.S2** Morpho-pathological characterization of APMAP-KO mice. **a** Organs and tissues analyzed to assess whether the biallelic deletion of the gene coding for APMAP induces macroscopic and/or microscopic morphological changes. **b** No significant morphological changes (graded from 0 to 6 according to their degree of severity) were recorded in the APMAP-KO groups compared to the age and sex-matched WT control animals, fed with chow or high fat diets. The phenotypic observations are not related to the specific genotype, as confirmed by the non-significant semi-quantitative histopathologic scores among the different groups, and by the intra- and intergroup low incidence. Mice on a chow diet were aged 7 to 9 months, with n=10 mice/group (equally distributed between males and females). Mice on a high fat diet were aged 4 months, with n=5 males/group. **c** APMAP deficiency does not affect morphology of neural tissues. Sagittal brain sections from 9 month-old WT and APMAP-KO mice stained with hematoxylin and eosin. Specific tissue is indicated at left of each pair of panels. Scale bars, 1 mm for brain and 200  $\mu$ m for hippocampus, cerebral cortex and thalamus.



**Fig.S3** Generation and selection of a CHO cell line stably overexpressing APMAP for the high-grade purification of APMAP and associated proteins. **a** Clonal selection of a CHO cell line stably overexpressing APMAP. Chinese hamster ovary adherent cells were transfected with a plasmid harboring APMAP1-Flag and selection was performed in DMEM containing 300  $\mu$ g/ml Geneticin G418. After 21 days of selection, single cell cultures were inoculated into 96-well plates by limiting dilution. Of all recovered clonal cell lines, 26 were screened for APMAP expression and the highest producers were maintained in culture for further analysis. **b, c** Whole cell extracts were prepared and analyzed by Western blot with anti-Flag (**b**) or anti-APMAP (**c**) antibodies. The highest producer (clone 5) was further adapted for cultures in suspension and used for the purification of APMAP and associated proteins.

## CP1

Q9HDC9 (100%), 46,481.5 Da

Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2

36 exclusive unique peptides, 50 exclusive unique spectra, 173 total spectra, 212/416 amino acids (51% coverage)

MSEADGLRQR	RPLRPPQVVT	DDGQAPEAKD	GSSFSGRVFR	VTFLMLAVSL	TVPLLGAAML
LESPIDPQPL	SFKPPLLLG	VLHPNTKLRQ	AERLFENQLV	GPESIAHIGD	VMFTGTADGR
VVKLENGEIE	TIARFGSGPC	KTRDDEPVCG	RPLGIRAGPN	GTLFVADAYK	GLFEVNPWKR
EVKLLLSSET	PIEGKNMSFV	NDLTVTQDGR	KIYFTDSSSK	WQRRDYLLLV	MEGTDDGRL
EYDTVTR	VLLDQLRFPN	GVQLSPAEDF	VLVAETTMR	IRRVYVSGLM	KGADL FVEN
MPGFPDNIRP	SSSGGYWVGM	STIRPNPGFS	MLDFLSERPW	IKRMIFKLF	QETVMK FVPR
YSLVLELSDS	GAFRRSLHDP	DGLVATYISE	VHEHDGHLYL	GSFRSPFLCR	LSLQAV

## CP2

Q9HDC9 (100%), 46,481.5 Da

Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2

32 exclusive unique peptides, 40 exclusive unique spectra, 126 total spectra, 196/416 amino acids (47% coverage)

MSEADGLRQR	RPLRPPQVVT	DDGQAPEAKD	GSSFSGRVFR	VTFLMLAVSL	TVPLLGAAML
LESPIDPQPL	SFKPPLLLG	VLHPNTKLRQ	AERLFENQLV	GPESIAHIGD	VMFTGTADGR
VVKLENGEIE	TIARFGSGPC	KTRDDEPVCG	RPLGIRAGPN	GTLFVADAYK	GLFEVNPWKR
EVKLLLSSET	PIEGKNMSFV	NDLTVTQDGR	KIYFTDSSSK	WQRRDYLLLV	MEGTDDGRL
EYDTVTR	VLLDQLRFPN	GVQLSPAEDF	VLVAETTMR	IRRVYVSGLM	KGADL FVEN
MPGFPDNIRP	SSSGGYWVGM	STIRPNPGFS	MLDFLSERPW	IKRMIFKLF	QETVMK FVPR
YSLVLELSDS	GAFRRSLHDP	DGLVATYISE	VHEHDGHLYL	GSFRSPFLCR	LSLQAV

P12763 (100%), 38,417.4 Da

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2

3 exclusive unique peptides, 3 exclusive unique spectra, 5 total spectra, 38/359 amino acids (11% coverage)

MKSFVLLFCL	AQLWGCHSIP	LDPVAGYKEP	ACDDPDTEQA	ALAAVDYINK	HLPRGYKHTL
NQIDSVKVP	RRPTGEVYDI	EIDTLETTCH	VLDPTPLANC	SVRQQTQHAV	EGDCDIHVLLK
QDGGQFSVLF	KCDSSPDSAE	DVRKLCPCDC	LLAPLNDSRV	VHAVEVALAT	FNAESNGSYL
QLVEISRQAF	VPLPVSVSVE	FAVAATDCIA	KEVVDPTKCN	LLAEKQYGF	KGSVIQKALG
GEDVRVTCTL	FQTQPVIPQP	QPDGAEAEAP	SAVPDAAGPT	PSAAGPPVAS	VVVGPSVVAV
PLPLHRAHYD	LRHTFSGVAS	VESSSGEAFH	VGKTPIVQGP	SIPGGPVR	LC PGRIRYFKI

## CP3

Q9HDC9 (100%), 46,481.5 Da

Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2

22 exclusive unique peptides, 25 exclusive unique spectra, 73 total spectra, 178/416 amino acids (43% coverage)

MSEADGLRQR	RPLRPPQVVT	DDGQAPEAKD	GSSFSGRVFR	VTFLMLAVSL	TVPLLGAAML
LESPIDPQPL	SFKPPLLLG	VLHPNTKLRQ	AERLFENQLV	GPESIAHIGD	VMFTGTADGR
VVKLENGEIE	TIARFGSGPC	KTRDDEPVCG	RPLGIRAGPN	GTLFVADAYK	GLFEVNPWKR
EVKLLLSSET	PIEGKNMSFV	NDLTVTQDGR	KIYFTDSSSK	WQRRDYLLLV	MEGTDDGRL
EYDTVTR	VLLDQLRFPN	GVQLSPAEDF	VLVAETTMR	IRRVYVSGLM	KGADL FVEN
MPGFPDNIRP	SSSGGYWVGM	STIRPNPGFS	MLDFLSERPW	IKRMIFKLF	QETVMK FVPR
YSLVLELSDS	GAFRRSLHDP	DGLVATYISE	VHEHDGHLYL	GSFRSPFLCR	LSLQAV



A0A061I3K8 (100%), 160,726.0 Da  
 Calnexin OS=Cricetulus griseus GN=H671\_7g18220 PE=3 SV=1  
 15 exclusive unique peptides, 18 exclusive unique spectra, 22 total spectra, 109/1479 amino acids (7% coverage)

