# Supplementary file

## Retinal Pathological Features and Proteome Signatures of Alzheimer's Disease

*Acta Neuropathologica*

Yosef Koronyo, MSc, Altan Rentsendorj, PhD, Nazanin Mirzaei, PhD, Giovanna C. Regis, BSc, Julia Sheyn, BSc, Haoshen Shi, PhD, Ernesto Barron, MSc, Galen Cook-Wiens, MSc, Anthony R. Rodriguez, BSc, Rodrigo Medeiros, PhD, Joao A. Paulo, PhD, Veer B. Gupta, PhD, Andrei A. Kramerov, MD, PhD, Alexander V. Ljubimov, PhD, Jennifer E. Van Eyk, PhD, Stuart L. Graham, MD, Vivek K. Gupta, PhD, John M. Ringman, MD, David R. Hinton, MD, PhD, Carol A. Miller, MD, Keith L. Black, MD, Antonino Cattaneo, MD, Giovanni Meli, PhD, Mehdi Mirzaei, PhD, Dieu-Trang Fuchs, MSc, and Maya Koronyo-Hamaoui, PhD

Corresponding author: Maya Koronyo-Hamaoui, PhD, Cedars-Sinai Medical Center, 127 S. San Vicente Blvd., Los Angeles, CA, USA 90048. E-mail: maya.koronyo@csmc.edu

**Supplementary Table 1.** List of human donors whose postmortem retinas and paired brains were used for histology and proteins.
**Supplementary Table 2.** List of human donors whose postmortem brains were used for mass spectrometry.
**Supplementary Table 3.** List of antibodies for immunohistochemistry.
**Supplementary Fig. 1.** Brain NFT and NT severity scores assigned based on Gallyas silver stain and immunofluorescence of retinal A$\beta_{42}$ and associated gliosis per subregion in human donors.
**Supplementary Fig. 2.** Extended data on retinal A$\beta_{42}$ deposition in relation to sex, age, and PMI in MCI and AD patients compared to NC controls.
**Supplementary Fig. 3.** Extended TEM analysis of retinal A$\beta_{42}$ deposits in AD patients.
**Supplementary Fig. 4.** Spatial distribution of A$\beta_{42}$ burden in retinal subregions and correlations with various brain regions and cognition.
**Supplementary Fig. 5.** Extended data on the intracellular scFvA13$^{+}$-Aβ oligomers (AβOi) distribution in the retinas of MCI and AD patients compared to retinas of NC controls and correlations with cerebral pathology and cognition.
**Supplementary Fig. 6.** Extended data on retinal S100β$^{+}$ and GFAP$^{+}$ macrogliosis distribution in MCI and AD patients and correlations to cerebral pathology and cognition.
**Supplementary Fig. 7.** Extended data on spatial distribution of retinal IBA1$^{+}$ microgliosis and correlations with retina and brain pathology and cognition.
**Supplementary Fig. 8.** Extended data on retinal atrophy and correlations with other cerebral biomarkers.
**Supplementary Fig. 9** Extended global proteomics data in retinas and brains from AD patients and NC controls.
**Supplementary Table 4.** Extended mass spectrometry data on significantly up-regulated proteins in the retina of Alzheimer's patients compared to cognitively normal controls.
**Supplementary Table 5.** Extended mass spectrometry data on significantly down-regulated proteins in the retina of Alzheimer's patients compared to cognitively normal controls.
**Supplementary Table 6.** Extended mass spectrometry data on significantly up-regulated proteins in the temporal cortex of Alzheimer's patients compared to cognitively normal controls.
**Supplementary Table 7.** Extended mass spectrometry data on significantly down-regulated proteins in the temporal cortex of Alzheimer's patients compared to cognitively normal controls
**Supplementary Table 8.** Extended mass spectrometry data on significantly up-regulated proteins in the hippocampus of Alzheimer's patients compared to cognitively normal controls.
**Supplementary Table 9.** Extended mass spectrometry data on significantly down-regulated proteins in the hippocampus of Alzheimer's patients compared to cognitively normal controls.
**Supplementary Table 10.** Extended mass spectrometry data on significantly up-regulated proteins in the cerebellum of Alzheimer's patients compared to cognitively normal controls.
**Supplementary Table 11.** Extended mass spectrometry data on significantly down-regulated proteins in the cerebellum of Alzheimer's patients compared to cognitively normal controls.
**Supplementary Table 12.** Common upregulated DEPs with previous brain datasets.
**Supplementary Table 13.** Common downregulated DEPs with previous brain datasets.

**Supplementary Table 1.** List of human donors whose postmortem retinas and paired brains were used for histology and proteins.

| Retinas | Diagnosis | Sex | Race | Age at death | Thal-A | Braak-B | CERAD-C | CAA | Co-morbid. [LB/ASVD] | Braak Stage | Braak Stage average | CDR score | MMSE score | APOE status | Study type |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | AD | F | W | 63 | 3 | 3 | 3 | 0 | −/+ | V | 5 | n.a. | 9 | n.a. | His |
| 2 | AD | F | W | 90 | 2 | 3 | 3 | 0 | −/+ | IV | 4 | n.a. | 16 | n.a. | His |
| 3 | AD | F | B | 94 | 3 | 3 | 3 | II | −/+ | V | 5 | n.a. | n.a. | n.a. | His |
| 4 | AD | F | A | 89 | 2 | 3 | 2 | II | −/+ | V-VI | 5.5 | n.a. | 6 | n.a. | His |
| 5 | AD | F | W | 64 | 3 | 3 | 2 | 0 | −/+ | VI | 6 | 3 | 5 | n.a. | His |
| 6 | AD | F | W | 90 | 2 | 3 | 3 | II | −/+ | V | 5 | 2 | 9 | n.a. | His |
| 7 | AD | F | A | 93 | 3 | 2 | 2 | 0 | −/+ | IV | 4 | 3 | n.a. | e3/e3 | His |
| 8 | AD | F | W | 81 | 3 | 3 | 3 | II | −/+ | VI | 6 | n.a. | 4 | n.a. | His |
| 9 | AD | F | W | 65 | 3 | 3 | 3 | II | −/+ | V-VI | 5.5 | n.a. | n.a. | n.a. | His |
| 10 | AD | F | B | 90 | 3 | 3 | 3 | II | −/+ | V-VI | 5.5 | n.a. | n.a. | n.a. | His |
| 11 | AD | F | W | 97 | 2 | 3 | 2 | 0 | −/+ | V | 5 | n.a. | 4 | n.a. | His |
| 12 | AD | F | W | 86 | 3 | 3 | 2 | I | −/+ | V-VI | 5.5 | n.a. | n.a. | n.a. | His |
| 13 | AD | M | W | 85 | 3 | 2 | 3 | I | −/+ | IV | 4 | n.a. | n.a. | n.a. | His |
| 14 | AD | M | W | 83 | 3 | 2 | 3 | II | −/+ | IV | 4 | n.a. | 15 | n.a. | His |
| 15 | AD | M | W | 88 | 2 | 2 | 2 | 0 | −/+ | III-IV | 3.5 | n.a. | 4 | n.a. | His |
| 16 | AD | M | W | 75 | 2 | 2 | 2 | 0 | −/+ | III-IV | 3.5 | n.a. | 4 | n.a. | His |
| 17 | AD | M | W | 71 | 3 | 3 | 3 | II | −/n.a. | VI | 6 | n.a. | 10 | n.a. | His |
| 18 | AD | M | W | 90 | 3 | 3 | 2 | II | −/+ | V | 5 | 2 | 18 | n.a. | His |
| 19 | AD | M | W | 66 | 3 | 3 | 3 | I-II | −/+ | V | 5 | 3 | n.a. | n.a. | His |
| 20 | AD/AD | M | A | 40 | 3 | 2 | 3 | I | −/− | III-IV | 3.5 | 3 | n.a. | e3/e3 | His |
| 21 | AD* | M | W | 85 | n.a. | n.a. | n.a. | n.a. | −/n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 22 | AD* | M | W | 79 | n.a. | n.a. | n.a. | n.a. | n.a./+ | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 23 | AD* | M | W | 59 | n.a. | n.a. | n.a. | n.a. | n.a./+ | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 24 | AD | M | W | 88 | 3 | 3 | 3 | I-II | −/+ | V-VI | 5.5 | n.a. | n.a. | n.a. | His |
| 25 | MCI | F | W | 91 | 2 | 2 | 2 | 0 | −/+ | III-IV | 3.5 | n.a. | 29 | n.a. | His |
| 26 | MCI | F | W | 80 | 3 | 3 | 3 | I | variant/n.a. | V | 5 | n.a. | n.a. | n.a. | His |
| 27 | MCI | F | W | 88 | 3 | 3 | 2 | II | −/+ | V | 5 | 2 | 15 | n.a. | His |
| 28 | MCI | F | W | 76 | 3 | 3 | 3 | II | −/+ | V | 5 | n.a. | 26 | e3/e4 | His |
| 29 | MCI | F | W | 93 | 3 | 2 | 2 | II | −/+ | IV | 4 | 3 | n.a. | e3/e3 | His |
| 30 | MCI | F | W | 86 | 3 | 1 | 3 | 0 | −/− | I-II | 1.5 | 0 | 26 | e3/e4 | His |
| 31 | MCI | F | W | 87 | 3 | 3 | 3 | I-II | −/+ | V-VI | 5.5 | 3 | n.a. | e3/e3 | His |
| 32 | MCI | M | W | 83 | 2 | 3 | 2 | I-II | −/+ | III-IV | 3.5 | n.a. | 28 | n.a. | His |
| 33 | MCI | M | W | 93 | 2 | 0 | 2 | 0 | −/+ | 0 | 0 | 3 | n.a. | n.a. | His |
| 34 | MCI | M | H | 80 | 3 | 3 | 2 | I | −/+ | V | 5 | 3 | n.a. | e3/e3 | His |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 35 | MCI | M | W | 97 | 2 | 3 | 3 | I | −/+ | V | 5 | n.a. | n.a. | e3/e3 | His |
| 36 | NC* | F | W | 71 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 37 | NC* | F | W | 86 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 38 | NC | F | W | 92 | 1 | 1 | 1 | I | −/n.a. | I-II | 1.5 | n.a. | 25 | n.a. | His |
| 39 | NC* | F | W | 70 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 40 | NC | F | W | 95 | 3 | 3 | 2 | I | −/+ | V | 5 | 0 | 30 | e3/e3 | His |
| 41 | NC* | F | W | 75 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 42 | NC* | F | W | 76 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 43 | NC* | F | W | 58 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | ^30 | n.a. | His |
| 44 | NC* | F | B | 73 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 45 | NC | F | H | 85 | 2 | 1 | 2 | 0 | −/+ | I-II | 1.5 | 0 | 30 | e3/e3 | His |
| 46 | NC | F | W | 93 | 3 | 2 | 3 | 0 | −/+ | III-IV | 3.5 | 1 | n.a. | e2/e3 | His |
| 47 | NC | F | W | 95 | 1 | 0 | 0 | I | −/− | I | 1 | 0 | 30 | n.a. | His |
| 48 | NC | M | W | 88 | 2 | 1 | 2 | 0 | −/n.a. | II | 2 | 0 | 30 | n.a. | His |
| 49 | NC* | M | W | 77 | n.a. | n.a. | n.a. | n.a. | n.a./+ | n.a. | n.a. | n.a. | ^30 | n.a. | His |
| 50 | NC* | M | W | 66 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | His |
| 51 | NC* | M | W | 84 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | ^30 | n.a. | His |
| 52 | NC | M | W | 70 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | 30 | n.a. | His |
| 53 | NC | M | W | 69 | 0 | 0 | 1 | 0 | −/+ | I | 1 | 1 | 28 | n.a. | His |
| 54 | NC* | M | W | 87 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | ^30 | n.a. | His |
| 55 | AD/AD | F | H | 48 | 3 | 3 | 3 | I-III | −/n.a. | V | 5 | n.a. | n.a. | n.a. | P/MS |
| 56 | AD | F | W | 81 | 3 | 3 | 3 | 0 | −/− | V | 5 | n.a. | 12 | n.a. | P/MS |
| 57 | AD | F | W | 93 | 2 | 3 | 3 | I | −/n.a. | V | 5 | 3 | n.a. | n.a. | P/MS |
| 58 | AD | M | W | 88 | 2 | 3 | 2. | I | −/+ | V-VI | 5.5 | 1 | 18 | n.a. | P/MS |
| 59 | AD | M | W | 88 | 1 | 2 | 2 | 0 | −/+ | III | 3 | n.a. | n.a. | n.a. | P/MS |
| 60 | AD | F | W | 94 | 3 | 3 | 3 | 0 | −/+ | V-VI | 5.5 | 3 | n.a. | n.a. | P/MS |
| 61 | AD | F | W | 100 | 2 | 3 | 3 | 0 | −/+ | V-VI | 5.5 | 2 | 16 | n.a. | P/MS |
| 62 | NC* | F | W | 75 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | P/MS |
| 63 | NC* | F | W | 72 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | P/MS |
| 64 | NC | M | H | 81 | 3 | 1 | 2 | 0 | −/n.a. | I-II | 1.5 | 0 | 23 | n.a. | P/MS |
| 65 | NC* | M | W | 69 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | P/MS |
| 66 | NC* | F | W | 79 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | P/MS |
| 67 | NC* | F | W | 76 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | P/MS |
| 68 | NC | M | W | 85 | 0 | 1 | 3 | I | −/+ | I-II | 1.5 | 0.5 | n.a. | n.a. | P/MS |

AD, Alzheimer's disease dementia; AD/AD, patient #20 with A260V mutation in presenilin-1 (PSEN1) and patient #55 with A431E mutation in PSEN1; MCI, mild cognitive impairment; NC, normal cognition (no dementia); F, female; M, male; A, Asian; B, Black; H, Hispanic; W, White; His, histology; P, proteins for ELISA; MS, mass spectrometry. ABC scores determined as: A, Aβ plaque score modified from Thal; B, NFT stage modified from Braak; C, Neuritic plaque score modified from CERAD; CAA, Cerebral amyloid angiopathy; LB, Lewy bodies; ASVD. Atherosclerosis; CDR, Clinical dementia rating; MMSE, Mini-Mental State Examination; ^Normal MMSE assigned per absence of dementia in NDRI cases in correlation analyses; n.a., not available; +: present; –: none; APOE, apolipoprotein alleles. Human donor tissues obtained from USC-ADRC, and *cases obtained from NDRI.

**Supplementary Table 2.** List of human donors whose postmortem brains were used for mass spectrometry.

| Brains | Diagnosis | Sex | Race | Age at death | Plaque Stage | Braak Stage | Neuritic Plaque | Prion | Co-morbidity | MMSE score | APOE status | Study type |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 69 | AD | M | W | 86 | C | 6 | 4 | M/M | none | 19 | 3/4 | MS |
| 70 | AD | F | W | 89 | C | 6 | 4 | n.a. | none | 15 | 3/4 | MS |
| 71 | AD | F | W | 95 | C | 6 | 3 | M/M | none | n.a. | 2/3 | MS |
| 72 | AD | F | W | 93 | C | 6 | 4 | M/M | none | 13 | 3/3 | MS |
| 73 | AD | F | W | 88 | C | 5 | 4 | V/V | HYCEPH | 10 | 3/3 | MS |
| 74 | AD | M | W | 92 | C | 5 | 4 | M/V | none | 12 | 3/3 | MS |
| 75 | AD | M | H | 86 | C | 5 | 4 | M/V | none | n.a. | 3/3 | MS |
| 76 | AD | F | W | 98 | C | 6 | 4 | M/V | none | 14 | 3/3 | MS |
| 77 | AD | F | W | 91 | C | 6 | 4 | M/V | none | 17 | 3/3 | MS |
| 78 | AD | F | W | 82 | C | 6 | 4 | n.a. | none | 17 | 3/3 | MS |
| 79 | NC | F | W | 87 | 0 | 2 | 1 | M/V | none | 30 | 2/3 | MS |
| 80 | NC | F | W | 91 | 0 | 4 | 1 | M/V | none | 29 | 2/3 | MS |
| 81 | NC | F | H/AI | 95 | 0 | 2 | 1 | V/V | none | n.a. | 3/3 | MS |
| 82 | NC | F | W | 90 | B | 3 | 3 | n.a. | LBD; DEP | 18 | 3/3 | MS |
| 83 | NC | M | W | 96 | 0 | 2 | 1 | M/V | none | 29 | 2/3 | MS |
| 84 | NC | M | W | 94 | 0 | 1 | 1 | n.a. | LBD; DEP | 27 | 3/3 | MS |
| 85 | NC | M | W | 86 | 0 | 2 | 2 | V/V | none | 27 | 3/3 | MS |
| 86 | NC | F | W | 91 | A | 2 | 2 | M/M | none | 29 | 3/3 | MS |

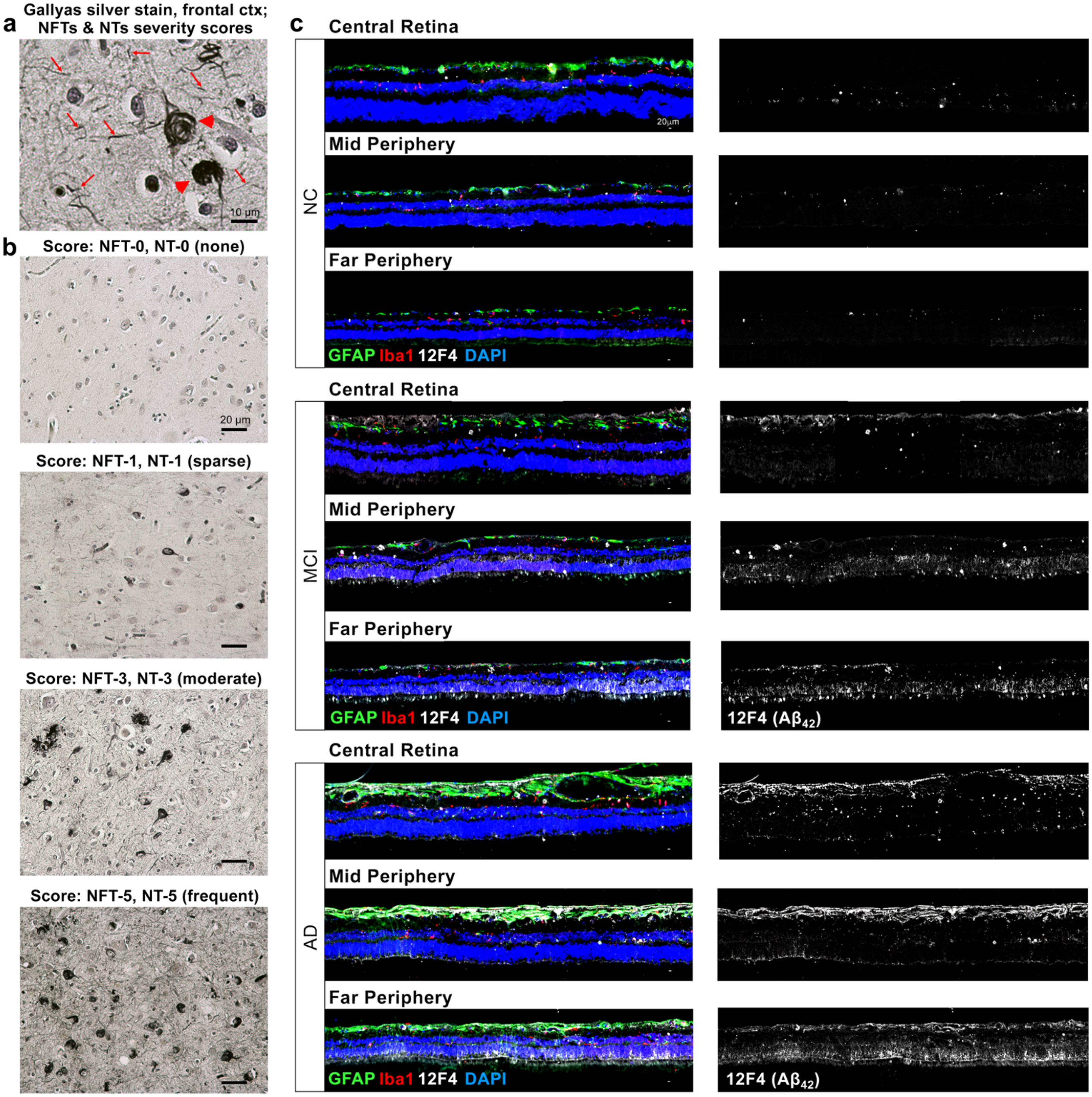
AD, Alzheimer's disease; NC, normal cognition; F, female; M, male; AI, American Indian; H, Hispanic; W, White; MS, mass spectrometry; MMSE, Mini-Mental State Examination; n.a., not available. Plaque Stage: 0, none; A, phase I-II; B, phase III; C, phase IV-V; Neuritic Plaque (NP) scores: 4, frequent NP; 3, moderate NP; 2, sparce NP; 1, no NPs. Prion polymorphisms: methionine/methionine (M/M), methionine/valine (M/V), valine/valine (V/V). Co-morbidities: LBD, Lewy body disease; Dep, Depression; HYCEPH, Normal-pressure hydrocephalus. APOE, apolipoprotein alleles. All human donor tissues obtained from UCI-ADRC.

**Supplementary Table 3.** List of antibodies for immunohistochemistry.

| ***Antibodies*** | **Source Species** | **Dilution** | **Application** | **Source** | **Catalog. #** |
|---|---|---|---|---|---|
| *Primary antibody* | | | | | |
| *$A\beta_{42}$-12F4 mAb* | Mouse | 1:500 | IF & Peroxidase | Biolegend | 805502 |
| *GFAP mAb* | Rat | 1:500 | IF | Invitrogen | 13-0300 |
| *Iba-1 mAb* | Rabbit | 1:200 | IF | Wako | 019-19741 |
| *AβOi - scFvA13 mAb* | Mouse* | 1:450 | IF | G. Meli Lab | scFvA13 |
| *β-III Tubulin pAb* | Rabbit | 1:500 | IF | Abcam | ab18207 |
| *S100β mAb* | Rabbit | 1:150 | IF | Abcam | ab52642 |
| *4G8 mAb* | Mouse | 1:250 | IF | Biolegend | 800702 |
| *$A\beta_{42}$ – JRF/cAβ 42/26* | Mouse | 1:5000 | Peroxidase | Janssen | 8151 |
| *JRF /Aβtot/17* | Mouse | 1:3500 | Peroxidase | Janssen | Pur 117-120 |
| *CCasp3 pAb* | Rabbit | 1:250 | IF | Cell Signaling | 9661 |
| *Secondary antibody* | | | | | |
| *Cy2 (anti-rat, anti-rabbit)* | Donkey | 1:200 | IF | Jackson ImmunoResearch Laboratories | 711-225-152<br>712-225-150 |
| *Cy3 (anti-mouse, anti-rat, anti-rabbit)* | Donkey | 1:200 | IF | Jackson ImmunoResearch Laboratories | 715-165-150<br>712-165-153<br>711-165-152 |
| *Cy5 (anti-mouse, anti-rabbit)* | Donkey | 1:200 | IF | Jackson ImmunoResearch Laboratories | 715-175-150<br>711-175-152 |
| *Anti-V5 Tag mAb Intermediate* | Mouse | 1:200 | IF | Invitrogen | R960-25 |
| *anti-mouse Ab - HRP* | Goat | Drop/25ul | Peroxidase | Dako Envision | K4000/1 |
| *anti-mouse 10nm gold conjugate (for EM)* | Goat | 1:100 | Immunogold labelling | Ted Pella, Inc. | 15736 |

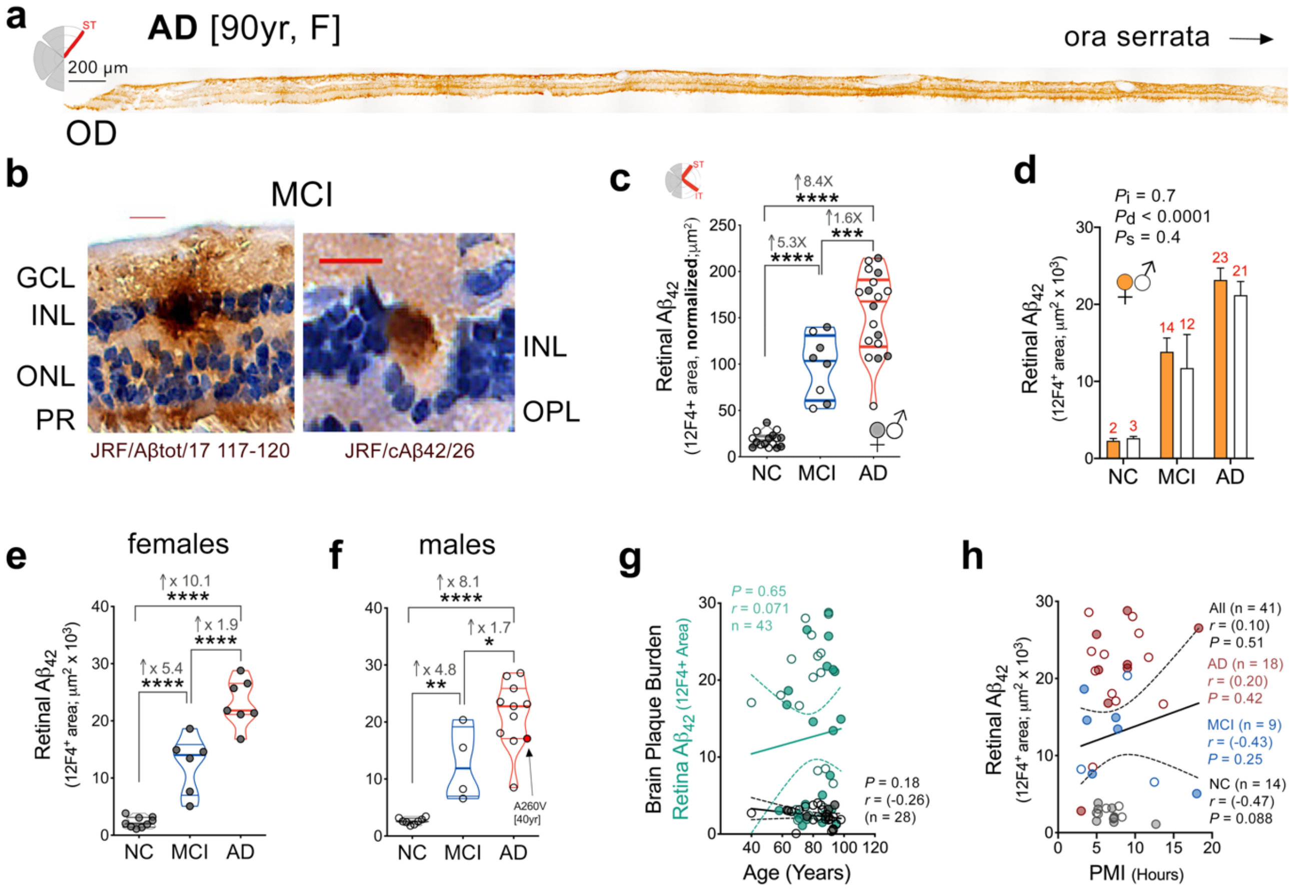
Aβ – amyloid β-protein; $A\beta_{42}$ – 42 amino acid-long Aβ alloform; AβOi – intracellular Aβ oligomers; EM – electron microscopy; GFAP – glial fibrillary acidic protein; Iba1 – ionized calcium binding adaptor molecule 1; CCasp3 – Cleaved Caspase-3; IF – immunofluorescence; mAb – monoclonal antibody; pAb – polyclonal antibody; Peroxidase – peroxidase-based immunostaining; S100β – S100 calcium-binding protein B; scFv – single chain Fv fragment; *mouse recombinant antibody fragment.

**Supplementary Fig. 1.** Brain NFT and NT severity scores assigned based on Gallyas silver stain and immunofluorescence of retinal A$\beta_{42}$ and associated gliosis per subregion in human donors.



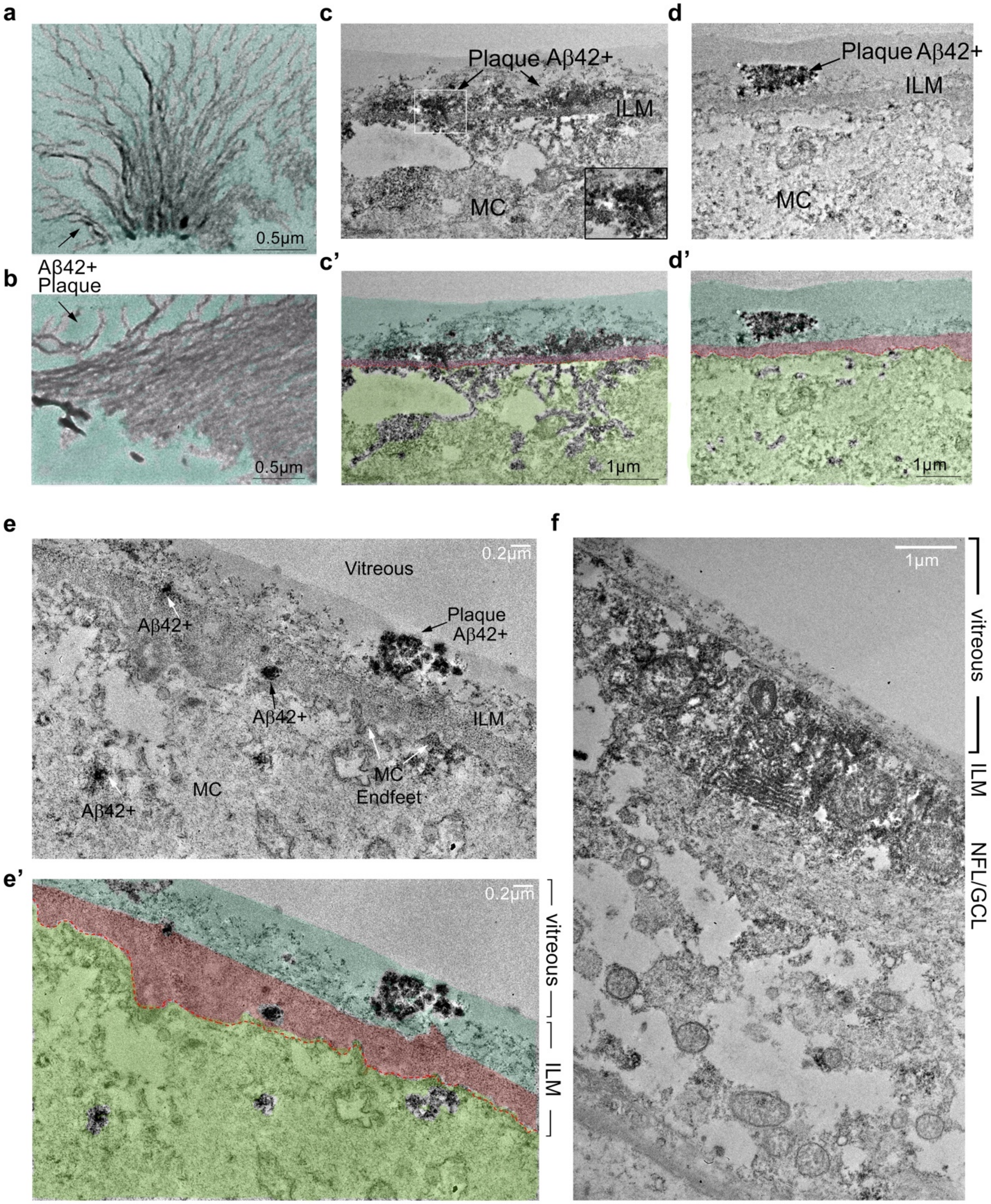
**a**. Gallyas silver stain detection of neurofibrillary tangles (NFTs, red arrowheads) and neuropil threads (NTs, red arrows) in a representative high-magnification microscopic image from the frontal cortex (ctx; superior frontal gyrus of the frontal lobe) of an AD patient. Scale bar: 10 µm. **b**. Brain NFT or NT severity scoring system was derived from observed burden of these AD neuropathologic changes detected here by Gallyas silver stain and measured per 1 mm$^2$ brain area. The assigned NFT or NT scores are as following: 0 = none; 1 = sparse (mild burden); 3 = moderate (intermediate burden); or 5 = frequent (severe burden). Representative microscopic images (20x; total magnification of 200x) of frontal cortices with assigned scores for each NFT or NT burdens, from NC subject (NFT-0, NT-0), MCI patient (NFT-1, NT-1), AD patient (NFT-3, NT-3), and another AD patient (NFT-5, NT-5). Scale bars: 20 µm. **c**. Representative tile scan fluorescence micrographs of retinal cross-sections from individuals with NC, MCI, or AD. Samples were immunolabeled for GFAP$^+$-macroglia (green), Iba1$^+$-microglia (red), 12F4$^+$-A$\beta_{42}$ (white), and nuclei (DAPI, blue), and are shown separately in central, mid- and far peripheral retinal subregions of the retina. AD = Alzheimer's disease, MCI = mild cognitive impairment, NC = normal cognition. Merge channels (left column), 12F4$^+$-A$\beta_{42}$ channel (white, right column). Scale bars = 20 µm.

**Supplementary Fig. 2.** Extended data on retinal $A\beta_{42}$ deposition in relation to sex, age, and PMI in MCI and AD patients compared to NC controls.



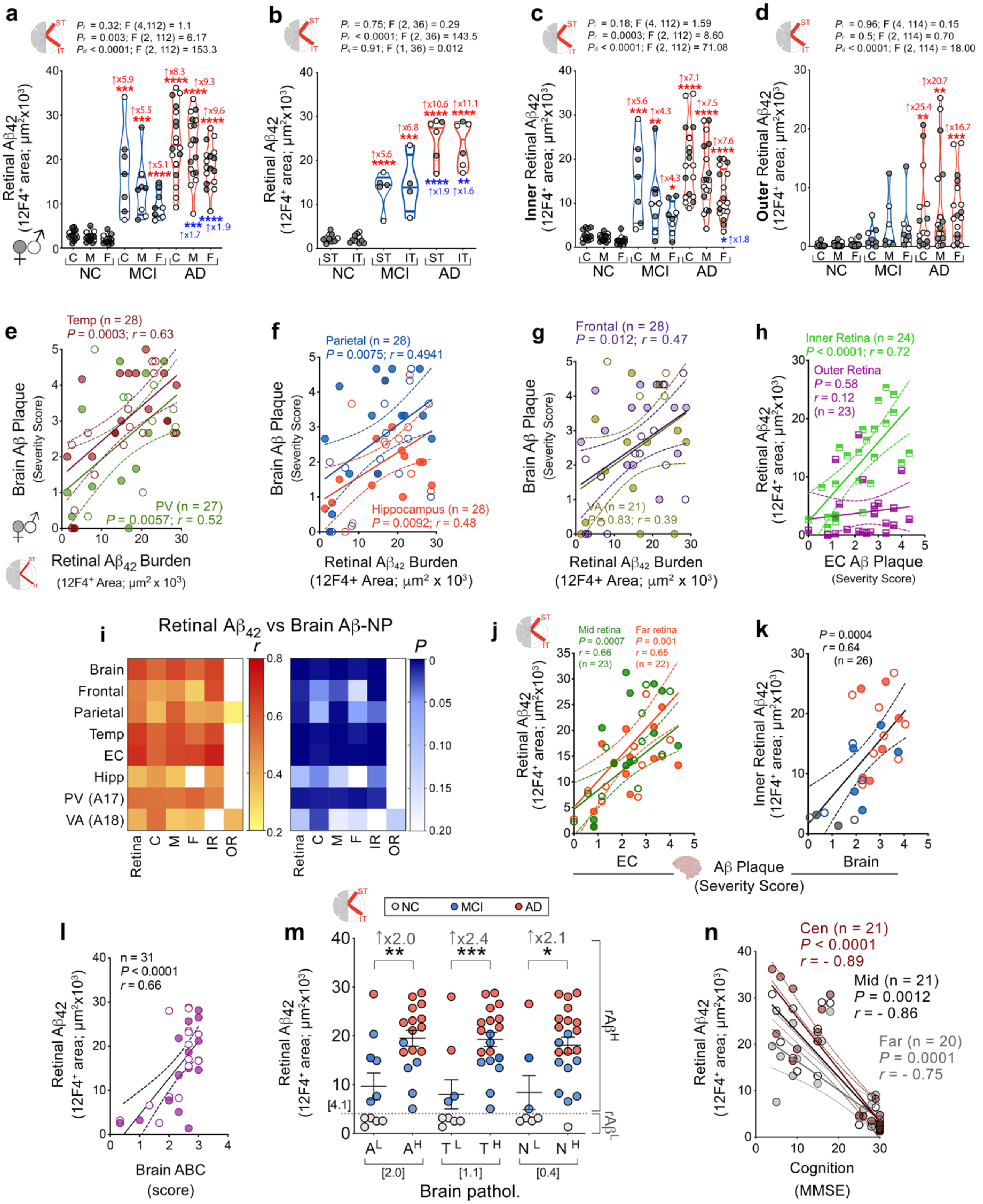
**a**. Representative tile image of the ST region extending from the optic disc (OD) to the ora serrata stained with 12F4 ($A\beta_{42}$) and peroxidase-based DAB. **b**. Micrographs of retinal cross-sections from an MCI patient that were stained with JRF/Aβtot/17 117-120 mAb (specific to the N′-terminus of Aβ; left image) and JRF/c$A\beta_{42/26}$ mAb (specific to the C′-terminus of $A\beta_{42}$; right image) with peroxidase-based DAB. Retinal Aβ plaques are seen in the INL. Scale bar: 20 µm. **c**. Quantitative IHC analysis of the retinal $A\beta_{42}$-immunoractive (IR) area normalized to retinal thickness in AD (n=18), MCI (n=8), or NC (n=16) patients. **d**. Bar graph displays retinal $A\beta_{42}$ burden separated by sex in the same cohort. Pd–diagnostic groups; Ps–females vs. males (sex groups); Pi–interactions. **e, f.** Quantitative retinal $A\beta_{42}$-IR areas in females with AD (n=7), MCI (n=6) or NC (n=9) and in males with AD (n=11), MCI (n=4), or NC (n=8). Red circle represents an ADAD patient with an A260V mutation in presenilin-1 (PSEN1). **g, h**. Pearson's correlation coefficient (*r*) analysis of (**g**) ages plotted against brain plaque burden or retina $12F4^+$-$A\beta_{42}$ IR area and (**h**) the retinal $12F4^+$-$A\beta_{42}$ IR area plotted against the postmortem interval (PMI). Violin plots show median and lower and upper quartiles, and individual data points are presented. $^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, $^{****}P < 0.0001$, by one-or two-way ANOVA and Tukey's post-hoc multiple comparison test. Filled and empty circles represent women and men, respectively.