MEGKWL LCLL	LVLGTVAVQA	HDGHDDDMID	IEDDLDDVIE	EVEDSK	<b>SKSD</b>	<b>SSTPPSPK</b>	VT
YK <b>APVPTGEV</b>	<b>YFADSFDR</b> GS	LSGWILSK	<b>AK</b>	<b>KDDTDDEIAK</b>	YDGKWEVDEM	KDTKLPDGDKG	
LVLMSRAKHH	AISAKLNKPF	LFDTKPLIVQ	YEVNFQNGIE	CGGAYVKLLS	K <b>TSELNLDQF</b>		
<b>HDK</b> TPYTIMF	GPDKCGEDYK	LHFI FRHKNP	KTGVYEEKHA	KRPDTDLKIY	FTDKKTHLYT		
LILNPDNSFE	ILVDQYVVNS	GNLLNDMTPA	VNPSREIEDP	EDQKPEDWDE	RPKIPDPDAV		
KPDDWDEDAP	GKIPDEEATK	PEGWLDDEPE	YIPDPDADKP	EDWDEMDDGE	WEAPQIANPK		
CESAPGCGVW	QR <b>PLIDNPY</b>	<b>KGKWKPPMID</b>	NPNYQGVWKP	RKIPNPDFFE	DLEPFKMTPF		
SAIGLELWSM	TSDIFFDNFI	ISGDRRVVDD	WANDGWGLK <b>K</b>	<b>AADGAAEPGV</b>	<b>VGHMLEAEE</b>		
RPWLWVYIL	TVALPVFLVI	LFCCSGKKQS	NAMEYK <b>KTDA</b>	<b>AQPDVKEDEG</b>	<b>KEEEKNKGD</b>		
<b>EEEEKLEEK</b>	QKSDAEEEDGG	TGSQDEEDRK	PTAEEDEILN	RSPRNRKPRR	ESWDLWHLHD		
TVKRNLD SAA	SPQNGDQNG	YGDLPFGHKK	TRREAPLGIS	VSANGLPPAS	PLGQPKPPG		
GDALQSGGKH	SLGLDPIINCK	CMADSSIEHLN	GSSNPNPFP	LSLSKELKQE	PVDDPLCMIA		
GAGGSVSSSN	LMPDLNLNEQ	EWKELIEELN	RSVPDEDMKD	LFTEDFEKKE	DPEPPGSATQ		
TPLAQDINIK	TEFSPA AFEQ	EQLGSPQVRA	GSAGQTFLLGP	SSAPVGTDS	SLGSSQTLFH		
TTGQPGADNP	SANLMPASAQ	AQNAQRALAS	VVLPSPQGG	ASELSSAHQL	QQIAAKQKRE		
QMLQNPQAA	SPAPAPQLST	WQQAQPSHSP	LDPVYPMEKP	ASPPGYKQDF	TNSKLLMMP		
VNKSSPRPGG	PYLQPSHNL	LSHQSPSNLN	QSSVNNQGA	LDYGNTKPLS	HYKADCQQG		
PGSGQSKPAL	MAYLPPQLPH	LSNEQNSLFL	MKQKAANMPF	RS LVP PGQE	NP SNV SPAQ		
TANVGTQPPS	VSVASTHNS	PYLSQQQAA	VMKQHQLLD	QQKQREQQQL	QQQQQQLQR		
QHLLAEQEKQ	QFQRPASAAP	GMNNLGPSS	SCPRVFPQPG	TLMSMGQPHA	PVSSLPSSSG		
PQDRGVAQFT	GSQSLPQSSL	YGITSGLPQI	VAQPPPQAAS	AHAHI PRQTS	VGQNASAPAA		
YGGNSLGSAG	LSQQAHNKGT	PPGLTKSQVP	RVSAAMGGQN	ASWQHKGMPN	LS SQT PGNSS		
VSPFAAPSS	HMQQAHLKIP	GQQFSQAMP	RPMAPMSAG	AAGSMLPPVS	TQRNSAPAP		
APPQAAPQQG	LPGLSPAGPE	LGAFSQSS	QMN SRAGLHC	TQAYPVRTMG	QELPFAFSGG		
PGSSGLSSVA	GHTDLIDSLL	KNRTSEEWIN	EELDDL LGSQ				

A0A061IIM78 (100%), 43,787.5 Da  
 Lysosome-associated membrane glycoprotein 1 OS=Cricetulus griseus GN=H671\_1g1762 PE=4 SV=1  
 2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 23/407 amino acids (6% coverage)

MAAPGAPRSL	LLLLLAGLAH	GASALFVVKD	SNGTACIMAN	FSASFFTIYE	TGHGSKNSTF
ELPSSAEVLN	SNSSCGRENV	SEPILTIAFG	SGYLLTLNFT	RNATRYSVQD	MYFAYNLSDT
QHFLNASNK <b>G</b>	<b>IHSVDSSTDI</b>	<b>KADINKTYRC</b>	LSA IQVHMGN	VTVTLSDATI	QAYLLNSNFS
KEETRCTQDG	PSPTTVPPSP	SPPLVPTNPT	VIKYNTGEN	GTCLLASMAL	QMNITYMKKD
NMTVTRALNI	SPNDTASGSC	SPHVVTLTVE	SKNSILD LKF	GMNGSSSLFF	LQEVRLNMTL
PDANVSS LMA	SNQSLR <b>ALQA</b>	<b>TVGNSYK</b> CNT	EEHIFVTKEF	SLNVF SVVQV	AFKVESDRFG
SVEECMQDGN	NMLIPIAVGG	ALAGLVLIVL	IAYLIGRKR S	HAGYQTI	

G3H7X9 (100%), 68,661.3 Da  
 Nicastrin OS=Cricetulus griseus GN=I79\_006475 PE=4 SV=1  
 3 exclusive unique peptides, 3 exclusive unique spectra, 3 total spectra, 35/615 amino acids (6% coverage)

MV LLEGLKLFN	RAVMEK LKGR	TSRIAGLAVT	LAKPNSTSS F	SPSVQCPNDG	FGIYSNSYGS
EFAHCKQTLW	NELGNGLAYE	DFSFPILFLE	DENETKVIKQ	CYQDHNLAQN	GSAPRFPLCA
MQLFSSHMHAV	I STATCMRRS	FIQSTFINS	EIVCDPLSDY	NVWSMLKPIN	TSGALFPDDR
VVVAATR LDS	RSFFWNVAPG	AESAVASYVT	QLAAAEALHK	<b>ASDVATLPRN</b>	VMFVFFQGET
FDYIGSSRMV	YDMENGFVP	RLENIDSFVE	LGQVALRTSL	DLWMHTDPM	QKNESVKNQV
EDLLVTLLEKS	GAGVPEVFLR	RQNQSDALPP	SSLQRFLRAR	NISGVVLADH	SGSFHNRYYQ
S IYDTAENIN	VTYPER <b>QSPE</b>	<b>EDLNFVTDTA</b>	<b>KALANVATVL</b>	<b>ARALYELAG</b>	TNFSDSIQAD
PQTVTRLLYG	FLVRANNSWF	QSI LRQDLRS	YLDGGLQHY	I AVTSPNTT	YVVQYALANL
TGKVTNL TRE	QCQDPSKVPN	ESKALYDYSW	VQGPLNSNKT	ERLPRCVRST	VRLARALSPA
FELSVQWGST	YSTWAESRWK	DIQARIFLVA	SKELEFITLT	VGFGILIFSL	IVTYCINAKA
DVLFVAPREP	GAVSY				

F1LQ3 (100%), 126,405.1 Da  
 Reticulon OS=Rattus norvegicus GN=Rtn4 PE=1 SV=1  
 2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 22/1163 amino acids (2% coverage)

MEDI DQSSLV	SSSTDSPPRP	PPAFKYQFVT	EPEDEEDEEEE	EDEDEEDEDED	LEELEVLERK
PAAGLSAAAV	PPAAAAPLL D	FSSDSVPPAP	RGPLPAAPP A	APERQPSWER	SPAAPAPSLP
PAAAVLPSKL	PEDDEPPARP	PPPPVAGASP	LAEPAAPST	PAAPKRRGSG	SVDET L FALP
AASEPVI PSS	AEKIMDLMEQ	PGNTVSSGQE	DFPVS LLETA	ASLPSLSPLS	TVSFKEHGYL
GNLSAVSSSE	GTIEETLNEA	SKELPERATN	PFFVNRDLAEF	SELEYSEMGS	SFKGSPKGES
AILVENTKEE	VIVRSKDKED	LVCSSAALHSP	QESPVGKEDR	VVSPEKTM DI	FNEMQMSVVA
PVREEYADF K	PFEQAWEVKD	TYEGS R D VLA	ARANVESKVD	RKCLLED SLEQ	KS LGKDS EGR
NEDASFPSTP	EPVKDSSRAY	ITCASFTSAT	ESTTANTFPL	LEDHTSENKT	DEKKIEERKA
QIITEKTS PK	TSNPFLVAVQ	DSEADYVTTD	TLSKVTEAAV	SNMPEGLTPD	LVQEACES EL
NEATGTKIAY	ETKVDLVQTS	EAIQESLYPT	AQLCPSFEAA	EATPSPVLPD	IVMEAPLNSL
LP SAGASVVQ	PVS SPL EAPP	PLSYDSIKLE	PENPPPYEEA	MNVALKALGT	KEGIKEPESF
NAAVQET EAP	YIS IACDLIK	ETKLKSTEPS	DFSNSSEIAK	FEKSVPEHAE	LVEDSSPSE
PVDLFSDDSI	PEVPPTQEEA	VMLMKESTE	VSETVAQHKE	ERLSASPEQL	GKPYLESFQP
NLHSTKDAAS	NDIPTLTKKE	KISLQMEEFN	TAIYSNDDLL	SSKEDKIKES	ETFS DSSPIE
IIDEFPTFVS	AKDIPSPKLAK	EYTDLEVSDK	SEIANIQSGA	DSLPCLELPC	DLSFKNIYPK
DEVHVSDEF S	ENRSSVSKAS	ISPSNVSALE	PQTEMGSIVK	SKSLTKAEAK	KLPSDTEKED
RSLSAVLSAE	LSKTSVV D LL	YWRD I KKTGV	VFGASLFLLL	SLTVFVSVSV	TAYIALALLS
VTISFRIYKVG	YIQAIQK <b>SDE</b>	<b>GHPFR</b> AYLES	EVAISEELVQ	<b>KYSNSALGHV</b>	<b>NSTIK</b> ELRR L
FLVDDLVDSL	KFAVLMWVFT	YVGA LFNGLT	LLILALISLF	SIPVIYERHQ	VQIDHYLGLA
NKSVK DAMAK	IQA KIPGLKR	KAD			



# CP6

Q9HDC9 (100%), 46,481.5 Da

Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2

31 exclusive unique peptides, 37 exclusive unique spectra, 59 total spectra, 204/416 amino acids (49% coverage)

MSEADGLRQR	RPLRPQVVTD	DDGQAPEAKD	GSSFSGRVFR	VTFLMLAVSL	TVPLLGAMML
LESPIDPQPL	SFKEPPLLLG	VLHPNPKLRQ	AERLLENQLV	GPESIAHIGD	VMFTGTADGR
VVKLENGEIE	TIARFGSGPC	KTRDDEPVCG	RPLGIRAGPN	GTLFVADAYK	GLFEVNPWKR
EVKLLLSSET	PIEGKNMSFV	NDLTVTQDGR	KIYFTDSSSK	WQRRDYLLLV	MEGTTDDGRLL
EYDVTREVK	VLLDQLRFPN	GVQLSPAEDF	VLVAETTMAR	IRRVYVSGLM	KGGADLFVEN
MPGFPDNIRP	SSSGGYWVGM	STIRPNPGFS	MLDFLSERPW	IKRMIFKLFSS	QETVMK FVPR
YSLVLELSDS	GAFRRSLHDP	DGLVATYISE	VHEHDGHLYL	GSRFRSFPFLCR	LSLQAV

A0A061M78 (100%), 43,787.5 Da

Lysosome-associated membrane glycoprotein 1 OS=Cricetulus griseus GN=H671\_1g1762 PE=4 SV=1

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 23/407 amino acids (6% coverage)

MAAPGAPRSL	L L L L L A G L A H	G A S A L F V V K D	S N G T A C I M A N	F S A S F F T I Y E	T G H G S K N S T F
E L P S S A E V L N	S N S S C G R E N V	S E P I L T I A F G	S G Y L L T L N F T	R N A T R Y S V Q D	M Y F A Y N L S D T
Q H F L N A S N K G	I H S V D S S T D I	K A D I N K T Y R C	L S A I Q V H M G N	V T V T L S D A T I	Q A Y L L N S N F S
K E E T R C T Q D G	P S P T T V P P S P	S P P L V P T N P T	V I K Y N V T G E N	G T C L L A S M A L	Q M N I T Y M K K D
N M T V T R A L N I	S P N D T A S G S C	S P H V V T L T V E	S K N S I L D L K F	G M N G S S S L F F	L Q E V R L N M T L
P D A N V S S L M A	S N Q S L R A L Q A	T V G N S Y K C N T	E E H I F V T K E F	S L N V F S V Q V Q	A F K V E S D R F G
S V E E C M Q D G N	N M L I P I A V G G	A L A G L V L I V L	I A Y L I G R K R S	H A G Y Q T I	

A0A061I3K8 (100%), 160,726.0 Da

Calnexin OS=Cricetulus griseus GN=H671\_7g18220 PE=3 SV=1

21 exclusive unique peptides, 24 exclusive unique spectra, 30 total spectra, 141/1479 amino acids (10% coverage)

M E G K W L L C L L	L V L G T V A V Q A	H D G H D D D M I D	I E D D L D D V I E	E V E D S K S K S D	S S T P P S P K V T
Y K A P V P T G E V	Y F A D S F D R G S	L S G W I L S K A K	K D D T D D E I A K	Y D G K W E V D E M	K D T K L P G D K G
L V L M S R A K H H	A I S A K L N K P F	L F D T K P L I V Q	Y E V N F Q N G I E	C G G A Y V K L L S	K T S E L N L D Q F
H D K T P Y T I M F	G P D K C G E D Y K	L H F I F R H K N P	K T G V Y E E K H A	K R P D T D L K I Y	F T D K K T H L Y T
L I L N P D N S F E	I L V D Q Y V V N S	G N L L N D M T P A	V N P S R E I E D P	E D Q K P E D W D E	R P K I P D P D A V
K P D D W D E D A P	G K I P D E E A T K	P E G W L D D E P E	Y I P D P D A D K P	E D W D E D M D G E	W E A P Q I A N P K
C E S A P G C G V P	Q R P L I D N P N Y	K G K W K P P M I D	N P N Y Q G V W K P	R K I P N P D F F E	D L E P F K M T P F
S A I G L E L W S M	T S D I F F D N F I	I S G D R R V V D D	W A N D G W G L K K	A A D G A A E P G V	V G H M L E A A E E
R P W L W V V I L L	T V A L P V F L V I	L F C C S G K K Q S	N A M E Y K K T D A	A Q P D V K E D E G	K E E E K N K G D E
E E E E E K L E E K	Q K S D A E E D G G	T G S Q D E E D R K	P T A E E D E I L N	R S P R N R K P R R	E S W D L W H L H D
T V K R N L D S A A	S P Q N G D Q Q N G	Y G D L F P G H K K	T R R E A P L G I S	V S A N G L P P A S	P L G Q D P K P P G
G D A L Q S G G K H	S L G L D P I N K K	C M A D S S I H L N	G S S N P N E P F P	L S L S K E L K Q E	P V D D L P C M I A
G A G G S V S Q S N	L M P D L N L N E Q	E W K E L I E E L N	R S V P D E D M K D	L F T E D F E E K K	D P E P P G S A T Q
T P L A Q D I N I K	T E F S P A A F E Q	E Q L G S P Q V R A	G S A G Q T F L G P	S S A P V G T D S P	S L G S S Q T L F H
T T G Q P G A D N P	S P N L M P A S A Q	A Q N A Q R A L A S	V V L P S Q G P G G	A S E L S A H A Q L	Q Q I A A K Q K R E
Q M L Q N P Q Q A A	S A P A P G Q L S T	W Q Q A G P S H S P	L D V Y P P M E K P	A S P P G Y K Q D F	T N S K L L M M P S
V N K S S P R P G P	P Y L Q P S H S N L	L S H Q S P S N L N	Q S S V N P Q G A V	L D Y G N T K P L S	H Y K A D C G Q G G
P G S G Q S K P A L	M A Y L P Q Q L P H	L S N E Q N S L F L	M K Q K A A N M P F	R S L V P P G Q E Q	N P S N V S V P A Q
T A N V G T Q P P S	V S V A S T H N S S	P Y L S S Q Q Q A A	V M K Q H Q L L L D	Q Q K Q R E Q Q Q L	Q Q Q Q Q Q L Q R
Q H L L A E Q E K Q	Q F Q R P S A A V P	G M N N L G P S N S	S C P R V F P Q P G	T L M S M G P G H A	P V S S L P S S S G
P Q D R G V A Q F T	G S Q S L P Q S S L	Y G I T S G L P Q I	V A Q P P P Q A A S	A H A H I P R Q T S	V G Q N A S A P A A
Y G Q N S L G S A G	L S Q Q H N K G T L	P P G L T K S Q V P	R V S A A M G G Q N	A S W Q H Q G M P N	L S S Q T P G N S S
V S P F A A P S S F	H M Q Q A H L K I P	G Q Q F S Q A M P S	R P M A P M S S A G	A A G S M L P P V S	T Q Q R N S A P A P
A P P Q A A P Q Q G	L P G L S P A G P E	L G A F S Q S S T S	Q M N S R A G L H C	T Q A Y P V R T M G	Q E L P F A F S G Q
P G S S G L S S V A	G H T D L I D S L L	K N R T S E E W I N	E L D D L L G S Q		