**Supplementary Fig. 3.** Extended TEM analysis of retinal $A\beta_{42}$ deposits in AD patients.



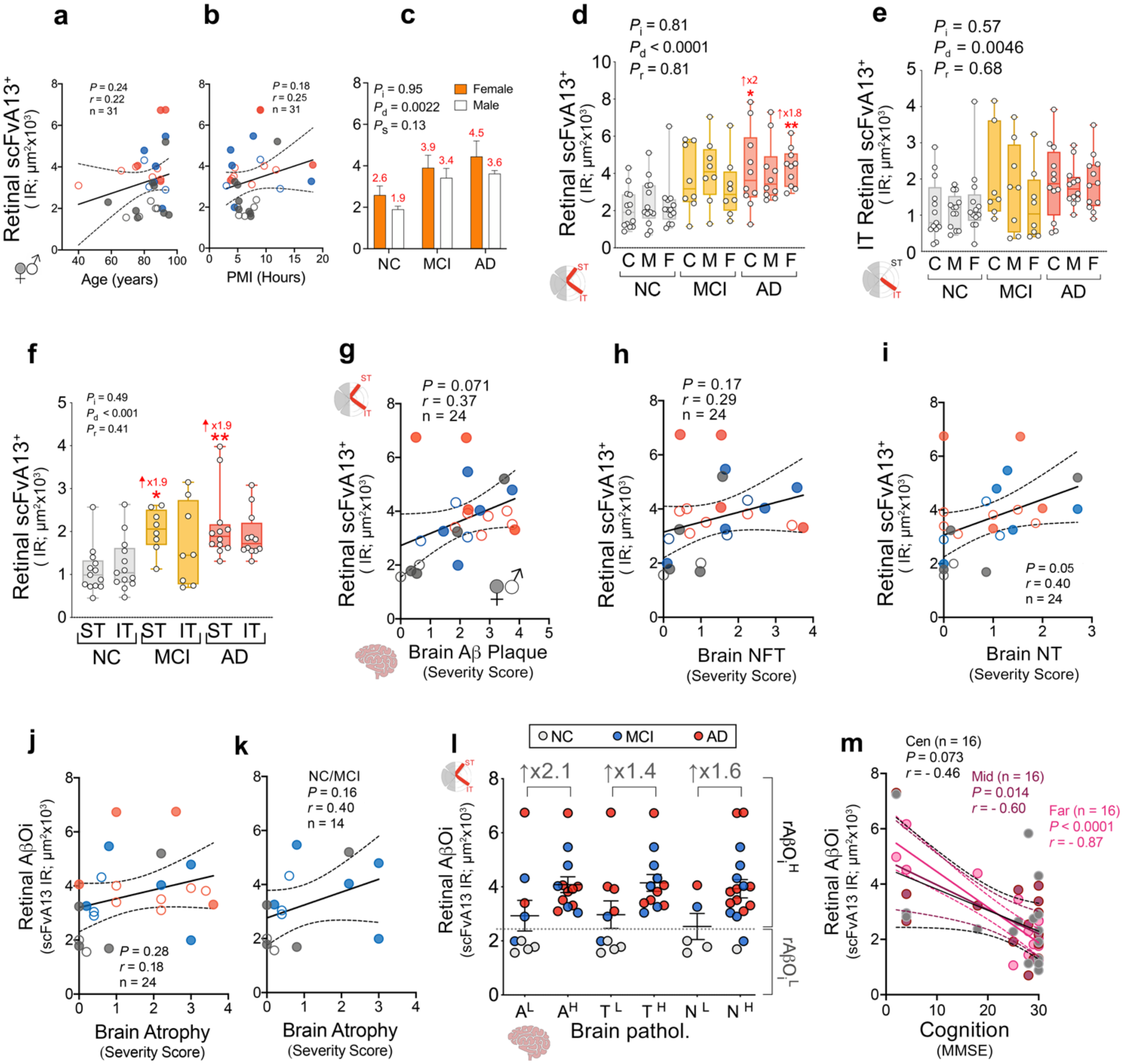
Human retinas from AD patients were pre-stained with anti-$A\beta_{42}$ mAb (12F4)-DAB. Transmission electron microscopy (TEM) analysis reveals the ultrastructure and location of retinal plaque $A\beta_{42}^{+}$ signals inside the inner limiting membrane (ILM) and Müller cell (MC) end feet (**a– e'**) as well as in the endoplasmic reticulum organelle in the GCL - ganglion cell layer (**f**). Pseudo colors were used to distinguish between the layers. Scale bars are indicated on each image. NFL = nerve fiber layer.

**Supplementary Fig. 4.** Spatial distribution of Aβ42 burden in retinal subregions and correlations with various brain regions and cognition.



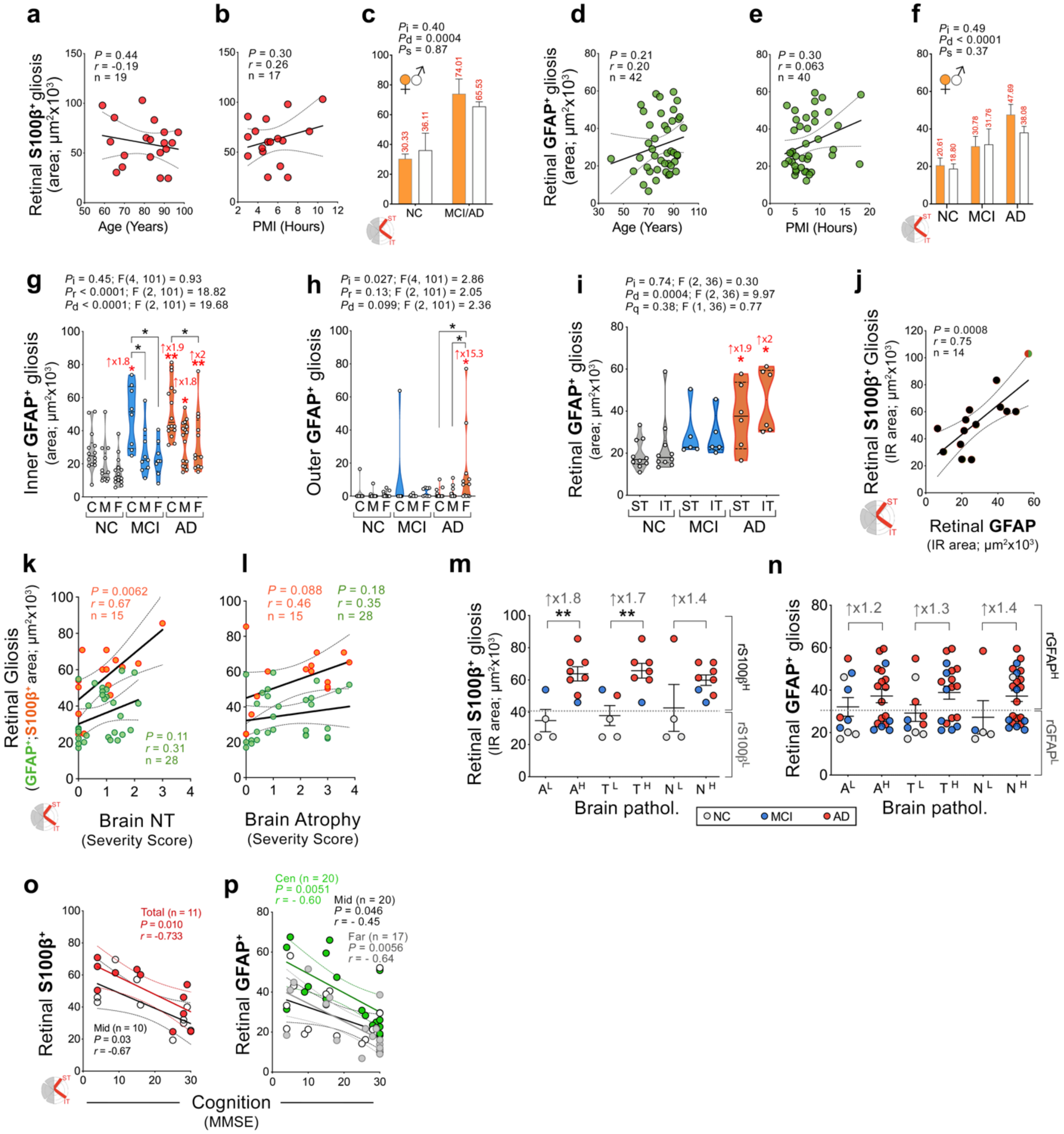
Stereological assessment of ST and IT retinal A$\beta_{42}$ (12F4$^+$-IR area) in age- and sex-matched patients with NC (n=15), MCI (n = 7, 8), or AD (n = 17, 18) within predetermined geometric subregions: **a**. Quantitative 12F4$^+$-IR from central (C), mid- (M), and far peripheral (F) retinal subregions. **b**. Retinal 12F4$^+$-IR area in ST versus IT regions in a subset of donors with NC (n=11), MCI (n=4, 5) or AD (n=6). **c**. Quantitative inner retinal A$\beta_{42}$-IR area extending from the inner limiting membrane to the inner nuclear layer per C/M/F subregions. **d**. Quantitative outer retinal 12F4$^+$-IR area extending from the outer plexiform layer to the outer limiting membrane per C/M/F subregions in the same cohort. Pd–diagnostic groups; Pr–regions; Pi–interactions. **e-g**. Pearson's correlation coefficient (r) analysis of retinal 12F4$^+$-IR area plotted against brain Aβ plaque burden in (**e)** the superior temporal (Temp) and the primary visual (PV) cortices, (**f**) the superior parietal cortex and hippocampus, and (**g)** the superior frontal and visual association (VA) cortices. **h**. Correlation analyses of inner or outer retinal A$\beta_{42}$ burden versus Aβ plaque in the entorhinal cortex (EC). **i**. Heatmaps summarizing Pearson's correlation coefficient (*r*) analyses between retinal A$\beta_{42}$ and the cerebral Aβ neuritic plaque (NP) score in all analyzed regions of the brain and retina (n=25); pseudo-color grading illustrates the strength and significance of 'r' (red) and 'P' (blue) values, respectively. **j-l**. Pearson's correlation coefficient (*r*) analysis of (**j**) the retinal 12F4$^+$-IR area in the mid- and far peripheral subregions plotted against Aβ plaque burden in the EC, (**k**) the inner retinal 12F4$^+$-IR area plotted against Aβ plaque burden in the brain, and (**l**) the retinal 12F4$^+$-IR area plotted against the cerebral ABC score derived from a 4-point scale based on the following brain pathologies: amyloid plaque – A, NFT by Braak – B, and NP by CERAD – C. **m**. Retinal A$\beta_{42}$ burden in patients stratified based on high (H) or low (L) brain ATN histopathology (severity scores) and color-labeled per diagnostic group (n=28); the extrapolated dotted-gray line marks the retinal A$\beta_{42}$ level separating ATN$^H$ from ATN$^L$ individuals. Individual data points are presented with group means ± SEMs. **n**. Pearson's correlations between retinal A$\beta_{42}$ burden per geometric subregion and MMSE cognitive scores. ST = superior-temporal, IT = inferior-temporal region of retina. Violin plots show median and lower and upper quartiles, and individual data points are presented. $^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, $^{****}P < 0.0001$, by one- or two-way ANOVA and Tukey's post-hoc multiple comparison test. Red and blue asterisks mark significance relative to NC and MCI, respectively. Filled and empty circles represent women and men, respectively.

**Supplementary Fig. 5.** Extended data on the intracellular scFvA13$^{+}$-Aβ oligomers (AβOi) distribution in the retinas of MCI and AD patients compared to retinas of NC controls and correlations with cerebral pathology and cognition.



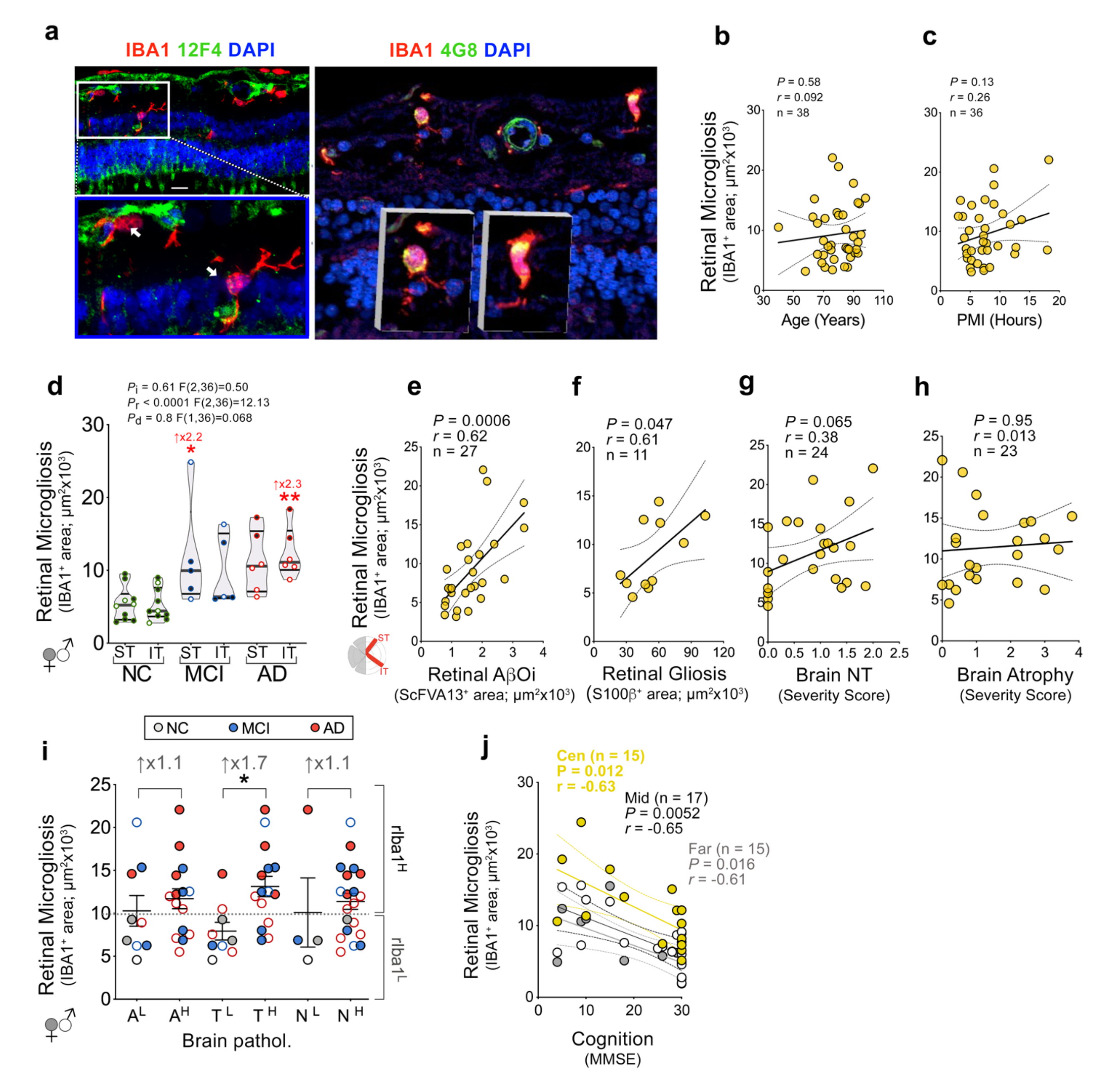
**a**-**b**. Pearson's correlation coefficient (r) analysis of retinal scFvA13$^{+}$ (AβOi)-IR versus (**a**) age and (**b**) PMI. **c.** Bar graph displays the retinal scFvA13-burden separated by sex in AD (n=12) and MCI (n=8) patients vs. NC controls (n=13). Pd–diagnostic groups; Ps–females vs. males (sex groups); Pi–interactions. **d**-**f**. Mapping of retinal scFvA13$^{+}$ in NC, MCI, and AD patient cohorts (n = 31–33) for (**d**) total ST/IT retina and (**e**) total IT, per C/ M/ F subregions, and (**f**) ST versus IT regions. Pd–diagnostic groups; Pr–regions; Pi–interactions. **g–k**. Pearson's correlation coefficient (*r*) analyses of retinal AβOi plotted against (**g**) cerebral Aβ plaque burden for all groups, (**h**) cerebral neurofibrillary tangle (NFT) pathology for all groups, (**i**) cerebral neuropil threads (NT) for all groups, (**j**) brain atrophy for all groups, and (**k**) NC and MCI groups. **l**. Analysis of the scFvA13$^{+}$-AβOi area in human retinas stratified based on high (H) or low (L) brain ATN histopathology and color-labeled per diagnostic group (n=22); extrapolated dotted-gray line marks the retinal AβOi level separating ATN$^{H}$ from ATN$^{L}$ individuals. **m**. Pearson's correlation between retinal AβOi per C/M/F subregions and MMSE cognitive scores. Median and lower and upper quartiles are indicated on each box plot, and individual data points are presented. $*P < 0.05$, $**P < 0.01$, by one- or two- way ANOVA and Tukey's post-hoc multiple comparison test. Red asterisks mark significance relative to NC. Filled and empty circles represent women and men, respectively. AβOi: intraneuronal Aβ oligomers.

**Supplementary Fig. 6.** Extended data on retinal S100β$^+$ and GFAP$^+$ macrogliosis distribution in MCI and AD patients and correlations to cerebral pathology and cognition.



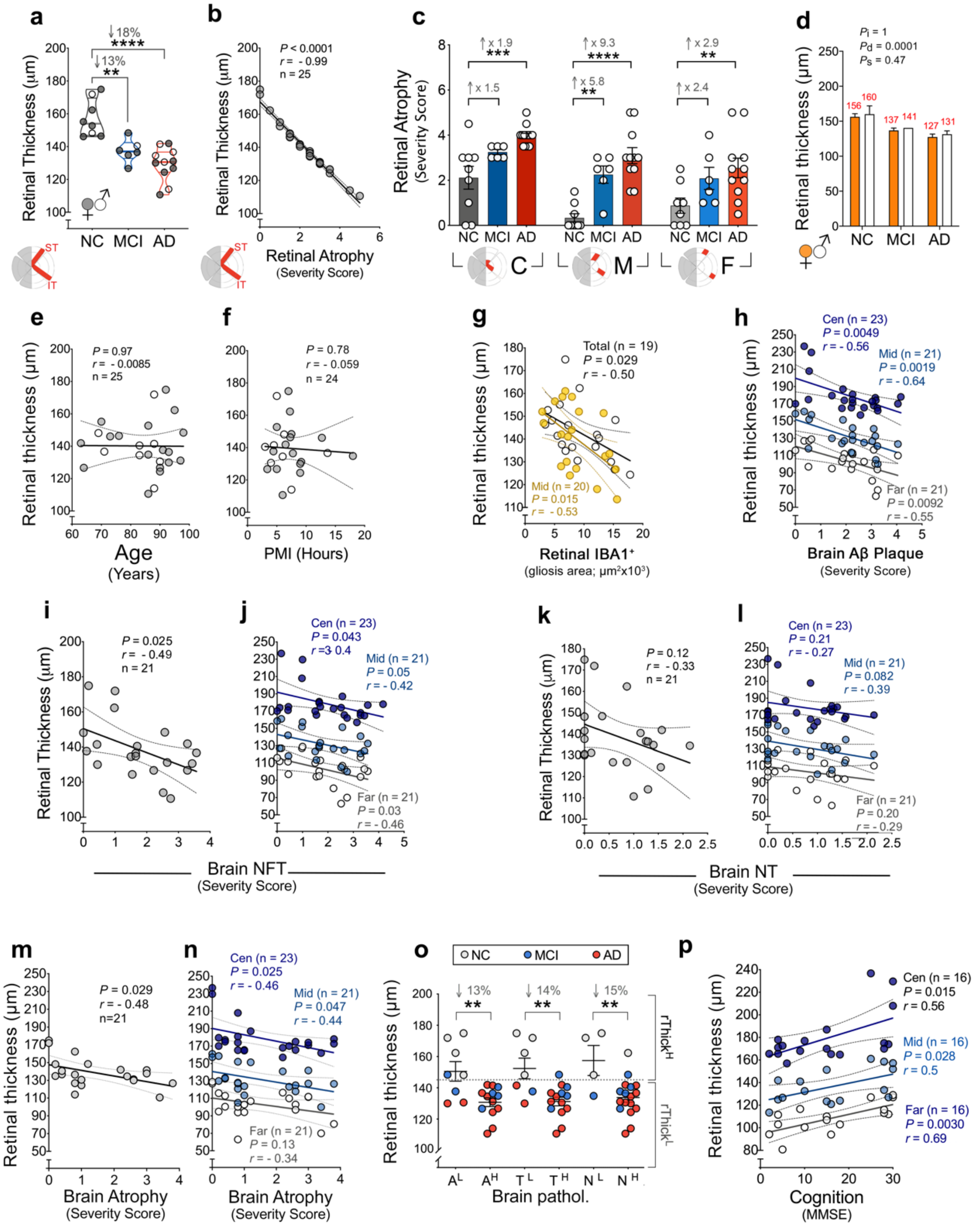
**a, b**. Pearson's correlation coefficient (*r*) analyses of the retinal gliosis S100β$^+$-IR area vs. (**a**) age and (**b**) PMI. **c**. Quantitative retinal S100β$^+$-IR area in males compared to females in NC (n = 5) vs. MCI/AD groups (n = 10-12). **d, e** Pearson's correlation coefficient (*r*) analyses of the retinal gliosis GFAP$^+$-IR area vs. (**d**) age and (**e**) PMI**. f**. Quantitative retinal GFAP$^+$-IR area in males compared to females in NC (n = 16), MCI (n = 9) and AD (n = 17) groups. **g–i**. Mapping of the retinal GFAP$^+$ gliosis-IR area in (**g**) the inner retinal layer from C/M/F subregions, (**h**) the outer retinal layer from C/M/F subregions, and (**i**) the ST vs. IT retina in the same cohort. Pd–diagnostic groups; Pr–regions; Pi–interactions. **j-l**. Pearson's correlation coefficient (r) analyses in a subset of NC, MCI, and AD patients between (**j**) reactive gliosis S100β$^+$ against GFAP$^+$, reactive gliosis (S100β$^+$; orange or GFAP$^+$; green) area against (**k**) brain NT, and (**l**) brain atrophy score. **m, n**. Retinal (**m**) S100β$^+$-IR area and (**n**) GFAP$^+$-IR area data in human donors stratified according to high (H) and low (L) brain ATN histopathology (severity scores) and color-labeled per diagnostic group (S100β$^+$, n=12; GFAP$^+$, n=28); extrapolated dotted-gray line signifies the level of retinal gliosis separating ATN$^H$ and ATN$^L$ individuals. **o, p**. Pearson's correlation coefficient (r) analyses between the retinal (**o**) S100β$^+$ area or (**p**) GFAP$^+$ area per C/M/F regions vs. MMSE score. Violin plots show median and lower and upper quartiles, and individual data points are presented. **P* < 0.05, ***P* < 0.01 by one- or two- way ANOVA and Tukey's post-hoc multiple comparison test. Red asterisks mark significance relative to NC.

**Supplementary Fig. 7.** Extended data on spatial distribution of retinal IBA1$^+$ microgliosis and correlations with retina and brain pathology and cognition.



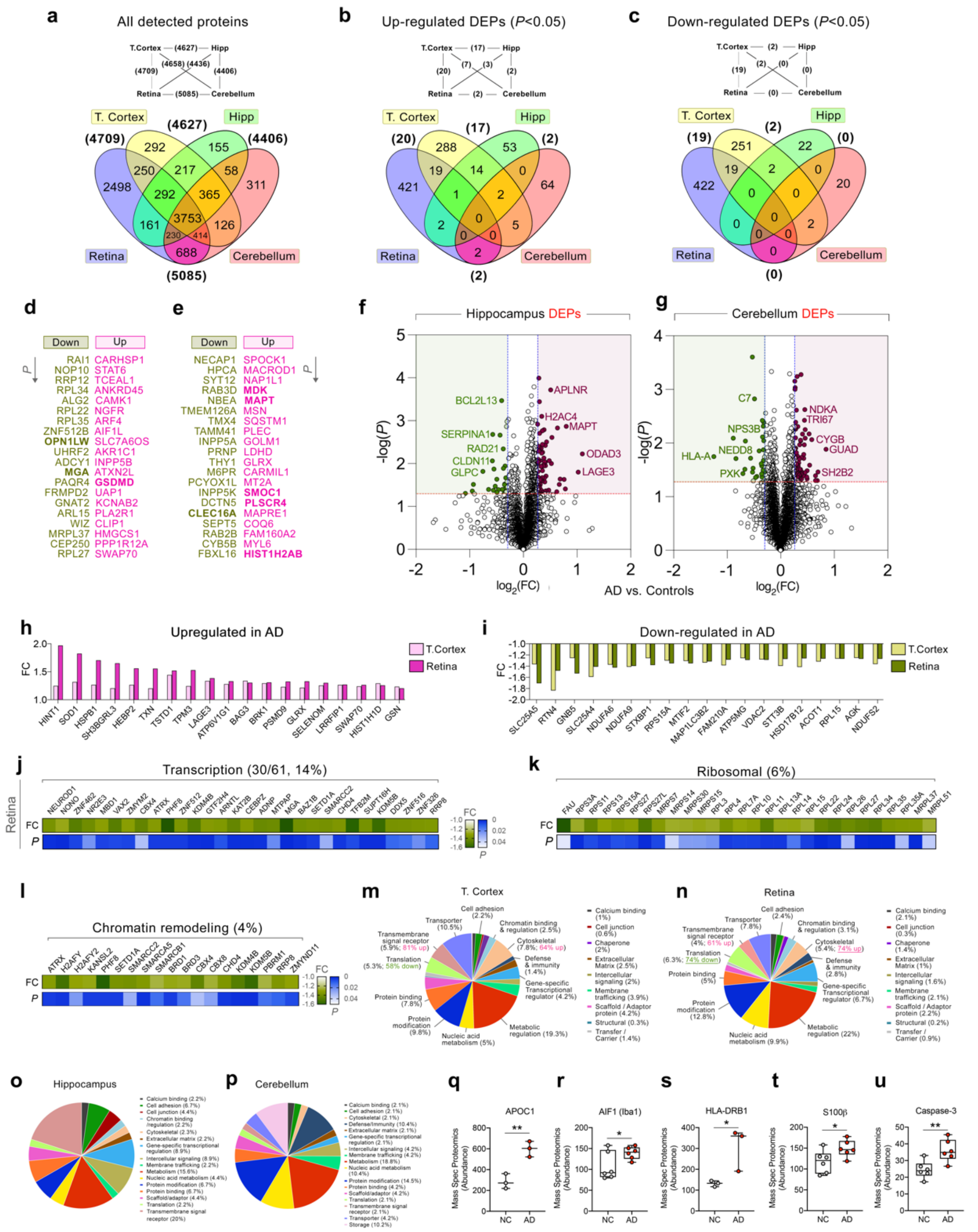
**a**. Representative immunofluorescence images of retinal cross-sections from AD patients showing IBA1$^+$-microgliosis (red), 12F4$^+$-A$\beta_{42}$ or 4G8$^+$-A$\beta_{42}$ deposits (green), and nuclei (DAPI, blue). Enlarged image depicts retinal microglia engulfing A$\beta_{42}$ deposits (white arrows). **b, c**. Pearson's correlation coefficient (*r*) analyses between Iba1$^+$ -microgliosis plotted against (**b**) age and (**c**) PMI in cohorts of donors with AD, MCI, or NC (n=36–38). **d**. Mapping of the retinal IBA1$^+$-IR area in the ST compared to the IT in NC controls (n=10) and MCI (n=5) and AD (n=6) patients. Pd–diagnostic groups; Pr–regions; Pi–interactions. **e-h.** Pearson's correlation coefficient (*r*) analyses of retinal IBA1$^+$-microgliosis in ST/IT regions plotted against (**e**) retinal AβOi, (**f**) retinal S100β$^+$ gliosis, (**g**) retinal brain neuropil threads (NT), and (**h**) brain atrophy scores**. i**. Analysis of the retinal IBA1$^+$-microgliosis area in individuals stratified according to high (H) or low (L) brain ATN histopathology and color-labeled per diagnostic group (n = 24); extrapolated dotted-gray line marks the level of retinal Iba1$^+$-microgliosis separating ATN$^H$ and ATN$^L$ individuals. **j**. Pearson's correlation between retinal IBA1 microgliosis per C/M/F subregions and MMSE cognitive score. Median and lower and upper quartiles are indicated on each violin plot, and individual data points are presented. *$P < 0.05$, **$P < 0.01$ by one- or two-way ANOVA and Tukey's post-hoc multiple comparison test. Red asterisks mark significance relative to NC group. Filled and empty circles represent women and men, respectively.

**Supplementary Figure 8.** Extended data on retinal atrophy and correlations with other cerebral biomarkers.



**a**. Quantification of retinal thickness (µm) in MCI and AD (n=17) patients and age- and sex-matched NC controls (n=8). **b**. Pearson's correlation coefficient (*r*) analysis of retinal thickness versus retinal atrophy severity score. **c**. Mapping of ST/IT retinal atrophy in this human cohort (n=26) in pre-defined central (C), mid- (M), and far (F) peripheral subregions. **d**. Quantitative retinal thickness per sex. **e-n**. Pearson's correlation coefficient (*r*) analysis of retinal thickness (µm) vs. (**e**) age, (**f**) PMI, (**g**) retinal IBA1$^+$-IR, (**h**) cerebral Aβ plaque burden per C/M/F subregions, (**i**) brain neurofibrillary tangles (NFTs)**,** (**j**) brain NFTs per C/M/F subregions, (**k**) brain neuropil threads, (**l**) brain neuropil threads per C/M/F subregions, (**m**) brain atrophy and (**n**) brain atrophy per C/M/F subregions. **o**. Analysis of retinal thickness stratified by high (H) or low (L) brain ATN histopathology and color-labeled per diagnostic group (n = 21); extrapolated dotted-gray line marks the level of retinal thickness (µm) separating ATN$^H$ and ATN$^L$ individuals. **p**. Correlations of retinal thickness in the 3 subregions vs. MMSE cognitive scores. Violin plots show median, lower and upper quartiles, and individual data points are presented. **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$ by one-or two-way ANOVA and Tukey's post-hoc multiple comparison test. Individual data points are presented with group means ± SEMs. Filled and empty circles represent women and men, respectively.

**Supplementary Fig. 9.** Extended global proteomics data in retinas and brains from AD patients and NC controls.



**a**–**c**. Venn diagrams showing (**a**) the total number of proteins detected by mass spectrometry and overlap between 3 CNS tissues as well as significantly (**b**) upregulated and (**c**) downregulated differentially expressed proteins (DEPs), based on statistical significance of $P<0.05$ and 1.2-fold change (FC) threshold criteria, with overlap between the 4 analyzed CNS tissues. The number of overlapping DEPs between each pair of CNS tissues is shown bolded in parentheses. **d**, **e**. Top 20 most significant (by p-value) upregulated (pink) and downregulated (green) proteins in the (**d**) temporal-hemiretina retina and (**e**) temporal cortex (T.Cortex) of AD patients compared to those of NC controls. DEPs are listed by ascending *P* values, with the upper DEPs having the lowest *P* values (most significant). Among these, the proteins most changed by FC are highlighted by bolded text. **f, g**. Volcano plots of all detected proteins in (**f**) the hippocampus and (**g**) cerebellum of AD patients compared to those in NC controls, with DEPs shown in red. **h, i.** Common (**h**) up- or (**i**) downregulated proteins between the retina and temporal cortex in AD patients versus controls. **j-l.** DAVID pathway analysis of AD retinas of top downregulated DEPs by FC related to the following functions: (**j**) transcription, (**k**) ribosome, and (**l**) chromatin remodeling, % proteins in a certain function of total downregulated DEPs). **m–p**. Pie charts from PANTHER functional classification analysis showing percentage of significant DEPs in (**m**) the temporal cortex, (**n**) retina, (**o**) hippocampus, and (**p**) cerebellum of AD patients compared to those in NC controls, grouped by protein class category. **q**–**u**. Box plot analysis of individual AD-associated DEPs—(**q**) APOC1, (**r**) AIF1/Iba1, (**s**) HLA-DRB1, (**t**) S100β, and (**u**) Caspase-3—related to neuroinflammation and atrophy in the retinas of AD patients vs. retinas of NC controls. Box and whiskers plots show median, lower and upper quartiles, and individual data points are presented. **P* < 0.05, ***P* < 0.01 by unpaired two-tailed Student's test.

**Supplementary Table 4.** Extended mass spectrometry data on significantly up-regulated proteins in the retina of Alzheimer's patients compared to cognitively normal controls.

| Accession | Description | AD (Means) | NC (Means) | FC | *P* |
|---|---|---|---|---|---|
| Q9Y2V2 | Calcium-regulated heat-stable protein 1 OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=2 | 262.44 | 153.78 | 1.71 | 8.643E-05 |
| P42226 | Signal transducer and activator of transcription 6 OS=Homo sapiens OX=9606 GN=STAT6 PE=1 SV=1 | 126.47 | 99.89 | 1.27 | 9.612E-05 |
| Q15170 | Isoform 2 of Transcription elongation factor A protein-like 1 OS=Homo sapiens OX=9606 GN=TCEAL1 | 121.35 | 76.26 | 1.59 | 0.00030 |
| Q5TZF3 | Isoform 2 of Ankyrin repeat domain-containing protein 45 OS=Homo sapiens OX=9606 GN=ANKRD45 | 22.38 | 14.49 | 1.54 | 0.00032 |
| Q14012 | Calcium/calmodulin-dependent protein kinase type 1 OS=Homo sapiens OX=9606 GN=CAMK1 PE=1 SV=1 | 143.38 | 108.58 | 1.32 | 0.00032 |
| P08138 | Isoform 2 of Tumor necrosis factor receptor superfamily member 16 OS=Homo sapiens OX=9606 GN=NGFR | 40.44 | 24.72 | 1.64 | 0.00065 |
| P18085 | ADP-ribosylation factor 4 OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=3 | 883.54 | 645.81 | 1.37 | 0.00065 |
| Q9BQI0 | Allograft inflammatory factor 1-like OS=Homo sapiens OX=9606 GN=AIF1L PE=1 SV=1 | 231.24 | 162.04 | 1.43 | 0.00066 |
| Q96CW6 | Probable RNA polymerase II nuclear localization protein SLC7A6OS OS=Homo sapiens OX=9606 GN=SLC7A6OS PE=1 SV=2 | 55.22 | 35.09 | 1.57 | 0.00070 |
| Q04828 | Aldo-keto reductase family 1 member C1 OS=Homo sapiens OX=9606 GN=AKR1C1 PE=1 SV=1 | 400.78 | 269.55 | 1.49 | 0.00074 |
| P32019 | Type II inositol 1,4,5-trisphosphate 5-phosphatase OS=Homo sapiens OX=9606 GN=INPP5B PE=1 SV=4 | 15.26 | 9.54 | 1.60 | 0.00080 |
| H3BUF6 | Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=1 | 30.04 | 21.65 | 1.39 | 0.00080 |
| G3V1A6 | Gasdermin domain containing 1, isoform CRA_d OS=Homo sapiens OX=9606 GN=GSDMD PE=1 SV=1 | 31.58 | 15.62 | 2.02 | 0.00090 |
| Q16222 | UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens OX=9606 GN=UAP1 PE=1 SV=3 | 14.51 | 9.33 | 1.55 | 0.00099 |
| Q13303 | Isoform 3 of Voltage-gated potassium channel subunit beta-2 OS=Homo sapiens OX=9606 GN=KCNAB2 | 122.11 | 83.92 | 1.46 | 0.00100 |
| Q13018 | Secretory phospholipase A2 receptor OS=Homo sapiens OX=9606 GN=PLA2R1 PE=1 SV=2 | 154.38 | 127.41 | 1.21 | 0.00112 |
| P30622 | CAP-Gly domain-containing linker protein 1 OS=Homo sapiens OX=9606 GN=CLIP1 PE=1 SV=2 | 1073.32 | 883.48 | 1.21 | 0.00124 |
| Q01581 | Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens OX=9606 GN=HMGCS1 PE=1 SV=2 | 123.62 | 90.34 | 1.37 | 0.00126 |
| O14974 | Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1 | 1259.97 | 1048.38 | 1.20 | 0.00128 |
| Q9UH65 | Switch-associated protein 70 OS=Homo sapiens OX=9606 GN=SWAP70 PE=1 SV=1 | 440.63 | 348.41 | 1.26 | 0.00147 |

| | | | | | |
|---|---|---|---|---|---|
| E9PSH4 | Repressor of RNA polymerase III transcription MAF1 OS=Homo sapiens OX=9606 GN=MAF1 PE=1 SV=1 | 57.64 | 36.07 | 1.60 | 0.00156 |
| O15514 | DNA-directed RNA polymerase II subunit RPB4 OS=Homo sapiens OX=9606 GN=POLR2D PE=1 SV=1 | 48.86 | 37.89 | 1.29 | 0.00158 |
| Q9H1P3 | Oxysterol-binding protein-related protein 2 OS=Homo sapiens OX=9606 GN=OSBPL2 PE=1 SV=1 | 475.60 | 393.03 | 1.21 | 0.00161 |
| Q9NRV9 | Heme-binding protein 1 OS=Homo sapiens OX=9606 GN=HEBP1 PE=1 SV=1 | 930.77 | 667.70 | 1.39 | 0.00171 |
| Q12841 | Follistatin-related protein 1 OS=Homo sapiens OX=9606 GN=FSTL1 PE=1 SV=1 | 114.74 | 90.64 | 1.27 | 0.00171 |
| Q9P287 | BRCA2 and CDKN1A-interacting protein OS=Homo sapiens OX=9606 GN=BCCIP PE=1 SV=1 | 260.96 | 149.99 | 1.74 | 0.00179 |
| A0A087WY62 | Neuroblastoma breakpoint family member 26 OS=Homo sapiens OX=9606 GN=NBPF26 PE=4 SV=3 | 99.18 | 59.84 | 1.66 | 0.00190 |
| Q14657 | EKC/KEOPS complex subunit LAGE3 OS=Homo sapiens OX=9606 GN=LAGE3 PE=1 SV=2 | 32.15 | 23.23 | 1.38 | 0.00202 |
| Q92995 | Ubiquitin carboxyl-terminal hydrolase 13 OS=Homo sapiens OX=9606 GN=USP13 PE=1 SV=2 | 14.83 | 10.03 | 1.48 | 0.00213 |
| A0A087X091 | WD repeat-containing protein 13 (Fragment) OS=Homo sapiens OX=9606 GN=WDR13 PE=1 SV=1 | 78.88 | 63.41 | 1.24 | 0.00234 |
| O15355 | Protein phosphatase 1G OS=Homo sapiens OX=9606 GN=PPM1G PE=1 SV=1 | 747.14 | 588.94 | 1.27 | 0.00251 |
| Q9UKW4 | Isoform 4 of Guanine nucleotide exchange factor VAV3 OS=Homo sapiens OX=9606 GN=VAV3 | 164.63 | 137.13 | 1.20 | 0.00272 |
| Q14376 | UDP-glucose 4-epimerase OS=Homo sapiens OX=9606 GN=GALE PE=1 SV=2 | 439.78 | 293.33 | 1.50 | 0.00279 |
| Q9H6X2 | Anthrax toxin receptor 1 OS=Homo sapiens OX=9606 GN=ANTXR1 PE=1 SV=2 | 52.50 | 40.64 | 1.29 | 0.00298 |
| Q9UK22 | F-box only protein 2 OS=Homo sapiens OX=9606 GN=FBXO2 PE=1 SV=2 | 982.04 | 778.07 | 1.26 | 0.00300 |
| P62330 | ADP-ribosylation factor 6 OS=Homo sapiens OX=9606 GN=ARF6 PE=1 SV=2 | 431.76 | 298.76 | 1.45 | 0.00312 |
| P00915 | Carbonic anhydrase 1 OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=2 | 2538.21 | 1397.54 | 1.82 | 0.00313 |
| Q9BW83 | Intraflagellar transport protein 27 homolog OS=Homo sapiens OX=9606 GN=IFT27 PE=1 SV=1 | 556.96 | 395.36 | 1.41 | 0.00316 |
| P02489 | Alpha-crystallin A chain OS=Homo sapiens OX=9606 GN=CRYAA PE=1 SV=2 | 13374.84 | 8743.41 | 1.53 | 0.00324 |
| P02042 | Hemoglobin subunit delta OS=Homo sapiens OX=9606 GN=HBD PE=1 SV=2 | 3439.58 | 1703.27 | 2.02 | 0.00331 |
| P05413 | Fatty acid-binding protein, heart OS=Homo sapiens OX=9606 GN=FABP3 PE=1 SV=4 | 918.93 | 601.21 | 1.53 | 0.00340 |
| O15405 | TOX high mobility group box family member 3 OS=Homo sapiens OX=9606 GN=TOX3 PE=1 SV=2 | 77.89 | 61.67 | 1.26 | 0.00354 |
| O15212 | Prefoldin subunit 6 OS=Homo sapiens OX=9606 GN=PFDN6 PE=1 SV=1 | 653.96 | 376.98 | 1.73 | 0.00357 |
| Q9Y5K3 | Choline-phosphate cytidylyltransferase B OS=Homo sapiens OX=9606 GN=PCYT1B PE=1 SV=1 | 166.76 | 121.81 | 1.37 | 0.00359 |
| P09497 | Isoform Non-brain of Clathrin light chain B OS=Homo sapiens OX=9606 GN=CLTB | 462.23 | 249.08 | 1.86 | 0.00362 |