G3H7X9 (100%), 68,661.3 Da

Nicastrin OS=Cricetulus griseus GN=I79\_006475 PE=4 SV=1

4 exclusive unique peptides, 4 exclusive unique spectra, 4 total spectra, 44/615 amino acids (7% coverage)

M V L L E G K L F N	R A V M E K L K G R	T S R I A G L A V T	L A K P N S T S S F	S P S V Q C P N D G	F G I Y S N S Y G S
E F A H C K Q T L W	N E L G N G L A Y E	D F S F P I F L L E	D E N E T K V I K Q	C Y Q D H N L A Q N	G S A P R F P L C A
M Q L F S H M H A V	I S T A T C M R R S	F I Q S T F S I N P	E I V C D P L S D Y	N V W S M L K P I N	T S G A L E P D D R
V V V A A T R L D S	R S F F W N V A P G	A E S A V A S Y V T	Q L A A A E A L H K	A S D V A T L P R N	V M F V F F Q G E T
F D Y I G S S R M V	Y D M E N G K F P V	R L E N I D S F V E	L G Q V A L R T S L	D L W M H T D P M S	Q K N E S V K N Q V
E D L L V T L E K S	G A G V P E V V L R	R Q N Q S Q A L P P	S S L Q R F L R A R	N I S G V V L A D H	S G S F H N R Y Y Q
S I Y D T A E N I N	V T Y P E R Q S P E	E D L N F V T D T A	K A L A N V A T V L	A R A L Y E L A G G	T N F S D S I Q A D
P Q T V T R L L Y G	F L V R A N N S W F	Q S I L R Q D L R S	Y L D D G P L Q H Y	I A V T S P T N T T	V V V Q Y A L A N L
T G K V T N L T R E	Q C Q D P S K V P N	E S K A L Y D Y S W	V Q G P L N S N K T	E R L P R C V R S T	V R L A R A L S P A
F E L S Q W G S T E	Y S T W A E S R W K	D I Q A R I F L V A	S K E L E F I T L T	V G F G I L I F S L	I V T Y C I N A K A
D V L F V A P R E P	G A V S Y				

G3H902 (100%), 93,714.9 Da  
 Prostaglandin F2 receptor negative regulator OS=Cricetulus griseus GN=I79\_006863 PE=4 SV=1  
 2 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 20/830 amino acids (2% coverage)

MASVCRGRVV	RVPSSGSLVRV	VGTELVIPC	VSDYDGP	IEQ	NFDWSFSSSG	SSFLELASTW
EPGFPAQLYR	ERLQRGDILL	RRTANDAVEL	HIKNVQPSDQ	GHYKCSTPST	DATVQGNVED	
TVQVKVLADA	LVLVGPSSRPP	PGLSLREGE	FELRCITSTM	SPLHTHLALR	WELHRGVPVHR	
SILALSHAGR	FHPGPGYEQ	YHSGDVR	<b>LDT</b>	<b>AGSDAYR</b>	LSV	ARALSADQGS
EQGNWQEQE	KAVEVATVVI	QPTALQLAVP	RTVSVTEGKD	LDLSCNITTD	RVDVDRPEVT	
WYFKKTPDAS	LLASHMLARL	DRDSLHSSP	HVALSHVDTR	SYHLLVRDAS	KENSGYLCCL	
VALWAPGHNR	SWHKVAEAMS	APSSVSVTWL	EPEYQVYVNA	SKVPGFSDDP	TELQCRVJDM	
KRVEAGVRLT	VSWYYRMRNR	IGDEVVASEL	LAVMDGDWTL	RYGERSKQRA	<b>QSGEFIFSK</b>	<b>E</b>
HTDTFSFRIQ	RTTEEDRGN	YCVVSAWTRQ	RNNSWVKSKD	VFSKPVNIFW	ASEDSVLVVR	
ARQPKPFAA	GNTFEMTCKV	SSKNIKSPRY	SVLITAEKPV	GDLTSPNETK	YIISLDQDSV	
VKLENWTDAS	RVDGCVLEKV	QEDEFRYRMY	QTQVSDAGLY	RCMVTAWSPI	GGSLWREAAAT	
SLSNPIEIDF	QTSDDMAFDV	SWFAVHSGFL	DKDPVLLSSL	DRKGVVTTGQ	RDWKSTLSLE	
RVSVLEFLLQ	VHGSSEDMQDFG	NYYCSVTPWV	RSPTGWSQRE	AEIHSRPIFI	TVKMDVLSNAF	
KYPLLLIGVGL	STVIGLLSCL	IGYCSSSHWC	KKEVRETRRE	RRRLMSMEMD		

CP7

Q9HDC9 (100%), 46,481.5 Da  
 Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2  
 19 exclusive unique peptides, 22 exclusive unique spectra, 26 total spectra, 146/416 amino acids (35% coverage)

MSEADGLR	<b>QR</b>	<b>RPLRPQVVTD</b>	<b>DDGQAPEAKD</b>	<b>GSSFSGRVFR</b>	VTFLMLAVSL	TVPLLGAMML
LESPIDPQPL	SFK <b>EPPLLLG</b>	<b>VLHPNTKLRQ</b>	<b>AERLFFENQLV</b>	<b>GPESIAHIGD</b>	VMFTGTADGR	
VVK <b>LENGEIE</b>	<b>TIA</b> RFGSGPC	<b>KTRDDEPVCG</b>	<b>RPLGIRAGPN</b>	GTFLFVADAYK	GLFEVNPWKR	
EVK <b>LLLSSET</b>	<b>PIEG</b> KNMSFV	NDLTVTQDGR	<b>KIYFTDSSSK</b>	WQR <b>RDYLLLV</b>	<b>MEGTD</b> <b>DDGRLL</b>	
<b>EYD</b> <b>TVTR</b> EVK	VLLDQLRFPN	GVQLSPAEDF	VLVAETTMAR	IRRV <b>YV</b> SGLM	<b>KGGADL</b> FVEN	
MPGFPDNIRP	SSSGGYWVGM	STIRPNPGFS	MLDFLSERPW	IKRMIFK <b>LF</b> S	<b>QETVM</b> <b>K</b> FVPR	
YSLVLELSDS	GAFRRS <b>LHDP</b>	DGLVATYISE	VHEHDGHLYL	GSRSPFLCR	LSLQAV	

A0A061I3K8 (100%), 160,726.0 Da  
 Calnexin OS=Cricetulus griseus GN=H671\_7g18220 PE=3 SV=1  
 10 exclusive unique peptides, 12 exclusive unique spectra, 14 total spectra, 115/1479 amino acids (8% coverage)