| | | | | | |
|---|---|---|---|---|---|
| O00233 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=3 | 565.79 | 427.45 | 1.32 | 0.00370 |
| P09936 | Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens OX=9606 GN=UCHL1 PE=1 SV=2 | 5218.63 | 3210.77 | 1.63 | 0.00379 |
| P68871 | Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2 | 13260.96 | 6808.23 | 1.95 | 0.00384 |
| P30085 | UMP-CMP kinase OS=Homo sapiens OX=9606 GN=CMPK1 PE=1 SV=3 | 1046.10 | 626.46 | 1.67 | 0.00386 |
| P36021 | Monocarboxylate transporter 8 OS=Homo sapiens OX=9606 GN=SLC16A2 PE=1 SV=2 | 25.83 | 20.70 | 1.25 | 0.00409 |
| Q14574 | Isoform 3B of Desmocollin-3 OS=Homo sapiens OX=9606 GN=DSC3 | 67.06 | 41.13 | 1.63 | 0.00419 |
| A6ZKI3 | Retrotransposon Gag-like protein 8C OS=Homo sapiens OX=9606 GN=RTL8C PE=1 SV=1 | 340.77 | 232.88 | 1.46 | 0.00422 |
| Q99584 | Protein S100-A13 OS=Homo sapiens OX=9606 GN=S100A13 PE=1 SV=1 | 1730.80 | 1073.04 | 1.61 | 0.00426 |
| O15217 | Glutathione S-transferase A4 OS=Homo sapiens OX=9606 GN=GSTA4 PE=1 SV=1 | 135.42 | 94.80 | 1.43 | 0.00435 |
| Q7Z449 | Cytochrome P450 2U1 OS=Homo sapiens OX=9606 GN=CYP2U1 PE=1 SV=1 | 133.60 | 108.12 | 1.24 | 0.00441 |
| A0A0U1RRM6 | Protein enabled homolog OS=Homo sapiens OX=9606 GN=ENAH PE=1 SV=1 | 310.29 | 235.12 | 1.32 | 0.00443 |
| P31749 | RAC-alpha serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=AKT1 PE=1 SV=2 | 506.93 | 420.35 | 1.21 | 0.00448 |
| Q96QA5 | Gasdermin-A OS=Homo sapiens OX=9606 GN=GSDMA PE=1 SV=4 | 125.32 | 65.57 | 1.91 | 0.00451 |
| Q9NX08 | COMM domain-containing protein 8 OS=Homo sapiens OX=9606 GN=COMMD8 PE=1 SV=1 | 45.31 | 33.39 | 1.36 | 0.00454 |
| A0A2R8Y7C0 | Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1 | 5429.62 | 2843.25 | 1.91 | 0.00456 |
| A0A087X0M8 | Neural cell adhesion molecule L1-like protein OS=Homo sapiens OX=9606 GN=CHL1 PE=1 SV=1 | 255.41 | 200.14 | 1.28 | 0.00459 |
| Q15370 | Elongin-B OS=Homo sapiens OX=9606 GN=ELOB PE=1 SV=1 | 1449.87 | 1066.65 | 1.36 | 0.00464 |
| P19971 | Isoform 2 of Thymidine phosphorylase OS=Homo sapiens OX=9606 GN=TYMP | 141.34 | 92.93 | 1.52 | 0.00524 |
| Q9BV86 | N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens OX=9606 GN=NTMT1 PE=1 SV=3 | 154.88 | 102.59 | 1.51 | 0.00525 |
| P04792 | Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2 | 3569.10 | 2093.53 | 1.70 | 0.00539 |
| O00499 | Isoform IIB of Myc box-dependent-interacting protein 1 OS=Homo sapiens OX=9606 GN=BIN1 | 79.67 | 61.50 | 1.30 | 0.00562 |
| P52566 | Rho GDP-dissociation inhibitor 2 OS=Homo sapiens OX=9606 GN=ARHGDIB PE=1 SV=3 | 393.32 | 281.16 | 1.40 | 0.00565 |
| O75368 | SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens OX=9606 GN=SH3BGRL PE=1 SV=1 | 1705.57 | 856.93 | 1.99 | 0.00568 |
| Q9H299 | SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens OX=9606 GN=SH3BGRL3 PE=1 SV=1 | 818.47 | 495.54 | 1.65 | 0.00577 |

| | | | | | |
|---|---|---|---|---|---|
| Q8IYD1 | Eukaryotic peptide chain release factor GTP-binding subunit ERF3B OS=Homo sapiens OX=9606 GN=GSPT2 PE=1 SV=2 | 112.56 | 90.67 | 1.24 | 0.00584 |
| O00273 | DNA fragmentation factor subunit alpha OS=Homo sapiens OX=9606 GN=DFFA PE=1 SV=1 | 501.47 | 380.95 | 1.32 | 0.00602 |
| H7C394 | Calcium/calmodulin-dependent protein kinase type II subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=CAMK2B PE=1 SV=1 | 54.35 | 41.07 | 1.32 | 0.00602 |
| P67936 | Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=3 | 2478.28 | 1531.27 | 1.62 | 0.00605 |
| Q9UJ68 | Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens OX=9606 GN=MSRA PE=1 SV=1 | 77.57 | 62.20 | 1.25 | 0.00606 |
| P69905 | Hemoglobin subunit alpha OS=Homo sapiens OX=9606 GN=HBA1 PE=1 SV=2 | 463.25 | 198.84 | 2.33 | 0.00613 |
| H7BZ14 | Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Homo sapiens OX=9606 GN=PPIL3 PE=1 SV=1 | 345.89 | 237.99 | 1.45 | 0.00616 |
| J3QRF4 | RNA binding protein fox-1 homolog OS=Homo sapiens OX=9606 GN=RBFOX3 PE=1 SV=1 | 33.06 | 26.92 | 1.23 | 0.00623 |
| Q9NZ08 | Isoform 2 of Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens OX=9606 GN=ERAP1 | 40.72 | 31.92 | 1.28 | 0.00651 |
| G8JLG2 | CDSN OS=Homo sapiens OX=9606 GN=CDSN PE=1 SV=1 | 126.01 | 78.81 | 1.60 | 0.00658 |
| P52306 | Isoform 4 of Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens OX=9606 GN=RAP1GDS1 | 2217.84 | 1630.59 | 1.36 | 0.00663 |
| A8MXB7 | Sorting nexin-24 OS=Homo sapiens OX=9606 GN=SNX24 PE=1 SV=1 | 54.56 | 37.15 | 1.47 | 0.00664 |
| P20472 | Parvalbumin alpha OS=Homo sapiens OX=9606 GN=PVALB PE=1 SV=2 | 2478.41 | 1017.20 | 2.44 | 0.00666 |
| P05154 | Plasma serine protease inhibitor OS=Homo sapiens OX=9606 GN=SERPINA5 PE=1 SV=3 | 52.47 | 32.42 | 1.62 | 0.00686 |
| Q9Y5F8 | Protocadherin gamma-B7 OS=Homo sapiens OX=9606 GN=PCDHGB7 PE=2 SV=1 | 18.30 | 14.01 | 1.31 | 0.00687 |
| P48436 | Transcription factor SOX-9 OS=Homo sapiens OX=9606 GN=SOX9 PE=1 SV=1 | 64.74 | 49.97 | 1.30 | 0.00689 |
| P17812 | CTP synthase 1 OS=Homo sapiens OX=9606 GN=CTPS1 PE=1 SV=2 | 372.46 | 300.89 | 1.24 | 0.00697 |
| Q9BRT3 | Migration and invasion enhancer 1 OS=Homo sapiens OX=9606 GN=MIEN1 PE=1 SV=1 | 374.40 | 266.73 | 1.40 | 0.00719 |
| Q9Y6K9 | Isoform 2 of NF-kappa-B essential modulator OS=Homo sapiens OX=9606 GN=IKBKG | 320.50 | 251.71 | 1.27 | 0.00721 |
| P42574 | Caspase-3 OS=Homo sapiens OX=9606 GN=CASP3 PE=1 SV=2 | 35.44 | 24.03 | 1.47 | 0.00733 |
| Q9BRQ8 | Apoptosis-inducing factor 2 OS=Homo sapiens OX=9606 GN=AIFM2 PE=1 SV=1 | 16.21 | 11.42 | 1.42 | 0.00744 |
| O75821 | Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens OX=9606 GN=EIF3G PE=1 SV=2 | 802.62 | 656.36 | 1.22 | 0.00772 |
| P04003 | C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2 | 178.85 | 146.54 | 1.22 | 0.00793 |
| Q9BU02 | Thiamine-triphosphatase OS=Homo sapiens OX=9606 GN=THTPA PE=1 SV=3 | 135.79 | 109.04 | 1.25 | 0.00821 |
| Q8NDI1 | Isoform 2 of EH domain-binding protein 1 OS=Homo sapiens OX=9606 GN=EHBP1 | 86.38 | 64.60 | 1.34 | 0.00849 |

| | | | | | |
|---|---|---|---|---|---|
| Q32MZ4 | Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens OX=9606 GN=LRRFIP1 | 406.39 | 320.01 | 1.27 | 0.00869 |
| Q9Y5B0 | RNA polymerase II subunit A C-terminal domain phosphatase OS=Homo sapiens OX=9606 GN=CTDP1 PE=1 SV=3 | 60.00 | 44.41 | 1.35 | 0.00870 |
| Q59EK9 | Isoform 2 of RUN domain-containing protein 3A OS=Homo sapiens OX=9606 GN=RUNDC3A | 129.38 | 88.76 | 1.46 | 0.00873 |
| O95433 | Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens OX=9606 GN=AHSA1 PE=1 SV=1 | 1320.18 | 944.06 | 1.40 | 0.00895 |
| A0A0A0MSS3 | SLAIN motif-containing protein 1 OS=Homo sapiens OX=9606 GN=SLAIN1 PE=1 SV=1 | 32.99 | 18.03 | 1.83 | 0.00896 |
| P62166 | Neuronal calcium sensor 1 OS=Homo sapiens OX=9606 GN=NCS1 PE=1 SV=2 | 124.19 | 91.92 | 1.35 | 0.00898 |
| Q8WWX9 | Selenoprotein M OS=Homo sapiens OX=9606 GN=SELENOM PE=1 SV=3 | 61.70 | 47.38 | 1.30 | 0.00926 |
| P02654 | Apolipoprotein C-I OS=Homo sapiens OX=9606 GN=APOC1 PE=1 SV=1 | 596.18 | 278.36 | 2.14 | 0.00931 |
| P45974 | Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 PE=1 SV=2 | 2537.62 | 2076.73 | 1.22 | 0.00934 |
| Q96BH1 | E3 ubiquitin-protein ligase RNF25 OS=Homo sapiens OX=9606 GN=RNF25 PE=1 SV=1 | 74.03 | 59.99 | 1.23 | 0.00935 |
| Q8IYB5 | Isoform 2 of Stromal membrane-associated protein 1 OS=Homo sapiens OX=9606 GN=SMAP1 | 238.94 | 174.64 | 1.37 | 0.00942 |
| Q96P47 | Isoform 4 of Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 OS=Homo sapiens OX=9606 GN=AGAP3 | 179.44 | 144.58 | 1.24 | 0.00975 |
| D3DSM0 | Integrin beta OS=Homo sapiens OX=9606 GN=ITGB2 PE=1 SV=1 | 49.29 | 39.12 | 1.26 | 0.00981 |
| Q9NRX4 | 14 kDa phosphohistidine phosphatase OS=Homo sapiens OX=9606 GN=PHPT1 PE=1 SV=1 | 1108.29 | 619.01 | 1.79 | 0.00988 |
| Q96RR4 | Calcium/calmodulin-dependent protein kinase kinase 2 OS=Homo sapiens OX=9606 GN=CAMKK2 PE=1 SV=2 | 19.25 | 15.08 | 1.28 | 0.00997 |
| Q15102 | Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens OX=9606 GN=PAFAH1B3 PE=1 SV=1 | 780.04 | 522.27 | 1.49 | 0.00998 |
| Q96DG6 | Carboxymethylenebutenolidase homolog OS=Homo sapiens OX=9606 GN=CMBL PE=1 SV=1 | 403.88 | 278.56 | 1.45 | 0.01008 |
| P15374 | Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens OX=9606 GN=UCHL3 PE=1 SV=1 | 227.05 | 156.66 | 1.45 | 0.01010 |
| Q86TP1 | Exopolyphosphatase PRUNE1 OS=Homo sapiens OX=9606 GN=PRUNE1 PE=1 SV=2 | 227.16 | 178.09 | 1.28 | 0.01022 |
| Q5T7Y6 | Protein S100 OS=Homo sapiens OX=9606 GN=S100A1 PE=1 SV=1 | 800.46 | 411.02 | 1.95 | 0.01028 |
| P49773 | Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=2 | 1325.92 | 673.28 | 1.97 | 0.01029 |
| Q96S19 | Methyltransferase-like 26 OS=Homo sapiens OX=9606 GN=METTL26 PE=1 SV=2 | 133.15 | 105.62 | 1.26 | 0.01046 |
| Q9BWD1 | Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens OX=9606 GN=ACAT2 PE=1 SV=2 | 1137.07 | 859.36 | 1.32 | 0.01052 |

| | | | | | |
|---|---|---|---|---|---|
| Q9UNZ2 | Isoform 3 of NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C | 2258.72 | 1688.00 | 1.34 | 0.01053 |
| Q5QJ74 | Tubulin-specific chaperone cofactor E-like protein OS=Homo sapiens OX=9606 GN=TBCEL PE=1 SV=2 | 54.46 | 41.05 | 1.33 | 0.01058 |
| Q13526 | Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens OX=9606 GN=PIN1 PE=1 SV=1 | 1031.81 | 719.37 | 1.43 | 0.01061 |
| P48507 | Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens OX=9606 GN=GCLM PE=1 SV=1 | 261.02 | 202.56 | 1.29 | 0.01062 |
| O75832 | 26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens OX=9606 GN=PSMD10 PE=1 SV=1 | 627.63 | 494.69 | 1.27 | 0.01077 |
| P51636 | Caveolin-2 OS=Homo sapiens OX=9606 GN=CAV2 PE=1 SV=2 | 116.44 | 85.53 | 1.36 | 0.01078 |
| O76003 | Glutaredoxin-3 OS=Homo sapiens OX=9606 GN=GLRX3 PE=1 SV=2 | 466.75 | 356.01 | 1.31 | 0.01078 |
| O75312 | Zinc finger protein ZPR1 OS=Homo sapiens OX=9606 GN=ZPR1 PE=1 SV=1 | 42.66 | 28.75 | 1.48 | 0.01081 |
| P54725 | Isoform 3 of UV excision repair protein RAD23 homolog A OS=Homo sapiens OX=9606 GN=RAD23A | 591.74 | 457.20 | 1.29 | 0.01098 |
| P0DI81 | Isoform 3 of Trafficking protein particle complex subunit 2 OS=Homo sapiens OX=9606 GN=TRAPPC2 | 67.81 | 51.34 | 1.32 | 0.01099 |
| Q92696 | Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens OX=9606 GN=RABGGTA PE=1 SV=2 | 550.76 | 451.60 | 1.22 | 0.01109 |
| Q13107 | Ubiquitin carboxyl-terminal hydrolase 4 OS=Homo sapiens OX=9606 GN=USP4 PE=1 SV=3 | 226.73 | 185.92 | 1.22 | 0.01115 |
| Q6FI81 | Anamorsin OS=Homo sapiens OX=9606 GN=CIAPIN1 PE=1 SV=2 | 868.18 | 605.79 | 1.43 | 0.01122 |
| Q8TCC7 | Isoform 2 of Solute carrier family 22 member 8 OS=Homo sapiens OX=9606 GN=SLC22A8 | 32.50 | 16.95 | 1.92 | 0.01126 |
| Q5SYC1 | Clavesin-2 OS=Homo sapiens OX=9606 GN=CLVS2 PE=2 SV=1 | 301.23 | 211.87 | 1.42 | 0.01128 |
| Q15785 | Mitochondrial import receptor subunit TOM34 OS=Homo sapiens OX=9606 GN=TOMM34 PE=1 SV=2 | 483.95 | 402.79 | 1.20 | 0.01128 |
| Q8TDH9 | Biogenesis of lysosome-related organelles complex 1 subunit 5 OS=Homo sapiens OX=9606 GN=BLOC1S5 PE=1 SV=1 | 53.76 | 42.00 | 1.28 | 0.01128 |
| Q6NW29 | RWD domain-containing protein 4 OS=Homo sapiens OX=9606 GN=RWDD4 PE=1 SV=3 | 121.98 | 90.50 | 1.35 | 0.01149 |
| P40123 | Adenylyl cyclase-associated protein 2 OS=Homo sapiens OX=9606 GN=CAP2 PE=1 SV=1 | 842.21 | 692.64 | 1.22 | 0.01153 |
| Q9UNI6 | Dual specificity protein phosphatase 12 OS=Homo sapiens OX=9606 GN=DUSP12 PE=1 SV=1 | 37.12 | 28.13 | 1.32 | 0.01162 |
| Q9NWV4 | UPF0587 protein C1orf123 OS=Homo sapiens OX=9606 GN=C1orf123 PE=1 SV=1 | 192.40 | 128.29 | 1.50 | 0.01177 |
| Q96PE1 | Adhesion G protein-coupled receptor A2 OS=Homo sapiens OX=9606 GN=ADGRA2 PE=1 SV=2 | 400.09 | 309.54 | 1.29 | 0.01177 |
| Q9UNN5 | FAS-associated factor 1 OS=Homo sapiens OX=9606 GN=FAF1 PE=1 SV=2 | 514.75 | 428.62 | 1.20 | 0.01182 |
| Q68CZ2 | Tensin-3 OS=Homo sapiens OX=9606 GN=TNS3 PE=1 SV=2 | 453.91 | 371.91 | 1.22 | 0.01185 |

| | | | | | |
|---|---|---|---|---|---|
| Q14515 | SPARC-like protein 1 OS=Homo sapiens OX=9606 GN=SPARCL1 PE=1 SV=2 | 552.86 | 420.47 | 1.31 | 0.01188 |
| Q15555 | Isoform 5 of Microtubule-associated protein RP/EB family member 2 OS=Homo sapiens OX=9606 GN=MAPRE2 | 1854.81 | 1469.12 | 1.26 | 0.01191 |
| P06732 | Creatine kinase M-type OS=Homo sapiens OX=9606 GN=CKM PE=1 SV=2 | 336.46 | 177.58 | 1.89 | 0.01205 |
| A0A0A0MSS8 | Aldo-keto reductase family 1 member C3 OS=Homo sapiens OX=9606 GN=AKR1C3 PE=1 SV=1 | 5088.56 | 3237.40 | 1.57 | 0.01209 |
| O43399 | Isoform 7 of Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 | 642.20 | 487.69 | 1.32 | 0.01245 |
| Q92882 | Osteoclast-stimulating factor 1 OS=Homo sapiens OX=9606 GN=OSTF1 PE=1 SV=2 | 257.38 | 206.19 | 1.25 | 0.01257 |
| Q01469 | Fatty acid-binding protein 5 OS=Homo sapiens OX=9606 GN=FABP5 PE=1 SV=3 | 2053.51 | 1176.32 | 1.75 | 0.01262 |
| P43487 | Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1 | 1344.99 | 875.65 | 1.54 | 0.01280 |
| P35754 | Glutaredoxin-1 OS=Homo sapiens OX=9606 GN=GLRX PE=1 SV=2 | 27.47 | 20.68 | 1.33 | 0.01285 |
| E5RJR5 | S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=1 | 2046.62 | 1575.94 | 1.30 | 0.01306 |
| O15498 | Synaptobrevin homolog YKT6 OS=Homo sapiens OX=9606 GN=YKT6 PE=1 SV=1 | 655.96 | 467.21 | 1.40 | 0.01312 |
| Q6GMV3 | Putative peptidyl-tRNA hydrolase PTRHD1 OS=Homo sapiens OX=9606 GN=PTRHD1 PE=1 SV=1 | 472.66 | 336.48 | 1.40 | 0.01328 |
| P10599 | Thioredoxin OS=Homo sapiens OX=9606 GN=TXN PE=1 SV=3 | 2044.74 | 1314.22 | 1.56 | 0.01340 |
| Q9BUT1 | 3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens OX=9606 GN=BDH2 PE=1 SV=2 | 1449.11 | 1073.46 | 1.35 | 0.01342 |
| Q8IVM0 | Isoform 2 of Coiled-coil domain-containing protein 50 OS=Homo sapiens OX=9606 GN=CCDC50 | 329.00 | 233.10 | 1.41 | 0.01345 |
| P62256 | Ubiquitin-conjugating enzyme E2 H OS=Homo sapiens OX=9606 GN=UBE2H PE=1 SV=1 | 294.12 | 211.92 | 1.39 | 0.01359 |
| P06753 | Isoform 6 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 | 125.65 | 89.61 | 1.40 | 0.01373 |
| P68032 | Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1 | 4806.37 | 3608.74 | 1.33 | 0.01384 |
| P12429 | Annexin A3 OS=Homo sapiens OX=9606 GN=ANXA3 PE=1 SV=3 | 944.41 | 763.07 | 1.24 | 0.01416 |
| Q96IU4 | Protein ABHD14B OS=Homo sapiens OX=9606 GN=ABHD14B PE=1 SV=1 | 487.88 | 288.37 | 1.69 | 0.01417 |
| Q96NT1 | Nucleosome assembly protein 1-like 5 OS=Homo sapiens OX=9606 GN=NAP1L5 PE=1 SV=1 | 420.40 | 268.61 | 1.57 | 0.01436 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens OX=9606 GN=KRT6B PE=1 SV=5 | 361.94 | 208.21 | 1.74 | 0.01447 |
| Q8NFU3 | Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 PE=1 SV=3 | 481.54 | 316.75 | 1.52 | 0.01448 |
| P62942 | Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens OX=9606 GN=FKBP1A PE=1 SV=2 | 209.95 | 120.26 | 1.75 | 0.01491 |
| Q6UUV9 | CREB-regulated transcription coactivator 1 OS=Homo sapiens OX=9606 GN=CRTC1 PE=1 SV=2 | 83.47 | 54.48 | 1.53 | 0.01508 |

| | | | | | |
|---|---|---|---|---|---|
| A0AVT1 | Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens OX=9606 GN=UBA6 PE=1 SV=1 | 1134.19 | 862.00 | 1.32 | 0.01533 |
| Q8WUY3 | Isoform 3 of Protein prune homolog 2 OS=Homo sapiens OX=9606 GN=PRUNE2 | 194.34 | 153.39 | 1.27 | 0.01535 |
| P00441 | Superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD1 PE=1 SV=2 | 8941.29 | 4901.83 | 1.82 | 0.01536 |
| O00287 | Regulatory factor X-associated protein OS=Homo sapiens OX=9606 GN=RFXAP PE=1 SV=1 | 11.53 | 7.35 | 1.57 | 0.01536 |
| P50225 | Sulfotransferase 1A1 OS=Homo sapiens OX=9606 GN=SULT1A1 PE=1 SV=3 | 1246.23 | 687.94 | 1.81 | 0.01557 |
| A0A0B4J2C3 | Translationally-controlled tumor protein OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1 | 1235.16 | 822.45 | 1.50 | 0.01565 |
| Q9Y3C6 | Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens OX=9606 GN=PPIL1 PE=1 SV=1 | 1666.88 | 1372.13 | 1.21 | 0.01575 |
| Q9NZN3 | EH domain-containing protein 3 OS=Homo sapiens OX=9606 GN=EHD3 PE=1 SV=2 | 1388.28 | 1149.33 | 1.21 | 0.01590 |
| P55283 | Cadherin-4 OS=Homo sapiens OX=9606 GN=CDH4 PE=2 SV=2 | 32.24 | 25.09 | 1.28 | 0.01591 |
| Q8WUW1 | Isoform 2 of Protein BRICK1 OS=Homo sapiens OX=9606 GN=BRK1 | 71.36 | 54.48 | 1.31 | 0.01610 |
| P31946 | 14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=3 | 3109.42 | 2450.13 | 1.27 | 0.01634 |
| Q9BVJ7 | Dual specificity protein phosphatase 23 OS=Homo sapiens OX=9606 GN=DUSP23 PE=1 SV=1 | 167.45 | 137.47 | 1.22 | 0.01645 |
| Q13542 | Eukaryotic translation initiation factor 4E-binding protein 2 OS=Homo sapiens OX=9606 GN=EIF4EBP2 PE=1 SV=1 | 18.90 | 11.30 | 1.67 | 0.01650 |
| P31939 | Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=3 | 3324.72 | 2451.98 | 1.36 | 0.01663 |
| F8WBA3 | Serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=PRKD1 PE=1 SV=1 | 21.28 | 17.00 | 1.25 | 0.01666 |
| O00764 | Pyridoxal kinase OS=Homo sapiens OX=9606 GN=PDXK PE=1 SV=1 | 878.05 | 692.86 | 1.27 | 0.01667 |
| Q13200 | 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PSMD2 PE=1 SV=3 | 5510.45 | 4577.83 | 1.20 | 0.01678 |
| Q9NPA8 | Transcription and mRNA export factor ENY2 OS=Homo sapiens OX=9606 GN=ENY2 PE=1 SV=1 | 223.02 | 174.99 | 1.27 | 0.01687 |
| Q15404 | Ras suppressor protein 1 OS=Homo sapiens OX=9606 GN=RSU1 PE=1 SV=3 | 775.98 | 646.36 | 1.20 | 0.01694 |
| Q9Y5N5 | Methyltransferase N6AMT1 OS=Homo sapiens OX=9606 GN=N6AMT1 PE=1 SV=4 | 63.32 | 46.73 | 1.36 | 0.01699 |
| P23763 | Vesicle-associated membrane protein 1 OS=Homo sapiens OX=9606 GN=VAMP1 PE=1 SV=1 | 157.11 | 117.05 | 1.34 | 0.01719 |
| P09493 | Isoform 9 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 | 5738.17 | 3811.32 | 1.51 | 0.01721 |
| Q16515 | Acid-sensing ion channel 2 OS=Homo sapiens OX=9606 GN=ASIC2 PE=1 SV=1 | 37.57 | 30.30 | 1.24 | 0.01722 |
| Q8WVJ2 | NudC domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NUDCD2 PE=1 SV=1 | 281.85 | 166.20 | 1.70 | 0.01737 |
| J3KN67 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=1 | 2389.74 | 1563.25 | 1.53 | 0.01743 |

| | | | | | |
|---|---|---|---|---|---|
| P07738 | Bisphosphoglycerate mutase OS=Homo sapiens OX=9606 GN=BPGM PE=1 SV=2 | 543.27 | 427.15 | 1.27 | 0.01747 |
| P0C6S8 | Leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 3 OS=Homo sapiens OX=9606 GN=LINGO3 PE=3 SV=1 | | 29.85 | 22.76 | 1.31173004 |
| E9PAV3 | Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 | 541.53 | 402.79 | 1.34 | 0.01754 |
| Q6PUV4 | Complexin-2 OS=Homo sapiens OX=9606 GN=CPLX2 PE=2 SV=2 | 213.96 | 131.18 | 1.63 | 0.01767 |
| Q96EI5 | Isoform 2 of Transcription elongation factor A protein-like 4 OS=Homo sapiens OX=9606 GN=TCEAL4 | 304.94 | 213.65 | 1.43 | 0.01769 |
| O75487 | Glypican-4 OS=Homo sapiens OX=9606 GN=GPC4 PE=1 SV=4 | 39.10 | 20.86 | 1.87 | 0.01785 |
| Q99733 | Isoform 2 of Nucleosome assembly protein 1-like 4 OS=Homo sapiens OX=9606 GN=NAP1L4 | 2060.27 | 1689.41 | 1.22 | 0.01786 |
| P52594 | Isoform 4 of Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=AGFG1 | 600.42 | 494.60 | 1.21 | 0.01788 |
| P52434 | DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H PE=1 SV=4 | 58.16 | 42.61 | 1.37 | 0.01789 |
| Q96RU3 | Formin-binding protein 1 OS=Homo sapiens OX=9606 GN=FNBP1 PE=1 SV=2 | 199.10 | 158.72 | 1.25 | 0.01846 |
| P30043 | Flavin reductase (NADPH) OS=Homo sapiens OX=9606 GN=BLVRB PE=1 SV=3 | 679.07 | 533.46 | 1.27 | 0.01847 |
| O95777 | U6 snRNA-associated Sm-like protein LSm8 OS=Homo sapiens OX=9606 GN=LSM8 PE=1 SV=3 | 526.83 | 419.00 | 1.26 | 0.01848 |
| O94888 | UBX domain-containing protein 7 OS=Homo sapiens OX=9606 GN=UBXN7 PE=1 SV=2 | 537.48 | 406.04 | 1.32 | 0.01851 |
| Q96FC7 | Phytanoyl-CoA hydroxylase-interacting protein-like OS=Homo sapiens OX=9606 GN=PHYHIPL PE=1 SV=3 | 3052.33 | 2221.45 | 1.37 | 0.01868 |
| Q9Y2Z0 | Protein SGT1 homolog OS=Homo sapiens OX=9606 GN=SUGT1 PE=1 SV=3 | 889.01 | 636.82 | 1.40 | 0.01871 |
| P13747 | HLA class I histocompatibility antigen, alpha chain E OS=Homo sapiens OX=9606 GN=HLA-E PE=1 SV=4 | 66.11 | 48.76 | 1.36 | 0.01884 |
| P46934 | Isoform 4 of E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens OX=9606 GN=NEDD4 | 19.32 | 14.43 | 1.34 | 0.01893 |
| P33241 | Isoform 3 of Lymphocyte-specific protein 1 OS=Homo sapiens OX=9606 GN=LSP1 | 68.78 | 46.00 | 1.50 | 0.01901 |
| Q96EB1 | Elongator complex protein 4 OS=Homo sapiens OX=9606 GN=ELP4 PE=1 SV=2 | 83.97 | 68.63 | 1.22 | 0.01904 |
| O43765 | Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens OX=9606 GN=SGTA PE=1 SV=1 | 1357.54 | 1074.89 | 1.26 | 0.01906 |
| Q08188 | Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens OX=9606 GN=TGM3 PE=1 SV=4 | 46.19 | 34.73 | 1.33 | 0.01917 |
| P16402 | Histone H1.3 OS=Homo sapiens OX=9606 GN=HIST1H1D PE=1 SV=2 | 82.42 | 65.56 | 1.26 | 0.01924 |
| P14324 | Farnesyl pyrophosphate synthase OS=Homo sapiens OX=9606 GN=FDPS PE=1 SV=4 | 944.67 | 660.04 | 1.43 | 0.01939 |
| Q8WVV4 | Isoform 1 of Protein POF1B OS=Homo sapiens OX=9606 GN=POF1B | 152.81 | 75.08 | 2.04 | 0.01951 |

| | | | | | |
|---|---|---|---|---|---|
| J3KPJ3 | Calcium/calmodulin-dependent protein kinase kinase 1 OS=Homo sapiens OX=9606 GN=CAMKK1 PE=1 SV=1 | 264.32 | 210.62 | 1.25 | 0.01971 |
| Q9UN36 | Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 PE=1 SV=2 | 1514.06 | 1220.32 | 1.24 | 0.01987 |
| Q7LG56 | Isoform 6 of Ribonucleoside-diphosphate reductase subunit M2 B OS=Homo sapiens OX=9606 GN=RRM2B | 420.22 | 339.50 | 1.24 | 0.01993 |
| Q9H2J4 | Phosducin-like protein 3 OS=Homo sapiens OX=9606 GN=PDCL3 PE=1 SV=1 | 115.08 | 81.65 | 1.41 | 0.01997 |
| Q6NZI2 | Caveolae-associated protein 1 OS=Homo sapiens OX=9606 GN=CAVIN1 PE=1 SV=1 | 1133.86 | 913.06 | 1.24 | 0.02000 |
| F5H211 | Ataxin-3 OS=Homo sapiens OX=9606 GN=ATXN3 PE=1 SV=2 | 36.80 | 25.58 | 1.44 | 0.02005 |
| O60493 | Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 PE=1 SV=3 | 317.87 | 239.98 | 1.32 | 0.02008 |
| P51668 | Ubiquitin-conjugating enzyme E2 D1 OS=Homo sapiens OX=9606 GN=UBE2D1 PE=1 SV=1 | 173.55 | 130.03 | 1.33 | 0.02017 |
| P08397 | Porphobilinogen deaminase OS=Homo sapiens OX=9606 GN=HMBS PE=1 SV=2 | 11.04 | 7.30 | 1.51 | 0.02027 |
| Q9GZP9 | Derlin-2 OS=Homo sapiens OX=9606 GN=DERL2 PE=1 SV=1 | 77.25 | 60.74 | 1.27 | 0.02029 |
| Q9P2X3 | Protein IMPACT OS=Homo sapiens OX=9606 GN=IMPACT PE=1 SV=2 | 174.19 | 137.56 | 1.27 | 0.02031 |
| Q9HBL8 | NmrA-like family domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NMRAL1 PE=1 SV=1 | 132.05 | 95.42 | 1.38 | 0.02032 |
| Q14643 | Inositol 1,4,5-trisphosphate receptor type 1 OS=Homo sapiens OX=9606 GN=ITPR1 PE=1 SV=3 | 14.20 | 10.66 | 1.33 | 0.02056 |
| Q8N806 | Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens OX=9606 GN=UBR7 PE=1 SV=2 | 342.00 | 277.05 | 1.23 | 0.02058 |
| Q6ZV70 | LanC-like protein 3 OS=Homo sapiens OX=9606 GN=LANCL3 PE=2 SV=2 | 9.15 | 4.55 | 2.01 | 0.02059 |
| Q9Y2Y0 | ADP-ribosylation factor-like protein 2-binding protein OS=Homo sapiens OX=9606 GN=ARL2BP PE=1 SV=1 | 126.64 | 98.19 | 1.29 | 0.02062 |
| Q96NL8 | Protein C8orf37 OS=Homo sapiens OX=9606 GN=C8orf37 PE=1 SV=1 | 205.81 | 132.73 | 1.55 | 0.02063 |
| Q05209 | Tyrosine-protein phosphatase non-receptor type 12 OS=Homo sapiens OX=9606 GN=PTPN12 PE=1 SV=3 | 35.49 | 27.45 | 1.29 | 0.02085 |
| P62328 | Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2 | 295.95 | 153.78 | 1.92 | 0.02087 |
| Q5SQI0 | Alpha-tubulin N-acetyltransferase 1 OS=Homo sapiens OX=9606 GN=ATAT1 PE=1 SV=1 | 231.81 | 175.67 | 1.32 | 0.02093 |
| I3L504 | Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=1 | 1338.85 | 956.16 | 1.40 | 0.02110 |
| P01040 | Cystatin-A OS=Homo sapiens OX=9606 GN=CSTA PE=1 SV=1 | 198.20 | 141.32 | 1.40 | 0.02124 |
| Q9UHD9 | Ubiquilin-2 OS=Homo sapiens OX=9606 GN=UBQLN2 PE=1 SV=2 | 988.40 | 801.92 | 1.23 | 0.02130 |
| A0A1B0GUS4 | Ubiquitin-conjugating enzyme E2 L5 OS=Homo sapiens OX=9606 GN=UBE2L5 PE=2 SV=1 | 43.70 | 29.83 | 1.47 | 0.02141 |
| Q969E8 | Pre-rRNA-processing protein TSR2 homolog OS=Homo sapiens OX=9606 GN=TSR2 PE=1 SV=1 | 310.82 | 236.58 | 1.31 | 0.02154 |

| | | | | | |
|---|---|---|---|---|---|
| O15145 | Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens OX=9606 GN=ARPC3 PE=1 SV=3 | 334.10 | 276.82 | 1.21 | 0.02161 |
| Q9BXS9 | Solute carrier family 26 member 6 OS=Homo sapiens OX=9606 GN=SLC26A6 PE=1 SV=1 | 9.46 | 6.65 | 1.42 | 0.02163 |
| Q9UI26 | Isoform 2 of Importin-11 OS=Homo sapiens OX=9606 GN=IPO11 | 99.11 | 76.42 | 1.30 | 0.02165 |
| O75223 | Gamma-glutamylcyclotransferase OS=Homo sapiens OX=9606 GN=GGCT PE=1 SV=1 | 838.28 | 511.58 | 1.64 | 0.02171 |
| P25391 | Laminin subunit alpha-1 OS=Homo sapiens OX=9606 GN=LAMA1 PE=1 SV=2 | 24.89 | 20.10 | 1.24 | 0.02178 |
| Q9UK45 | U6 snRNA-associated Sm-like protein LSm7 OS=Homo sapiens OX=9606 GN=LSM7 PE=1 SV=1 | 432.90 | 345.80 | 1.25 | 0.02185 |
| Q04323 | UBX domain-containing protein 1 OS=Homo sapiens OX=9606 GN=UBXN1 PE=1 SV=2 | 662.96 | 485.60 | 1.37 | 0.02188 |
| A6NGJ0 | Dynein light chain Tctex-type 3 OS=Homo sapiens OX=9606 GN=DYNLT3 PE=1 SV=1 | 8.39 | 4.77 | 1.76 | 0.02209 |
| Q9HAB8 | Phosphopantothenate--cysteine ligase OS=Homo sapiens OX=9606 GN=PPCS PE=1 SV=2 | 456.39 | 327.88 | 1.39 | 0.02219 |
| Q96GX2 | Ataxin-7-like protein 3B OS=Homo sapiens OX=9606 GN=ATXN7L3B PE=1 SV=2 | 51.49 | 40.80 | 1.26 | 0.02219 |
| Q99961 | Endophilin-A2 OS=Homo sapiens OX=9606 GN=SH3GL1 PE=1 SV=1 | 565.35 | 453.68 | 1.25 | 0.02228 |
| P31751 | RAC-beta serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=AKT2 PE=1 SV=2 | 118.23 | 97.80 | 1.21 | 0.02233 |
| O95817 | BAG family molecular chaperone regulator 3 OS=Homo sapiens OX=9606 GN=BAG3 PE=1 SV=3 | 1493.09 | 1144.22 | 1.30 | 0.02252 |
| O14933 | Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens OX=9606 GN=UBE2L6 PE=1 SV=4 | 54.85 | 40.67 | 1.35 | 0.02254 |
| Q8N9V3 | WD repeat, SAM and U-box domain-containing protein 1 OS=Homo sapiens OX=9606 GN=WDSUB1 PE=1 SV=3 | 48.04 | 32.99 | 1.46 | 0.02270 |
| Q9UJY1 | Heat shock protein beta-8 OS=Homo sapiens OX=9606 GN=HSPB8 PE=1 SV=1 | 1119.54 | 905.68 | 1.24 | 0.02284 |
| Q9NR19 | Isoform 2 of Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens OX=9606 GN=ACSS2 | 264.03 | 211.87 | 1.25 | 0.02297 |
| P34913 | Bifunctional epoxide hydrolase 2 OS=Homo sapiens OX=9606 GN=EPHX2 PE=1 SV=2 | 3171.92 | 2341.45 | 1.35 | 0.02298 |
| P42773 | Cyclin-dependent kinase 4 inhibitor C OS=Homo sapiens OX=9606 GN=CDKN2C PE=1 SV=1 | 62.40 | 45.01 | 1.39 | 0.02301 |
| Q8TAA9 | Vang-like protein 1 OS=Homo sapiens OX=9606 GN=VANGL1 PE=1 SV=1 | 41.58 | 30.67 | 1.36 | 0.02301 |
| P20039 | HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens OX=9606 GN=HLA-DRB1 PE=1 SV=1 | 294.89 | 130.80 | 2.25 | 0.02316 |
| Q13158 | FAS-associated death domain protein OS=Homo sapiens OX=9606 GN=FADD PE=1 SV=1 | 118.59 | 85.52 | 1.39 | 0.02337 |
| Q14118 | Dystroglycan OS=Homo sapiens OX=9606 GN=DAG1 PE=1 SV=2 | 436.47 | 355.64 | 1.23 | 0.02420 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| P51965 | Ubiquitin-conjugating enzyme E2 E1 OS=Homo sapiens OX=9606 GN=UBE2E1 PE=1 SV=1 | 369.01 | 239.14 | 1.54 | 0.02422 |
| P20591 | Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens OX=9606 GN=MX1 PE=1 SV=4 | 70.00 | 57.46 | 1.22 | 0.02423 |
| P43250 | Isoform GRK6B of G protein-coupled receptor kinase 6 OS=Homo sapiens OX=9606 GN=GRK6 | 34.21 | 26.81 | 1.28 | 0.02435 |
| Q7Z6K5 | Isoform C15orf38-AP3S2 of Arpin OS=Homo sapiens OX=9606 GN=ARPIN | 561.07 | 426.69 | 1.31 | 0.02442 |
| A6NKN8 | Purkinje cell protein 4-like protein 1 OS=Homo sapiens OX=9606 GN=PCP4L1 PE=3 SV=3 | 251.18 | 145.43 | 1.73 | 0.02462 |
| A0A2R8YFE2 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 | 211.72 | 160.99 | 1.32 | 0.02468 |
| Q9BTV5 | Fibronectin type III and SPRY domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FSD1 PE=1 SV=1 | 280.54 | 228.71 | 1.23 | 0.02473 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3 | 4832.84 | 2921.26 | 1.65 | 0.02473 |
| Q9NUP1 | Biogenesis of lysosome-related organelles complex 1 subunit 4 OS=Homo sapiens OX=9606 GN=BLOC1S4 PE=1 SV=1 | 133.99 | 110.25 | 1.22 | 0.02490 |
| Q86WV7 | CCDC43 protein OS=Homo sapiens OX=9606 GN=CCDC43 PE=1 SV=1 | 276.11 | 179.55 | 1.54 | 0.02493 |
| Q93045 | Isoform 2 of Stathmin-2 OS=Homo sapiens OX=9606 GN=STMN2 | 47.31 | 39.33 | 1.20 | 0.02551 |
| Q5JS54 | Isoform 2 of Proteasome assembly chaperone 4 OS=Homo sapiens OX=9606 GN=PSMG4 | 9.78 | 6.98 | 1.40 | 0.02556 |
| O76070 | Gamma-synuclein OS=Homo sapiens OX=9606 GN=SNCG PE=1 SV=2 | 3826.18 | 2568.81 | 1.49 | 0.02565 |
| P40855 | Peroxisomal biogenesis factor 19 OS=Homo sapiens OX=9606 GN=PEX19 PE=1 SV=1 | 664.76 | 477.10 | 1.39 | 0.02573 |
| Q8WV99 | AN1-type zinc finger protein 2B OS=Homo sapiens OX=9606 GN=ZFAND2B PE=1 SV=1 | 26.35 | 21.03 | 1.25 | 0.02601 |
| Q9UBE0 | SUMO-activating enzyme subunit 1 OS=Homo sapiens OX=9606 GN=SAE1 PE=1 SV=1 | 1328.42 | 976.11 | 1.36 | 0.02615 |
| A6NDU8 | UPF0600 protein C5orf51 OS=Homo sapiens OX=9606 GN=C5orf51 PE=1 SV=1 | 237.13 | 180.63 | 1.31 | 0.02620 |
| O60443 | Gasdermin-E OS=Homo sapiens OX=9606 GN=GSDME PE=1 SV=2 | 172.99 | 135.62 | 1.28 | 0.02642 |
| A0MZ66 | Isoform 3 of Shootin-1 OS=Homo sapiens OX=9606 GN=SHTN1 | 774.52 | 609.52 | 1.27 | 0.02644 |
| Q712K3 | Ubiquitin-conjugating enzyme E2 R2 OS=Homo sapiens OX=9606 GN=UBE2R2 PE=1 SV=1 | 125.34 | 91.63 | 1.37 | 0.02652 |
| Q96K17 | Transcription factor BTF3 homolog 4 OS=Homo sapiens OX=9606 GN=BTF3L4 PE=1 SV=1 | 118.58 | 83.83 | 1.41 | 0.02659 |
| P84085 | ADP-ribosylation factor 5 OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=2 | 489.18 | 398.02 | 1.23 | 0.02666 |
| Q9UI15 | Transgelin-3 OS=Homo sapiens OX=9606 GN=TAGLN3 PE=1 SV=2 | 2887.73 | 2231.51 | 1.29 | 0.02692 |
| Q8WZA0 | Isoform 2 of Protein LZIC OS=Homo sapiens OX=9606 GN=LZIC | 875.67 | 513.65 | 1.70 | 0.02697 |
| Q9UPR0 | Inactive phospholipase C-like protein 2 OS=Homo sapiens OX=9606 GN=PLCL2 PE=1 SV=2 | 71.79 | 59.11 | 1.21 | 0.02699 |