MEGKWL	LCLL	LVLGTVAVQA	HDGHDDDMID	IEDDLDDVIE	EVEDSKSK	<b>SD</b>	<b>SSTPPSPK</b>	VT
YK <b>APVPTGEV</b>	<b>YFADSFDR</b>	GS	LSGWILSKAK	<b>KDDTDDEIAK</b>	YDGKWEVDEM		KDTKLP	GDKG
LVLMSRAKHH	AISAKLNKPF	LFDTKPLIVQ	LHFIFRHKNP	YEVNFQNGIE	CGGAYVKLLS		K <b>TSELNLDQF</b>	
<b>HDKT</b> <b>PYTIMF</b>	<b>GPDK</b> CGEDYK	LHFLFRHKNP	GNLNDMTPA	KTGVYEEKHA	KRPDSDLKIY		FTDKKTHLYT	
LILNPDNSFE	ILVDQYVNS	PEGWLDDEPE	YIPDPDADKP	VNPSREIEDP	EDQKPEDWGE		RPKIPDPDAV	
KPDDWDEDAP	GKIPDEEATK	PEGWLDDEPE	NPNYQGVWKP	WANDGWGLKK	EDWDEDMDGE		WEAPQIANPK	
CESAPGCGVW	QR <b>PLIDNPNY</b>	KGKWKPPMID	NPNYQGVWKP	NAMEYK <b>KTDA</b>	RKIPNPDFFE		DLEPFKMTPF	
SAIGLELWSM	TSDIFFDNFI	ISGDRRVVDD	WANDGWGLKK	PTAEEDEILN	<b>AADGAAEPGV</b>		<b>VGHM</b> LEAAEE	
RPWLWVVYIL	TVALPVFLVI	LFCCSGKKQS	NAMEYK <b>KTDA</b>	TRREAPLGIS	<b>AQPDVKEDEG</b>		<b>KEEEEK</b> <b>KNK</b> <b>GDE</b>	
<b>EEEEEKLEEK</b>	QKSDAEEEDGG	TGSQDEEDRK	PTAEEDEILN	VSANGLPPAS	RSPRNRKPRR		ESWDLWHLHD	
TVKRNLDSAA	SPQNGDQQNG	YGDLPFGHKK	TRREAPLGIS	LSLSKELKQE	VSANGLPPAS		PLGQPDKPPG	
GDALQSGGKH	SLGLDPINKK	CMADSSIHLLN	GSSNPNEPFP	LFTEDFEEKK	LSLSKELKQE		PVDDLPCMIA	
GAGGSVQSNS	LMPDLNLEEQ	EWKELIEELN	RSVPDEDMKD	SSAPVGTDS	LFTEDFEEKK		DPEPPGSATQ	
TPLAQDINIK	TEFSPAAFEQ	EQLGSPQVRA	GSAGQTFLLG	ASSELSSAHQL	SSAPVGTDS		SLGSSQTLFH	
TTGQPGADNP	SPNLMPASAAQ	AQNAQRALAS	VVLPSQGGG	LDVYPMEKP	ASSELSSAHQL		QQIAAKQKRE	
QMLQNPQAAA	SAPAPGQLST	WQQAGPSHSP	LDVYPMEKP	QSSVNNQGA	ASPPGYKQDF		TNSKLLMMPS	
VNKSSPRPGG	PYLQPSHSNL	LSHQSPSNLN	QSSVNNQGA	LDYGNTPKPLS	LDYGNTPKPLS		HYKADCGQGG	
PGSGQSKPAL	MAYLPQQLPH	LSNEQNSLFL	MKQKAAANMPF	RSLVPPGQEQ	LDYGNTPKPLS		NPSNVSVPAQ	
TANVGTQPPS	VSAVSTHNS	PYLSNSQQA	VMKQHQLLLD	QQKQREQQQL	RSLVPPGQEQ		QQQQQVFLQR	
QHLLEAEQEKQ	QFQRPSAAVP	GMNLLGPSNS	SACPRVFPQPG	TLMMSMGPGHA	QQKQREQQQL		PVSSLPSSSG	
PQDRGVAQFT	GSQSLPQSSSL	YGITSGLPQI	VAGPPPPQAS	AHAHAPRQTS	TLMMSMGPGHA		VGQNASAPAA	
YGQNSLGSAG	LSQQHNLKGT	PPGLTKSQVP	RVSAAAMGGQN	ASWQHQGMPN	AHAHAPRQTS		LSSQTPGNS	
VSPFAAPSFF	HMQQAHLKIP	GQQFSGQMP	RPMAAMSGAG	AAGSMPLPV	ASWQHQGMPN		TQQRNSAPAP	
APPQAAPOQG	LPGLSPAGPE	LGAFSQSSTS	QMNSRAGLHC	TQAYPVRTMG	AAGSMPLPV		QELPFAFSGQ	
PGSSGLSVA	GHTDLIDSL	KNRTSEEWIN	ELDDL	LG	TQAYPVRTMG			

**G3HQ1 (100%), 186,663.3 Da**

Cation-independent mannose-6-phosphate receptor OS=Cricetulus griseus GN=i79\_009791 PE=4 SV=1

14 exclusive unique peptides, 14 exclusive unique spectra, 14 total spectra, 152/1700 amino acids (9% coverage)

MPLVCSLYVH	PLP L L I G D S L	LRSSSRSLLE	FNTTTDCQPS	DSQHR	<b>TQTSI</b>	<b>TFLCGK</b>	T L G T
PEFVTATDCV	HYFEWRTTAA	CKKDIKADK	EVPCYAFDDK	LKKHDLNPLI		KLSSGGYLVDD	
SDPETS L F I N	VCR <b>DIDSLRD</b>	<b>PSTQLRACPA</b>	<b>GTAACLKGD</b>	QAFDVGGRPKE		GLKLVSKDRLL	
VL SY VKEEAE	KPDFCNGHSP	AVTITFVCP S	ERRREGTIPKL	TASSNCRYEVE		EWITEYACHR	
DYLESETCSL	SSEQHDI A I D	LSPLAQGGGS	SYVSDGREYT	FYINVCGNAT		VPLCNLKE SA	
VCQVKKADST	QVKIAGRHNQ	QTLRYSDGDL	TLIYSGGDEC	SSGFQRM SVI		NFECNKTAGN	
DGRGEPVFTG	EVDCTYFFTW	DTRYACVKEK	<b>EDLLCGVSDG</b>	<b>KKRYDLSVLA</b>	<b>RHSESEKNWE</b>		
AVDGDQAES E	KKYFFINVC H	RVLQEGKARS	CPEDAAVCAV	DKNGSKNLGK	FVSSPTSEK G		
YIQLSYSDGD	DCGSDKKIT T	NITLVCKPGD	LESAPVLRTA	GPDGCFYEF E	WHTAAA CVLS		
KTEGENCTVF	DAQAGFSFDL	SPLTKKNGAY	KVGT EKYDFY	INVC GPVSDV	LCQPN SGACQ		
VAKRQEEEDNS	TYNFRWYTSY	ACPEEPL E CM	VTDPSMMEQY	DLSSLVKSEG	RSGGNWAYME		
NSREHVT R R K	YYINVC R <b>PLN</b>	<b>PVPGCDRYAA</b>	ACQMRYENSE	GSLAETVSI S	NLGVAKTG P V		
VEESGSL L L E	YVNGSACTTS	DGRLTTYSTR	IHLVCGRGS L	NTHPIFTY NW	ECVVSFLWNT		
EACAPIQITIT	DTDQACSIRD	PNSGFVFNLS	PLNR <b>SQGYVV</b>	<b>PGIGK</b>	ICGAMPECGT		
IAGNPAFGCE	AGTQTELES L	KPERPVGMEK	SLQLSTEGFL	TLYKGS SPS	DKGTAFAIR <b>F</b>		
<b>ICNDDIYPGT</b>	<b>AKFLHQDIDS</b>	TRGIRNTFFE	FETALACVPS	RVDCQVTDPA	GNEYDL SALS		
MAGK PWTAVD	TSVDGKKR SF	YLSVCTPLPY	IPGCHGSAVG	SCMVLPAEDR	GLNLGVVQIS		
PQADANGSLS	ILYVNGDKCF	NQR FSTR I I F	ECAQT LGS PV	FQFVKDCEYM	<b>FVWRTVEACP</b>		
<b>VVR</b> EEGDNCQ	VKDP RHGNFY	DLKPLALS DT	IITAGEYTY Y	FRVCGK <b>LSSN</b>	<b>VCHVRD</b> GSKV		
VSSCQEKKGS	QGFQKVA GLL	TQKLT YENGL	LKMNYTGGDT	CHQVYQRSTT	IYFYCDRSTQ		
KPVFLRETTD	CSYL F EWR T Q	YACPPFNVTE	CSTQD GAGNS	IDLSSL S RYS	DNWEAVTRTG		
ATEHYLINIC	KSLS P RAGGG	EPCPPEAAVC	LLDGS KPLNL	GKVRDGPQWT	GGVTVLK <b>YVD</b>		
<b>GDLCPDQIRK</b>	RST I I R <b>FTCS</b>	<b>ESQVSSRPLF</b>	ISAVQDC EYT	FSWPTPAACP	VKNSTHDDCQ		
VTNPSTGHLF	DLSSLSGEGAG	<b>VTVSYSEKGL</b>	VYMS ICGENE	NCGAGV GACF	GQTRISV GKA		
SKR LSYVDQV	LQLVYEEGSL	CPSKSGLR YK	SVISFVCRPE	AGPTNR PMLI	SLDKQCT L F		
FSWHTPLACE	QVTECTVRNG	SSIIDLSP LI	HRTGGYEAYD	ESEDGTS DTT	PDFYINICQP		
LNP MHG V P C P	AGAAVCK <b>VPV</b>	<b>NGPPIDIGRV</b>	TG P P I F N P V A	NEVYLN FESS	TPCLADKHMN		
YTS L IAFHCK	RGVSMGTPK L	I R T N D C D F V F	EWET P I V C P D	E V K T Q G C S V T	DEQLLYS FNL		
TSLS T S T FKA	RLPS IARGSD						

**P10909 (100%), 52,495.0 Da**

Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 19/449 amino acids (4% coverage)