| | | | | | |
|---|---|---|---|---|---|
| P81605 | Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2 | 344.22 | 228.39 | 1.51 | 0.02764 |
| Q15056 | Eukaryotic translation initiation factor 4H OS=Homo sapiens OX=9606 GN=EIF4H PE=1 SV=5 | 1466.23 | 1015.93 | 1.44 | 0.02798 |
| U3KQP1 | Asparagine synthetase domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ASNSD1 PE=1 SV=1 | 175.68 | 97.40 | 1.80 | 0.02798 |
| E9PGN7 | Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 PE=1 SV=1 | 413.30 | 290.92 | 1.42 | 0.02801 |
| Q13228 | Isoform 4 of Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 | 3216.48 | 2278.79 | 1.41 | 0.02813 |
| P07992 | DNA excision repair protein ERCC-1 OS=Homo sapiens OX=9606 GN=ERCC1 PE=1 SV=1 | 61.09 | 42.17 | 1.45 | 0.02819 |
| P55899 | IgG receptor FcRn large subunit p51 OS=Homo sapiens OX=9606 GN=FCGRT PE=1 SV=1 | 30.23 | 19.50 | 1.55 | 0.02823 |
| P28676 | Grancalcin OS=Homo sapiens OX=9606 GN=GCA PE=1 SV=2 | 574.29 | 465.20 | 1.23 | 0.02870 |
| J3KR44 | Ubiquitin thioesterase OS=Homo sapiens OX=9606 GN=OTUB1 PE=1 SV=2 | 789.81 | 587.72 | 1.34 | 0.02879 |
| O60927 | E3 ubiquitin-protein ligase PPP1R11 OS=Homo sapiens OX=9606 GN=PPP1R11 PE=1 SV=1 | 156.67 | 126.28 | 1.24 | 0.02885 |
| P52564 | Dual specificity mitogen-activated protein kinase kinase 6 OS=Homo sapiens OX=9606 GN=MAP2K6 PE=1 SV=1 | 755.76 | 564.72 | 1.34 | 0.02923 |
| P45985 | Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens OX=9606 GN=MAP2K4 | 463.04 | 359.87 | 1.29 | 0.02933 |
| P78560 | Death domain-containing protein CRADD OS=Homo sapiens OX=9606 GN=CRADD PE=1 SV=1 | 95.79 | 74.65 | 1.28 | 0.02935 |
| F8W031 | DUF3456 domain-containing protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 | 1160.13 | 915.99 | 1.27 | 0.02938 |
| O14907 | Tax1-binding protein 3 OS=Homo sapiens OX=9606 GN=TAX1BP3 PE=1 SV=2 | 89.59 | 70.08 | 1.28 | 0.02945 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3 | 4034.84 | 2131.10 | 1.89 | 0.02950 |
| P14317 | Hematopoietic lineage cell-specific protein OS=Homo sapiens OX=9606 GN=HCLS1 PE=1 SV=3 | 93.07 | 64.47 | 1.44 | 0.02969 |
| P60842 | Eukaryotic initiation factor 4A-I OS=Homo sapiens OX=9606 GN=EIF4A1 PE=1 SV=1 | 2488.42 | 2027.15 | 1.23 | 0.03003 |
| P31944 | Caspase-14 OS=Homo sapiens OX=9606 GN=CASP14 PE=1 SV=2 | 76.33 | 57.56 | 1.33 | 0.03062 |
| Q15714 | TSC22 domain family protein 1 OS=Homo sapiens OX=9606 GN=TSC22D1 PE=1 SV=3 | 426.74 | 307.19 | 1.39 | 0.03065 |
| Q15121 | Isoform 2 of Astrocytic phosphoprotein PEA-15 OS=Homo sapiens OX=9606 GN=PEA15 | 1974.43 | 1233.39 | 1.60 | 0.03080 |
| A8MUM1 | EARP and GARP complex-interacting protein 1 OS=Homo sapiens OX=9606 GN=EIPR1 PE=1 SV=2 | 510.04 | 421.59 | 1.21 | 0.03091 |
| Q9BRG1 | Vacuolar protein-sorting-associated protein 25 OS=Homo sapiens OX=9606 GN=VPS25 PE=1 SV=1 | 534.56 | 440.77 | 1.21 | 0.03113 |

| | | | | | |
|---|---|---|---|---|---|
| Q9BPY3 | Protein FAM118B OS=Homo sapiens OX=9606 GN=FAM118B PE=1 SV=1 | 145.27 | 119.26 | 1.22 | 0.03134 |
| P46439 | Glutathione S-transferase Mu 5 OS=Homo sapiens OX=9606 GN=GSTM5 PE=1 SV=3 | 560.41 | 354.95 | 1.58 | 0.03136 |
| E9PSI1 | Transmembrane 9 superfamily member OS=Homo sapiens OX=9606 PE=3 SV=1 | 313.85 | 233.32 | 1.35 | 0.03162 |
| Q9H425 | Uncharacterized protein C1orf198 OS=Homo sapiens OX=9606 GN=C1orf198 PE=1 SV=1 | 134.06 | 105.33 | 1.27 | 0.03174 |
| Q8WUX9 | Charged multivesicular body protein 7 OS=Homo sapiens OX=9606 GN=CHMP7 PE=1 SV=1 | 8.28 | 5.60 | 1.48 | 0.03192 |
| P13797 | Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4 | 1562.55 | 1183.35 | 1.32 | 0.03218 |
| P11215 | Isoform 2 of Integrin alpha-M OS=Homo sapiens OX=9606 GN=ITGAM | 79.11 | 62.72 | 1.26 | 0.03222 |
| A0A1B0GWK2 | Kazrin OS=Homo sapiens OX=9606 GN=KAZN PE=1 SV=1 | 265.05 | 210.82 | 1.26 | 0.03224 |
| Q969G6 | Riboflavin kinase OS=Homo sapiens OX=9606 GN=RFK PE=1 SV=2 | 277.71 | 213.14 | 1.30 | 0.03226 |
| P00966 | Argininosuccinate synthase OS=Homo sapiens OX=9606 GN=ASS1 PE=1 SV=2 | 1994.42 | 1544.51 | 1.29 | 0.03241 |
| Q8WTS6 | Histone-lysine N-methyltransferase SETD7 OS=Homo sapiens OX=9606 GN=SETD7 PE=1 SV=1 | 195.29 | 151.71 | 1.29 | 0.03250 |
| P98172 | Ephrin-B1 OS=Homo sapiens OX=9606 GN=EFNB1 PE=1 SV=1 | 168.84 | 139.67 | 1.21 | 0.03252 |
| P06396 | Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1 | 8635.00 | 7169.94 | 1.20 | 0.03259 |
| Q02413 | Desmoglein-1 OS=Homo sapiens OX=9606 GN=DSG1 PE=1 SV=2 | 434.04 | 298.91 | 1.45 | 0.03271 |
| P51570 | Isoform 2 of Galactokinase OS=Homo sapiens OX=9606 GN=GALK1 | 726.70 | 535.20 | 1.36 | 0.03295 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6 | 10437.18 | 6494.34 | 1.61 | 0.03298 |
| Q9Y342 | Plasmolipin OS=Homo sapiens OX=9606 GN=PLLP PE=1 SV=1 | 35.61 | 29.30 | 1.22 | 0.03380 |
| Q86TA1 | MOB kinase activator 3B OS=Homo sapiens OX=9606 GN=MOB3B PE=1 SV=2 | 30.99 | 20.28 | 1.53 | 0.03385 |
| O60268 | Uncharacterized protein KIAA0513 OS=Homo sapiens OX=9606 GN=KIAA0513 PE=1 SV=1 | 871.30 | 720.07 | 1.21 | 0.03400 |
| P48539 | Calmodulin regulator protein PCP4 OS=Homo sapiens OX=9606 GN=PCP4 PE=1 SV=3 | 514.38 | 317.59 | 1.62 | 0.03410 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2 | 10383.09 | 6164.24 | 1.68 | 0.03418 |
| Q15126 | Phosphomevalonate kinase OS=Homo sapiens OX=9606 GN=PMVK PE=1 SV=3 | 660.06 | 481.19 | 1.37 | 0.03432 |
| P61204 | ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=2 | 2786.01 | 1835.24 | 1.52 | 0.03440 |
| Q8TED1 | Probable glutathione peroxidase 8 OS=Homo sapiens OX=9606 GN=GPX8 PE=1 SV=2 | 82.24 | 62.44 | 1.32 | 0.03469 |
| Q14240 | Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 | 1031.39 | 789.42 | 1.31 | 0.03475 |
| J3QLJ5 | MIF4G domain-containing protein OS=Homo sapiens OX=9606 GN=MIF4GD PE=1 SV=1 | 130.29 | 104.18 | 1.25 | 0.03497 |

| | | | | | |
|---|---|---|---|---|---|
| Q9BTL3 | RNA guanine-N7 methyltransferase activating subunit OS=Homo sapiens OX=9606 GN=RAMAC PE=1 SV=1 | 224.64 | 120.09 | 1.87 | 0.03497 |
| Q9UHV9 | Prefoldin subunit 2 OS=Homo sapiens OX=9606 GN=PFDN2 PE=1 SV=1 | 1293.85 | 975.68 | 1.33 | 0.03500 |
| Q99447 | Isoform 3 of Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens OX=9606 GN=PCYT2 | 693.88 | 528.01 | 1.31 | 0.03510 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4 | 6367.18 | 3638.68 | 1.75 | 0.03515 |
| P40616 | ADP-ribosylation factor-like protein 1 OS=Homo sapiens OX=9606 GN=ARL1 PE=1 SV=1 | 165.49 | 114.22 | 1.45 | 0.03521 |
| Q9Y5Z4 | Heme-binding protein 2 OS=Homo sapiens OX=9606 GN=HEBP2 PE=1 SV=1 | 1379.74 | 884.12 | 1.56 | 0.03524 |
| Q6ZVX7 | F-box only protein 50 OS=Homo sapiens OX=9606 GN=NCCRP1 PE=1 SV=1 | 59.00 | 45.25 | 1.30 | 0.03524 |
| Q9UBT2 | SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 GN=UBA2 PE=1 SV=2 | 1166.84 | 902.58 | 1.29 | 0.03551 |
| A0AVF1 | Intraflagellar transport protein 56 OS=Homo sapiens OX=9606 GN=TTC26 PE=2 SV=1 | 13.21 | 8.35 | 1.58 | 0.03556 |
| P12277 | Creatine kinase B-type OS=Homo sapiens OX=9606 GN=CKB PE=1 SV=1 | 35126.72 | 23959.06 | 1.47 | 0.03582 |
| P19256 | Lymphocyte function-associated antigen 3 OS=Homo sapiens OX=9606 GN=CD58 PE=1 SV=1 | 70.69 | 58.24 | 1.21 | 0.03586 |
| P13646 | Keratin, type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 PE=1 SV=4 | 253.72 | 180.84 | 1.40 | 0.03613 |
| O95999 | B-cell lymphoma/leukemia 10 OS=Homo sapiens OX=9606 GN=BCL10 PE=1 SV=1 | 23.49 | 18.33 | 1.28 | 0.03646 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3 | 9921.25 | 5593.39 | 1.77 | 0.03667 |
| Q5JVS0 | Intracellular hyaluronan-binding protein 4 OS=Homo sapiens OX=9606 GN=HABP4 PE=1 SV=1 | 116.04 | 90.64 | 1.28 | 0.03670 |
| O75506 | Heat shock factor-binding protein 1 OS=Homo sapiens OX=9606 GN=HSBP1 PE=1 SV=1 | 17.43 | 9.84 | 1.77 | 0.03691 |
| P30414 | NK-tumor recognition protein OS=Homo sapiens OX=9606 GN=NKTR PE=1 SV=2 | 20.08 | 15.05 | 1.33 | 0.03692 |
| Q9NV35 | Nucleotide triphosphate diphosphatase NUDT15 OS=Homo sapiens OX=9606 GN=NUDT15 PE=1 SV=1 | 71.20 | 38.17 | 1.87 | 0.03697 |
| P0C870 | Bifunctional peptidase and (3S)-lysyl hydroxylase JMJD7 OS=Homo sapiens OX=9606 GN=JMJD7 PE=1 SV=1 | 186.36 | 134.88 | 1.38 | 0.03718 |
| Q9H3K6 | BolA-like protein 2 OS=Homo sapiens OX=9606 GN=BOLA2 PE=1 SV=1 | 306.06 | 241.59 | 1.27 | 0.03720 |
| Q8NFH8 | RalBP1-associated Eps domain-containing protein 2 OS=Homo sapiens OX=9606 GN=REPS2 PE=1 SV=2 | 89.44 | 35.85 | 2.49 | 0.03721 |
| Q9NP86 | Calcium-binding protein 5 OS=Homo sapiens OX=9606 GN=CABP5 PE=1 SV=1 | 46.90 | 38.17 | 1.23 | 0.03723 |
| Q86YZ3 | Hornerin OS=Homo sapiens OX=9606 GN=HRNR PE=1 SV=2 | 113.61 | 62.79 | 1.81 | 0.03737 |
| Q5D862 | Filaggrin-2 OS=Homo sapiens OX=9606 GN=FLG2 PE=1 SV=1 | 128.65 | 78.32 | 1.64 | 0.03746 |
| O14618 | Copper chaperone for superoxide dismutase OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1 | 1308.90 | 962.41 | 1.36 | 0.03752 |

| | | | | | |
|---|---|---|---|---|---|
| O43657 | Tetraspanin-6 OS=Homo sapiens OX=9606 GN=TSPAN6 PE=1 SV=1 | 99.96 | 73.20 | 1.37 | 0.03809 |
| B0QZ18 | Copine-1 OS=Homo sapiens OX=9606 GN=CPNE1 PE=1 SV=1 | 610.40 | 477.34 | 1.28 | 0.03824 |
| Q9Y259 | Choline/ethanolamine kinase OS=Homo sapiens OX=9606 GN=CHKB PE=1 SV=3 | 176.56 | 143.65 | 1.23 | 0.03848 |
| P15531 | Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 | 146.42 | 83.44 | 1.75 | 0.03862 |
| B8ZZ50 | Eukaryotic translation initiation factor 4E type 2 OS=Homo sapiens OX=9606 GN=EIF4E2 PE=1 SV=1 | 156.85 | 112.61 | 1.39 | 0.03869 |
| P13929 | Isoform 2 of Beta-enolase OS=Homo sapiens OX=9606 GN=ENO3 | 20.90 | 17.15 | 1.22 | 0.03876 |
| P23443 | Ribosomal protein S6 kinase beta-1 OS=Homo sapiens OX=9606 GN=RPS6KB1 PE=1 SV=2 | 113.58 | 87.96 | 1.29 | 0.03893 |
| P36404 | ADP-ribosylation factor-like protein 2 OS=Homo sapiens OX=9606 GN=ARL2 PE=1 SV=4 | 433.15 | 339.88 | 1.27 | 0.03916 |
| P36639 | 7,8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens OX=9606 GN=NUDT1 PE=1 SV=3 | 58.19 | 36.59 | 1.59 | 0.03938 |
| E9PNP3 | Mth938 domain-containing protein OS=Homo sapiens OX=9606 GN=AAMDC PE=1 SV=1 | 214.37 | 115.64 | 1.85 | 0.03961 |
| Q5VW32 | BRO1 domain-containing protein BROX OS=Homo sapiens OX=9606 GN=BROX PE=1 SV=1 | 640.64 | 470.31 | 1.36 | 0.03991 |
| P23490 | Loricrin OS=Homo sapiens OX=9606 GN=LOR PE=1 SV=2 | 93.17 | 46.84 | 1.99 | 0.03991 |
| P24666 | Isoform 2 of Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 | 8.23 | 5.08 | 1.62 | 0.03997 |
| Q9Y243 | RAC-gamma serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=AKT3 PE=1 SV=1 | 123.26 | 94.52 | 1.30 | 0.04008 |
| A0A087WSV8 | Nucleobindin 2, isoform CRA_b OS=Homo sapiens OX=9606 GN=NUCB2 PE=1 SV=1 | 1430.99 | 1120.89 | 1.28 | 0.04018 |
| P29762 | Cellular retinoic acid-binding protein 1 OS=Homo sapiens OX=9606 GN=CRABP1 PE=1 SV=2 | 14415.60 | 8282.52 | 1.74 | 0.04022 |
| P51452 | Dual specificity protein phosphatase 3 OS=Homo sapiens OX=9606 GN=DUSP3 PE=1 SV=1 | 475.50 | 334.88 | 1.42 | 0.04037 |
| P28161 | Glutathione S-transferase Mu 2 OS=Homo sapiens OX=9606 GN=GSTM2 PE=1 SV=2 | 3962.76 | 2277.58 | 1.74 | 0.04060 |
| P12004 | Proliferating cell nuclear antigen OS=Homo sapiens OX=9606 GN=PCNA PE=1 SV=1 | 1124.53 | 833.21 | 1.35 | 0.04061 |
| P47813 | Eukaryotic translation initiation factor 1A, X-chromosomal OS=Homo sapiens OX=9606 GN=EIF1AX PE=1 SV=2 | 1280.23 | 961.91 | 1.33 | 0.04073 |
| P09668 | Pro-cathepsin H OS=Homo sapiens OX=9606 GN=CTSH PE=1 SV=4 | 104.62 | 82.52 | 1.27 | 0.04103 |
| Q5TIG5 | Afadin OS=Homo sapiens OX=9606 GN=AFDN PE=1 SV=1 | 8.50 | 5.74 | 1.48 | 0.04111 |
| Q9NYB0 | Telomeric repeat-binding factor 2-interacting protein 1 OS=Homo sapiens OX=9606 GN=TERF2IP PE=1 SV=1 | 1488.03 | 1190.90 | 1.25 | 0.04114 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| A0A0B4J2B5 | Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3OR16-9 PE=1 SV=1 | 168.23 | 105.74 | 1.59 | 0.04116 |
| P35813 | Isoform 3 of Protein phosphatase 1A OS=Homo sapiens OX=9606 GN=PPM1A | 1577.44 | 1205.51 | 1.31 | 0.04121 |
| P49189 | Isoform 3 of 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1 | 24.97 | 20.39 | 1.22 | 0.04135 |
| Q9HAT2 | Sialate O-acetylesterase OS=Homo sapiens OX=9606 GN=SIAE PE=1 SV=1 | 151.30 | 119.24 | 1.27 | 0.04142 |
| P07858 | Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3 | 1220.13 | 1010.73 | 1.21 | 0.04143 |
| P43034 | Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens OX=9606 GN=PAFAH1B1 PE=1 SV=2 | 2589.92 | 2101.44 | 1.23 | 0.04143 |
| Q9NT62 | Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens OX=9606 GN=ATG3 PE=1 SV=1 | 412.08 | 329.13 | 1.25 | 0.04156 |
| E9PC47 | LIM domain kinase 1 OS=Homo sapiens OX=9606 GN=LIMK1 PE=1 SV=1 | 38.26 | 30.56 | 1.25 | 0.04167 |
| Q13043 | Serine/threonine-protein kinase 4 OS=Homo sapiens OX=9606 GN=STK4 PE=1 SV=2 | 83.53 | 68.29 | 1.22 | 0.04175 |
| A0A0A0MS69 | Phosphodiesterase OS=Homo sapiens OX=9606 GN=PDE1C PE=1 SV=1 | 105.93 | 86.04 | 1.23 | 0.04178 |
| Q5KU26 | Collectin-12 OS=Homo sapiens OX=9606 GN=COLEC12 PE=1 SV=3 | 802.09 | 544.68 | 1.47 | 0.04204 |
| A0A087X0R6 | Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 PE=1 SV=1 | 711.04 | 536.29 | 1.33 | 0.04230 |
| P60981 | Destrin OS=Homo sapiens OX=9606 GN=DSTN PE=1 SV=3 | 1974.07 | 1553.94 | 1.27 | 0.04231 |
| P36507 | Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens OX=9606 GN=MAP2K2 PE=1 SV=1 | 1446.42 | 1144.63 | 1.26 | 0.04235 |
| O95372 | Acyl-protein thioesterase 2 OS=Homo sapiens OX=9606 GN=LYPLA2 PE=1 SV=1 | 649.73 | 526.50 | 1.23 | 0.04250 |
| P49354 | Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens OX=9606 GN=FNTA PE=1 SV=1 | 141.23 | 108.31 | 1.30 | 0.04259 |
| O15540 | Fatty acid-binding protein, brain OS=Homo sapiens OX=9606 GN=FABP7 PE=1 SV=3 | 5465.08 | 3199.43 | 1.71 | 0.04267 |
| Q00169 | Phosphatidylinositol transfer protein alpha isoform OS=Homo sapiens OX=9606 GN=PITPNA PE=1 SV=2 | 2235.76 | 1794.18 | 1.25 | 0.04282 |
| P54727 | UV excision repair protein RAD23 homolog B OS=Homo sapiens OX=9606 GN=RAD23B PE=1 SV=1 | 2026.91 | 1628.90 | 1.24 | 0.04306 |
| Q9NWY4 | Histone PARylation factor 1 OS=Homo sapiens OX=9606 GN=HPF1 PE=1 SV=2 | 194.51 | 152.21 | 1.28 | 0.04307 |
| A0A087WYT3 | Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 PE=1 SV=1 | 1395.13 | 931.29 | 1.50 | 0.04363 |
| P55285 | Cadherin-6 OS=Homo sapiens OX=9606 GN=CDH6 PE=1 SV=1 | 53.52 | 38.05 | 1.41 | 0.04370 |
| P49441 | Inositol polyphosphate 1-phosphatase OS=Homo sapiens OX=9606 GN=INPP1 PE=1 SV=1 | 429.04 | 321.00 | 1.34 | 0.04405 |
| P20930 | Filaggrin OS=Homo sapiens OX=9606 GN=FLG PE=1 SV=3 | 237.67 | 167.91 | 1.42 | 0.04424 |
| J3KPD3 | RNA binding motif protein 7, isoform CRA_c OS=Homo sapiens OX=9606 GN=RBM7 PE=1 SV=1 | 57.02 | 39.37 | 1.45 | 0.04429 |

| | | | | | |
|---|---|---|---|---|---|
| Q96MH2 | Protein HEXIM2 OS=Homo sapiens OX=9606 GN=HEXIM2 PE=1 SV=1 | 47.02 | 38.79 | 1.21 | 0.04438 |
| O95154 | Aflatoxin B1 aldehyde reductase member 3 OS=Homo sapiens OX=9606 GN=AKR7A3 PE=1 SV=2 | 207.44 | 153.24 | 1.35 | 0.04463 |
| P12271 | Retinaldehyde-binding protein 1 OS=Homo sapiens OX=9606 GN=RLBP1 PE=1 SV=2 | 12553.86 | 8152.54 | 1.54 | 0.04464 |
| P29508 | Serpin B3 OS=Homo sapiens OX=9606 GN=SERPINB3 PE=1 SV=2 | 142.21 | 102.68 | 1.38 | 0.04472 |
| P20810 | Isoform 6 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST | 1405.33 | 943.52 | 1.49 | 0.04493 |
| Q08554 | Isoform 1B of Desmocollin-1 OS=Homo sapiens OX=9606 GN=DSC1 | 197.63 | 106.71 | 1.85 | 0.04497 |
| O75348 | V-type proton ATPase subunit G 1 OS=Homo sapiens OX=9606 GN=ATP6V1G1 PE=1 SV=3 | 1372.85 | 1032.46 | 1.33 | 0.04513 |
| O43396 | Thioredoxin-like protein 1 OS=Homo sapiens OX=9606 GN=TXNL1 PE=1 SV=3 | 1165.52 | 951.25 | 1.23 | 0.04514 |
| P23434 | Glycine cleavage system H protein, mitochondrial OS=Homo sapiens OX=9606 GN=GCSH PE=1 SV=2 | 468.64 | 370.74 | 1.26 | 0.04516 |
| Q6NYC1 | Isoform 3 of Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Homo sapiens OX=9606 GN=JMJD6 | 145.67 | 120.56 | 1.21 | 0.04525 |
| Q8NBR6 | Ubiquitin carboxyl-terminal hydrolase MINDY-2 OS=Homo sapiens OX=9606 GN=MINDY2 PE=1 SV=2 | 74.04 | 61.16 | 1.21 | 0.04547 |
| P04271 | Protein S100-B OS=Homo sapiens OX=9606 GN=S100B PE=1 SV=2 | 147.67 | 114.52 | 1.29 | 0.04580 |
| P06753 | Isoform 4 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 | 503.78 | 379.93 | 1.33 | 0.04591 |
| O43852 | Isoform 3 of Calumenin OS=Homo sapiens OX=9606 GN=CALU | 1210.20 | 910.59 | 1.33 | 0.04595 |
| A0A2R8Y5P1 | Receptor expression-enhancing protein (Fragment) OS=Homo sapiens OX=9606 GN=REEP1 PE=1 SV=1 | 137.34 | 99.00 | 1.39 | 0.04603 |
| Q5STX8 | Allograft inflammatory factor 1 (Fragment) OS=Homo sapiens OX=9606 GN=AIF1 PE=1 SV=1 | 138.67 | 103.75 | 1.34 | 0.04615 |
| Q96EQ0 | Small glutamine-rich tetratricopeptide repeat-containing protein beta OS=Homo sapiens OX=9606 GN=SGTB PE=1 SV=1 | 263.09 | 201.41 | 1.31 | 0.04647 |
| P35270 | Sepiapterin reductase OS=Homo sapiens OX=9606 GN=SPR PE=1 SV=1 | 709.60 | 540.19 | 1.31 | 0.04672 |
| O60437 | Periplakin OS=Homo sapiens OX=9606 GN=PPL PE=1 SV=4 | 965.19 | 753.12 | 1.28 | 0.04682 |
| P21266 | Glutathione S-transferase Mu 3 OS=Homo sapiens OX=9606 GN=GSTM3 PE=1 SV=3 | 4161.69 | 2492.01 | 1.67 | 0.04685 |
| Q9HAF1 | Isoform 3 of Chromatin modification-related protein MEAF6 OS=Homo sapiens OX=9606 GN=MEAF6 | 164.49 | 122.30 | 1.34 | 0.04688 |
| P55327 | Isoform 4 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 | 852.68 | 562.49 | 1.52 | 0.04733 |
| Q9BZ67 | FERM domain-containing protein 8 OS=Homo sapiens OX=9606 GN=FRMD8 PE=1 SV=1 | 57.05 | 46.56 | 1.23 | 0.04764 |
| P47224 | Guanine nucleotide exchange factor MSS4 OS=Homo sapiens OX=9606 GN=RABIF PE=1 SV=2 | 91.18 | 71.52 | 1.27 | 0.04791 |
| P09467 | Fructose-1,6-bisphosphatase 1 OS=Homo sapiens OX=9606 GN=FBP1 PE=1 SV=5 | 220.21 | 168.40 | 1.31 | 0.04794 |

| | | | | | |
|---|---|---|---|---|---|
| P30047 | GTP cyclohydrolase 1 feedback regulatory protein OS=Homo sapiens OX=9606 GN=GCHFR PE=1 SV=3 | 272.18 | 208.34 | 1.31 | 0.04839 |
| P27482 | Calmodulin-like protein 3 OS=Homo sapiens OX=9606 GN=CALML3 PE=1 SV=2 | 150.30 | 116.71 | 1.29 | 0.04846 |
| Q06323 | Proteasome activator complex subunit 1 OS=Homo sapiens OX=9606 GN=PSME1 PE=1 SV=1 | 2321.33 | 1673.46 | 1.39 | 0.04868 |
| Q99497 | Protein/nucleic acid deglycase DJ-1 OS=Homo sapiens OX=9606 GN=PARK7 PE=1 SV=2 | 10619.07 | 6552.39 | 1.62 | 0.04878 |
| Q7Z4H3 | HD domain-containing protein 2 OS=Homo sapiens OX=9606 GN=HDDC2 PE=1 SV=1 | 377.34 | 265.61 | 1.42 | 0.04890 |
| Q8WVY7 | Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens OX=9606 GN=UBLCP1 PE=1 SV=2 | 864.37 | 640.17 | 1.35 | 0.04901 |
| Q86V88 | Magnesium-dependent phosphatase 1 OS=Homo sapiens OX=9606 GN=MDP1 PE=1 SV=1 | 99.17 | 77.10 | 1.29 | 0.04918 |
| Q9HB40 | Retinoid-inducible serine carboxypeptidase OS=Homo sapiens OX=9606 GN=SCPEP1 PE=1 SV=1 | 62.53 | 39.79 | 1.57 | 0.04926 |
| Q96IZ7 | Serine/Arginine-related protein 53 OS=Homo sapiens OX=9606 GN=RSRC1 PE=1 SV=1 | 30.55 | 24.64 | 1.24 | 0.04982 |
| P41219 | Isoform 2 of Peripherin OS=Homo sapiens OX=9606 GN=PRPH | 1227.43 | 731.78 | 1.68 | 0.04994 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; $P<0.05$

**Supplementary Table 5.** Extended mass spectrometry data on significantly down-regulated proteins in the retina of Alzheimer's patients compared to cognitively normal controls.

| **Accession** | **Description** | **AD (Means)** | **NC (Means)** | **FC (*-1)** | ***P*** |
|---|---|---|---|---|---|
| Q7Z5J4 | Retinoic acid-induced protein 1 OS=Homo sapiens OX=9606 GN=RAI1 PE=1 SV=2 | 137.76 | 191.14 | 1.39 | 2.211E-05 |
| Q9NPE3 | H/ACA ribonucleoprotein complex subunit 3 OS=Homo sapiens OX=9606 GN=NOP10 PE=1 SV=1 | 45.27 | 59.72 | 1.32 | 2.673E-05 |
| Q5JTH9 | RRP12-like protein OS=Homo sapiens OX=9606 GN=RRP12 PE=1 SV=2 | 346.19 | 524.04 | 1.51 | 4.516E-05 |
| P49207 | 60S ribosomal protein L34 OS=Homo sapiens OX=9606 GN=RPL34 PE=1 SV=3 | 1135.67 | 1669.64 | 1.47 | 0.00013 |
| Q9H553 | Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Homo sapiens OX=9606 GN=ALG2 PE=1 SV=1 | 593.09 | 755.64 | 1.27 | 0.00018 |
| P35268 | 60S ribosomal protein L22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=2 | 429.55 | 613.96 | 1.43 | 0.00019 |
| P42766 | 60S ribosomal protein L35 OS=Homo sapiens OX=9606 GN=RPL35 PE=1 SV=2 | 1558.92 | 2123.74 | 1.36 | 0.00022 |
| Q96KM6 | Zinc finger protein 512B OS=Homo sapiens OX=9606 GN=ZNF512B PE=1 SV=1 | 336.70 | 441.77 | 1.31 | 0.00029 |
| P04000 | Long-wave-sensitive opsin 1 OS=Homo sapiens OX=9606 GN=OPN1LW PE=1 SV=1 | 821.14 | 1552.94 | 1.89 | 0.00035 |
| Q96PU4 | E3 ubiquitin-protein ligase UHRF2 OS=Homo sapiens OX=9606 GN=UHRF2 PE=1 SV=1 | 251.73 | 337.09 | 1.34 | 0.00038 |
| Q08828 | Adenylate cyclase type 1 OS=Homo sapiens OX=9606 GN=ADCY1 PE=1 SV=2 | 394.82 | 582.32 | 1.47 | 0.00038 |
| Q8IWI9 | MAX gene-associated protein OS=Homo sapiens OX=9606 GN=MGA PE=1 SV=4 | 15.10 | 31.80 | 2.11 | 0.00046 |
| Q8N4S7 | Progestin and adipoQ receptor family member 4 OS=Homo sapiens OX=9606 GN=PAQR4 PE=2 SV=3 | 213.99 | 279.32 | 1.31 | 0.00047 |
| A0A1B0GUQ4 | FERM and PDZ domain-containing protein 2 OS=Homo sapiens OX=9606 GN=FRMPD2 PE=1 SV=1 | 242.91 | 351.85 | 1.45 | 0.00048 |
| P19087 | Guanine nucleotide-binding protein G(t) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAT2 PE=2 SV=4 | 1071.16 | 1600.60 | 1.49 | 0.00052 |
| A0A087WUW9 | ADP-ribosylation factor-like protein 15 OS=Homo sapiens OX=9606 GN=ARL15 PE=1 SV=1 | 30.52 | 41.99 | 1.38 | 0.00052 |
| M0QXA7 | Protein Wiz OS=Homo sapiens OX=9606 GN=WIZ PE=1 SV=1 | 160.17 | 216.70 | 1.35 | 0.00056 |
| Q9BZE1 | 39S ribosomal protein L37, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL37 PE=1 SV=2 | 287.75 | 387.20 | 1.35 | 0.00064 |
| Q9BV73 | Centrosome-associated protein CEP250 OS=Homo sapiens OX=9606 GN=CEP250 PE=1 SV=2 | 227.57 | 326.12 | 1.43 | 0.00065 |
| P61353 | 60S ribosomal protein L27 OS=Homo sapiens OX=9606 GN=RPL27 PE=1 SV=2 | 1376.63 | 1992.62 | 1.45 | 0.00069 |
| Q15233 | Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NONO PE=1 SV=4 | 7052.67 | 9062.23 | 1.28 | 0.00069 |
| H0YMV8 | 40S ribosomal protein S27 OS=Homo sapiens OX=9606 GN=RPS27L PE=1 SV=1 | 64.34 | 96.38 | 1.50 | 0.00078 |
| Q96QC0 | Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Homo sapiens OX=9606 GN=PPP1R10 PE=1 SV=1 | 310.60 | 405.29 | 1.30 | 0.00083 |

| | | | | | |
|---|---|---|---|---|---|
| O75916 | Isoform 3 of Regulator of G-protein signaling 9 OS=Homo sapiens OX=9606 GN=RGS9 | 1385.37 | 3024.08 | 2.18 | 0.00086 |
| A0A0A0MS41 | Sidoreflexin OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=1 | 2188.85 | 3028.99 | 1.38 | 0.00086 |
| A0A0C4DH72 | Immunoglobulin kappa variable 1-6 OS=Homo sapiens OX=9606 GN=IGKV1-6 PE=3 SV=1 | 17.62 | 34.62 | 1.97 | 0.00088 |
| Q9BZV3 | Interphotoreceptor matrix proteoglycan 2 OS=Homo sapiens OX=9606 GN=IMPG2 PE=1 SV=3 | 3876.18 | 9847.49 | 2.54 | 0.00092 |
| Q14028 | Isoform GARP2 of Cyclic nucleotide-gated cation channel beta-1 OS=Homo sapiens OX=9606 GN=CNGB1 | 115.79 | 212.66 | 1.84 | 0.00096 |
| Q13523 | Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3 | 1300.35 | 1696.36 | 1.30 | 0.00100 |
| Q14721 | Potassium voltage-gated channel subfamily B member 1 OS=Homo sapiens OX=9606 GN=KCNB1 PE=1 SV=2 | 568.65 | 763.06 | 1.34 | 0.00103 |
| P39210 | Protein Mpv17 OS=Homo sapiens OX=9606 GN=MPV17 PE=1 SV=1 | 70.41 | 91.18 | 1.29 | 0.00103 |
| Q96JM3 | Chromosome alignment-maintaining phosphoprotein 1 OS=Homo sapiens OX=9606 GN=CHAMP1 PE=1 SV=2 | 885.42 | 1210.08 | 1.37 | 0.00107 |
| O60721 | Isoform 2 of Sodium/potassium/calcium exchanger 1 OS=Homo sapiens OX=9606 GN=SLC24A1 | 278.87 | 658.72 | 2.36 | 0.00109 |
| Q86TX2 | Acyl-coenzyme A thioesterase 1 OS=Homo sapiens OX=9606 GN=ACOT1 PE=1 SV=1 | 1406.26 | 1781.28 | 1.27 | 0.00117 |
| O60725 | Protein-S-isoprenylcysteine O-methyltransferase OS=Homo sapiens OX=9606 GN=ICMT PE=1 SV=1 | 56.43 | 90.29 | 1.60 | 0.00119 |
| P78363 | Retinal-specific phospholipid-transporting ATPase ABCA4 OS=Homo sapiens OX=9606 GN=ABCA4 PE=1 SV=3 | 4963.73 | 9186.12 | 1.85 | 0.00119 |
| O14775 | Guanine nucleotide-binding protein subunit beta-5 OS=Homo sapiens OX=9606 GN=GNB5 PE=1 SV=2 | 1144.84 | 1751.26 | 1.53 | 0.00119 |
| D3DWX8 | Family with sequence similarity 3, member A, isoform CRA_c OS=Homo sapiens OX=9606 GN=FAM3A PE=1 SV=1 | 40.98 | 62.95 | 1.54 | 0.00123 |
| P61247 | 40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=2 | 3383.30 | 4305.64 | 1.27 | 0.00124 |
| Q92759 | General transcription factor IIH subunit 4 OS=Homo sapiens OX=9606 GN=GTF2H4 PE=1 SV=1 | 42.86 | 57.46 | 1.34 | 0.00124 |
| Q6ZXV5 | Protein O-mannosyl-transferase TMTC3 OS=Homo sapiens OX=9606 GN=TMTC3 PE=1 SV=2 | 411.20 | 528.65 | 1.29 | 0.00126 |
| Q15067 | Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens OX=9606 GN=ACOX1 PE=1 SV=3 | 745.13 | 953.53 | 1.28 | 0.00128 |
| Q14318 | Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens OX=9606 GN=FKBP8 | 1404.77 | 1803.87 | 1.28 | 0.00131 |
| Q8NCY6 | Myb/SANT-like DNA-binding domain-containing protein 4 OS=Homo sapiens OX=9606 GN=MSANTD4 PE=1 SV=1 | 54.76 | 70.46 | 1.29 | 0.00135 |
| P51531 | Probable global transcription activator SNF2L2 OS=Homo sapiens OX=9606 GN=SMARCA2 PE=1 SV=2 | 1653.49 | 2089.63 | 1.26 | 0.00136 |
| Q9H4B0 | Probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=OSGEPL1 PE=2 SV=2 | 115.66 | 160.62 | 1.39 | 0.00136 |