MMKTL L L F V G	LLLTWES GQV	LGDQTVSDNE	LQEMSNQGS K	YVNKEIQNAV	NGVKQIK TLI
EKTNEERKTL	LSNLEEA KKK	KEDALNETRE	SETK LKELPG	VCNETMMALW	EECKPCLKQT
CMKFYARVCR	<b>SGSGLVGR</b> QL	EEFLNQSSPF	YFWMNGDRID	S LLENDRQQT	HMLDVMQDHF
SRASS I I DEL	FQDRFFTR EP	QDTYHYLSPFS	LPHRRPHFFF	PKSRIVRSLM	PFSPEQLNLF
HAMFQ P F L E M	IHEAQQAMDI	HFHSPAFOHP	PTEF I R E G D D	DRTVCREIRH	NSTGCLR MKD
QCCKCREILS	VDCSTNNPSQ	AKLR <b>ELDES</b>	<b>LQVAER</b> LTRK	YNELLKSYQW	KMLNTSS LLE
QLNEQFNWVS	RLANLTQGED	QYYLRVTVA	SHTSDSDVPS	GVTEVVVKLF	DSDPITVTV P
VEVSRKNPKF	METVAEKALQ	EYRKKHREE			

**F1LPC5 (100%), 63,343.8 Da**

Protein Tmem259 OS=Rattus norvegicus GN=Tmem259 PE=1 SV=2

3 exclusive unique peptides, 3 exclusive unique spectra, 3 total spectra, 30/574 amino acids (5% coverage)

MSEHAAPGP	GPNGGGGGGA	APVGRPR <b>GPN</b>	<b>LNPNPLINVR</b>	DRLFHALFFK	MAVTYSRLF P
PAFRRLFEFF	VLLKALFVLF	VLAYIHIVFS	RSPINCLEHV	RDRWPREGLV	RVEVTRHNSR
APVILQFCDG	GLGGDLLEPG	GLELEEELS	VEMFTNSSIK	<b>FELDIEPK</b> VF	KPPGGADALN
DSQDFPFPE T	PAKAWPQDEY	IVEYSLEYGF	LRLSQATRQR	LSIPVMVVT L	DPTR EQCFGD
RFSRL L L L D F G	LYGDDVLMSS	VKGLAENEEN	KGFLR <b>NVVS G</b>	<b>EHYR</b> FVSMWM	ARTSYLAAFV
IMVIFTLSVS	MLLRYSHHQI	FVFIVDL LQM	LEMNMAIAFP	AAPLTLVILA	LVGMEAIMSE
FFNDT T T A F Y	IILIVWLADQ	YDAICCHTNT	SKRHWR LFFY	LYHFAFYAYH	YRFNGQYSS L
ALVTSWLFIQ	HSMIYFFHHY	ELPALQQRIR	IQEMLLQTPP	LGPPTPTALP	DDLNNNSGSP
ATPDPSPLA	LGPS SSPAPT	GGASGPGSLG	AGASVSGSDL	GWVAETA A I I	S D A S F L S G L S
ASLLER R P A A	PSAPDSARPD	P GAS L E D A P A	PAGS		

**CP8**

**Q9HDC9 (100%), 46,481.5 Da**

Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2

8 exclusive unique peptides, 10 exclusive unique spectra, 10 total spectra, 100/416 amino acids (24% coverage)

MSEADGLRQR	<b>RPLRPQVVT D</b>	<b>DDGQAPEAKD</b>	GSSFSGRVFR	VTF LMLAVS L	TVPLLGAMML
LESPI DPQPL	SFKEPPLLLG	VLHPNTKLRQ	AER <b>LFENQLV</b>	<b>GPESIAH</b> IGD	VMFTGTADGR
VVK <b>LENGEIE</b>	<b>TIA</b> RFGSGPC	KTRDDEPVCG	RPLGIRAGPN	GTLFVADAYK	GLFEVNPWKR
EVK <b>LLLSSET</b>	<b>PIE</b> GKNMSFV	NDLTVTQDGR	KIYFTDSSSK	WQRR <b>DYLLLV</b>	<b>MEGTD DGRLL</b>
EYDVT TREVK	<b>VLLDQLR</b> FPN	GVQLSPAEDF	LVAETTMR	IRRVYVSGLM	KGGADLFVEN
MPGFPDNI RP	SSSGGYWVGM	STIRPNPGFS	MLDFLSERPW	IKRMIFK <b>LFS</b>	<b>QETVMK</b> FVPR
YSLVLELSDS	GAFRRSLHDP	DGLVATYISE	VHEHDGHL YL	G S F R S P F L C R	L S L Q A V

A0A096P063 (100%), 34,826.0 Da

Arginase OS=Papio anubis GN=ARG1 PE=3 SV=1

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 22/323 amino acids (7% coverage)

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MSAKSR TIGI IGAPFSK GQP RGGVEEGPTV LRKAGLLEKL EEQECDVKDY GDLSFADIPN
DSPFQIVKNP RSVGKATEQL AGKVAEVKKN GRISLVLGGD HRS LAIGSIS GHASVHPDLG
VIWVDAHTDI NTPLTTTGN LHGQPVSFLL KELKGIIPDV PGFSWVTPCI SAKDIVYIGL
RDVDPGEHYI LKTLGIKYFS MTEVDRLLGIG KVMEETLSYL LGRKKRPIHL SFDVDGLDPS
FTPATGTPVV GGLSYREGLY ITEEIKTGL LSGLDIMEVN PSLGKTPEEV TRTVNTAVA I
ILACFGVARE GNHKPIDYLN PPK
```

G3HZE5 (100%), 69,919.3 Da

Heat shock 70 kDa protein 1A OS=Cricetulus griseus GN=I79\_016446 PE=3 SV=1

6 exclusive unique peptides, 6 exclusive unique spectra, 14 total spectra, 81/641 amino acids (13% coverage)

```
MAKSTAIGID LGTTYSCVGV FQHGKVEIIA NDQGNRTTPS YVAFTDTERL IGDAAKNQVA
LNPNQNTVFDA KRLLGRKFGD AVVQADMKHW PFQVVDGDK PKVQVSYKGE TRAFYPPEEIS
SMVLTCKMKEV AEAYLGHVPV NAVITVPAYF NDSQRQATKD AGVIAGLNVL R IINEPTAAA
IAYGLDRSGK GERNVLI FDL GGGTFDVSIL TIDDGIFEVK ATAGDTHLGG EDFDNRLVSH
FVEEFKRKHK KDISQNKRAV RRLRTACERA KRTLSSSTQA NLEIDSLFEG IDFYTSITRA
RFEELCADLF RGTLEPVEKS LRDAKMDKAK IHDIVLVGGS TRIPKVQKLL QDFFNGRDLN
KSI NPDEAVA YGAAVQAAIL MGDKSENVD LLLLDVAPLS LGLETAGGVM TALIKRNSTI
PTKQTQTFIT YSDNQPGVLI QVYEGER AMT RDNNLLGRFE LSGIPPA PRG VPQIEVTFDI
DANGILNVTATDKSTGKANK ITITNDKGR L SKEEIER MVQ EAERYKAEDE VQRERVA AKN
ALESYAFNMK SAVEDEGLKG KISEADRKKV LDGCQEVISW LDANTLADKE EFVHKRQELE
RVCGP I V SGL YQGAGAPGAG GFGAQAPKGG SSGSPTIEEV D
```

P29508 (100%), 44,565.9 Da

Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2

22 exclusive unique peptides, 27 exclusive unique spectra, 28 total spectra, 194/390 amino acids (50% coverage)

```
MNSLSEANTK FMFDL FQQR KSKENNI FYS PISITSA LGM VLLGAKDNTA QQIK KVLHFD
QVTENTTGKA ATYHVDRSGN VHHQFQKLLT EFNK STDAYE LKIANKL FGE KTYLFLQEYL
DAIKKFYQTS VESVDFANAP EESRKKINSW VESQTNEKIK NLIPEGNIGS NTTLVLVNAI
YFKGQWEKKF NKEDTKEEKF WPNKNTYKSI QMMRQYTSFH FASLEDVQAK VLEIPYKGGD
LSMIV LLPNE IDGLQKLEEK LTAEK LMEWT SLQNMRETRV DLHLPRFKVE ESYDLKDTLR
TMGMVDIFNG DADLSGMTGS RGLVLSGVLH KAFVEVTEEG AEAAAATAVV GFGSSPTSTN
EEFHCHNHPFL FFIR QNK TNS ILFYGRFSSP
```

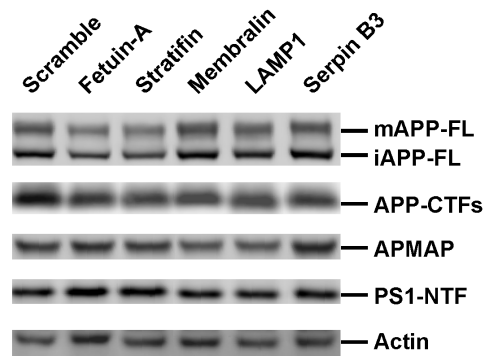
G3HYQ1 (100%), 27,689.8 Da

14-3-3 protein sigma OS=Cricetulus griseus GN=I79\_016192 PE=3 SV=1

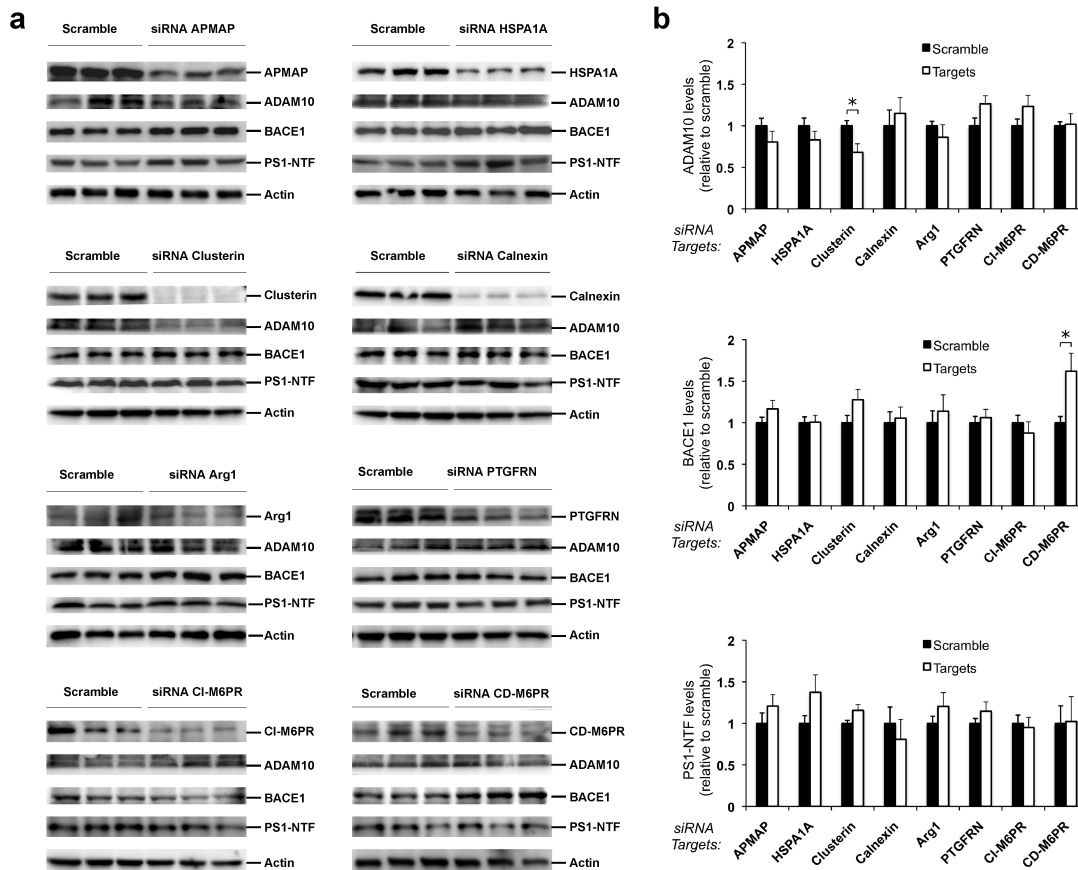
6 exclusive unique peptides, 8 exclusive unique spectra, 9 total spectra, 51/248 amino acids (21% coverage)