| | | | | | |
|---|---|---|---|---|---|
| Q5T1C6 | Acyl-coenzyme A thioesterase THEM4 OS=Homo sapiens OX=9606 GN=THEM4 PE=1 SV=1 | 267.13 | 385.44 | 1.44 | 0.00136 |
| P61764 | Syntaxin-binding protein 1 OS=Homo sapiens OX=9606 GN=STXBP1 PE=1 SV=1 | 1209.71 | 1670.29 | 1.38 | 0.00141 |
| Q5T3J3 | Ligand-dependent nuclear receptor-interacting factor 1 OS=Homo sapiens OX=9606 GN=LRIF1 PE=1 SV=1 | 239.56 | 304.88 | 1.27 | 0.00143 |
| Q9Y5B9 | FACT complex subunit SPT16 OS=Homo sapiens OX=9606 GN=SUPT16H PE=1 SV=1 | 1721.89 | 2382.39 | 1.38 | 0.00144 |
| Q9UGL1 | Isoform 2 of Lysine-specific demethylase 5B OS=Homo sapiens OX=9606 GN=KDM5B | 454.20 | 707.33 | 1.56 | 0.00146 |
| Q96AG4 | Leucine-rich repeat-containing protein 59 OS=Homo sapiens OX=9606 GN=LRRC59 PE=1 SV=1 | 1202.76 | 1693.98 | 1.41 | 0.00148 |
| F5GX28 | Lysine-specific demethylase 4B OS=Homo sapiens OX=9606 GN=KDM4B PE=1 SV=2 | 243.38 | 360.78 | 1.48 | 0.00151 |
| Q6NUK1 | Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens OX=9606 GN=SLC25A24 PE=1 SV=2 | 3060.37 | 5023.55 | 1.64 | 0.00152 |
| Q02880 | Isoform Beta-1 of DNA topoisomerase 2-beta OS=Homo sapiens OX=9606 GN=TOP2B | 6484.20 | 9188.47 | 1.42 | 0.00160 |
| P63211 | Guanine nucleotide-binding protein G(T) subunit gamma-T1 OS=Homo sapiens OX=9606 GN=GNGT1 PE=1 SV=2 | 1963.86 | 3028.85 | 1.54 | 0.00163 |
| P29973 | Isoform 2 of cGMP-gated cation channel alpha-1 OS=Homo sapiens OX=9606 GN=CNGA1 | 792.46 | 1841.01 | 2.32 | 0.00164 |
| K7EKE6 | Lon protease homolog, mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 PE=1 SV=1 | 2977.31 | 4024.30 | 1.35 | 0.00164 |
| Q13562 | Neurogenic differentiation factor 1 OS=Homo sapiens OX=9606 GN=NEUROD1 PE=1 SV=3 | 19.95 | 27.43 | 1.38 | 0.00165 |
| Q92831 | Histone acetyltransferase KAT2B OS=Homo sapiens OX=9606 GN=KAT2B PE=1 SV=3 | 132.01 | 190.27 | 1.44 | 0.00166 |
| Q08945 | FACT complex subunit SSRP1 OS=Homo sapiens OX=9606 GN=SSRP1 PE=1 SV=1 | 1160.96 | 1471.93 | 1.27 | 0.00170 |
| Q17R60 | Interphotoreceptor matrix proteoglycan 1 OS=Homo sapiens OX=9606 GN=IMPG1 PE=1 SV=2 | 4962.91 | 11887.91 | 2.40 | 0.00171 |
| P19367 | Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1 PE=1 SV=3 | 159.78 | 258.75 | 1.62 | 0.00174 |
| O94806 | Serine/threonine-protein kinase D3 OS=Homo sapiens OX=9606 GN=PRKD3 PE=1 SV=1 | 25.74 | 34.32 | 1.33 | 0.00179 |
| Q9BSJ5 | Uncharacterized protein C17orf80 OS=Homo sapiens OX=9606 GN=C17orf80 PE=2 SV=2 | 278.25 | 364.65 | 1.31 | 0.00180 |
| Q03701 | CCAAT/enhancer-binding protein zeta OS=Homo sapiens OX=9606 GN=CEBPZ PE=1 SV=3 | 56.18 | 75.44 | 1.34 | 0.00187 |
| Q5SSJ5 | Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1 | 7121.93 | 10412.01 | 1.46 | 0.00187 |
| Q8TCG5 | Carnitine O-palmitoyltransferase 1, brain isoform OS=Homo sapiens OX=9606 GN=CPT1C PE=1 SV=1 | 378.60 | 488.72 | 1.29 | 0.00189 |
| P22087 | rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens OX=9606 GN=FBL PE=1 SV=2 | 762.38 | 1061.22 | 1.39 | 0.00189 |
| P83731 | 60S ribosomal protein L24 OS=Homo sapiens OX=9606 GN=RPL24 PE=1 SV=1 | 1601.02 | 2353.30 | 1.47 | 0.00195 |
| P35914 | Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens OX=9606 GN=HMGCL PE=1 SV=2 | 741.00 | 939.73 | 1.27 | 0.00195 |

| | | | | | |
|---|---|---|---|---|---|
| I3L4I4 | TOM1-like protein 1 OS=Homo sapiens OX=9606 GN=TOM1L1 PE=1 SV=1 | 156.18 | 260.00 | 1.66 | 0.00198 |
| Q9NVH0 | Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens OX=9606 GN=EXD2 PE=1 SV=2 | 216.29 | 270.72 | 1.25 | 0.00201 |
| Q12923 | Isoform 4 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens OX=9606 GN=PTPN13 | 969.04 | 1487.03 | 1.53 | 0.00202 |
| O94874 | E3 UFM1-protein ligase 1 OS=Homo sapiens OX=9606 GN=UFL1 PE=1 SV=2 | 2551.36 | 3285.43 | 1.29 | 0.00205 |
| Q4R9M9 | Kinesin family member 1Bbeta isoform II OS=Homo sapiens OX=9606 GN=KIF1B PE=1 SV=1 | 763.96 | 982.72 | 1.29 | 0.00207 |
| A6NHR9 | Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SMCHD1 PE=1 SV=2 | 1687.32 | 2233.41 | 1.32 | 0.00207 |
| Q8TB37 | Iron-sulfur protein NUBPL OS=Homo sapiens OX=9606 GN=NUBPL PE=1 SV=3 | 115.06 | 147.24 | 1.28 | 0.00208 |
| Q7L592 | Protein arginine methyltransferase NDUFAF7, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFAF7 PE=1 SV=1 | 355.20 | 461.61 | 1.30 | 0.00210 |
| Q9BUJ2 | Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=2 | 2473.33 | 3273.79 | 1.32 | 0.00215 |
| Q9H2P0 | Activity-dependent neuroprotector homeobox protein OS=Homo sapiens OX=9606 GN=ADNP PE=1 SV=1 | 1163.70 | 1657.90 | 1.42 | 0.00220 |
| Q9UIG0 | Tyrosine-protein kinase BAZ1B OS=Homo sapiens OX=9606 GN=BAZ1B PE=1 SV=2 | 1923.85 | 2682.48 | 1.39 | 0.00222 |
| P17480 | Nucleolar transcription factor 1 OS=Homo sapiens OX=9606 GN=UBTF PE=1 SV=1 | 1107.77 | 1431.42 | 1.29 | 0.00225 |
| O60264 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 SV=1 | 3371.65 | 4562.95 | 1.35 | 0.00225 |
| P38432 | Coilin OS=Homo sapiens OX=9606 GN=COIL PE=1 SV=1 | 88.63 | 132.66 | 1.50 | 0.00228 |
| Q6UB98 | Ankyrin repeat domain-containing protein 12 OS=Homo sapiens OX=9606 GN=ANKRD12 PE=1 SV=3 | 33.32 | 43.13 | 1.29 | 0.00237 |
| Q8IXT5 | RNA-binding protein 12B OS=Homo sapiens OX=9606 GN=RBM12B PE=1 SV=2 | 652.16 | 901.76 | 1.38 | 0.00238 |
| Q9HCE3 | Zinc finger protein 532 OS=Homo sapiens OX=9606 GN=ZNF532 PE=1 SV=2 | 32.92 | 42.14 | 1.28 | 0.00241 |
| Q96CQ1 | Solute carrier family 25 member 36 OS=Homo sapiens OX=9606 GN=SLC25A36 PE=1 SV=1 | 78.74 | 103.28 | 1.31 | 0.00242 |
| Q15717 | ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=2 | 2237.03 | 2854.27 | 1.28 | 0.00249 |
| Q9NTN3 | UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter OS=Homo sapiens OX=9606 GN=SLC35D1 PE=2 SV=1 | 510.77 | 696.77 | 1.36 | 0.00253 |
| Q49A26 | Putative oxidoreductase GLYR1 OS=Homo sapiens OX=9606 GN=GLYR1 PE=1 SV=3 | 800.43 | 1027.47 | 1.28 | 0.00254 |
| Q96I24 | Far upstream element-binding protein 3 OS=Homo sapiens OX=9606 GN=FUBP3 PE=1 SV=2 | 1206.80 | 1519.38 | 1.26 | 0.00260 |
| Q8NCC3 | Group XV phospholipase A2 OS=Homo sapiens OX=9606 GN=PLA2G15 PE=1 SV=2 | 55.19 | 88.42 | 1.60 | 0.00263 |
| Q9NW64 | Pre-mRNA-splicing factor RBM22 OS=Homo sapiens OX=9606 GN=RBM22 PE=1 SV=1 | 852.61 | 1098.69 | 1.29 | 0.00263 |
| Q96SK2 | Isoform 2 of Transmembrane protein 209 OS=Homo sapiens OX=9606 GN=TMEM209 | 280.86 | 371.59 | 1.32 | 0.00265 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| Q6KCM7 | Isoform 5 of Calcium-binding mitochondrial carrier protein SCaMC-2 OS=Homo sapiens OX=9606 GN=SLC25A25 | 1590.61 | 2373.72 | 1.49 | 0.00268 |
| P55265 | Isoform 4 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens OX=9606 GN=ADAR | 3695.65 | 4739.66 | 1.28 | 0.00272 |
| Q02846 | Retinal guanylyl cyclase 1 OS=Homo sapiens OX=9606 GN=GUCY2D PE=1 SV=2 | 1519.22 | 2334.86 | 1.54 | 0.00277 |
| P23942 | Peripherin-2 OS=Homo sapiens OX=9606 GN=PRPH2 PE=1 SV=1 | 1926.55 | 5266.71 | 2.73 | 0.00279 |
| Q9P1Z0 | Zinc finger and BTB domain-containing protein 4 OS=Homo sapiens OX=9606 GN=ZBTB4 PE=1 SV=3 | 99.21 | 130.59 | 1.32 | 0.00280 |
| Q14690 | Protein RRP5 homolog OS=Homo sapiens OX=9606 GN=PDCD11 PE=1 SV=3 | 129.96 | 183.72 | 1.41 | 0.00280 |
| O75367 | Core histone macro-H2A.1 OS=Homo sapiens OX=9606 GN=H2AFY PE=1 SV=4 | 9523.66 | 14529.77 | 1.53 | 0.00282 |
| Q9NPI0 | Transmembrane protein 138 OS=Homo sapiens OX=9606 GN=TMEM138 PE=1 SV=1 | 40.63 | 54.75 | 1.35 | 0.00285 |
| Q14839 | Isoform 2 of Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens OX=9606 GN=CHD4 | 3338.60 | 4536.76 | 1.36 | 0.00290 |
| L0R6Q1 | SLC35A4 upstream open reading frame protein OS=Homo sapiens OX=9606 GN=SLC35A4 PE=3 SV=1 | 494.59 | 641.62 | 1.30 | 0.00291 |
| Q7Z3K3 | Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=2 | 670.13 | 880.37 | 1.31 | 0.00294 |
| P08100 | Rhodopsin OS=Homo sapiens OX=9606 GN=RHO PE=1 SV=1 | 4543.76 | 11529.48 | 2.54 | 0.00307 |
| P03999 | Short-wave-sensitive opsin 1 OS=Homo sapiens OX=9606 GN=OPN1SW PE=1 SV=1 | 214.41 | 336.65 | 1.57 | 0.00316 |
| P40429 | 60S ribosomal protein L13a OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2 | 1913.84 | 2466.83 | 1.29 | 0.00320 |
| Q9Y426 | C2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=C2CD2 PE=1 SV=2 | 812.55 | 1051.76 | 1.29 | 0.00320 |
| P62913 | 60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 PE=1 SV=2 | 1122.02 | 1642.98 | 1.46 | 0.00322 |
| Q9BT22 | Chitobiosyldiphosphodolichol beta-mannosyltransferase OS=Homo sapiens OX=9606 GN=ALG1 PE=1 SV=2 | 387.48 | 496.90 | 1.28 | 0.00331 |
| Q9NVJ2 | ADP-ribosylation factor-like protein 8B OS=Homo sapiens OX=9606 GN=ARL8B PE=1 SV=1 | 870.22 | 1105.28 | 1.27 | 0.00334 |
| Q8NDX5 | Isoform 7 of Polyhomeotic-like protein 3 OS=Homo sapiens OX=9606 GN=PHC3 | 171.23 | 233.13 | 1.36 | 0.00337 |
| Q53GS7 | Nucleoporin GLE1 OS=Homo sapiens OX=9606 GN=GLE1 PE=1 SV=2 | 51.66 | 71.76 | 1.39 | 0.00337 |
| Q15118 | [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial OS=Homo sapiens OX=9606 GN=PDK1 PE=1 SV=1 | 715.14 | 924.65 | 1.29 | 0.00358 |
| Q56VL3 | OCIA domain-containing protein 2 OS=Homo sapiens OX=9606 GN=OCIAD2 PE=1 SV=1 | 366.92 | 543.96 | 1.48 | 0.00360 |
| Q9GZT6 | Coiled-coil domain-containing protein 90B, mitochondrial OS=Homo sapiens OX=9606 GN=CCDC90B PE=1 SV=2 | 624.64 | 814.13 | 1.30 | 0.00363 |
| Q6N043 | Zinc finger protein 280D OS=Homo sapiens OX=9606 GN=ZNF280D PE=1 SV=3 | 120.61 | 155.48 | 1.29 | 0.00364 |
| O43264 | Centromere/kinetochore protein zw10 homolog OS=Homo sapiens OX=9606 GN=ZW10 PE=1 SV=3 | 471.75 | 602.10 | 1.28 | 0.00366 |

| | | | | | |
|---|---|---|---|---|---|
| P62277 | 40S ribosomal protein S13 OS=Homo sapiens OX=9606 GN=RPS13 PE=1 SV=2 | 1696.70 | 2212.39 | 1.30 | 0.00367 |
| O15047 | Histone-lysine N-methyltransferase SETD1A OS=Homo sapiens OX=9606 GN=SETD1A PE=1 SV=3 | 46.59 | 64.30 | 1.38 | 0.00373 |
| Q96ME7 | Zinc finger protein 512 OS=Homo sapiens OX=9606 GN=ZNF512 PE=1 SV=2 | 1137.00 | 1553.94 | 1.37 | 0.00380 |
| P36578 | 60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5 | 3224.08 | 4413.76 | 1.37 | 0.00380 |
| Q8WWQ0 | PH-interacting protein OS=Homo sapiens OX=9606 GN=PHIP PE=1 SV=2 | 1291.81 | 1646.77 | 1.27 | 0.00382 |
| O14832 | Phytanoyl-CoA dioxygenase, peroxisomal OS=Homo sapiens OX=9606 GN=PHYH PE=1 SV=1 | 160.07 | 213.78 | 1.34 | 0.00384 |
| P46100 | Transcriptional regulator ATRX OS=Homo sapiens OX=9606 GN=ATRX PE=1 SV=5 | 1007.01 | 1349.78 | 1.34 | 0.00388 |
| F8VX10 | KAT8 regulatory NSL complex subunit 2 OS=Homo sapiens OX=9606 GN=KANSL2 PE=1 SV=1 | 53.23 | 68.44 | 1.29 | 0.00389 |
| Q9UPP1 | Histone lysine demethylase PHF8 OS=Homo sapiens OX=9606 GN=PHF8 PE=1 SV=3 | 121.42 | 194.70 | 1.60 | 0.00393 |
| O95696 | Isoform 2 of Bromodomain-containing protein 1 OS=Homo sapiens OX=9606 GN=BRD1 | 194.32 | 250.07 | 1.29 | 0.00393 |
| P54819 | Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=2 | 2347.29 | 3595.15 | 1.53 | 0.00398 |
| P56715 | Oxygen-regulated protein 1 OS=Homo sapiens OX=9606 GN=RP1 PE=1 SV=1 | 459.79 | 694.24 | 1.51 | 0.00401 |
| P52272 | Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=3 | 13023.51 | 17928.54 | 1.38 | 0.00408 |
| P61313 | 60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2 | 890.01 | 1127.90 | 1.27 | 0.00427 |
| Q9UH99 | Isoform 2 of SUN domain-containing protein 2 OS=Homo sapiens OX=9606 GN=SUN2 | 564.44 | 736.67 | 1.31 | 0.00440 |
| A0A087WXF8 | Nucleolar protein of 40 kDa OS=Homo sapiens OX=9606 GN=ZCCHC17 PE=1 SV=1 | 68.44 | 87.62 | 1.28 | 0.00446 |
| P56182 | Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens OX=9606 GN=RRP1 PE=1 SV=1 | 80.54 | 108.00 | 1.34 | 0.00448 |
| Q2TB10 | Zinc finger protein 800 OS=Homo sapiens OX=9606 GN=ZNF800 PE=1 SV=1 | 147.53 | 192.00 | 1.30 | 0.00455 |
| A0A087X117 | Nodal modulator 1 OS=Homo sapiens OX=9606 GN=NOMO1 PE=1 SV=1 | 64.14 | 96.00 | 1.50 | 0.00473 |
| Q1KMD3 | Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens OX=9606 GN=HNRNPUL2 PE=1 SV=1 | 4147.45 | 5206.04 | 1.26 | 0.00478 |
| P61026 | Ras-related protein Rab-10 OS=Homo sapiens OX=9606 GN=RAB10 PE=1 SV=1 | 1555.61 | 2012.13 | 1.29 | 0.00480 |
| Q14683 | Structural maintenance of chromosomes protein 1A OS=Homo sapiens OX=9606 GN=SMC1A PE=1 SV=2 | 4639.03 | 5827.76 | 1.26 | 0.00487 |
| P27635 | 60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=4 | 1193.92 | 1574.73 | 1.32 | 0.00491 |
| P62424 | 60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=2 | 2268.97 | 2942.17 | 1.30 | 0.00496 |
| K7ELF7 | Retinol dehydrogenase 8 OS=Homo sapiens OX=9606 GN=RDH8 PE=1 SV=1 | 256.17 | 439.26 | 1.71 | 0.00500 |
| Q9UIS9 | Isoform 9 of Methyl-CpG-binding domain protein 1 OS=Homo sapiens OX=9606 GN=MBD1 | 508.26 | 672.28 | 1.32 | 0.00503 |
| Q03395 | Rod outer segment membrane protein 1 OS=Homo sapiens OX=9606 GN=ROM1 PE=1 SV=2 | 1005.87 | 1942.72 | 1.93 | 0.00505 |

| | | | | | |
|---|---|---|---|---|---|
| Q9H936 | Mitochondrial glutamate carrier 1 OS=Homo sapiens OX=9606 GN=SLC25A22 PE=1 SV=1 | 2796.50 | 3992.80 | 1.43 | 0.00506 |
| P35610 | Sterol O-acyltransferase 1 OS=Homo sapiens OX=9606 GN=SOAT1 PE=1 SV=3 | 25.93 | 33.75 | 1.30 | 0.00507 |
| Q9NXE4 | Isoform 4 of Sphingomyelin phosphodiesterase 4 OS=Homo sapiens OX=9606 GN=SMPD4 | 279.95 | 363.42 | 1.30 | 0.00508 |
| Q9HCC8 | Isoform 3 of Glycerophosphoinositol inositolphosphodiesterase GDPD2 OS=Homo sapiens OX=9606 GN=GDPD2 | 153.18 | 199.04 | 1.30 | 0.00515 |
| Q9Y6A9 | Signal peptidase complex subunit 1 OS=Homo sapiens OX=9606 GN=SPCS1 PE=1 SV=4 | 243.63 | 343.80 | 1.41 | 0.00519 |
| A3KMH1 | von Willebrand factor A domain-containing protein 8 OS=Homo sapiens OX=9606 GN=VWA8 PE=1 SV=2 | 957.82 | 1287.97 | 1.34 | 0.00522 |
| Q9BQ39 | ATP-dependent RNA helicase DDX50 OS=Homo sapiens OX=9606 GN=DDX50 PE=1 SV=1 | 528.68 | 718.44 | 1.36 | 0.00524 |
| Q9HBH5 | Retinol dehydrogenase 14 OS=Homo sapiens OX=9606 GN=RDH14 PE=1 SV=1 | 353.01 | 481.91 | 1.37 | 0.00525 |
| Q9UBW7 | Zinc finger MYM-type protein 2 OS=Homo sapiens OX=9606 GN=ZMYM2 PE=1 SV=1 | 306.51 | 406.62 | 1.33 | 0.00526 |
| Q96JM2 | Isoform 3 of Zinc finger protein 462 OS=Homo sapiens OX=9606 GN=ZNF462 | 168.94 | 249.91 | 1.48 | 0.00529 |
| Q8IZD4 | mRNA-decapping enzyme 1B OS=Homo sapiens OX=9606 GN=DCP1B PE=1 SV=2 | 16.36 | 21.55 | 1.32 | 0.00541 |
| Q6ZS82 | Regulator of G-protein signaling 9-binding protein OS=Homo sapiens OX=9606 GN=RGS9BP PE=2 SV=1 | 180.83 | 331.88 | 1.84 | 0.00544 |
| O95159 | Zinc finger protein-like 1 OS=Homo sapiens OX=9606 GN=ZFPL1 PE=1 SV=2 | 101.53 | 146.00 | 1.44 | 0.00544 |
| P21397 | Amine oxidase [flavin-containing] A OS=Homo sapiens OX=9606 GN=MAOA PE=1 SV=1 | 2747.05 | 3780.61 | 1.38 | 0.00549 |
| Q9UG56 | Phosphatidylserine decarboxylase proenzyme, mitochondrial OS=Homo sapiens OX=9606 GN=PISD PE=2 SV=4 | 145.74 | 192.42 | 1.32 | 0.00563 |
| A0A0A0MSV9 | Tapasin OS=Homo sapiens OX=9606 GN=TAPBP PE=1 SV=1 | 292.01 | 375.63 | 1.29 | 0.00565 |
| J3QLS3 | 28S ribosomal protein S7, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS7 PE=1 SV=1 | 389.96 | 523.36 | 1.34 | 0.00566 |
| O94826 | Mitochondrial import receptor subunit TOM70 OS=Homo sapiens OX=9606 GN=TOMM70 PE=1 SV=1 | 5428.78 | 7579.92 | 1.40 | 0.00567 |
| Q96NR8 | Retinol dehydrogenase 12 OS=Homo sapiens OX=9606 GN=RDH12 PE=1 SV=3 | 1829.75 | 3089.46 | 1.69 | 0.00567 |
| Q00839 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU | 3442.14 | 4906.01 | 1.43 | 0.00569 |
| Q96NB2 | Sideroflexin-2 OS=Homo sapiens OX=9606 GN=SFXN2 PE=1 SV=2 | 46.59 | 75.61 | 1.62 | 0.00572 |
| Q6YN16 | Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens OX=9606 GN=HSDL2 PE=1 SV=1 | 1468.35 | 1968.12 | 1.34 | 0.00575 |
| Q8IXI1 | Mitochondrial Rho GTPase 2 OS=Homo sapiens OX=9606 GN=RHOT2 PE=1 SV=2 | 834.56 | 1215.25 | 1.46 | 0.00577 |
| Q9UIW0 | Ventral anterior homeobox 2 OS=Homo sapiens OX=9606 GN=VAX2 PE=1 SV=1 | 35.11 | 51.94 | 1.48 | 0.00590 |
| A0A0A0MRM8 | Unconventional myosin-VI OS=Homo sapiens OX=9606 GN=MYO6 PE=1 SV=1 | 1038.10 | 1382.20 | 1.33 | 0.00597 |

| | | | | | |
|---|---|---|---|---|---|
| Q9HC21 | Mitochondrial thiamine pyrophosphate carrier OS=Homo sapiens OX=9606 GN=SLC25A19 PE=1 SV=1 | 58.27 | 75.05 | 1.29 | 0.00600 |
| Q15326 | Zinc finger MYND domain-containing protein 11 OS=Homo sapiens OX=9606 GN=ZMYND11 PE=1 SV=2 | 205.80 | 269.15 | 1.31 | 0.00606 |
| P42677 | 40S ribosomal protein S27 OS=Homo sapiens OX=9606 GN=RPS27 PE=1 SV=3 | 516.62 | 683.11 | 1.32 | 0.00608 |
| Q96E39 | RNA binding motif protein, X-linked-like-1 OS=Homo sapiens OX=9606 GN=RBMXL1 PE=1 SV=1 | 593.13 | 820.41 | 1.38 | 0.00610 |
| P51160 | Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha' OS=Homo sapiens OX=9606 GN=PDE6C PE=1 SV=2 | 1073.08 | 1638.32 | 1.53 | 0.00618 |
| P05141 | ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC25A5 PE=1 SV=7 | 3059.45 | 5217.90 | 1.71 | 0.00626 |
| P62280 | 40S ribosomal protein S11 OS=Homo sapiens OX=9606 GN=RPS11 PE=1 SV=3 | 1944.23 | 2800.11 | 1.44 | 0.00630 |
| Q9H5Q4 | Dimethyladenosine transferase 2, mitochondrial OS=Homo sapiens OX=9606 GN=TFB2M PE=1 SV=1 | 12.56 | 20.09 | 1.60 | 0.00633 |
| Q7Z3H4 | Sterile alpha motif domain-containing protein 7 OS=Homo sapiens OX=9606 GN=SAMD7 PE=1 SV=1 | 161.75 | 218.59 | 1.35 | 0.00650 |
| Q5VZL5 | Zinc finger MYM-type protein 4 OS=Homo sapiens OX=9606 GN=ZMYM4 PE=1 SV=1 | 163.47 | 258.68 | 1.58 | 0.00652 |
| Q13151 | Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens OX=9606 GN=HNRNPA0 PE=1 SV=1 | 2351.07 | 3023.49 | 1.29 | 0.00667 |
| Q9GZY4 | Cytochrome c oxidase assembly factor 1 homolog OS=Homo sapiens OX=9606 GN=COA1 PE=1 SV=1 | 54.72 | 75.69 | 1.38 | 0.00667 |
| Q96A26 | Protein FAM162A OS=Homo sapiens OX=9606 GN=FAM162A PE=1 SV=2 | 1199.35 | 1739.09 | 1.45 | 0.00670 |
| O75152 | Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens OX=9606 GN=ZC3H11A PE=1 SV=3 | 1022.93 | 1358.09 | 1.33 | 0.00687 |
| P32243 | Homeobox protein OTX2 OS=Homo sapiens OX=9606 GN=OTX2 PE=1 SV=1 | 170.27 | 242.89 | 1.43 | 0.00703 |
| P62244 | 40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 SV=2 | 801.52 | 1082.17 | 1.35 | 0.00710 |
| Q8NBN7 | Retinol dehydrogenase 13 OS=Homo sapiens OX=9606 GN=RDH13 PE=1 SV=2 | 561.69 | 818.18 | 1.46 | 0.00716 |
| Q53GQ0 | Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens OX=9606 GN=HSD17B12 PE=1 SV=2 | 2307.29 | 2907.23 | 1.26 | 0.00716 |
| Q969S2 | Endonuclease 8-like 2 OS=Homo sapiens OX=9606 GN=NEIL2 PE=1 SV=3 | 224.86 | 285.29 | 1.27 | 0.00718 |
| P51659 | Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=3 | 2684.32 | 3420.04 | 1.27 | 0.00741 |
| Q9NQC3 | Isoform C of Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 | 290.93 | 430.93 | 1.48 | 0.00761 |
| O95831 | Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 PE=1 SV=1 | 3094.56 | 4916.30 | 1.59 | 0.00763 |
| Q9HC07 | Transmembrane protein 165 OS=Homo sapiens OX=9606 GN=TMEM165 PE=1 SV=1 | 96.07 | 132.91 | 1.38 | 0.00772 |
| O00327 | Aryl hydrocarbon receptor nuclear translocator-like protein 1 OS=Homo sapiens OX=9606 GN=ARNTL PE=1 SV=2 | 73.43 | 99.38 | 1.35 | 0.00782 |
| P49916 | DNA ligase 3 OS=Homo sapiens OX=9606 GN=LIG3 PE=1 SV=2 | 694.19 | 874.70 | 1.26 | 0.00790 |

| | | | | | |
|---|---|---|---|---|---|
| Q6ZNB6 | NF-X1-type zinc finger protein NFXL1 OS=Homo sapiens OX=9606 GN=NFXL1 PE=1 SV=2 | 136.94 | 180.31 | 1.32 | 0.00796 |
| Q96CB8 | Integrator complex subunit 12 OS=Homo sapiens OX=9606 GN=INTS12 PE=1 SV=1 | 150.70 | 211.05 | 1.40 | 0.00803 |
| Q5SY16 | Polynucleotide 5'-hydroxyl-kinase NOL9 OS=Homo sapiens OX=9606 GN=NOL9 PE=1 SV=1 | 64.82 | 90.73 | 1.40 | 0.00837 |
| P42126 | Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens OX=9606 GN=ECI1 PE=1 SV=1 | 1261.55 | 1674.27 | 1.33 | 0.00852 |
| A0A286YEX2 | Synaptotagmin VI, isoform CRA_b OS=Homo sapiens OX=9606 GN=SYT6 PE=1 SV=1 | 28.57 | 44.37 | 1.55 | 0.00880 |
| M0R2Z9 | SURP and G-patch domain-containing protein 2 OS=Homo sapiens OX=9606 GN=SUGP2 PE=1 SV=1 | 3446.26 | 4619.53 | 1.34 | 0.00888 |
| Q9H6K4 | Optic atrophy 3 protein OS=Homo sapiens OX=9606 GN=OPA3 PE=1 SV=1 | 277.06 | 383.94 | 1.39 | 0.00892 |
| Q13557 | Isoform Delta 12 of Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens OX=9606 GN=CAMK2D | 75.28 | 115.98 | 1.54 | 0.00901 |
| A0A0J9YXJ0 | CUGBP Elav-like family member 2 OS=Homo sapiens OX=9606 GN=CELF2 PE=1 SV=1 | 825.94 | 1112.66 | 1.35 | 0.00904 |
| O43913 | Origin recognition complex subunit 5 OS=Homo sapiens OX=9606 GN=ORC5 PE=1 SV=1 | 209.90 | 264.16 | 1.26 | 0.00916 |
| O95573 | Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens OX=9606 GN=ACSL3 PE=1 SV=3 | 3396.69 | 4474.53 | 1.32 | 0.00919 |
| Q9UEG4 | Zinc finger protein 629 OS=Homo sapiens OX=9606 GN=ZNF629 PE=1 SV=2 | 438.75 | 577.93 | 1.32 | 0.00927 |
| P16499 | Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha OS=Homo sapiens OX=9606 GN=PDE6A PE=1 SV=4 | 5665.39 | 9688.89 | 1.71 | 0.00936 |
| Q7Z7K6 | Isoform 3 of Centromere protein V OS=Homo sapiens OX=9606 GN=CENPV | 1164.57 | 1456.85 | 1.25 | 0.00940 |
| Q6UX98 | Probable palmitoyltransferase ZDHHC24 OS=Homo sapiens OX=9606 GN=ZDHHC24 PE=1 SV=1 | 60.01 | 79.57 | 1.33 | 0.00958 |
| P12236 | ADP/ATP translocase 3 OS=Homo sapiens OX=9606 GN=SLC25A6 PE=1 SV=4 | 3963.69 | 5987.79 | 1.51 | 0.00963 |
| O95563 | Mitochondrial pyruvate carrier 2 OS=Homo sapiens OX=9606 GN=MPC2 PE=1 SV=1 | 788.34 | 1117.64 | 1.42 | 0.00976 |
| Q9UI40 | Sodium/potassium/calcium exchanger 2 OS=Homo sapiens OX=9606 GN=SLC24A2 PE=1 SV=1 | 255.79 | 376.11 | 1.47 | 0.00984 |
| Q5T3F8 | CSC1-like protein 2 OS=Homo sapiens OX=9606 GN=TMEM63B PE=1 SV=1 | 445.29 | 593.43 | 1.33 | 0.00985 |
| Q8WTQ7 | Rhodopsin kinase OS=Homo sapiens OX=9606 GN=GRK7 PE=1 SV=1 | 339.33 | 448.62 | 1.32 | 0.00986 |
| Q8N5G0 | Isoform 2 of Small integral membrane protein 20 OS=Homo sapiens OX=9606 GN=SMIM20 | 217.36 | 293.38 | 1.35 | 0.00988 |
| Q8TCJ2 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens OX=9606 GN=STT3B PE=1 SV=1 | 787.93 | 1002.15 | 1.27 | 0.00999 |
| Q9BQQ3 | Golgi reassembly-stacking protein 1 OS=Homo sapiens OX=9606 GN=GORASP1 PE=1 SV=3 | 55.20 | 70.65 | 1.28 | 0.01004 |
| Q10471 | Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens OX=9606 GN=GALNT2 PE=1 SV=1 | 871.64 | 1205.72 | 1.38 | 0.01006 |
| Q96KR6 | Protein FAM210B, mitochondrial OS=Homo sapiens OX=9606 GN=FAM210B PE=1 SV=2 | 10.54 | 20.83 | 1.98 | 0.01010 |

| | | | | | |
|---|---|---|---|---|---|
| P0C7P0 | CDGSH iron-sulfur domain-containing protein 3, mitochondrial OS=Homo sapiens OX=9606 GN=CISD3 PE=1 SV=1 | 175.58 | 229.71 | 1.31 | 0.01014 |
| A0A2R8YFG2 | Nicotinamide-nucleotide adenylyltransferase OS=Homo sapiens OX=9606 GN=NMNAT3 PE=1 SV=1 | 131.44 | 199.89 | 1.52 | 0.01023 |
| Q9NPJ3 | Acyl-coenzyme A thioesterase 13 OS=Homo sapiens OX=9606 GN=ACOT13 PE=1 SV=1 | 581.91 | 786.90 | 1.35 | 0.01028 |
| O43521 | Bcl-2-like protein 11 OS=Homo sapiens OX=9606 GN=BCL2L11 PE=1 SV=1 | 8.04 | 13.14 | 1.63 | 0.01032 |
| Q96SI9 | Spermatid perinuclear RNA-binding protein OS=Homo sapiens OX=9606 GN=STRBP PE=1 SV=1 | 1235.05 | 1555.53 | 1.26 | 0.01046 |
| O43159 | Ribosomal RNA-processing protein 8 OS=Homo sapiens OX=9606 GN=RRP8 PE=1 SV=2 | 285.81 | 388.10 | 1.36 | 0.01072 |
| Q9UHQ9 | NADH-cytochrome b5 reductase 1 OS=Homo sapiens OX=9606 GN=CYB5R1 PE=1 SV=1 | 1946.11 | 2486.74 | 1.28 | 0.01083 |
| P12532 | Creatine kinase U-type, mitochondrial OS=Homo sapiens OX=9606 GN=CKMT1A PE=1 SV=1 | 4658.90 | 6782.95 | 1.46 | 0.01085 |
| A0A0D9SEI0 | Uncharacterized protein C6orf203 OS=Homo sapiens OX=9606 GN=C6orf203 PE=1 SV=1 | 31.75 | 41.87 | 1.32 | 0.01091 |
| I3L0E3 | HCG1984214, isoform CRA_a OS=Homo sapiens OX=9606 GN=hCG_1984214 PE=4 SV=1 | 146.35 | 194.17 | 1.33 | 0.01110 |
| J3KTA4 | Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1 | 3427.64 | 4738.96 | 1.38 | 0.01116 |
| Q6PD62 | RNA polymerase-associated protein CTR9 homolog OS=Homo sapiens OX=9606 GN=CTR9 PE=1 SV=1 | 599.73 | 755.58 | 1.26 | 0.01125 |
| P84243 | Histone H3.3 OS=Homo sapiens OX=9606 GN=H3F3A PE=1 SV=2 | 10890.96 | 14793.45 | 1.36 | 0.01127 |
| O76081 | Regulator of G-protein signaling 20 OS=Homo sapiens OX=9606 GN=RGS20 PE=1 SV=4 | 219.53 | 294.44 | 1.34 | 0.01149 |
| Q9UKU0 | Long-chain-fatty-acid--CoA ligase 6 OS=Homo sapiens OX=9606 GN=ACSL6 PE=2 SV=4 | 2997.24 | 3799.15 | 1.27 | 0.01152 |
| O00567 | Nucleolar protein 56 OS=Homo sapiens OX=9606 GN=NOP56 PE=1 SV=4 | 1421.10 | 1826.79 | 1.29 | 0.01154 |
| F8VVT9 | Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens OX=9606 GN=AGAP2 PE=1 SV=1 | 17.50 | 24.49 | 1.40 | 0.01159 |
| A0A140TA86 | MICOS complex subunit MIC13 OS=Homo sapiens OX=9606 GN=C19orf70 PE=1 SV=1 | 689.77 | 1028.51 | 1.49 | 0.01160 |
| Q9BPW8 | Protein NipSnap homolog 1 OS=Homo sapiens OX=9606 GN=NIPSNAP1 PE=1 SV=1 | 2389.62 | 3133.30 | 1.31 | 0.01170 |
| Q96AN5 | Transmembrane protein 143 OS=Homo sapiens OX=9606 GN=TMEM143 PE=2 SV=1 | 116.48 | 149.12 | 1.28 | 0.01194 |
| O60506 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP | 26.41 | 33.51 | 1.27 | 0.01195 |
| P21675 | Isoform 4 of Transcription initiation factor TFIID subunit 1 OS=Homo sapiens OX=9606 GN=TAF1 | 83.91 | 109.09 | 1.30 | 0.01198 |
| Q8WUY8 | N-acetyltransferase 14 OS=Homo sapiens OX=9606 GN=NAT14 PE=1 SV=1 | 455.46 | 571.80 | 1.26 | 0.01198 |
| Q5T8D3 | Acyl-CoA-binding domain-containing protein 5 OS=Homo sapiens OX=9606 GN=ACBD5 PE=1 SV=1 | 621.92 | 782.82 | 1.26 | 0.01204 |
| Q9UNL2 | Isoform 2 of Translocon-associated protein subunit gamma OS=Homo sapiens OX=9606 GN=SSR3 | 148.11 | 186.53 | 1.26 | 0.01207 |