```
MEKASLIQKA KLA EQAERYE DMAAFMKGAV EKGEELSCEE RNLLSVAYKN VVGGQRAAWR
VLS SIEQKSN EEGSEEK GPE VKE YREKVET ELRGVCDTVL GLLD SHLIKE AGEAGSRV FY
LKMKG DYRY LAEVATGDDK KRIID SARSA YQEAMDISKK EMPPTNPIRL GLALNFSV FH
YEIANSPEEA ISLAKTTFDE AMADLHTLNE DSYK DSTLIM QLLRDNLTLW TADSAGEEGG
EAP EEPQS
```

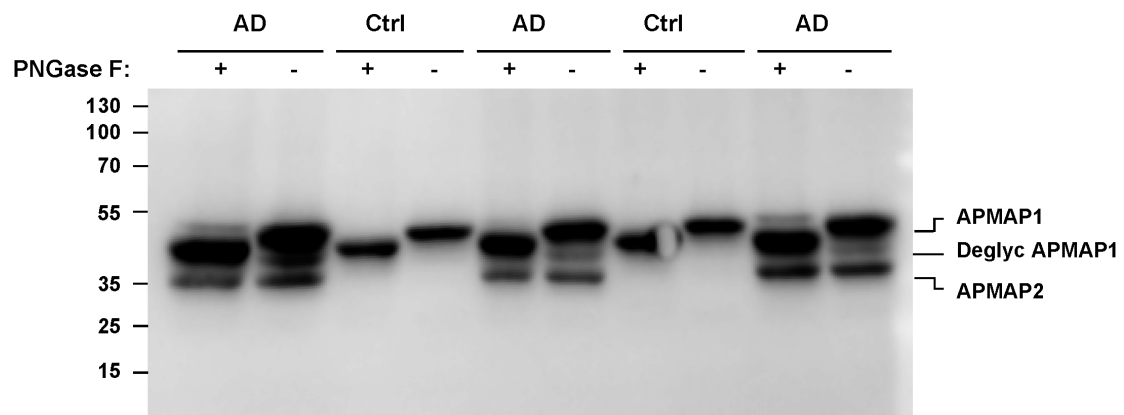
**Fig.S4** Mass spectrometric identification of APMAP-interacting proteins. Peptides identified by LC-MS/MS after tryptic digestion of eight different APMAP-containing low and high molecular weight protein complexes (CP1-CP8) from selected SEC fractions resolved by native-PAGE (see Fig.3) are highlighted in yellow in the primary sequences. Modifications are highlighted in green.



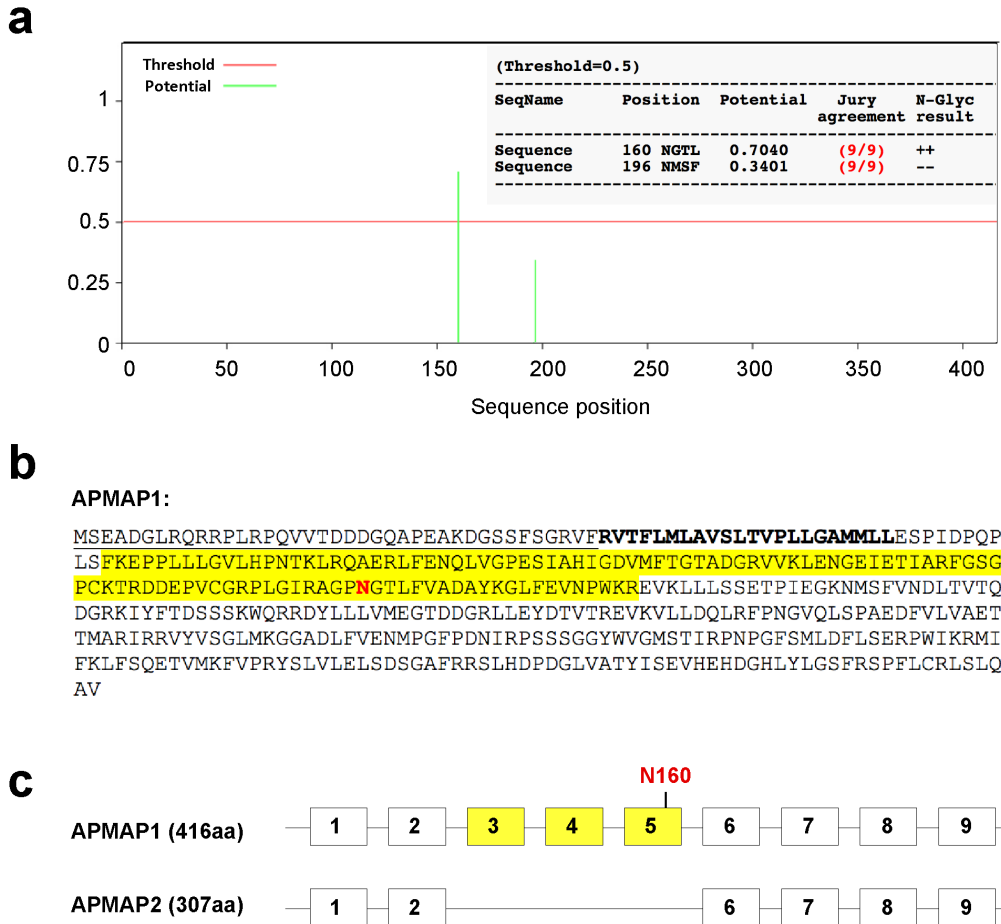
**Fig.S5** Treatments with siRNAs targeting fetuin-A, serpinB3, stratifin, LAMP-1 and membralin do not affect APP-FL, APP-CTFs, or APMAP. The knockdown of the indicated APMAP-interacting proteins was performed as described in Fig.4 by small interfering RNA (siRNA) in HEK cells overexpressing APP bearing the Swedish mutation that causes early-onset familial Alzheimer's disease (HEK-APPswe). Cells were treated for 3 days with siRNA duplexes (listed in the Materials and Methods section) complexed with Lipofectamine RNAiMax (Invitrogen). Whole cell extracts were prepared in HEPES buffer containing 1% NP40 and analyzed by Western blot for the siRNA protein targets APP-FL, APP-CTFs and APMAP. Cells transfected with the allstar control siRNA (scramble) served as negative controls while actin served as a protein loading control. APP-FL: APP full-length; APP-CTFs: APP-C-terminal fragments.



**Fig.S6** Depletion of individual APMAP interacting proteins does not affect the level of  $\alpha$ -,  $\beta$ - or  $\gamma$ -secretases. **a** The same whole-cell extracts as in Fig.4a, prepared from biological triplicates of HEK-APP<sup>Swe</sup> cells treated for three days with siRNA duplexes targeting the indicated APMAP-interacting proteins were analyzed by Western blot for the siRNA proteins targets,  $\alpha$ -secretase ADAM10,  $\beta$ -secretase BACE1 and  $\gamma$ -secretase catalytic site protein presenilin-1 N-terminal fragment (PS1-NTF). Cells transfected with the allstar control siRNA (scramble) served as negative controls while actin served as a protein loading control. **b** Densitometric analysis of the ADAM10, BACE1 and PS1-NTF Western blot bands in (a). Student's *t*-test was applied for statistical analysis; significance is shown as the mean  $\pm$  SEM, \**P*<0.05; ADAM10, BACE1 and PS1-NTF: *n*=3/group.

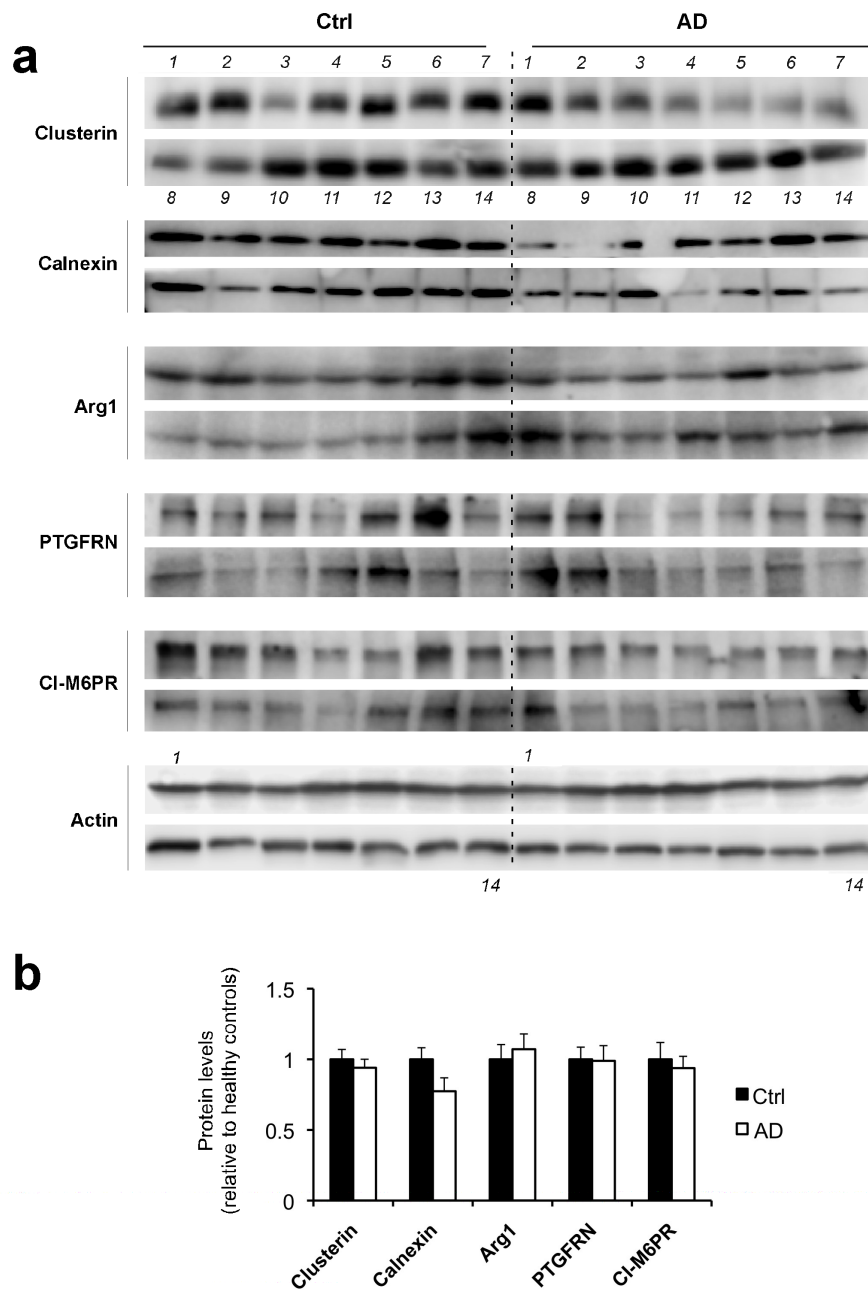


**Fig.S7** N-linked glycosylation of APMAP1 and absence of glycosylation of APMAP2. The glycosylation profiles of APMAP1 and APMAP2 were estimated by Western blot analysis of denatured human cortical lysates of two control brains and three neuropathologically verified AD brains treated for one hour at 37°C in the presence (+) or absence (-) of Peptide-N-glycosidase F (PNGase F) to catalyze the cleavage of N-linked oligosaccharides. For APMAP1, the PNGase-dependent band shift (from APMAP1 to Deglyc APMAP1) reveals an N-linked glycosylation. For APMAP2, the absence of a band shift confirms an unglycosylated protein.



**Fig.S8** APMAP1 predicted N-glycosylation at residue Asn160, while APMAP2 is unglycosylated. **a** Glycosylation site prediction in human APMAP1 with NetNGlyc 1.0 (<http://www.cbs.dtu.dk/services/NetNGlyc/>), by using artificial neural networks that analyzed the sequence context of Asn-Xaa-Ser/Thr. Asn160 was the only site with a predicted high probability N-glycosylation (potential > 0.5 and Jury agreement 9/9). **b** Primary sequence of human APMAP1 with the cytosolic N-terminal domain underlined, the transmembrane domain in bold and exons 3, 4 and 5 in yellow. The predicted N-glycosylated residue Asn160 on exon 5 is displayed in red. **c** The human alternative splicing variant APMAP2 lacks exons 3 and 4 and exon 5 containing the predicted glycosylation site Asn160.





**Fig.S9** The protein levels of the APMAP interactomers clusterin, calnexin, Arg1, PTGFRN and CI-M6PR are unchanged in AD brains. **a** The protein levels of the indicated APMAP interactomers were estimated by Western blot analysis in cortical lysates of 14 control brains and 14 neuropathologically verified AD brains (same samples as in Figure 5). **b** The densitometric analysis of the Western blot bands in (a) revealed no statistically relevant changes (Student's t-test) in the control and AD brains.