| | | | | | |
|---|---|---|---|---|---|
| Q9NSE4 | Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=IARS2 PE=1 SV=2 | 4132.84 | 5203.64 | 1.26 | 0.01233 |
| Q08211 | ATP-dependent RNA helicase A OS=Homo sapiens OX=9606 GN=DHX9 PE=1 SV=4 | 7425.00 | 9505.02 | 1.28 | 0.01234 |
| Q8N4Q0 | Prostaglandin reductase 3 OS=Homo sapiens OX=9606 GN=ZADH2 PE=1 SV=1 | 311.09 | 426.11 | 1.37 | 0.01250 |
| Q8N4T8 | Carbonyl reductase family member 4 OS=Homo sapiens OX=9606 GN=CBR4 PE=1 SV=3 | 734.05 | 962.15 | 1.31 | 0.01254 |
| Q96HJ9 | Protein FMC1 homolog OS=Homo sapiens OX=9606 GN=FMC1 PE=1 SV=2 | 87.75 | 120.80 | 1.38 | 0.01263 |
| Q12824 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens OX=9606 GN=SMARCB1 PE=1 SV=2 | 208.95 | 261.32 | 1.25 | 0.01265 |
| Q9H7B2 | Ribosome production factor 2 homolog OS=Homo sapiens OX=9606 GN=RPF2 PE=1 SV=2 | 40.52 | 68.28 | 1.68 | 0.01270 |
| Q92618 | Zinc finger protein 516 OS=Homo sapiens OX=9606 GN=ZNF516 PE=1 SV=1 | 128.54 | 177.34 | 1.38 | 0.01273 |
| O95168 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Homo sapiens OX=9606 GN=NDUFB4 PE=1 SV=3 | 974.42 | 1348.82 | 1.38 | 0.01275 |
| P00505 | Aspartate aminotransferase, mitochondrial OS=Homo sapiens OX=9606 GN=GOT2 PE=1 SV=3 | 9965.94 | 12975.28 | 1.30 | 0.01277 |
| J3QR07 | YTH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=YTHDC1 PE=1 SV=1 | 838.93 | 1065.40 | 1.27 | 0.01278 |
| P15880 | 40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2 | 2971.84 | 3731.89 | 1.26 | 0.01295 |
| P11488 | Guanine nucleotide-binding protein G(t) subunit alpha-1 OS=Homo sapiens OX=9606 GN=GNAT1 PE=1 SV=5 | 6093.27 | 8679.41 | 1.42 | 0.01295 |
| Q14938 | Isoform 6 of Nuclear factor 1 X-type OS=Homo sapiens OX=9606 GN=NFIX | 85.11 | 108.55 | 1.28 | 0.01314 |
| Q5TZA2 | Rootletin OS=Homo sapiens OX=9606 GN=CROCC PE=1 SV=1 | 10601.83 | 15821.05 | 1.49 | 0.01323 |
| Q96T37 | RNA-binding protein 15 OS=Homo sapiens OX=9606 GN=RBM15 PE=1 SV=2 | 673.82 | 845.85 | 1.26 | 0.01327 |
| Q86U86 | Protein polybromo-1 OS=Homo sapiens OX=9606 GN=PBRM1 PE=1 SV=1 | 585.33 | 734.28 | 1.25 | 0.01344 |
| Q9NP73 | Isoform 2 of Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13 OS=Homo sapiens OX=9606 GN=ALG13 | | 267.18 | 346.60 | 1.29724745 |
| P35913 | Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta OS=Homo sapiens OX=9606 GN=PDE6B PE=1 SV=2 | 1415.37 | 2168.90 | 1.53 | 0.01370 |
| Q96AQ8 | Mitochondrial calcium uniporter regulator 1 OS=Homo sapiens OX=9606 GN=MCUR1 PE=1 SV=1 | 159.84 | 263.64 | 1.65 | 0.01385 |
| Q02318 | Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens OX=9606 GN=CYP27A1 PE=1 SV=1 | 485.52 | 652.06 | 1.34 | 0.01392 |
| P42167 | Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2 | 260.55 | 338.35 | 1.30 | 0.01394 |
| Q9Y5A9 | YTH domain-containing family protein 2 OS=Homo sapiens OX=9606 GN=YTHDF2 PE=1 SV=2 | 278.90 | 378.80 | 1.36 | 0.01399 |
| O95164 | Ubiquitin-like protein 3 OS=Homo sapiens OX=9606 GN=UBL3 PE=1 SV=1 | 174.64 | 225.64 | 1.29 | 0.01409 |
| E7ESZ7 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFA10 PE=1 SV=1 | 1518.87 | 2342.73 | 1.54 | 0.01411 |

| | | | | | |
|---|---|---|---|---|---|
| Q5SNT2 | Transmembrane protein 201 OS=Homo sapiens OX=9606 GN=TMEM201 PE=1 SV=1 | 685.19 | 923.77 | 1.35 | 0.01415 |
| Q15059 | Bromodomain-containing protein 3 OS=Homo sapiens OX=9606 GN=BRD3 PE=1 SV=1 | 697.01 | 889.63 | 1.28 | 0.01417 |
| P51553 | Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial OS=Homo sapiens OX=9606 GN=IDH3G PE=1 SV=1 | 1546.46 | 2003.09 | 1.30 | 0.01424 |
| A0A0G2JPF8 | Heterogeneous nuclear ribonucleoprotein C-like 4 OS=Homo sapiens OX=9606 GN=HNRNPCL4 PE=4 SV=1 | 334.34 | 463.55 | 1.39 | 0.01441 |
| Q96RK4 | Isoform 2 of Bardet-Biedl syndrome 4 protein OS=Homo sapiens OX=9606 GN=BBS4 | 242.29 | 307.05 | 1.27 | 0.01448 |
| P20700 | Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2 | 8343.65 | 11350.53 | 1.36 | 0.01464 |
| Q9GZR5 | Elongation of very long chain fatty acids protein 4 OS=Homo sapiens OX=9606 GN=ELOVL4 PE=1 SV=1 | 557.56 | 740.06 | 1.33 | 0.01482 |
| P50914 | 60S ribosomal protein L14 OS=Homo sapiens OX=9606 GN=RPL14 PE=1 SV=4 | 925.47 | 1194.18 | 1.29 | 0.01501 |
| P50416 | Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens OX=9606 GN=CPT1A PE=1 SV=2 | 954.47 | 1271.01 | 1.33 | 0.01507 |
| P12235 | ADP/ATP translocase 1 OS=Homo sapiens OX=9606 GN=SLC25A4 PE=1 SV=4 | 2006.89 | 2831.13 | 1.41 | 0.01507 |
| Q14119 | Vascular endothelial zinc finger 1 OS=Homo sapiens OX=9606 GN=VEZF1 PE=1 SV=2 | 412.55 | 539.88 | 1.31 | 0.01522 |
| Q5VU43 | Isoform 2 of Myomegalin OS=Homo sapiens OX=9606 GN=PDE4DIP | 681.84 | 856.97 | 1.26 | 0.01524 |
| Q9ULX7 | Carbonic anhydrase 14 OS=Homo sapiens OX=9606 GN=CA14 PE=1 SV=1 | 1337.80 | 1812.15 | 1.35 | 0.01530 |
| Q9H5V9 | UPF0428 protein CXorf56 OS=Homo sapiens OX=9606 GN=CXorf56 PE=1 SV=1 | 118.56 | 148.28 | 1.25 | 0.01552 |
| A0A0R4J2E9 | Interphotoreceptor matrix proteoglycan 1 OS=Homo sapiens OX=9606 GN=IMPG1 PE=1 SV=1 | 92.73 | 139.98 | 1.51 | 0.01560 |
| O14681 | Etoposide-induced protein 2.4 homolog OS=Homo sapiens OX=9606 GN=EI24 PE=1 SV=4 | 75.86 | 109.58 | 1.44 | 0.01571 |
| Q8TDN2 | Potassium voltage-gated channel subfamily V member 2 OS=Homo sapiens OX=9606 GN=KCNV2 PE=1 SV=1 | 249.16 | 371.18 | 1.49 | 0.01576 |
| Q02040 | A-kinase anchor protein 17A OS=Homo sapiens OX=9606 GN=AKAP17A PE=1 SV=2 | 245.87 | 311.72 | 1.27 | 0.01597 |
| O75880 | Protein SCO1 homolog, mitochondrial OS=Homo sapiens OX=9606 GN=SCO1 PE=1 SV=1 | 394.97 | 515.12 | 1.30 | 0.01611 |
| Q9NV79 | Protein-L-isoaspartate O-methyltransferase domain-containing protein 2 OS=Homo sapiens OX=9606 GN=PCMTD2 PE=2 SV=2 | 161.27 | 226.06 | 1.40 | 0.01646 |
| Q9UGM6 | Tryptophan--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=WARS2 PE=1 SV=1 | 169.56 | 234.18 | 1.38 | 0.01650 |
| A8MXP9 | Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 | 8964.81 | 11239.55 | 1.25 | 0.01651 |
| Q9BXC9 | Bardet-Biedl syndrome 2 protein OS=Homo sapiens OX=9606 GN=BBS2 PE=1 SV=1 | 567.02 | 709.82 | 1.25 | 0.01659 |
| B4DR61 | cDNA FLJ59739, highly similar to Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens OX=9606 GN=SEC61A1 PE=1 SV=1 | 456.85 | 600.92 | 1.32 | 0.01687 |
| Q8TBF4 | Zinc finger CCHC-type and RNA-binding motif-containing protein 1 OS=Homo sapiens OX=9606 GN=ZCRB1 PE=1 SV=2 | 113.95 | 153.35 | 1.35 | 0.01704 |

| | | | | | |
|---|---|---|---|---|---|
| O43766 | Lipoyl synthase, mitochondrial OS=Homo sapiens OX=9606 GN=LIAS PE=1 SV=3 | 9.67 | 12.79 | 1.32 | 0.01710 |
| Q96ER9 | Coiled-coil domain-containing protein 51 OS=Homo sapiens OX=9606 GN=CCDC51 PE=1 SV=2 | 278.69 | 350.81 | 1.26 | 0.01732 |
| P51970 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Homo sapiens OX=9606 GN=NDUFA8 PE=1 SV=3 | 1087.43 | 1631.25 | 1.50 | 0.01732 |
| Q8IW92 | Beta-galactosidase-1-like protein 2 OS=Homo sapiens OX=9606 GN=GLB1L2 PE=2 SV=1 | 146.73 | 194.41 | 1.32 | 0.01743 |
| P62917 | 60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=2 | 2031.33 | 2556.63 | 1.26 | 0.01744 |
| Q6ZU65 | Ubinuclein-2 OS=Homo sapiens OX=9606 GN=UBN2 PE=1 SV=2 | 70.68 | 90.12 | 1.27 | 0.01750 |
| P43897 | Elongation factor Ts, mitochondrial OS=Homo sapiens OX=9606 GN=TSFM PE=1 SV=2 | 821.75 | 1267.79 | 1.54 | 0.01779 |
| Q9NVH1 | DnaJ homolog subfamily C member 11 OS=Homo sapiens OX=9606 GN=DNAJC11 PE=1 SV=2 | 1604.84 | 2040.62 | 1.27 | 0.01787 |
| P48047 | ATP synthase subunit O, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PO PE=1 SV=1 | 4586.82 | 6567.65 | 1.43 | 0.01806 |
| Q99766 | ATP synthase subunit s, mitochondrial OS=Homo sapiens OX=9606 GN=DMAC2L PE=1 SV=3 | 453.22 | 590.28 | 1.30 | 0.01809 |
| Q8TC12 | Retinol dehydrogenase 11 OS=Homo sapiens OX=9606 GN=RDH11 PE=1 SV=2 | 1330.02 | 1692.86 | 1.27 | 0.01819 |
| Q8IV63 | Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens OX=9606 GN=VRK3 PE=1 SV=2 | 200.20 | 261.20 | 1.30 | 0.01822 |
| P09874 | Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4 | 9120.96 | 12247.68 | 1.34 | 0.01829 |
| Q12791 | Isoform 7 of Calcium-activated potassium channel subunit alpha-1 OS=Homo sapiens OX=9606 GN=KCNMA1 | 69.85 | 125.61 | 1.80 | 0.01870 |
| O15537 | Retinoschisin OS=Homo sapiens OX=9606 GN=RS1 PE=1 SV=2 | 3679.26 | 5144.49 | 1.40 | 0.01879 |
| Q8NBU5 | ATPase family AAA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ATAD1 PE=1 SV=1 | 986.91 | 1262.03 | 1.28 | 0.01941 |
| H7C1N3 | BET1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=BET1 PE=1 SV=1 | 232.18 | 304.81 | 1.31 | 0.01943 |
| P56381 | ATP synthase subunit epsilon, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1E PE=1 SV=2 | 574.24 | 840.50 | 1.46 | 0.01944 |
| Q9NVV4 | Poly(A) RNA polymerase, mitochondrial OS=Homo sapiens OX=9606 GN=MTPAP PE=1 SV=1 | 344.21 | 485.88 | 1.41 | 0.01955 |
| P49821 | NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFV1 PE=1 SV=4 | 4213.15 | 5757.12 | 1.37 | 0.01958 |
| Q9Y6M9 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens OX=9606 GN=NDUFB9 PE=1 SV=3 | 946.06 | 1199.22 | 1.27 | 0.01970 |
| F5GXJ1 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS7 PE=1 SV=1 | 1174.69 | 1632.12 | 1.39 | 0.01986 |
| Q01538 | Isoform 2 of Myelin transcription factor 1 OS=Homo sapiens OX=9606 GN=MYT1 | 150.39 | 190.15 | 1.26 | 0.02007 |
| P50213 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1 | 3685.57 | 4729.34 | 1.28 | 0.02011 |

| | | | | | |
|---|---|---|---|---|---|
| P40926 | Malate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3 | 7026.53 | 9236.31 | 1.31 | 0.02024 |
| Q5BKZ1 | DBIRD complex subunit ZNF326 OS=Homo sapiens OX=9606 GN=ZNF326 PE=1 SV=2 | 818.26 | 1115.44 | 1.36 | 0.02031 |
| Q9NW81 | Isoform 4 of Distal membrane-arm assembly complex protein 2 OS=Homo sapiens OX=9606 GN=DMAC2 | 103.53 | 140.94 | 1.36 | 0.02037 |
| P21589 | 5'-nucleotidase OS=Homo sapiens OX=9606 GN=NT5E PE=1 SV=1 | 1411.74 | 1832.40 | 1.30 | 0.02112 |
| P35250 | Replication factor C subunit 2 OS=Homo sapiens OX=9606 GN=RFC2 PE=1 SV=3 | 168.94 | 221.13 | 1.31 | 0.02117 |
| A0A0G2JPT5 | Cell cycle checkpoint protein RAD17 OS=Homo sapiens OX=9606 GN=RAD17 PE=1 SV=1 | 44.77 | 60.08 | 1.34 | 0.02117 |
| Q53H12 | Acylglycerol kinase, mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=2 | 1586.43 | 2012.75 | 1.27 | 0.02132 |
| P55809 | Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens OX=9606 GN=OXCT1 PE=1 SV=1 | 3830.84 | 5097.67 | 1.33 | 0.02135 |
| Q9Y5X4 | Photoreceptor-specific nuclear receptor OS=Homo sapiens OX=9606 GN=NR2E3 PE=1 SV=1 | 350.86 | 493.98 | 1.41 | 0.02165 |
| P09669 | Cytochrome c oxidase subunit 6C OS=Homo sapiens OX=9606 GN=COX6C PE=1 SV=2 | 1630.25 | 2263.91 | 1.39 | 0.02173 |
| P24539 | ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PB PE=1 SV=2 | 3354.29 | 4531.22 | 1.35 | 0.02187 |
| Q7Z3D6 | Isoform 2 of D-glutamate cyclase, mitochondrial OS=Homo sapiens OX=9606 GN=DGLUCY | 838.71 | 1135.88 | 1.35 | 0.02196 |
| P39023 | 60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2 | 3527.34 | 4503.28 | 1.28 | 0.02196 |
| P24310 | Cytochrome c oxidase subunit 7A1, mitochondrial OS=Homo sapiens OX=9606 GN=COX7A1 PE=1 SV=2 | 142.06 | 185.56 | 1.31 | 0.02204 |
| Q8N8Y2 | V-type proton ATPase subunit d 2 OS=Homo sapiens OX=9606 GN=ATP6V0D2 PE=2 SV=1 | 12.85 | 18.61 | 1.45 | 0.02232 |
| P21912 | Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens OX=9606 GN=SDHB PE=1 SV=3 | 2373.88 | 3233.29 | 1.36 | 0.02284 |
| Q9BQ75 | Protein CMSS1 OS=Homo sapiens OX=9606 GN=CMSS1 PE=1 SV=2 | 198.62 | 248.66 | 1.25 | 0.02287 |
| A0A087WUC6 | Signal peptidase complex subunit 2 OS=Homo sapiens OX=9606 GN=SPCS2 PE=1 SV=1 | 1038.68 | 1341.35 | 1.29 | 0.02325 |
| Q9P0M6 | Core histone macro-H2A.2 OS=Homo sapiens OX=9606 GN=H2AFY2 PE=1 SV=3 | 2055.40 | 2670.11 | 1.30 | 0.02333 |
| P14866 | Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=2 | 8054.42 | 10695.98 | 1.33 | 0.02345 |
| Q9NP92 | 39S ribosomal protein S30, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS30 PE=1 SV=2 | 237.94 | 303.61 | 1.28 | 0.02381 |
| P82914 | 28S ribosomal protein S15, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS15 PE=1 SV=1 | 359.90 | 463.56 | 1.29 | 0.02389 |
| Q9BYV7 | Beta,beta-carotene 9',10'-oxygenase OS=Homo sapiens OX=9606 GN=BCO2 PE=1 SV=5 | 173.67 | 226.24 | 1.30 | 0.02406 |
| H3BN98 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=2 | 1218.14 | 1550.85 | 1.27 | 0.02423 |
| Q9Y2D8 | Afadin- and alpha-actinin-binding protein OS=Homo sapiens OX=9606 GN=SSX2IP PE=1 SV=3 | 440.93 | 580.45 | 1.32 | 0.02441 |

| | | | | | |
|---|---|---|---|---|---|
| Q8N565 | Isoform 2 of Melanoregulin OS=Homo sapiens OX=9606 GN=MREG | 47.78 | 62.05 | 1.30 | 0.02465 |
| O96000 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens OX=9606 GN=NDUFB10 PE=1 SV=3 | 1689.40 | 2336.24 | 1.38 | 0.02466 |
| Q16795 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFA9 PE=1 SV=2 | 3946.99 | 5509.63 | 1.40 | 0.02477 |
| Q9BVA0 | Katanin p80 WD40 repeat-containing subunit B1 OS=Homo sapiens OX=9606 GN=KATNB1 PE=1 SV=1 | 41.81 | 52.88 | 1.26 | 0.02491 |
| P28331 | Isoform 2 of NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS1 | 7383.60 | 9577.38 | 1.30 | 0.02493 |
| Q16718 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=3 | 908.78 | 1300.59 | 1.43 | 0.02503 |
| O43324 | Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens OX=9606 GN=EEF1E1 PE=1 SV=1 | 308.89 | 392.12 | 1.27 | 0.02537 |
| Q08AF3 | Schlafen family member 5 OS=Homo sapiens OX=9606 GN=SLFN5 PE=1 SV=1 | 64.58 | 88.01 | 1.36 | 0.02542 |
| Q9HC52 | Chromobox protein homolog 8 OS=Homo sapiens OX=9606 GN=CBX8 PE=1 SV=3 | 746.02 | 942.06 | 1.26 | 0.02548 |
| Q14149 | MORC family CW-type zinc finger protein 3 OS=Homo sapiens OX=9606 GN=MORC3 PE=1 SV=3 | 16.25 | 23.32 | 1.44 | 0.02568 |
| P35398 | Isoform 2 of Nuclear receptor ROR-alpha OS=Homo sapiens OX=9606 GN=RORA | 80.34 | 108.53 | 1.35 | 0.02570 |
| D6RGC4 | E3 ubiquitin-protein ligase MARCH1 OS=Homo sapiens OX=9606 GN=MARCH1 PE=1 SV=1 | 22.26 | 31.00 | 1.39 | 0.02579 |
| Q9H7N4 | Splicing factor, arginine/serine-rich 19 OS=Homo sapiens OX=9606 GN=SCAF1 PE=1 SV=3 | 649.15 | 824.12 | 1.27 | 0.02640 |
| Q9NRC6 | Spectrin beta chain, non-erythrocytic 5 OS=Homo sapiens OX=9606 GN=SPTBN5 PE=1 SV=2 | 1119.69 | 1456.17 | 1.30 | 0.02720 |
| P25445 | Tumor necrosis factor receptor superfamily member 6 OS=Homo sapiens OX=9606 GN=FAS PE=1 SV=1 | 64.73 | 93.16 | 1.44 | 0.02726 |
| Q96A23-2 | Isoform 2 of Copine-4 OS=Homo sapiens OX=9606 GN=CPNE4 | 20.00 | 28.66 | 1.43 | 0.02766 |
| A0A0B4J2F0 | Protein PIGBOS1 OS=Homo sapiens OX=9606 GN=PIGBOS1 PE=3 SV=1 | 83.66 | 186.85 | 2.23 | 0.02767 |
| Q01850 | Cerebellar degeneration-related protein 2 OS=Homo sapiens OX=9606 GN=CDR2 PE=1 SV=2 | 138.95 | 193.95 | 1.40 | 0.02770 |
| Q9BVV7 | Mitochondrial import inner membrane translocase subunit Tim21 OS=Homo sapiens OX=9606 GN=TIMM21 PE=1 SV=1 | 118.01 | 150.15 | 1.27 | 0.02781 |
| P86397 | Hydroxyacyl-thioester dehydratase type 2, mitochondrial OS=Homo sapiens OX=9606 GN=HTD2 PE=1 SV=1 | 124.44 | 165.96 | 1.33 | 0.02806 |
| A0A2U3TZT0 | Zinc finger protein 385B OS=Homo sapiens OX=9606 GN=ZNF385B PE=1 SV=1 | 300.66 | 384.93 | 1.28 | 0.02864 |
| Q8N8R7 | ARL14 effector protein OS=Homo sapiens OX=9606 GN=ARL14EP PE=1 SV=1 | 114.81 | 158.66 | 1.38 | 0.02867 |
| Q96A72 | Protein mago nashi homolog 2 OS=Homo sapiens OX=9606 GN=MAGOHB PE=1 SV=1 | 725.32 | 953.53 | 1.31 | 0.02889 |
| Q8TAQ2 | SWI/SNF complex subunit SMARCC2 OS=Homo sapiens OX=9606 GN=SMARCC2 PE=1 SV=1 | 17.85 | 24.79 | 1.39 | 0.02903 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| A0A075B6Q7 | Disrupted in schizophrenia 1 protein OS=Homo sapiens OX=9606 GN=DISC1 PE=1 SV=1 | 53.56 | 71.24 | 1.33 | 0.02923 |
| D6RDH5 | Guanine nucleotide-binding protein subunit gamma OS=Homo sapiens OX=9606 GN=GNGT2 PE=1 SV=1 | 493.66 | 664.79 | 1.35 | 0.02937 |
| F8W930 | Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2 PE=1 SV=1 | 1514.45 | 1975.42 | 1.30 | 0.02956 |
| Q9NX40 | OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 | 896.12 | 1142.06 | 1.27 | 0.02982 |
| P17568 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Homo sapiens OX=9606 GN=NDUFB7 PE=1 SV=4 | 991.53 | 1313.44 | 1.32 | 0.02995 |
| Q8IWN7 | Retinitis pigmentosa 1-like 1 protein OS=Homo sapiens OX=9606 GN=RP1L1 PE=1 SV=5 | 374.50 | 477.47 | 1.27 | 0.03000 |
| O43920 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens OX=9606 GN=NDUFS5 PE=1 SV=3 | 551.80 | 750.25 | 1.36 | 0.03162 |
| P49411 | Elongation factor Tu, mitochondrial OS=Homo sapiens OX=9606 GN=TUFM PE=1 SV=2 | 4369.87 | 6022.78 | 1.38 | 0.03172 |
| Q9ULU4 | Isoform 10 of Protein kinase C-binding protein 1 OS=Homo sapiens OX=9606 GN=ZMYND8 | 776.07 | 995.12 | 1.28 | 0.03182 |
| P18077 | 60S ribosomal protein L35a OS=Homo sapiens OX=9606 GN=RPL35A PE=1 SV=2 | 858.11 | 1158.87 | 1.35 | 0.03214 |
| O95182 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens OX=9606 GN=NDUFA7 PE=1 SV=3 | 1481.76 | 1968.81 | 1.33 | 0.03217 |
| Q9BWE0 | Isoform 2 of Replication initiator 1 OS=Homo sapiens OX=9606 GN=REPIN1 | 246.48 | 353.16 | 1.43 | 0.03234 |
| P61254 | 60S ribosomal protein L26 OS=Homo sapiens OX=9606 GN=RPL26 PE=1 SV=1 | 790.13 | 1117.43 | 1.41 | 0.03242 |
| Q9BVG8 | Isoform 5 of Kinesin-like protein KIFC3 OS=Homo sapiens OX=9606 GN=KIFC3 | 60.30 | 79.70 | 1.32 | 0.03247 |
| O00257 | E3 SUMO-protein ligase CBX4 OS=Homo sapiens OX=9606 GN=CBX4 PE=1 SV=3 | 121.17 | 175.49 | 1.45 | 0.03304 |
| Q96ND0 | Protein FAM210A OS=Homo sapiens OX=9606 GN=FAM210A PE=1 SV=2 | 525.75 | 675.19 | 1.28 | 0.03305 |
| A0A2Y9D025 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens OX=9606 GN=NDUFA6 PE=4 SV=1 | 1085.90 | 1548.14 | 1.43 | 0.03310 |
| Q8IY26 | Phospholipid phosphatase 6 OS=Homo sapiens OX=9606 GN=PLPP6 PE=1 SV=3 | 40.46 | 51.61 | 1.28 | 0.03337 |
| A6NDA9 | Isoform 2 of Leucine-rich repeat, immunoglobulin-like domain and transmembrane domain-containing protein 2 OS=Homo sapiens OX=9606 GN=LRIT2 | 190.45 | 301.63 | 1.58 | 0.03376 |
| E9PN58 | NAD-dependent protein deacetylase sirtuin-3, mitochondrial OS=Homo sapiens OX=9606 GN=SIRT3 PE=1 SV=1 | 14.48 | 19.64 | 1.36 | 0.03418 |
| Q96JP9 | Cadherin-related family member 1 OS=Homo sapiens OX=9606 GN=CDHR1 PE=1 SV=2 | 93.20 | 133.60 | 1.43 | 0.03424 |
| A6NCE7 | Microtubule-associated proteins 1A/1B light chain 3 beta 2 OS=Homo sapiens OX=9606 GN=MAP1LC3B2 PE=2 SV=1 | 758.11 | 997.87 | 1.32 | 0.03443 |
| Q9UIV1 | CCR4-NOT transcription complex subunit 7 OS=Homo sapiens OX=9606 GN=CNOT7 PE=1 SV=3 | 35.00 | 44.95 | 1.28 | 0.03469 |
| P61129 | Zinc finger CCCH domain-containing protein 6 OS=Homo sapiens OX=9606 GN=ZC3H6 PE=1 SV=2 | 41.59 | 54.47 | 1.31 | 0.03528 |
| P23786 | Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens OX=9606 GN=CPT2 PE=1 SV=2 | 1846.74 | 2412.11 | 1.31 | 0.03554 |

| | | | | | |
|---|---|---|---|---|---|
| H0Y886 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=NDUFB5 PE=1 SV=1 | 686.26 | 930.55 | 1.36 | 0.03583 |
| O75306 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS2 PE=1 SV=2 | 3339.43 | 4239.08 | 1.27 | 0.03609 |
| A6NCL7 | Ankyrin repeat domain-containing protein 33B OS=Homo sapiens OX=9606 GN=ANKRD33B PE=3 SV=1 | 112.12 | 143.49 | 1.28 | 0.03611 |
| Q4U2R6 | 39S ribosomal protein L51, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL51 PE=1 SV=1 | 65.30 | 82.45 | 1.26 | 0.03621 |
| Q5T9L3 | Isoform 2 of Protein wntless homolog OS=Homo sapiens OX=9606 GN=WLS | 209.52 | 265.35 | 1.27 | 0.03652 |
| Q96DA6 | Mitochondrial import inner membrane translocase subunit TIM14 OS=Homo sapiens OX=9606 GN=DNAJC19 PE=1 SV=3 | 659.50 | 831.13 | 1.26 | 0.03684 |
| Q6UW78 | Ubiquinol-cytochrome-c reductase complex assembly factor 3 OS=Homo sapiens OX=9606 GN=UQCC3 PE=1 SV=2 | 4.60 | 6.78 | 1.47 | 0.03693 |
| Q96EK4 | THAP domain-containing protein 11 OS=Homo sapiens OX=9606 GN=THAP11 PE=1 SV=2 | 40.34 | 53.56 | 1.33 | 0.03707 |
| Q9Y6M7 | Isoform 13 of Sodium bicarbonate cotransporter 3 OS=Homo sapiens OX=9606 GN=SLC4A7 | 986.63 | 1253.29 | 1.27 | 0.03721 |
| Q9H0M0 | NEDD4-like E3 ubiquitin-protein ligase WWP1 OS=Homo sapiens OX=9606 GN=WWP1 PE=1 SV=1 | 58.12 | 73.06 | 1.26 | 0.03769 |
| O43490 | Isoform 6 of Prominin-1 OS=Homo sapiens OX=9606 GN=PROM1 | 1373.75 | 2156.33 | 1.57 | 0.03829 |
| P14415 | Sodium/potassium-transporting ATPase subunit beta-2 OS=Homo sapiens OX=9606 GN=ATP1B2 PE=1 SV=3 | 3856.77 | 4906.22 | 1.27 | 0.03844 |
| Q96FJ2 | Dynein light chain 2, cytoplasmic OS=Homo sapiens OX=9606 GN=DYNLL2 PE=1 SV=1 | 1738.55 | 2206.07 | 1.27 | 0.03844 |
| Q5TEC6 | Histone H3 OS=Homo sapiens OX=9606 GN=HIST2H3PS2 PE=1 SV=1 | 1995.02 | 2639.12 | 1.32 | 0.03846 |
| Q92522 | Histone H1x OS=Homo sapiens OX=9606 GN=H1FX PE=1 SV=1 | 3692.40 | 4733.97 | 1.28 | 0.03874 |
| P46199 | Translation initiation factor IF-2, mitochondrial OS=Homo sapiens OX=9606 GN=MTIF2 PE=1 SV=2 | 298.78 | 403.10 | 1.35 | 0.03885 |
| O60783 | 28S ribosomal protein S14, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS14 PE=1 SV=1 | 15.81 | 20.10 | 1.27 | 0.03888 |
| P45880 | Isoform 1 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2 | 9309.14 | 11981.46 | 1.29 | 0.03903 |
| P13073 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens OX=9606 GN=COX4I1 PE=1 SV=1 | 3735.93 | 5071.00 | 1.36 | 0.03960 |
| O94925 | Glutaminase kidney isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS PE=1 SV=1 | 2301.15 | 3158.11 | 1.37 | 0.03970 |
| P03928 | ATP synthase protein 8 OS=Homo sapiens OX=9606 GN=MT-ATP8 PE=1 SV=1 | 607.08 | 835.02 | 1.38 | 0.04006 |
| Q9UJS0 | Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens OX=9606 GN=SLC25A13 PE=1 SV=2 | 2378.74 | 3155.24 | 1.33 | 0.04022 |
| Q9BWS9 | Isoform 2 of Chitinase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CHID1 | 417.77 | 559.38 | 1.34 | 0.04092 |

| | | | | | |
|---|---|---|---|---|---|
| O14730 | Serine/threonine-protein kinase RIO3 OS=Homo sapiens OX=9606 GN=RIOK3 PE=1 SV=2 | 7.62 | 11.06 | 1.45 | 0.04094 |
| Q9NWT8 | Aurora kinase A-interacting protein OS=Homo sapiens OX=9606 GN=AURKAIP1 PE=1 SV=1 | 96.36 | 137.27 | 1.42 | 0.04117 |
| P38159 | RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=3 | 6283.71 | 8055.48 | 1.28 | 0.04129 |
| O43676 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 OS=Homo sapiens OX=9606 GN=NDUFB3 PE=1 SV=3 | 632.75 | 888.93 | 1.40 | 0.04177 |
| C9JFV4 | Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens OX=9606 GN=PELP1 PE=1 SV=2 | 296.23 | 383.23 | 1.29 | 0.04289 |
| Q5JTZ9 | Alanine--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=AARS2 PE=1 SV=1 | 905.91 | 1152.73 | 1.27 | 0.04309 |
| Q9ULG6 | Isoform 5 of Cell cycle progression protein 1 OS=Homo sapiens OX=9606 GN=CCPG1 | 26.84 | 45.87 | 1.71 | 0.04313 |
| Q9BWF3 | RNA-binding protein 4 OS=Homo sapiens OX=9606 GN=RBM4 PE=1 SV=1 | 106.36 | 139.05 | 1.31 | 0.04350 |
| E9PR30 | 40S ribosomal protein S30 OS=Homo sapiens OX=9606 GN=FAU PE=1 SV=1 | 182.70 | 295.32 | 1.62 | 0.04362 |
| O94929 | Actin-binding LIM protein 3 OS=Homo sapiens OX=9606 GN=ABLIM3 PE=1 SV=3 | 558.81 | 736.30 | 1.32 | 0.04386 |
| O95139 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Homo sapiens OX=9606 GN=NDUFB6 PE=1 SV=3 | 1285.82 | 1611.76 | 1.25 | 0.04495 |
| O60563 | Cyclin-T1 OS=Homo sapiens OX=9606 GN=CCNT1 PE=1 SV=1 | 19.04 | 24.51 | 1.29 | 0.04542 |
| Q13627 | Isoform 1 of Dual specificity tyrosine-phosphorylation-regulated kinase 1A OS=Homo sapiens OX=9606 GN=DYRK1A | 206.01 | 259.04 | 1.26 | 0.04595 |
| A8CG34 | Nuclear envelope pore membrane protein POM 121C OS=Homo sapiens OX=9606 GN=POM121C PE=1 SV=3 | 153.47 | 195.31 | 1.27 | 0.04671 |
| O75964 | ATP synthase subunit g, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5MG PE=1 SV=3 | 1412.52 | 1819.90 | 1.29 | 0.04704 |
| Q5VST6 | Isoform 2 of Alpha/beta hydrolase domain-containing protein 17B OS=Homo sapiens OX=9606 GN=ABHD17B | 29.79 | 42.10 | 1.41 | 0.04774 |
| Q03001 | Isoform 8 of Dystonin OS=Homo sapiens OX=9606 GN=DST | 159.52 | 215.65 | 1.35 | 0.04826 |
| O15042 | U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens OX=9606 GN=U2SURP PE=1 SV=2 | 1291.63 | 1624.79 | 1.26 | 0.04839 |
| O60907 | Isoform 2 of F-box-like/WD repeat-containing protein TBL1X OS=Homo sapiens OX=9606 GN=TBL1X | 27.97 | 35.49 | 1.27 | 0.04851 |
| O15523 | ATP-dependent RNA helicase DDX3Y OS=Homo sapiens OX=9606 GN=DDX3Y PE=1 SV=2 | 98.58 | 187.93 | 1.91 | 0.04900 |
| Q15696 | U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit-related protein 2 OS=Homo sapiens OX=9606 GN=ZRSR2 PE=1 SV=2 | 61.37 | 82.41 | 1.34 | 0.04906 |
| P11169 | Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens OX=9606 GN=SLC2A3 PE=1 SV=1 | 586.42 | 762.08 | 1.30 | 0.04975 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; *P*<0.05

**Supplementary Table 6.** Extended mass spectrometry data on significantly up-regulated proteins in the temporal cortex of Alzheimer's patients compared to cognitively normal controls.

| **Accession** | **Description** | **AD (Means)** | **NC (Means)** | **FC** | ***P*** |
|---|---|---|---|---|---|
| Q08629 | Testican-1 OS=Homo sapiens OX=9606 GN=SPOCK1 PE=1 SV=1 | 105.77 | 75.72 | 1.40 | 3.473E-06 |
| Q9BQ69 | ADP-ribose glycohydrolase MACROD1 OS=Homo sapiens OX=9606 GN=MACROD1 PE=1 SV=2 | 536.38 | 352.00 | 1.52 | 7.918E-06 |
| P55209 | Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 | 898.47 | 724.28 | 1.24 | 1.185E-05 |
| E9PLM6 | Midkine OS=Homo sapiens OX=9606 GN=MDK PE=1 SV=1 | 252.71 | 64.77 | 3.90 | 1.708E-05 |
| P10636 | Isoform Tau-B of Microtubule-associated protein tau OS=Homo sapiens OX=9606 GN=MAPT | 1314.76 | 775.57 | 1.70 | 4.838E-05 |
| P26038 | Moesin OS=Homo sapiens OX=9606 GN=MSN PE=1 SV=3 | 5392.89 | 4063.81 | 1.33 | 4.862E-05 |
| Q13501 | Sequestosome-1 OS=Homo sapiens OX=9606 GN=SQSTM1 PE=1 SV=1 | 569.61 | 384.19 | 1.48 | 8.192E-05 |
| Q15149 | Isoform 3 of Plectin OS=Homo sapiens OX=9606 GN=PLEC | 54659.35 | 45015.76 | 1.21 | 8.867E-05 |
| Q8NBJ4 | Golgi membrane protein 1 OS=Homo sapiens OX=9606 GN=GOLM1 PE=1 SV=1 | 113.85 | 85.93 | 1.32 | 9.491E-05 |
| Q86WU2 | Probable D-lactate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=LDHD PE=1 SV=1 | 267.92 | 212.95 | 1.26 | 0.00010 |
| P35754 | Glutaredoxin-1 OS=Homo sapiens OX=9606 GN=GLRX PE=1 SV=2 | 137.25 | 112.96 | 1.22 | 0.00014 |
| Q5VZK9 | F-actin-uncapping protein LRRC16A OS=Homo sapiens OX=9606 GN=CARMIL1 PE=1 SV=1 | 290.16 | 241.33 | 1.20 | 0.00015 |
| P02795 | Metallothionein-2 OS=Homo sapiens OX=9606 GN=MT2A PE=1 SV=1 | 1151.26 | 742.94 | 1.55 | 0.00016 |
| Q9H4F8 | Isoform 2 of SPARC-related modular calcium-binding protein 1 OS=Homo sapiens OX=9606 GN=SMOC1 | 502.37 | 316.93 | 1.59 | 0.00017 |
| Q9NRQ2 | Phospholipid scramblase 4 OS=Homo sapiens OX=9606 GN=PLSCR4 PE=1 SV=2 | 25.40 | 15.74 | 1.61 | 0.00019 |
| Q15691 | Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens OX=9606 GN=MAPRE1 PE=1 SV=3 | 205.72 | 168.37 | 1.22 | 0.00020 |
| Q9Y2Z9 | Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial OS=Homo sapiens OX=9606 GN=COQ6 PE=1 SV=2 | 91.33 | 69.77 | 1.31 | 0.00025 |
| Q8N612 | Isoform 2 of FTS and Hook-interacting protein OS=Homo sapiens OX=9606 GN=FAM160A2 | 56.64 | 41.74 | 1.36 | 0.00029 |
| G3V1V0 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 | 2766.74 | 2069.34 | 1.34 | 0.00031 |
| P04908 | Histone H2A type 1-B/E OS=Homo sapiens OX=9606 GN=HIST1H2AB PE=1 SV=2 | 1078.32 | 570.92 | 1.89 | 0.00031 |
| Q9Y4J8 | Isoform 10 of Dystrobrevin alpha OS=Homo sapiens OX=9606 GN=DTNA | 313.27 | 246.66 | 1.27 | 0.00034 |
| Q9ULH7 | Myocardin-related transcription factor B OS=Homo sapiens OX=9606 GN=MRTFB PE=1 SV=3 | 1149.42 | 945.51 | 1.22 | 0.00035 |
| F6UJY1 | Putative hydroxypyruvate isomerase OS=Homo sapiens OX=9606 GN=HYI PE=1 SV=1 | 111.91 | 89.75 | 1.25 | 0.00040 |

| | | | | | |
|---|---|---|---|---|---|
| Q96AQ6 | Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens OX=9606 GN=PBXIP1 PE=1 SV=1 | 1994.79 | 1570.55 | 1.27 | 0.00044 |
| P50552 | Vasodilator-stimulated phosphoprotein OS=Homo sapiens OX=9606 GN=VASP PE=1 SV=3 | 293.35 | 238.10 | 1.23 | 0.00046 |
| O75348 | V-type proton ATPase subunit G 1 OS=Homo sapiens OX=9606 GN=ATP6V1G1 PE=1 SV=3 | 645.45 | 504.41 | 1.28 | 0.00047 |
| F6SYF8 | Dickkopf-related protein 3 OS=Homo sapiens OX=9606 GN=DKK3 PE=1 SV=1 | 662.78 | 496.04 | 1.34 | 0.00047 |
| J3KPP4 | Cisplatin resistance-associated overexpressed protein, isoform CRA_b OS=Homo sapiens OX=9606 GN=LUC7L3 PE=1 SV=1 | 93.64 | 70.94 | 1.32 | 0.00049 |
| P14649 | Myosin light chain 6B OS=Homo sapiens OX=9606 GN=MYL6B PE=1 SV=1 | 1100.43 | 915.51 | 1.20 | 0.00052 |
| O14558 | Heat shock protein beta-6 OS=Homo sapiens OX=9606 GN=HSPB6 PE=1 SV=2 | 348.88 | 275.31 | 1.27 | 0.00053 |
| A0A0G2JPD5 | Microtubule-associated protein OS=Homo sapiens OX=9606 GN=MAPT PE=1 SV=1 | 17974.26 | 13117.27 | 1.37 | 0.00055 |
| Q9H299 | SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens OX=9606 GN=SH3BGRL3 PE=1 SV=1 | 673.91 | 559.75 | 1.20 | 0.00057 |
| P21246 | Pleiotrophin OS=Homo sapiens OX=9606 GN=PTN PE=1 SV=1 | 342.76 | 241.05 | 1.42 | 0.00058 |
| P24043 | Laminin subunit alpha-2 OS=Homo sapiens OX=9606 GN=LAMA2 PE=1 SV=4 | 496.79 | 400.82 | 1.24 | 0.00059 |
| P56277 | Cx9C motif-containing protein 4 OS=Homo sapiens OX=9606 GN=CMC4 PE=1 SV=1 | 232.85 | 190.25 | 1.22 | 0.00062 |
| P02792 | Ferritin light chain OS=Homo sapiens OX=9606 GN=FTL PE=1 SV=2 | 3409.31 | 2727.13 | 1.25 | 0.00064 |
| Q9NWH9 | SAFB-like transcription modulator OS=Homo sapiens OX=9606 GN=SLTM PE=1 SV=2 | 163.59 | 122.92 | 1.33 | 0.00064 |
| P24593 | Insulin-like growth factor-binding protein 5 OS=Homo sapiens OX=9606 GN=IGFBP5 PE=1 SV=1 | 105.30 | 68.40 | 1.54 | 0.00065 |
| Q9UGM6 | Tryptophan--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=WARS2 PE=1 SV=1 | 183.36 | 152.28 | 1.20 | 0.00069 |
| Q6DD88 | Atlastin-3 OS=Homo sapiens OX=9606 GN=ATL3 PE=1 SV=1 | 216.04 | 173.65 | 1.24 | 0.00070 |
| H7BYT1 | Casein kinase I isoform delta OS=Homo sapiens OX=9606 GN=CSNK1D PE=1 SV=2 | 262.03 | 211.19 | 1.24 | 0.00071 |
| Q9UQE7 | Structural maintenance of chromosomes protein 3 OS=Homo sapiens OX=9606 GN=SMC3 PE=1 SV=2 | 810.43 | 672.43 | 1.21 | 0.00072 |
| Q9Y2R0 | Cytochrome c oxidase assembly factor 3 homolog, mitochondrial OS=Homo sapiens OX=9606 GN=COA3 PE=1 SV=1 | 512.25 | 411.97 | 1.24 | 0.00072 |
| Q96DF8 | Splicing factor ESS-2 homolog OS=Homo sapiens OX=9606 GN=ESS2 PE=1 SV=1 | 52.93 | 38.36 | 1.38 | 0.00074 |
| P07108 | Isoform 5 of Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI | 5776.54 | 4084.47 | 1.41 | 0.00083 |
| F8VWL3 | FYVE, RhoGEF and PH domain-containing protein 4 OS=Homo sapiens OX=9606 GN=FGD4 PE=1 SV=1 | 224.62 | 187.00 | 1.20 | 0.00086 |
| P08670 | Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4 | 24462.10 | 16885.08 | 1.45 | 0.00089 |
| P28838 | Cytosol aminopeptidase OS=Homo sapiens OX=9606 GN=LAP3 PE=1 SV=3 | 2818.43 | 2321.38 | 1.21 | 0.00091 |
| Q14019 | Coactosin-like protein OS=Homo sapiens OX=9606 GN=COTL1 PE=1 SV=3 | 1528.92 | 1197.70 | 1.28 | 0.00093 |
| O15061 | Synemin OS=Homo sapiens OX=9606 GN=SYNM PE=1 SV=2 | 1298.68 | 985.61 | 1.32 | 0.00093 |

| | | | | | |
|---|---|---|---|---|---|
| Q96ME1 | F-box/LRR-repeat protein 18 OS=Homo sapiens OX=9606 GN=FBXL18 PE=1 SV=2 | 401.29 | 286.78 | 1.40 | 0.00095 |
| A0A1B0GV68 | FERM, ARHGEF and pleckstrin domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FARP1 PE=1 SV=1 | 138.96 | 107.24 | 1.30 | 0.00101 |
| Q15149 | Isoform 8 of Plectin OS=Homo sapiens OX=9606 GN=PLEC | 299.89 | 212.07 | 1.41 | 0.00102 |
| O75882 | Attractin OS=Homo sapiens OX=9606 GN=ATRN PE=1 SV=2 | 161.48 | 126.25 | 1.28 | 0.00103 |
| P17931 | Galectin-3 OS=Homo sapiens OX=9606 GN=LGALS3 PE=1 SV=5 | 918.05 | 727.10 | 1.26 | 0.00112 |
| P26599 | Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 | 403.90 | 306.40 | 1.32 | 0.00125 |
| O00461 | Golgi integral membrane protein 4 OS=Homo sapiens OX=9606 GN=GOLIM4 PE=1 SV=1 | 25.52 | 15.70 | 1.63 | 0.00133 |
| P00441 | Superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD1 PE=1 SV=2 | 10641.47 | 8078.98 | 1.32 | 0.00141 |
| O94779 | Contactin-5 OS=Homo sapiens OX=9606 GN=CNTN5 PE=1 SV=2 | 169.94 | 124.36 | 1.37 | 0.00142 |
| O00115 | Deoxyribonuclease-2-alpha OS=Homo sapiens OX=9606 GN=DNASE2 PE=1 SV=2 | 328.90 | 265.01 | 1.24 | 0.00148 |
| Q9UPY8 | Isoform 2 of Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens OX=9606 GN=MAPRE3 | 131.86 | 107.13 | 1.23 | 0.00149 |
| P05067 | Amyloid-beta A4 protein OS=Homo sapiens OX=9606 GN=APP PE=1 SV=3 | 2645.65 | 2009.13 | 1.32 | 0.00154 |
| Q9UIK5 | Tomoregulin-2 OS=Homo sapiens OX=9606 GN=TMEFF2 PE=1 SV=1 | 124.38 | 103.22 | 1.21 | 0.00157 |
| Q6UXK2 | Immunoglobulin superfamily containing leucine-rich repeat protein 2 OS=Homo sapiens OX=9606 GN=ISLR2 PE=2 SV=1 | 240.09 | 188.73 | 1.27 | 0.00165 |
| Q09470 | Potassium voltage-gated channel subfamily A member 1 OS=Homo sapiens OX=9606 GN=KCNA1 PE=1 SV=2 | 91.20 | 73.72 | 1.24 | 0.00165 |
| Q9Y6M5 | Zinc transporter 1 OS=Homo sapiens OX=9606 GN=SLC30A1 PE=1 SV=3 | 177.86 | 137.04 | 1.30 | 0.00176 |
| P08294 | Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD3 PE=1 SV=2 | 483.50 | 398.39 | 1.21 | 0.00177 |
| Q53GG5 | PDZ and LIM domain protein 3 OS=Homo sapiens OX=9606 GN=PDLIM3 PE=1 SV=1 | 75.93 | 49.61 | 1.53 | 0.00179 |
| Q641Q2 | WASH complex subunit 2A OS=Homo sapiens OX=9606 GN=WASHC2A PE=1 SV=3 | 562.14 | 460.26 | 1.22 | 0.00179 |
| Q9GZM7 | Tubulointerstitial nephritis antigen-like OS=Homo sapiens OX=9606 GN=TINAGL1 PE=1 SV=1 | 128.70 | 92.63 | 1.39 | 0.00182 |
| Q9Y4J8 | Isoform 15 of Dystrobrevin alpha OS=Homo sapiens OX=9606 GN=DTNA | 1226.01 | 930.39 | 1.32 | 0.00185 |
| P16403 | Histone H1.2 OS=Homo sapiens OX=9606 GN=HIST1H1C PE=1 SV=2 | 793.01 | 534.84 | 1.48 | 0.00188 |
| Q96KQ4 | Apoptosis-stimulating of p53 protein 1 OS=Homo sapiens OX=9606 GN=PPP1R13B PE=1 SV=3 | 144.02 | 115.17 | 1.25 | 0.00191 |
| Q92522 | Histone H1x OS=Homo sapiens OX=9606 GN=H1FX PE=1 SV=1 | 1349.25 | 1089.10 | 1.24 | 0.00193 |
| Q15651 | High mobility group nucleosome-binding domain-containing protein 3 OS=Homo sapiens OX=9606 GN=HMGN3 PE=1 SV=2 | 57.15 | 41.13 | 1.39 | 0.00197 |
| P05362 | Intercellular adhesion molecule 1 OS=Homo sapiens OX=9606 GN=ICAM1 PE=1 SV=2 | 433.15 | 251.28 | 1.72 | 0.00204 |
| Q9NQ92 | Coordinator of PRMT5 and differentiation stimulator OS=Homo sapiens OX=9606 GN=COPRS PE=1 SV=3 | 104.51 | 75.32 | 1.39 | 0.00207 |

| | | | | | |
|---|---|---|---|---|---|
| Q9HCB6 | Spondin-1 OS=Homo sapiens OX=9606 GN=SPON1 PE=1 SV=2 | 107.07 | 74.17 | 1.44 | 0.00209 |
| Q8IX12 | Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens OX=9606 GN=CCAR1 PE=1 SV=2 | 46.09 | 36.75 | 1.25 | 0.00223 |
| Q9Y676 | 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS18B PE=1 SV=1 | 86.96 | 64.83 | 1.34 | 0.00226 |
| O43294 | Transforming growth factor beta-1-induced transcript 1 protein OS=Homo sapiens OX=9606 GN=TGFB1I1 PE=1 SV=2 | 149.57 | 122.97 | 1.22 | 0.00227 |
| A0A0G2JPP5 | Protein scribble homolog OS=Homo sapiens OX=9606 GN=SCRIB PE=1 SV=1 | 266.82 | 218.88 | 1.22 | 0.00227 |
| Q92562 | Polyphosphoinositide phosphatase OS=Homo sapiens OX=9606 GN=FIG4 PE=1 SV=1 | 186.94 | 142.23 | 1.31 | 0.00235 |
| Q9Y3D0 | Cytosolic iron-sulfur assembly component 2B OS=Homo sapiens OX=9606 GN=CIAO2B PE=1 SV=1 | 81.17 | 61.81 | 1.31 | 0.00239 |
| Q8NHP8 | Putative phospholipase B-like 2 OS=Homo sapiens OX=9606 GN=PLBD2 PE=1 SV=2 | 40.04 | 25.05 | 1.60 | 0.00255 |
| P09493 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2 | 266.25 | 209.96 | 1.27 | 0.00257 |
| P02545 | Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1 | 8480.83 | 6570.30 | 1.29 | 0.00261 |
| Q8N5G2 | Macoilin OS=Homo sapiens OX=9606 GN=MACO1 PE=1 SV=1 | 118.75 | 91.21 | 1.30 | 0.00264 |
| P62072 | Mitochondrial import inner membrane translocase subunit Tim10 OS=Homo sapiens OX=9606 GN=TIMM10 PE=1 SV=1 | 924.94 | 728.11 | 1.27 | 0.00269 |
| B7Z1P2 | F-box only protein 44 OS=Homo sapiens OX=9606 GN=FBXO44 PE=1 SV=1 | 116.35 | 95.64 | 1.22 | 0.00271 |
| Q9C0C2 | 182 kDa tankyrase-1-binding protein OS=Homo sapiens OX=9606 GN=TNKS1BP1 PE=1 SV=4 | 772.31 | 640.65 | 1.21 | 0.00288 |
| P04733 | Metallothionein-1F OS=Homo sapiens OX=9606 GN=MT1F PE=1 SV=1 | 1251.57 | 847.80 | 1.48 | 0.00288 |
| P55290 | Isoform 4 of Cadherin-13 OS=Homo sapiens OX=9606 GN=CDH13 | 1432.05 | 1057.68 | 1.35 | 0.00292 |
| P0C0S5 | Histone H2A.Z OS=Homo sapiens OX=9606 GN=H2AFZ PE=1 SV=2 | 235.78 | 162.07 | 1.45 | 0.00304 |
| Q93052 | Lipoma-preferred partner OS=Homo sapiens OX=9606 GN=LPP PE=1 SV=1 | 401.76 | 292.98 | 1.37 | 0.00319 |
| P04080 | Cystatin-B OS=Homo sapiens OX=9606 GN=CSTB PE=1 SV=2 | 1288.63 | 1019.59 | 1.26 | 0.00337 |
| J3KN67 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=1 | 1647.11 | 1325.05 | 1.24 | 0.00348 |
| Q9ULL4 | Isoform 2 of Plexin-B3 OS=Homo sapiens OX=9606 GN=PLXNB3 | 29.04 | 21.77 | 1.33 | 0.00354 |
| P10412 | Histone H1.4 OS=Homo sapiens OX=9606 GN=HIST1H1E PE=1 SV=2 | 4345.19 | 3164.51 | 1.37 | 0.00355 |
| A0A2R8Y4T1 | Tensin-1 OS=Homo sapiens OX=9606 GN=TNS1 PE=1 SV=1 | 1133.38 | 939.53 | 1.21 | 0.00358 |
| P62266 | 40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3 | 253.83 | 198.87 | 1.28 | 0.00361 |
| Q8TE77 | Protein phosphatase Slingshot homolog 3 OS=Homo sapiens OX=9606 GN=SSH3 PE=1 SV=2 | 50.20 | 32.70 | 1.54 | 0.00372 |
| Q9H5X1 | Cytosolic iron-sulfur assembly component 2A OS=Homo sapiens OX=9606 GN=CIAO2A PE=1 SV=1 | 102.59 | 76.99 | 1.33 | 0.00380 |
| P16519 | Neuroendocrine convertase 2 OS=Homo sapiens OX=9606 GN=PCSK2 PE=1 SV=2 | 217.32 | 174.37 | 1.25 | 0.00405 |
| P04792 | Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2 | 3745.17 | 2957.65 | 1.27 | 0.00406 |

| | | | | | |
|---|---|---|---|---|---|
| Q8WWX9 | Selenoprotein M OS=Homo sapiens OX=9606 GN=SELENOM PE=1 SV=3 | 102.86 | 81.96 | 1.26 | 0.00420 |
| Q9BRA0 | Isoform 2 of N-alpha-acetyltransferase 38, NatC auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA38 | 20.37 | 13.55 | 1.50 | 0.00422 |
| P06753 | Isoform 4 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 | 2977.57 | 2445.64 | 1.22 | 0.00427 |
| U3KQK0 | Histone H2B OS=Homo sapiens OX=9606 GN=HIST1H2BN PE=1 SV=1 | 7643.94 | 5760.87 | 1.33 | 0.00437 |
| Q9NQZ5 | StAR-related lipid transfer protein 7, mitochondrial OS=Homo sapiens OX=9606 GN=STARD7 PE=1 SV=2 | 226.13 | 180.73 | 1.25 | 0.00441 |
| P27987 | Inositol-trisphosphate 3-kinase B OS=Homo sapiens OX=9606 GN=ITPKB PE=1 SV=5 | 455.55 | 343.11 | 1.33 | 0.00450 |
| E7ERK9 | Translation initiation factor eIF-2B subunit delta OS=Homo sapiens OX=9606 GN=EIF2B4 PE=1 SV=1 | 33.34 | 16.25 | 2.05 | 0.00451 |
| A0A0U1RRH7 | Histone H2A OS=Homo sapiens OX=9606 PE=3 SV=1 | 4150.26 | 3332.62 | 1.25 | 0.00475 |
| Q4VCS5 | Angiomotin OS=Homo sapiens OX=9606 GN=AMOT PE=1 SV=1 | 232.50 | 187.82 | 1.24 | 0.00475 |
| O00625 | Pirin OS=Homo sapiens OX=9606 GN=PIR PE=1 SV=1 | 220.75 | 170.52 | 1.29 | 0.00492 |
| P98160 | Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens OX=9606 GN=HSPG2 PE=1 SV=4 | 1143.43 | 845.82 | 1.35 | 0.00494 |
| O60245 | Isoform B of Protocadherin-7 OS=Homo sapiens OX=9606 GN=PCDH7 | 194.80 | 150.86 | 1.29 | 0.00505 |
| Q96HC4 | PDZ and LIM domain protein 5 OS=Homo sapiens OX=9606 GN=PDLIM5 PE=1 SV=5 | 732.52 | 583.87 | 1.25 | 0.00511 |
| P40121 | Macrophage-capping protein OS=Homo sapiens OX=9606 GN=CAPG PE=1 SV=2 | 1477.09 | 1199.39 | 1.23 | 0.00524 |
| Q9BPY8 | Isoform 3 of Homeodomain-only protein OS=Homo sapiens OX=9606 GN=HOPX | 290.22 | 231.42 | 1.25 | 0.00530 |
| G3V3A4 | SNW domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SNW1 PE=1 SV=1 | 247.85 | 193.32 | 1.28 | 0.00537 |
| Q9BZ72 | Membrane-associated phosphatidylinositol transfer protein 2 OS=Homo sapiens OX=9606 GN=PITPNM2 PE=1 SV=1 | 364.36 | 282.29 | 1.29 | 0.00556 |
| Q02779 | Mitogen-activated protein kinase kinase kinase 10 OS=Homo sapiens OX=9606 GN=MAP3K10 PE=1 SV=3 | 43.93 | 32.24 | 1.36 | 0.00563 |
| Q9H019 | Mitochondrial fission regulator 1-like OS=Homo sapiens OX=9606 GN=MTFR1L PE=1 SV=2 | 118.16 | 94.57 | 1.25 | 0.00574 |
| Q9UII2 | ATPase inhibitor, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5IF1 PE=1 SV=1 | 3307.04 | 2618.00 | 1.26 | 0.00574 |
| H0YI08 | Protein MRVI1 OS=Homo sapiens OX=9606 GN=MRVI1 PE=1 SV=1 | 78.42 | 60.34 | 1.30 | 0.00575 |
| P34896 | Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens OX=9606 GN=SHMT1 PE=1 SV=1 | 148.39 | 119.92 | 1.24 | 0.00589 |
| P31483 | Nucleolysin TIA-1 isoform p40 OS=Homo sapiens OX=9606 GN=TIA1 PE=1 SV=3 | 103.45 | 77.69 | 1.33 | 0.00598 |
| P09486 | SPARC OS=Homo sapiens OX=9606 GN=SPARC PE=1 SV=1 | 56.82 | 43.96 | 1.29 | 0.00600 |
| Q9UH65 | Switch-associated protein 70 OS=Homo sapiens OX=9606 GN=SWAP70 PE=1 SV=1 | 267.43 | 215.74 | 1.24 | 0.00601 |
| Q9NR28 | Diablo homolog, mitochondrial OS=Homo sapiens OX=9606 GN=DIABLO PE=1 SV=1 | 591.61 | 488.40 | 1.21 | 0.00607 |
| P56385 | ATP synthase subunit e, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5ME PE=1 SV=2 | 837.30 | 660.79 | 1.27 | 0.00620 |
| Q8NHG7 | Small VCP/p97-interacting protein OS=Homo sapiens OX=9606 GN=SVIP PE=1 SV=1 | 744.07 | 577.43 | 1.29 | 0.00628 |

| | | | | | |
|---|---|---|---|---|---|
| A1X283 | SH3 and PX domain-containing protein 2B OS=Homo sapiens OX=9606 GN=SH3PXD2B PE=1 SV=3 | 120.52 | 97.61 | 1.23 | 0.00628 |
| Q8TEB1 | DDB1- and CUL4-associated factor 11 OS=Homo sapiens OX=9606 GN=DCAF11 PE=1 SV=1 | 12.07 | 6.16 | 1.96 | 0.00638 |
| P19838 | Isoform 2 of Nuclear factor NF-kappa-B p105 subunit OS=Homo sapiens OX=9606 GN=NFKB1 | 21.67 | 16.23 | 1.34 | 0.00640 |
| Q96RT1 | Isoform 8 of Erbin OS=Homo sapiens OX=9606 GN=ERBIN | 383.82 | 315.25 | 1.22 | 0.00651 |
| P10909 | Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU | 3019.46 | 2366.84 | 1.28 | 0.00652 |
| Q9UBI6 | Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens OX=9606 GN=GNG12 PE=1 SV=3 | 436.75 | 344.54 | 1.27 | 0.00665 |
| Q9NRR5 | Ubiquilin-4 OS=Homo sapiens OX=9606 GN=UBQLN4 PE=1 SV=2 | 325.87 | 257.88 | 1.26 | 0.00672 |
| Q96QE2 | Proton myo-inositol cotransporter OS=Homo sapiens OX=9606 GN=SLC2A13 PE=1 SV=3 | 282.08 | 222.62 | 1.27 | 0.00673 |
| P49773 | Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=2 | 1430.14 | 1145.91 | 1.25 | 0.00683 |
| Q8NEY1 | Neuron navigator 1 OS=Homo sapiens OX=9606 GN=NAV1 PE=1 SV=2 | 249.58 | 196.94 | 1.27 | 0.00692 |
| P04839 | Cytochrome b-245 heavy chain OS=Homo sapiens OX=9606 GN=CYBB PE=1 SV=2 | 126.87 | 101.88 | 1.25 | 0.00702 |
| M0QXZ5 | Zinc finger protein 428 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF428 PE=1 SV=1 | 23.62 | 16.38 | 1.44 | 0.00739 |
| K7EMC7 | Cytoglobin OS=Homo sapiens OX=9606 GN=CYGB PE=1 SV=1 | 41.76 | 28.36 | 1.47 | 0.00751 |
| Q9UEE9 | Craniofacial development protein 1 OS=Homo sapiens OX=9606 GN=CFDP1 PE=1 SV=1 | 403.16 | 325.66 | 1.24 | 0.00792 |
| P41227 | N-alpha-acetyltransferase 10 OS=Homo sapiens OX=9606 GN=NAA10 PE=1 SV=1 | 295.04 | 242.33 | 1.22 | 0.00794 |
| Q15375 | Ephrin type-A receptor 7 OS=Homo sapiens OX=9606 GN=EPHA7 PE=1 SV=3 | 71.15 | 45.81 | 1.55 | 0.00817 |
| Q9Y371 | Endophilin-B1 OS=Homo sapiens OX=9606 GN=SH3GLB1 PE=1 SV=1 | 53.42 | 43.46 | 1.23 | 0.00829 |
| Q9Y2S6 | Translation machinery-associated protein 7 OS=Homo sapiens OX=9606 GN=TMA7 PE=1 SV=1 | 412.93 | 248.99 | 1.66 | 0.00873 |
| Q9NWB6 | Arginine and glutamate-rich protein 1 OS=Homo sapiens OX=9606 GN=ARGLU1 PE=1 SV=1 | 739.84 | 607.26 | 1.22 | 0.00887 |
| Q9Y5Z4 | Heme-binding protein 2 OS=Homo sapiens OX=9606 GN=HEBP2 PE=1 SV=1 | 1155.34 | 913.17 | 1.27 | 0.00888 |
| F5H7S3 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2 | 1690.85 | 1276.31 | 1.32 | 0.00900 |
| Q08379 | Golgin subfamily A member 2 OS=Homo sapiens OX=9606 GN=GOLGA2 PE=1 SV=3 | 86.25 | 58.64 | 1.47 | 0.00902 |
| Q9HBT6 | Cadherin-20 OS=Homo sapiens OX=9606 GN=CDH20 PE=2 SV=2 | 39.15 | 30.94 | 1.27 | 0.00918 |
| A6NIW2 | Dedicator of cytokinesis protein 11 OS=Homo sapiens OX=9606 GN=DOCK11 PE=1 SV=2 | 59.82 | 43.36 | 1.38 | 0.00938 |
| Q8N1K5 | Isoform 4 of Protein THEMIS OS=Homo sapiens OX=9606 GN=THEMIS | 149.35 | 121.33 | 1.23 | 0.00961 |
| O75509 | Tumor necrosis factor receptor superfamily member 21 OS=Homo sapiens OX=9606 GN=TNFRSF21 PE=1 SV=1 | 27.65 | 17.28 | 1.60 | 0.00969 |
| P02462 | Collagen alpha-1(IV) chain OS=Homo sapiens OX=9606 GN=COL4A1 PE=1 SV=4 | 60.61 | 48.38 | 1.25 | 0.00980 |
| P08123 | Collagen alpha-2(I) chain OS=Homo sapiens OX=9606 GN=COL1A2 PE=1 SV=7 | 1642.41 | 1157.67 | 1.42 | 0.00987 |

| | | | | | |
|---|---|---|---|---|---|
| P06703 | Protein S100-A6 OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1 | 905.02 | 676.92 | 1.34 | 0.00992 |
| P20309 | Muscarinic acetylcholine receptor M3 OS=Homo sapiens OX=9606 GN=CHRM3 PE=1 SV=1 | 109.77 | 90.56 | 1.21 | 0.01004 |
| M0QZI3 | F-BAR domain only protein 1 OS=Homo sapiens OX=9606 GN=FCHO1 PE=1 SV=1 | 257.16 | 165.14 | 1.56 | 0.01007 |
| O00233 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=3 | 1094.79 | 890.46 | 1.23 | 0.01021 |
| A0A096LNH6 | Dedicator of cytokinesis protein 1 OS=Homo sapiens OX=9606 GN=DOCK1 PE=1 SV=1 | 459.34 | 371.19 | 1.24 | 0.01022 |
| Q9NVK5 | FGFR1 oncogene partner 2 OS=Homo sapiens OX=9606 GN=FGFR1OP2 PE=1 SV=1 | 123.61 | 97.52 | 1.27 | 0.01064 |
| Q9BZL4 | Protein phosphatase 1 regulatory subunit 12C OS=Homo sapiens OX=9606 GN=PPP1R12C PE=1 SV=1 | 93.48 | 64.74 | 1.44 | 0.01066 |
| Q96E39 | RNA binding motif protein, X-linked-like-1 OS=Homo sapiens OX=9606 GN=RBMXL1 PE=1 SV=1 | 607.57 | 454.38 | 1.34 | 0.01074 |
| Q8IY22 | C-Maf-inducing protein OS=Homo sapiens OX=9606 GN=CMIP PE=1 SV=3 | 111.00 | 89.49 | 1.24 | 0.01096 |
| Q9NR46 | Isoform 2 of Endophilin-B2 OS=Homo sapiens OX=9606 GN=SH3GLB2 | 495.62 | 400.03 | 1.24 | 0.01105 |
| O95817 | BAG family molecular chaperone regulator 3 OS=Homo sapiens OX=9606 GN=BAG3 PE=1 SV=3 | 645.72 | 482.68 | 1.34 | 0.01114 |
| A0A0X1KG71 | Negative elongation factor B OS=Homo sapiens OX=9606 GN=NELFB PE=1 SV=1 | 145.38 | 112.41 | 1.29 | 0.01114 |
| Q9H098 | Isoform 2 of Protein FAM107B OS=Homo sapiens OX=9606 GN=FAM107B | 191.85 | 138.38 | 1.39 | 0.01156 |
| Q8NDI1 | Isoform 3 of EH domain-binding protein 1 OS=Homo sapiens OX=9606 GN=EHBP1 | 677.85 | 564.60 | 1.20 | 0.01168 |
| Q9H0D6 | 5'-3' exoribonuclease 2 OS=Homo sapiens OX=9606 GN=XRN2 PE=1 SV=1 | 68.30 | 47.22 | 1.45 | 0.01188 |
| Q9NX24 | H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens OX=9606 GN=NHP2 PE=1 SV=1 | 65.03 | 50.06 | 1.30 | 0.01196 |
| Q86YR7 | Probable guanine nucleotide exchange factor MCF2L2 OS=Homo sapiens OX=9606 GN=MCF2L2 PE=2 SV=3 | 38.25 | 28.07 | 1.36 | 0.01228 |
| P06396 | Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1 | 9802.51 | 7948.33 | 1.23 | 0.01232 |
| Q9UPY6 | Isoform 2 of Wiskott-Aldrich syndrome protein family member 3 OS=Homo sapiens OX=9606 GN=WASF3 | 40.78 | 27.09 | 1.51 | 0.01235 |
| Q9UJU6 | Isoform 3 of Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL | 77.29 | 60.10 | 1.29 | 0.01236 |
| A0A2R8Y760 | Collagen alpha-1(XXV) chain OS=Homo sapiens OX=9606 GN=COL25A1 PE=1 SV=1 | 87.37 | 39.07 | 2.24 | 0.01248 |
| P61956 | Small ubiquitin-related modifier 2 OS=Homo sapiens OX=9606 GN=SUMO2 PE=1 SV=3 | 1105.54 | 894.88 | 1.24 | 0.01321 |
| Q10589 | Bone marrow stromal antigen 2 OS=Homo sapiens OX=9606 GN=BST2 PE=1 SV=1 | 99.37 | 77.18 | 1.29 | 0.01341 |
| Q15052 | Rho guanine nucleotide exchange factor 6 OS=Homo sapiens OX=9606 GN=ARHGEF6 PE=1 SV=2 | 193.39 | 161.09 | 1.20 | 0.01347 |
| Q13433 | Zinc transporter ZIP6 OS=Homo sapiens OX=9606 GN=SLC39A6 PE=1 SV=3 | 73.51 | 59.38 | 1.24 | 0.01351 |
| Q9Y3D2 | Methionine-R-sulfoxide reductase B2, mitochondrial OS=Homo sapiens OX=9606 GN=MSRB2 PE=1 SV=2 | 73.45 | 60.11 | 1.22 | 0.01360 |
| Q9ULX6 | A-kinase anchor protein 8-like OS=Homo sapiens OX=9606 GN=AKAP8L PE=1 SV=4 | 85.25 | 66.17 | 1.29 | 0.01372 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| A0A087X0I6 | Non-specific serine/threonine protein kinase OS=Homo sapiens OX=9606 GN=MARK1 PE=1 SV=1 | 20.66 | 15.49 | 1.33 | 0.01374 |
| P21333 | Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4 | 10917.17 | 8601.05 | 1.27 | 0.01383 |
| P09429 | High mobility group protein B1 OS=Homo sapiens OX=9606 GN=HMGB1 PE=1 SV=3 | 1200.72 | 986.44 | 1.22 | 0.01386 |
| O95263 | High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B OS=Homo sapiens OX=9606 GN=PDE8B PE=1 SV=2 | 338.01 | 280.25 | 1.21 | 0.01410 |
| Q96CT7 | Coiled-coil domain-containing protein 124 OS=Homo sapiens OX=9606 GN=CCDC124 PE=1 SV=1 | 325.57 | 266.67 | 1.22 | 0.01425 |
| P15259 | Phosphoglycerate mutase 2 OS=Homo sapiens OX=9606 GN=PGAM2 PE=1 SV=3 | 143.77 | 100.85 | 1.43 | 0.01456 |
| Q9HC36 | rRNA methyltransferase 3, mitochondrial OS=Homo sapiens OX=9606 GN=MRM3 PE=1 SV=2 | 173.08 | 126.78 | 1.37 | 0.01482 |
| P12110 | Collagen alpha-2(VI) chain OS=Homo sapiens OX=9606 GN=COL6A2 PE=1 SV=4 | 368.85 | 229.80 | 1.61 | 0.01538 |
| Q12797 | Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3 | 463.92 | 384.07 | 1.21 | 0.01560 |
| Q6GQQ9 | OTU domain-containing protein 7B OS=Homo sapiens OX=9606 GN=OTUD7B PE=1 SV=1 | 293.06 | 244.05 | 1.20 | 0.01576 |
| Q13177 | Serine/threonine-protein kinase PAK 2 OS=Homo sapiens OX=9606 GN=PAK2 PE=1 SV=3 | 372.16 | 307.63 | 1.21 | 0.01607 |
| Q9UJC3 | Protein Hook homolog 1 OS=Homo sapiens OX=9606 GN=HOOK1 PE=1 SV=2 | 64.12 | 52.87 | 1.21 | 0.01630 |
| Q8N4Q1 | Isoform 2 of Mitochondrial intermembrane space import and assembly protein 40 OS=Homo sapiens OX=9606 GN=CHCHD4 | 269.77 | 198.29 | 1.36 | 0.01640 |
| Q8NFU3 | Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 PE=1 SV=3 | 278.44 | 192.97 | 1.44 | 0.01720 |
| Q9H9J2 | 39S ribosomal protein L44, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL44 PE=1 SV=1 | 162.78 | 135.22 | 1.20 | 0.01736 |
| O14497 | AT-rich interactive domain-containing protein 1A OS=Homo sapiens OX=9606 GN=ARID1A PE=1 SV=3 | 175.22 | 127.30 | 1.38 | 0.01742 |
| E9PND2 | Cysteine and glycine-rich protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CSRP1 PE=1 SV=1 | 66.56 | 48.51 | 1.37 | 0.01781 |
| Q8NFW9 | Rab effector MyRIP OS=Homo sapiens OX=9606 GN=MYRIP PE=1 SV=2 | 89.26 | 69.25 | 1.29 | 0.01785 |
| P53384 | Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens OX=9606 GN=NUBP1 PE=1 SV=2 | 23.66 | 13.58 | 1.74 | 0.01787 |
| G3V4P8 | Glia maturation factor beta (Fragment) OS=Homo sapiens OX=9606 GN=GMFB PE=1 SV=1 | 1596.94 | 1322.68 | 1.21 | 0.01792 |
| P28906 | Hematopoietic progenitor cell antigen CD34 OS=Homo sapiens OX=9606 GN=CD34 PE=1 SV=2 | 29.13 | 20.15 | 1.45 | 0.01836 |
| P10599 | Thioredoxin OS=Homo sapiens OX=9606 GN=TXN PE=1 SV=3 | 3058.50 | 2544.00 | 1.20 | 0.01852 |
| Q96JN2 | Isoform 4 of Coiled-coil domain-containing protein 136 OS=Homo sapiens OX=9606 GN=CCDC136 | 126.85 | 104.73 | 1.21 | 0.01868 |
| Q86Y22 | Collagen alpha-1(XXIII) chain OS=Homo sapiens OX=9606 GN=COL23A1 PE=1 SV=1 | 345.92 | 200.10 | 1.73 | 0.01869 |

| | | | | | |
|---|---|---|---|---|---|
| O43291 | Kunitz-type protease inhibitor 2 OS=Homo sapiens OX=9606 GN=SPINT2 PE=1 SV=2 | 81.30 | 55.93 | 1.45 | 0.01870 |
| Q7Z422 | SUZ domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SZRD1 PE=1 SV=1 | 29.44 | 23.45 | 1.26 | 0.01872 |
| Q8NFD5 | Isoform 3 of AT-rich interactive domain-containing protein 1B OS=Homo sapiens OX=9606 GN=ARID1B | 63.25 | 48.71 | 1.30 | 0.01926 |
| Q96EU6 | Ribosomal RNA processing protein 36 homolog OS=Homo sapiens OX=9606 GN=RRP36 PE=1 SV=1 | 67.09 | 48.32 | 1.39 | 0.01953 |
| Q09666 | Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens OX=9606 GN=AHNAK PE=1 SV=2 | 13004.97 | 10807.21 | 1.20 | 0.01953 |
| P82914 | 28S ribosomal protein S15, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS15 PE=1 SV=1 | 214.40 | 170.46 | 1.26 | 0.01965 |
| Q15847 | Adipogenesis regulatory factor OS=Homo sapiens OX=9606 GN=ADIRF PE=1 SV=1 | 718.18 | 531.69 | 1.35 | 0.01973 |
| Q9BRP8 | Partner of Y14 and mago OS=Homo sapiens OX=9606 GN=PYM1 PE=1 SV=1 | 292.11 | 227.37 | 1.28 | 0.01993 |
| A0A2R8Y596 | Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens OX=9606 GN=BCAR1 PE=1 SV=1 | 71.70 | 50.43 | 1.42 | 0.02006 |
| P62847 | Isoform 4 of 40S ribosomal protein S24 OS=Homo sapiens OX=9606 GN=RPS24 | 660.47 | 547.04 | 1.21 | 0.02007 |
| O75167 | Isoform 4 of Phosphatase and actin regulator 2 OS=Homo sapiens OX=9606 GN=PHACTR2 | 56.71 | 41.84 | 1.36 | 0.02046 |
| A0A1B0GTU4 | Paxillin OS=Homo sapiens OX=9606 GN=PXN PE=1 SV=1 | 237.13 | 188.40 | 1.26 | 0.02047 |
| Q9UGU0 | Transcription factor 20 OS=Homo sapiens OX=9606 GN=TCF20 PE=1 SV=3 | 53.46 | 42.93 | 1.25 | 0.02064 |
| Q13523 | Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3 | 171.33 | 142.33 | 1.20 | 0.02084 |
| O75369 | Isoform 8 of Filamin-B OS=Homo sapiens OX=9606 GN=FLNB | 2012.73 | 1608.61 | 1.25 | 0.02119 |
| Q96Q15 | Serine/threonine-protein kinase SMG1 OS=Homo sapiens OX=9606 GN=SMG1 PE=1 SV=3 | 122.24 | 98.57 | 1.24 | 0.02132 |
| P57721 | Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 PE=2 SV=2 | 92.24 | 74.44 | 1.24 | 0.02139 |
| P61254 | 60S ribosomal protein L26 OS=Homo sapiens OX=9606 GN=RPL26 PE=1 SV=1 | 212.64 | 173.55 | 1.23 | 0.02140 |
| Q96SZ5 | 2-aminoethanethiol dioxygenase OS=Homo sapiens OX=9606 GN=ADO PE=1 SV=2 | 451.48 | 376.04 | 1.20 | 0.02145 |
| P02649 | Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1 | 4225.28 | 3443.42 | 1.23 | 0.02198 |
| E5RJD8 | Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=1 | 2039.19 | 1302.25 | 1.57 | 0.02208 |
| P49619 | Diacylglycerol kinase gamma OS=Homo sapiens OX=9606 GN=DGKG PE=2 SV=3 | 385.46 | 320.26 | 1.20 | 0.02211 |
| B7Z2U2 | TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 PE=1 SV=1 | 26.20 | 19.17 | 1.37 | 0.02237 |
| Q8WVF1 | Protein OSCP1 OS=Homo sapiens OX=9606 GN=OSCP1 PE=1 SV=4 | 126.70 | 102.63 | 1.23 | 0.02243 |
| O95631 | Netrin-1 OS=Homo sapiens OX=9606 GN=NTN1 PE=1 SV=2 | 26.30 | 18.76 | 1.40 | 0.02275 |
| A0A2R8YDH4 | Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 PE=3 SV=1 | 1288.19 | 1016.10 | 1.27 | 0.02290 |
| Q15287 | RNA-binding protein with serine-rich domain 1 OS=Homo sapiens OX=9606 GN=RNPS1 PE=1 SV=1 | 208.50 | 166.66 | 1.25 | 0.02315 |
| Q5TZA2 | Rootletin OS=Homo sapiens OX=9606 GN=CROCC PE=1 SV=1 | 237.49 | 197.77 | 1.20 | 0.02331 |

| | | | | | |
|---|---|---|---|---|---|
| Q5GH76 | XK-related protein 4 OS=Homo sapiens OX=9606 GN=XKR4 PE=2 SV=1 | 350.38 | 289.48 | 1.21 | 0.02335 |
| Q14657 | EKC/KEOPS complex subunit LAGE3 OS=Homo sapiens OX=9606 GN=LAGE3 PE=1 SV=2 | 31.65 | 23.71 | 1.34 | 0.02355 |
| E9PGZ1 | Caldesmon OS=Homo sapiens OX=9606 GN=CALD1 PE=1 SV=1 | 1532.30 | 1154.65 | 1.33 | 0.02362 |
| P07919 | Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRH PE=1 SV=2 | 925.28 | 695.52 | 1.33 | 0.02379 |
| A0A0J9YY34 | NHS-like protein 2 OS=Homo sapiens OX=9606 GN=NHSL2 PE=1 SV=1 | 33.37 | 26.39 | 1.26 | 0.02417 |
| Q15796 | Mothers against decapentaplegic homolog 2 OS=Homo sapiens OX=9606 GN=SMAD2 PE=1 SV=1 | 75.95 | 55.92 | 1.36 | 0.02439 |
| P28288 | ATP-binding cassette sub-family D member 3 OS=Homo sapiens OX=9606 GN=ABCD3 PE=1 SV=1 | 142.36 | 115.42 | 1.23 | 0.02506 |
| A0A096LP25 | AP2-associated protein kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=AAK1 PE=1 SV=1 | 19.54 | 15.66 | 1.25 | 0.02549 |
| Q14254 | Flotillin-2 OS=Homo sapiens OX=9606 GN=FLOT2 PE=1 SV=2 | 2909.79 | 2115.91 | 1.38 | 0.02637 |
| O95490 | Isoform 6 of Adhesion G protein-coupled receptor L2 OS=Homo sapiens OX=9606 GN=ADGRL2 | 52.06 | 40.47 | 1.29 | 0.02662 |
| Q86UU1 | Pleckstrin homology-like domain family B member 1 OS=Homo sapiens OX=9606 GN=PHLDB1 PE=1 SV=1 | 315.93 | 262.95 | 1.20 | 0.02682 |
| Q17R31 | Isoform 3 of Putative deoxyribonuclease TATDN3 OS=Homo sapiens OX=9606 GN=TATDN3 | 137.61 | 111.81 | 1.23 | 0.02718 |
| O43815 | Striatin OS=Homo sapiens OX=9606 GN=STRN PE=1 SV=4 | 109.04 | 78.70 | 1.39 | 0.02751 |
| P14209 | CD99 antigen OS=Homo sapiens OX=9606 GN=CD99 PE=1 SV=1 | 392.15 | 290.47 | 1.35 | 0.02758 |
| O15230 | Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8 | 226.87 | 185.75 | 1.22 | 0.02767 |
| Q6ZU35 | Uncharacterized protein KIAA1211 OS=Homo sapiens OX=9606 GN=KIAA1211 PE=1 SV=3 | 26.62 | 19.81 | 1.34 | 0.02778 |
| Q6KB66 | Isoform 3 of Keratin, type II cytoskeletal 80 OS=Homo sapiens OX=9606 GN=KRT80 | 27.64 | 20.25 | 1.36 | 0.02785 |
| Q53FA7 | Quinone oxidoreductase PIG3 OS=Homo sapiens OX=9606 GN=TP53I3 PE=1 SV=2 | 234.87 | 177.64 | 1.32 | 0.02817 |
| P20933 | N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase OS=Homo sapiens OX=9606 GN=AGA PE=1 SV=2 | 55.56 | 44.60 | 1.25 | 0.02830 |
| Q96DC8 | Enoyl-CoA hydratase domain-containing protein 3, mitochondrial OS=Homo sapiens OX=9606 GN=ECHDC3 PE=1 SV=2 | 108.00 | 77.52 | 1.39 | 0.02861 |
| H0Y449 | Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=YBX1 PE=1 SV=1 | 32.69 | 21.10 | 1.55 | 0.02864 |
| A1L188 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 8 OS=Homo sapiens OX=9606 GN=NDUFAF8 PE=1 SV=1 | 18.25 | 14.23 | 1.28 | 0.02870 |
| Q86WG5 | Myotubularin-related protein 13 OS=Homo sapiens OX=9606 GN=SBF2 PE=1 SV=1 | 108.24 | 88.79 | 1.22 | 0.02916 |
| Q9Y6N7 | Isoform 2 of Roundabout homolog 1 OS=Homo sapiens OX=9606 GN=ROBO1 | 47.52 | 36.66 | 1.30 | 0.02950 |
| Q13409 | Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=3 | 1582.12 | 1282.21 | 1.23 | 0.02958 |

| | | | | | |
|---|---|---|---|---|---|
| P10636 | Isoform Tau-F of Microtubule-associated protein tau OS=Homo sapiens OX=9606 GN=MAPT | 11.55 | 6.87 | 1.68 | 0.03021 |
| F5H757 | Cytochrome b561 OS=Homo sapiens OX=9606 GN=CYB561 PE=1 SV=1 | 114.48 | 94.49 | 1.21 | 0.03062 |
| Q9H446 | RWD domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RWDD1 PE=1 SV=1 | 319.45 | 252.05 | 1.27 | 0.03073 |
| Q9UD71 | Protein phosphatase 1 regulatory subunit 1B OS=Homo sapiens OX=9606 GN=PPP1R1B PE=1 SV=2 | 313.57 | 260.38 | 1.20 | 0.03085 |
| P48509 | CD151 antigen OS=Homo sapiens OX=9606 GN=CD151 PE=1 SV=3 | 120.07 | 85.33 | 1.41 | 0.03120 |
| Q9BQT9 | Isoform 2 of Calsyntenin-3 OS=Homo sapiens OX=9606 GN=CLSTN3 | 159.67 | 132.35 | 1.21 | 0.03143 |
| P98095 | Isoform 2 of Fibulin-2 OS=Homo sapiens OX=9606 GN=FBLN2 | 12.35 | 6.36 | 1.94 | 0.03149 |
| Q9H3Q1 | Cdc42 effector protein 4 OS=Homo sapiens OX=9606 GN=CDC42EP4 PE=1 SV=1 | 949.90 | 775.98 | 1.22 | 0.03150 |
| Q9P2U8 | Vesicular glutamate transporter 2 OS=Homo sapiens OX=9606 GN=SLC17A6 PE=2 SV=1 | 79.35 | 41.12 | 1.93 | 0.03160 |
| Q9UJU6 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 | 2030.02 | 1533.91 | 1.32 | 0.03201 |
| Q8WUW1 | Isoform 2 of Protein BRICK1 OS=Homo sapiens OX=9606 GN=BRK1 | 268.72 | 207.54 | 1.29 | 0.03204 |
| P17612 | cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens OX=9606 GN=PRKACA PE=1 SV=2 | 93.89 | 70.94 | 1.32 | 0.03256 |
| Q92835 | Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Homo sapiens OX=9606 GN=INPP5D PE=1 SV=2 | 77.16 | 60.45 | 1.28 | 0.03304 |
| A0A087WY08 | Thrombospondin type-1 domain-containing protein 7A OS=Homo sapiens OX=9606 GN=THSD7A PE=1 SV=1 | 62.46 | 49.99 | 1.25 | 0.03359 |
| E3W994 | CLIP-associating protein 2 OS=Homo sapiens OX=9606 GN=CLASP2 PE=1 SV=2 | 19.87 | 16.52 | 1.20 | 0.03377 |
| Q5VWP3 | Isoform 3 of Muscular LMNA-interacting protein OS=Homo sapiens OX=9606 GN=MLIP | 205.69 | 169.18 | 1.22 | 0.03429 |
| A0A0J9YX94 | Paraneoplastic antigen Ma6F OS=Homo sapiens OX=9606 GN=PNMA6F PE=4 SV=1 | 56.30 | 46.67 | 1.21 | 0.03479 |
| G3V164 | Glutamate receptor 4 OS=Homo sapiens OX=9606 GN=GRIA4 PE=1 SV=1 | 21.78 | 10.11 | 2.15 | 0.03511 |
| Q6UX71 | Plexin domain-containing protein 2 OS=Homo sapiens OX=9606 GN=PLXDC2 PE=1 SV=1 | 38.71 | 28.01 | 1.38 | 0.03603 |
| Q8IUE6 | Histone H2A type 2-B OS=Homo sapiens OX=9606 GN=HIST2H2AB PE=1 SV=3 | 88.21 | 64.16 | 1.37 | 0.03616 |
| Q96JN8 | Neuralized-like protein 4 OS=Homo sapiens OX=9606 GN=NEURL4 PE=1 SV=2 | 43.64 | 34.52 | 1.26 | 0.03662 |
| Q68CP4 | Heparan-alpha-glucosaminide N-acetyltransferase OS=Homo sapiens OX=9606 GN=HGSNAT PE=1 SV=2 | 33.64 | 25.17 | 1.34 | 0.03689 |
| Q9H1U4 | Multiple epidermal growth factor-like domains protein 9 OS=Homo sapiens OX=9606 GN=MEGF9 PE=2 SV=3 | 42.11 | 31.89 | 1.32 | 0.03697 |
| A0A0U1RQV1 | Endogenous retrovirus group K3 member 1 (Fragment) OS=Homo sapiens OX=9606 GN=ERVK3-1 PE=1 SV=1 | 229.56 | 181.78 | 1.26 | 0.03708 |
| O75347 | Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=3 | 699.36 | 524.96 | 1.33 | 0.03721 |
| P30876 | DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=1 | 65.86 | 51.30 | 1.28 | 0.03732 |
| Q7Z2W4 | Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens OX=9606 GN=ZC3HAV1 PE=1 SV=3 | 270.06 | 214.66 | 1.26 | 0.03739 |

| | | | | | |
|---|---|---|---|---|---|
| O60551 | Glycylpeptide N-tetradecanoyltransferase 2 OS=Homo sapiens OX=9606 GN=NMT2 PE=1 SV=1 | 607.23 | 496.98 | 1.22 | 0.03809 |
| Q13938 | Calcyphosin OS=Homo sapiens OX=9606 GN=CAPS PE=1 SV=2 | 761.24 | 557.10 | 1.37 | 0.03854 |
| E9PFU5 | Pituitary adenylate cyclase-activating polypeptide type I receptor OS=Homo sapiens OX=9606 GN=ADCYAP1R1 PE=1 SV=1 | 88.83 | 68.21 | 1.30 | 0.03876 |
| Q5VZ89 | Isoform 2 of DENN domain-containing protein 4C OS=Homo sapiens OX=9606 GN=DENND4C | 8.76 | 5.69 | 1.54 | 0.03926 |
| P09132 | Signal recognition particle 19 kDa protein OS=Homo sapiens OX=9606 GN=SRP19 PE=1 SV=3 | 341.06 | 273.35 | 1.25 | 0.03980 |
| A0A0U1RQN6 | Ankyrin-2 (Fragment) OS=Homo sapiens OX=9606 GN=ANK2 PE=1 SV=2 | 147.91 | 115.07 | 1.29 | 0.04001 |
| P16402 | Histone H1.3 OS=Homo sapiens OX=9606 GN=HIST1H1D PE=1 SV=2 | 2552.69 | 1973.97 | 1.29 | 0.04020 |
| P29279 | CCN family member 2 OS=Homo sapiens OX=9606 GN=CCN2 PE=1 SV=2 | 98.74 | 73.66 | 1.34 | 0.04143 |
| P18615 | Isoform 2 of Negative elongation factor E OS=Homo sapiens OX=9606 GN=NELFE | 37.79 | 29.01 | 1.30 | 0.04213 |
| Q5T200 | Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens OX=9606 GN=ZC3H13 PE=1 SV=1 | 68.32 | 54.12 | 1.26 | 0.04221 |
| A0A0U1RQS6 | Transmembrane protein 275 OS=Homo sapiens OX=9606 GN=TMEM275 PE=3 SV=1 | 53.00 | 43.14 | 1.23 | 0.04230 |
| Q7Z7L8 | Uncharacterized protein C11orf96 OS=Homo sapiens OX=9606 GN=C11orf96 PE=1 SV=3 | 168.41 | 138.38 | 1.22 | 0.04295 |
| P09012 | U1 small nuclear ribonucleoprotein A OS=Homo sapiens OX=9606 GN=SNRPA PE=1 SV=3 | 475.51 | 395.11 | 1.20 | 0.04390 |
| P63092 | Isoform 4 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens OX=9606 GN=GNAS | 151.91 | 125.14 | 1.21 | 0.04413 |
| Q15437 | Protein transport protein Sec23B OS=Homo sapiens OX=9606 GN=SEC23B PE=1 SV=2 | 98.58 | 81.55 | 1.21 | 0.04440 |
| B0YIW2 | Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1 | 23.51 | 14.11 | 1.67 | 0.04444 |
| Q69YU3 | Ankyrin repeat domain-containing protein 34A OS=Homo sapiens OX=9606 GN=ANKRD34A PE=2 SV=2 | 32.05 | 26.37 | 1.22 | 0.04448 |
| P12109 | Collagen alpha-1(VI) chain OS=Homo sapiens OX=9606 GN=COL6A1 PE=1 SV=3 | 716.08 | 484.40 | 1.48 | 0.04494 |
| Q32MZ4 | Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens OX=9606 GN=LRRFIP1 | 153.01 | 120.93 | 1.27 | 0.04524 |
| P00519 | Isoform IB of Tyrosine-protein kinase ABL1 OS=Homo sapiens OX=9606 GN=ABL1 | 97.88 | 75.82 | 1.29 | 0.04546 |
| Q5T011 | KICSTOR complex protein SZT2 OS=Homo sapiens OX=9606 GN=SZT2 PE=1 SV=3 | 57.35 | 47.61 | 1.20 | 0.04552 |
| Q9NPF0 | CD320 antigen OS=Homo sapiens OX=9606 GN=CD320 PE=1 SV=1 | 88.70 | 73.91 | 1.20 | 0.04577 |
| A0A2R8YFG2 | Nicotinamide-nucleotide adenylyltransferase OS=Homo sapiens OX=9606 GN=NMNAT3 PE=1 SV=1 | 194.50 | 155.89 | 1.25 | 0.04587 |
| P08908 | 5-hydroxytryptamine receptor 1A OS=Homo sapiens OX=9606 GN=HTR1A PE=1 SV=3 | 61.01 | 41.17 | 1.48 | 0.04596 |
| O60925 | Prefoldin subunit 1 OS=Homo sapiens OX=9606 GN=PFDN1 PE=1 SV=2 | 269.32 | 223.33 | 1.21 | 0.04661 |
| Q63ZY3 | Isoform 2 of KN motif and ankyrin repeat domain-containing protein 2 OS=Homo sapiens OX=9606 GN=KANK2 | 88.53 | 73.71 | 1.20 | 0.04664 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| A0A087WTE6 | SRC kinase-signaling inhibitor 1 (Fragment) OS=Homo sapiens OX=9606 GN=SRCIN1 PE=1 SV=1 | 33.93 | 23.51 | 1.44 | 0.04729 |
| P04083 | Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2 | 1124.28 | 910.62 | 1.23 | 0.04789 |
| A9Z1X7 | Serine/arginine repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1 PE=1 SV=1 | 111.47 | 89.16 | 1.25 | 0.04791 |
| Q96AE4 | Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=3 | 806.68 | 669.36 | 1.21 | 0.04795 |
| Q9BQ70 | Transcription factor 25 OS=Homo sapiens OX=9606 GN=TCF25 PE=1 SV=1 | 107.48 | 87.96 | 1.22 | 0.04824 |
| A0A1X7SBR1 | Prickle-like protein 2 OS=Homo sapiens OX=9606 GN=PRICKLE2 PE=1 SV=1 | 263.97 | 195.51 | 1.35 | 0.04872 |
| P05107 | Integrin beta-2 OS=Homo sapiens OX=9606 GN=ITGB2 PE=1 SV=2 | 203.83 | 167.00 | 1.22 | 0.04913 |
| Q9NRX2 | 39S ribosomal protein L17, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL17 PE=1 SV=1 | 215.06 | 175.83 | 1.22 | 0.04915 |
| P84101 | Small EDRK-rich factor 2 OS=Homo sapiens OX=9606 GN=SERF2 PE=1 SV=1 | 453.48 | 356.96 | 1.27 | 0.04951 |
| Q14247 | Isoform 3 of Src substrate cortactin OS=Homo sapiens OX=9606 GN=CTTN | 223.90 | 141.65 | 1.58 | 0.04953 |
| Q9Y3Q8 | TSC22 domain family protein 4 OS=Homo sapiens OX=9606 GN=TSC22D4 PE=1 SV=2 | 36.88 | 28.00 | 1.32 | 0.04994 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; $P<0.05$

**Supplementary Table 7.** Extended mass spectrometry data on significantly down-regulated proteins in the temporal cortex of Alzheimer's patients compared to cognitively normal controls.

| **Accession** | **Description** | **AD (Means)** | **NC (Means)** | **FC (*-1)** | ***P*** |
|---|---|---|---|---|---|
| Q8NC96 | Adaptin ear-binding coat-associated protein 1 OS=Homo sapiens OX=9606 GN=NECAP1 PE=1 SV=2 | 822.75 | 1065.81 | 1.30 | 1.894E-06 |
| P84074 | Neuron-specific calcium-binding protein hippocalcin OS=Homo sapiens OX=9606 GN=HPCA PE=1 SV=2 | 947.51 | 1322.95 | 1.40 | 9.479E-06 |
| Q8IV01 | Synaptotagmin-12 OS=Homo sapiens OX=9606 GN=SYT12 PE=1 SV=1 | 248.15 | 356.33 | 1.44 | 6.293E-05 |
| O95716 | Ras-related protein Rab-3D OS=Homo sapiens OX=9606 GN=RAB3D PE=1 SV=1 | 242.01 | 330.27 | 1.36 | 9.729E-05 |
| F5GXV7 | Neurobeachin OS=Homo sapiens OX=9606 GN=NBEA PE=1 SV=2 | 619.75 | 776.31 | 1.25 | 0.00017 |
| Q9H061 | Transmembrane protein 126A OS=Homo sapiens OX=9606 GN=TMEM126A PE=1 SV=1 | 600.37 | 839.21 | 1.40 | 0.00019 |
| Q9H1E5 | Thioredoxin-related transmembrane protein 4 OS=Homo sapiens OX=9606 GN=TMX4 PE=1 SV=1 | 82.50 | 114.56 | 1.39 | 0.00023 |
| Q96BW9 | Phosphatidate cytidylyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=TAMM41 PE=1 SV=2 | 154.42 | 238.23 | 1.54 | 0.00029 |
| Q14642 | Inositol polyphosphate-5-phosphatase A OS=Homo sapiens OX=9606 GN=INPP5A PE=1 SV=1 | 388.11 | 512.79 | 1.32 | 0.00030 |
| P04156 | Major prion protein OS=Homo sapiens OX=9606 GN=PRNP PE=1 SV=1 | 949.10 | 1207.63 | 1.27 | 0.00034 |
| E9PNQ8 | Thy-1 membrane glycoprotein (Fragment) OS=Homo sapiens OX=9606 GN=THY1 PE=1 SV=1 | 763.29 | 995.79 | 1.30 | 0.00042 |
| P20645 | Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=M6PR PE=1 SV=1 | 476.46 | 597.18 | 1.25 | 0.00045 |
| Q8NBM8 | Prenylcysteine oxidase-like OS=Homo sapiens OX=9606 GN=PCYOX1L PE=1 SV=2 | 140.59 | 189.15 | 1.35 | 0.00045 |
| Q9BT40 | Inositol polyphosphate 5-phosphatase K OS=Homo sapiens OX=9606 GN=INPP5K PE=1 SV=3 | 133.11 | 169.93 | 1.28 | 0.00046 |
| Q9BTE1 | Dynactin subunit 5 OS=Homo sapiens OX=9606 GN=DCTN5 PE=1 SV=1 | 249.45 | 312.29 | 1.25 | 0.00047 |
| Q2KHT3 | Protein CLEC16A OS=Homo sapiens OX=9606 GN=CLEC16A PE=1 SV=2 | 42.51 | 78.22 | 1.84 | 0.00050 |
| Q99719 | Septin-5 OS=Homo sapiens OX=9606 GN=SEPT5 PE=1 SV=1 | 1643.12 | 2357.81 | 1.43 | 0.00050 |
| P61225 | Ras-related protein Rap-2b OS=Homo sapiens OX=9606 GN=RAP2B PE=1 SV=1 | 862.47 | 1209.87 | 1.40 | 0.00051 |
| J3KNF8 | Cytochrome b5 type B (Outer mitochondrial membrane), isoform CRA_a OS=Homo sapiens OX=9606 GN=CYB5B PE=1 SV=1 | 244.39 | 327.41 | 1.34 | 0.00066 |
| Q8N461 | F-box/LRR-repeat protein 16 OS=Homo sapiens OX=9606 GN=FBXL16 PE=2 SV=2 | 210.97 | 264.37 | 1.25 | 0.00067 |
| Q9H3Z4 | DnaJ homolog subfamily C member 5 OS=Homo sapiens OX=9606 GN=DNAJC5 PE=1 SV=1 | 837.53 | 1160.09 | 1.39 | 0.00071 |
| Q5VT52 | Regulation of nuclear pre-mRNA domain-containing protein 2 OS=Homo sapiens OX=9606 GN=RPRD2 PE=1 SV=1 | 15.48 | 30.78 | 1.99 | 0.00073 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| P57740 | Nuclear pore complex protein Nup107 OS=Homo sapiens OX=9606 GN=NUP107 PE=1 SV=1 | 116.01 | 146.03 | 1.26 | 0.00073 |
| Q96AA8 | Isoform 3 of Janus kinase and microtubule-interacting protein 2 OS=Homo sapiens OX=9606 GN=JAKMIP2 | 59.96 | 80.78 | 1.35 | 0.00077 |
| P62166 | Neuronal calcium sensor 1 OS=Homo sapiens OX=9606 GN=NCS1 PE=1 SV=2 | 524.46 | 737.21 | 1.41 | 0.00081 |
| O75390 | Citrate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=2 | 4381.71 | 5495.39 | 1.25 | 0.00092 |
| F2Z2X4 | Exportin-4 OS=Homo sapiens OX=9606 GN=XPO4 PE=1 SV=1 | 27.38 | 35.98 | 1.31 | 0.00093 |
| O95163 | Elongator complex protein 1 OS=Homo sapiens OX=9606 GN=ELP1 PE=1 SV=3 | 21.73 | 33.41 | 1.54 | 0.00094 |
| Q00325 | Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=2 | 4191.96 | 5823.39 | 1.39 | 0.00095 |
| Q93050 | V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens OX=9606 GN=ATP6V0A1 PE=1 SV=3 | 4724.70 | 5996.51 | 1.27 | 0.00095 |
| Q9NVA1 | Ubiquinol-cytochrome-c reductase complex assembly factor 1 OS=Homo sapiens OX=9606 GN=UQCC1 PE=1 SV=3 | 157.71 | 228.43 | 1.45 | 0.00097 |
| Q9H2U2 | Isoform 2 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 | 370.66 | 477.22 | 1.29 | 0.00102 |
| P36542 | ATP synthase subunit gamma, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1C PE=1 SV=1 | 3478.55 | 4463.32 | 1.28 | 0.00103 |
| P0C7M8 | C-type lectin domain family 2 member L OS=Homo sapiens OX=9606 GN=CLEC2L PE=3 SV=1 | 106.75 | 243.36 | 2.28 | 0.00116 |
| Q9UDW1 | Cytochrome b-c1 complex subunit 9 OS=Homo sapiens OX=9606 GN=UQCR10 PE=1 SV=3 | 197.02 | 300.30 | 1.52 | 0.00129 |
| Q53H12 | Acylglycerol kinase, mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=2 | 1188.82 | 1488.52 | 1.25 | 0.00131 |
| P21579 | Synaptotagmin-1 OS=Homo sapiens OX=9606 GN=SYT1 PE=1 SV=1 | 6183.22 | 8012.52 | 1.30 | 0.00133 |
| J3QSW6 | Kalirin OS=Homo sapiens OX=9606 GN=KALRN PE=1 SV=1 | 233.70 | 381.69 | 1.63 | 0.00148 |
| Q16531 | DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DDB1 PE=1 SV=1 | 2261.76 | 2948.49 | 1.30 | 0.00154 |
| P30048 | Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens OX=9606 GN=PRDX3 PE=1 SV=3 | 1718.20 | 2279.42 | 1.33 | 0.00161 |
| Q9UK22 | F-box only protein 2 OS=Homo sapiens OX=9606 GN=FBXO2 PE=1 SV=2 | 795.58 | 999.13 | 1.26 | 0.00170 |
| P42704 | Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens OX=9606 GN=LRPPRC PE=1 SV=3 | 3261.35 | 4128.66 | 1.27 | 0.00175 |
| Q86UY8 | 5'-nucleotidase domain-containing protein 3 OS=Homo sapiens OX=9606 GN=NT5DC3 PE=1 SV=1 | 347.33 | 506.85 | 1.46 | 0.00181 |
| B5MDU6 | Lipid droplet-associated hydrolase OS=Homo sapiens OX=9606 GN=LDAH PE=1 SV=1 | 252.83 | 329.71 | 1.30 | 0.00181 |
| H7BYZ3 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 | 473.39 | 736.33 | 1.56 | 0.00184 |
| Q8WWI5 | Isoform 2 of Choline transporter-like protein 1 OS=Homo sapiens OX=9606 GN=SLC44A1 | 854.84 | 1302.93 | 1.52 | 0.00188 |
| Q96S97 | Myeloid-associated differentiation marker OS=Homo sapiens OX=9606 GN=MYADM PE=1 SV=2 | 256.66 | 366.47 | 1.43 | 0.00189 |
| Q9NQC3 | Isoform C of Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 | 75.50 | 138.56 | 1.84 | 0.00191 |

| | | | | | |
|---|---|---|---|---|---|
| P46736 | Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens OX=9606 GN=BRCC3 PE=1 SV=2 | 61.29 | 78.33 | 1.28 | 0.00192 |
| Q8N9R8 | Isoform 2 of Protein SCAI OS=Homo sapiens OX=9606 GN=SCAI | 587.99 | 767.36 | 1.31 | 0.00200 |
| Q7L1V2 | Vacuolar fusion protein MON1 homolog B OS=Homo sapiens OX=9606 GN=MON1B PE=1 SV=1 | 35.25 | 56.22 | 1.59 | 0.00207 |
| Q15904 | V-type proton ATPase subunit S1 OS=Homo sapiens OX=9606 GN=ATP6AP1 PE=1 SV=2 | 252.13 | 368.51 | 1.46 | 0.00208 |
| Q9H845 | Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens OX=9606 GN=ACAD9 PE=1 SV=1 | 838.08 | 1118.02 | 1.33 | 0.00210 |
| O75306 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS2 PE=1 SV=2 | 1156.89 | 1576.62 | 1.36 | 0.00211 |
| P45880 | Isoform 1 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2 | 6722.43 | 8604.01 | 1.28 | 0.00211 |
| Q02978 | Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens OX=9606 GN=SLC25A11 PE=1 SV=3 | 2289.49 | 3470.47 | 1.52 | 0.00214 |
| P15531 | Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 | 239.63 | 307.61 | 1.28 | 0.00215 |
| Q16795 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFA9 PE=1 SV=2 | 2107.21 | 2975.15 | 1.41 | 0.00225 |
| O75689 | Arf-GAP with dual PH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ADAP1 PE=1 SV=2 | 1512.04 | 1978.18 | 1.31 | 0.00229 |
| Q96F07 | Isoform 2 of Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens OX=9606 GN=CYFIP2 | 3728.54 | 4723.96 | 1.27 | 0.00229 |
| A0A087WT12 | Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX4 PE=1 SV=1 | 1217.90 | 1524.79 | 1.25 | 0.00229 |
| P27701 | CD82 antigen OS=Homo sapiens OX=9606 GN=CD82 PE=1 SV=1 | 86.19 | 165.41 | 1.92 | 0.00230 |
| A0A087WWT2 | Neuritin OS=Homo sapiens OX=9606 GN=NRN1 PE=1 SV=1 | 333.47 | 450.12 | 1.35 | 0.00258 |
| Q9NR31 | GTP-binding protein SAR1a OS=Homo sapiens OX=9606 GN=SAR1A PE=1 SV=1 | 722.82 | 992.88 | 1.37 | 0.00270 |
| P23469 | Receptor-type tyrosine-protein phosphatase epsilon OS=Homo sapiens OX=9606 GN=PTPRE PE=1 SV=1 | 108.03 | 156.94 | 1.45 | 0.00273 |
| P61601 | Neurocalcin-delta OS=Homo sapiens OX=9606 GN=NCALD PE=1 SV=2 | 394.03 | 516.84 | 1.31 | 0.00292 |
| P62244 | 40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 SV=2 | 190.92 | 248.23 | 1.30 | 0.00302 |
| Q969L2 | Protein MAL2 OS=Homo sapiens OX=9606 GN=MAL2 PE=1 SV=1 | 136.09 | 176.31 | 1.30 | 0.00308 |
| P54803 | Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC PE=1 SV=3 | 121.16 | 362.06 | 2.99 | 0.00315 |
| Q16186 | Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens OX=9606 GN=ADRM1 PE=1 SV=2 | 308.10 | 389.11 | 1.26 | 0.00318 |
| Q9GZN7 | Protein rogdi homolog OS=Homo sapiens OX=9606 GN=ROGDI PE=1 SV=1 | 663.05 | 865.97 | 1.31 | 0.00318 |
| P63096 | Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens OX=9606 GN=GNAI1 PE=1 SV=2 | 937.27 | 1246.15 | 1.33 | 0.00321 |
| Q12981 | Isoform 3 of Vesicle transport protein SEC20 OS=Homo sapiens OX=9606 GN=BNIP1 | 132.39 | 179.95 | 1.36 | 0.00323 |
| Q9Y276 | Mitochondrial chaperone BCS1 OS=Homo sapiens OX=9606 GN=BCS1L PE=1 SV=1 | 429.73 | 608.00 | 1.41 | 0.00324 |

| | | | | | |
|---|---|---|---|---|---|
| K7EJH8 | Alpha-actinin-4 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=1 | 31.74 | 42.20 | 1.33 | 0.00331 |
| J3KQA9 | Microtubule-associated tumor suppressor candidate 2 OS=Homo sapiens OX=9606 GN=MTUS2 PE=1 SV=1 | 26.50 | 45.22 | 1.71 | 0.00336 |
| P0CG08 | Golgi pH regulator B OS=Homo sapiens OX=9606 GN=GPR89B PE=1 SV=1 | 95.98 | 130.34 | 1.36 | 0.00337 |
| A0A2R8YFE2 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 | 95.52 | 126.57 | 1.33 | 0.00338 |
| J3KR44 | Ubiquitin thioesterase OS=Homo sapiens OX=9606 GN=OTUB1 PE=1 SV=2 | 1233.71 | 1550.46 | 1.26 | 0.00339 |
| Q9Y376 | Calcium-binding protein 39 OS=Homo sapiens OX=9606 GN=CAB39 PE=1 SV=1 | 677.67 | 986.55 | 1.46 | 0.00350 |
| P21796 | Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens OX=9606 GN=VDAC1 PE=1 SV=2 | 9820.98 | 12600.37 | 1.28 | 0.00354 |
| P04179 | Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens OX=9606 GN=SOD2 PE=1 SV=3 | 2948.09 | 3753.25 | 1.27 | 0.00355 |
| P20337 | Ras-related protein Rab-3B OS=Homo sapiens OX=9606 GN=RAB3B PE=1 SV=2 | 31.56 | 54.85 | 1.74 | 0.00362 |
| Q96ND0 | Protein FAM210A OS=Homo sapiens OX=9606 GN=FAM210A PE=1 SV=2 | 91.82 | 127.12 | 1.38 | 0.00370 |
| A6NMU8 | Neuroligin 4, Y-linked, isoform CRA_c OS=Homo sapiens OX=9606 GN=NLGN4Y PE=4 SV=1 | 99.11 | 127.41 | 1.29 | 0.00384 |
| Q16799 | Isoform RTN1-C of Reticulon-1 OS=Homo sapiens OX=9606 GN=RTN1 | 420.65 | 756.50 | 1.80 | 0.00403 |
| P27449 | V-type proton ATPase 16 kDa proteolipid subunit OS=Homo sapiens OX=9606 GN=ATP6V0C PE=1 SV=1 | 560.53 | 746.40 | 1.33 | 0.00426 |
| C9JV77 | Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1 | 172.48 | 217.79 | 1.26 | 0.00443 |
| P32189 | Glycerol kinase OS=Homo sapiens OX=9606 GN=GK PE=1 SV=3 | 616.42 | 772.26 | 1.25 | 0.00479 |
| A0A1X7SBR8 | Voltage-dependent calcium channel gamma-8 subunit OS=Homo sapiens OX=9606 GN=CACNG8 PE=1 SV=1 | 574.17 | 730.12 | 1.27 | 0.00483 |
| Q96DI7 | Isoform 2 of U5 small nuclear ribonucleoprotein 40 kDa protein OS=Homo sapiens OX=9606 GN=SNRNP40 | 176.37 | 225.54 | 1.28 | 0.00486 |
| F8WB74 | Selenoprotein W OS=Homo sapiens OX=9606 GN=SELENOW PE=1 SV=1 | 139.92 | 177.39 | 1.27 | 0.00487 |
| Q9UGP8 | Translocation protein SEC63 homolog OS=Homo sapiens OX=9606 GN=SEC63 PE=1 SV=2 | 19.24 | 32.63 | 1.70 | 0.00516 |
| Q9Y6A2 | Cholesterol 24-hydroxylase OS=Homo sapiens OX=9606 GN=CYP46A1 PE=1 SV=1 | 84.69 | 109.21 | 1.29 | 0.00518 |
| Q86V21 | Acetoacetyl-CoA synthetase OS=Homo sapiens OX=9606 GN=AACS PE=1 SV=1 | 63.67 | 90.04 | 1.41 | 0.00523 |
| Q14232 | Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens OX=9606 GN=EIF2B1 PE=1 SV=1 | 431.34 | 653.33 | 1.51 | 0.00524 |
| E9PFW3 | AP-2 complex subunit mu OS=Homo sapiens OX=9606 GN=AP2M1 PE=1 SV=1 | 4684.31 | 5868.05 | 1.25 | 0.00524 |
| P20336 | Ras-related protein Rab-3A OS=Homo sapiens OX=9606 GN=RAB3A PE=1 SV=1 | 3071.40 | 4157.31 | 1.35 | 0.00524 |
| Q9NUJ1 | Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens OX=9606 GN=ABHD10 PE=1 SV=1 | 720.66 | 998.03 | 1.38 | 0.00527 |
| Q9HD34 | LYR motif-containing protein 4 OS=Homo sapiens OX=9606 GN=LYRM4 PE=1 SV=1 | 126.81 | 161.99 | 1.28 | 0.00528 |
| Q96PB7 | Noelin-3 OS=Homo sapiens OX=9606 GN=OLFM3 PE=1 SV=1 | 142.65 | 180.25 | 1.26 | 0.00539 |

| | | | | | |
|---|---|---|---|---|---|
| Q5T0D9 | Tumor protein p63-regulated gene 1-like protein OS=Homo sapiens OX=9606 GN=TPRG1L PE=1 SV=1 | 411.43 | 567.89 | 1.38 | 0.00545 |
| P23396 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=2 | 1401.53 | 1908.79 | 1.36 | 0.00551 |
| P19075 | Tetraspanin-8 OS=Homo sapiens OX=9606 GN=TSPAN8 PE=1 SV=1 | 214.96 | 338.43 | 1.57 | 0.00561 |
| P20339 | Ras-related protein Rab-5A OS=Homo sapiens OX=9606 GN=RAB5A PE=1 SV=2 | 604.03 | 779.75 | 1.29 | 0.00565 |
| P14678 | Isoform SM-B1 of Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens OX=9606 GN=SNRPB | 372.64 | 500.55 | 1.34 | 0.00573 |
| O00232 | 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens OX=9606 GN=PSMD12 PE=1 SV=3 | 875.38 | 1200.39 | 1.37 | 0.00582 |
| O15260 | Surfeit locus protein 4 OS=Homo sapiens OX=9606 GN=SURF4 PE=1 SV=3 | 63.36 | 87.17 | 1.38 | 0.00589 |
| A8MUM1 | EARP and GARP complex-interacting protein 1 OS=Homo sapiens OX=9606 GN=EIPR1 PE=1 SV=2 | 439.07 | 587.81 | 1.34 | 0.00591 |
| P18085 | ADP-ribosylation factor 4 OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=3 | 159.05 | 264.41 | 1.66 | 0.00600 |
| Q00169 | Phosphatidylinositol transfer protein alpha isoform OS=Homo sapiens OX=9606 GN=PITPNA PE=1 SV=2 | 1270.28 | 1776.64 | 1.40 | 0.00602 |
| O95858 | Tetraspanin-15 OS=Homo sapiens OX=9606 GN=TSPAN15 PE=1 SV=1 | 85.10 | 134.30 | 1.58 | 0.00603 |
| Q13491 | Isoform 4 of Neuronal membrane glycoprotein M6-b OS=Homo sapiens OX=9606 GN=GPM6B | 1790.54 | 2280.03 | 1.27 | 0.00616 |
| O14775 | Guanine nucleotide-binding protein subunit beta-5 OS=Homo sapiens OX=9606 GN=GNB5 PE=1 SV=2 | 567.68 | 712.36 | 1.25 | 0.00624 |
| P12235 | ADP/ATP translocase 1 OS=Homo sapiens OX=9606 GN=SLC25A4 PE=1 SV=4 | 948.42 | 1509.10 | 1.59 | 0.00632 |
| Q15119 | [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial OS=Homo sapiens OX=9606 GN=PDK2 PE=1 SV=2 | 555.80 | 728.35 | 1.31 | 0.00637 |
| A0A1W2PPJ5 | Protein cereblon OS=Homo sapiens OX=9606 GN=CRBN PE=1 SV=1 | 296.85 | 402.70 | 1.36 | 0.00646 |
| P61204 | ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=2 | 1222.31 | 1795.71 | 1.47 | 0.00652 |
| Q86Y39 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens OX=9606 GN=NDUFA11 PE=1 SV=3 | 301.35 | 498.15 | 1.65 | 0.00652 |
| A0A024R4M0 | 40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=1 | 1279.78 | 1629.30 | 1.27 | 0.00659 |
| Q9Y277 | Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606 GN=VDAC3 | 549.42 | 737.88 | 1.34 | 0.00668 |
| Q53H82 | Endoribonuclease LACTB2 OS=Homo sapiens OX=9606 GN=LACTB2 PE=1 SV=2 | 16.76 | 27.02 | 1.61 | 0.00679 |
| Q9BXS5 | Isoform 2 of AP-1 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP1M1 | 782.34 | 991.58 | 1.27 | 0.00682 |
| Q8TCJ2 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens OX=9606 GN=STT3B PE=1 SV=1 | 286.40 | 399.42 | 1.39 | 0.00694 |
| Q99873 | Protein arginine N-methyltransferase 1 OS=Homo sapiens OX=9606 GN=PRMT1 PE=1 SV=3 | 165.83 | 240.45 | 1.45 | 0.00711 |
| O15144 | Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1 | 1016.03 | 1343.09 | 1.32 | 0.00717 |
| Q96RD7 | Pannexin-1 OS=Homo sapiens OX=9606 GN=PANX1 PE=1 SV=4 | 25.82 | 42.10 | 1.63 | 0.00739 |

| | | | | | |
|---|---|---|---|---|---|
| O95197 | Isoform 3 of Reticulon-3 OS=Homo sapiens OX=9606 GN=RTN3 | 102.85 | 150.41 | 1.46 | 0.00763 |
| Q9Y6X5 | Bis(5'-adenosyl)-triphosphatase ENPP4 OS=Homo sapiens OX=9606 GN=ENPP4 PE=1 SV=3 | 107.55 | 174.91 | 1.63 | 0.00769 |
| P22694 | cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens OX=9606 GN=PRKACB PE=1 SV=2 | 913.56 | 1356.86 | 1.49 | 0.00780 |
| P56545 | Isoform 2 of C-terminal-binding protein 2 OS=Homo sapiens OX=9606 GN=CTBP2 | 79.41 | 108.94 | 1.37 | 0.00813 |
| A0A0A0MQT0 | Retinol binding protein 1, cellular OS=Homo sapiens OX=9606 GN=RBP1 PE=1 SV=1 | 386.06 | 484.95 | 1.26 | 0.00818 |
| Q9UIQ6 | Leucyl-cystinyl aminopeptidase OS=Homo sapiens OX=9606 GN=LNPEP PE=1 SV=3 | 118.23 | 170.43 | 1.44 | 0.00820 |
| O95772 | STARD3 N-terminal-like protein OS=Homo sapiens OX=9606 GN=STARD3NL PE=1 SV=1 | 105.04 | 150.44 | 1.43 | 0.00823 |
| Q9UBQ5 | Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens OX=9606 GN=EIF3K PE=1 SV=1 | 366.95 | 466.17 | 1.27 | 0.00823 |
| Q9Y277 | Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606 GN=VDAC3 PE=1 SV=1 | 3781.00 | 5405.35 | 1.43 | 0.00830 |
| P05141 | ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC25A5 PE=1 SV=7 | 7252.71 | 9907.02 | 1.37 | 0.00833 |
| Q7Z7H5 | Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens OX=9606 GN=TMED4 PE=1 SV=1 | 237.73 | 311.26 | 1.31 | 0.00850 |
| Q7Z5G4 | Golgin subfamily A member 7 OS=Homo sapiens OX=9606 GN=GOLGA7 PE=1 SV=2 | 387.60 | 491.86 | 1.27 | 0.00854 |
| Q9NRZ5 | 1-acyl-sn-glycerol-3-phosphate acyltransferase delta OS=Homo sapiens OX=9606 GN=AGPAT4 PE=1 SV=1 | 131.26 | 175.30 | 1.34 | 0.00867 |
| Q13936 | Isoform 2 of Voltage-dependent L-type calcium channel subunit alpha-1C OS=Homo sapiens OX=9606 GN=CACNA1C | 22.98 | 35.41 | 1.54 | 0.00885 |
| P28676 | Grancalcin OS=Homo sapiens OX=9606 GN=GCA PE=1 SV=2 | 151.92 | 205.78 | 1.35 | 0.00907 |
| Q14240 | Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=2 | 1815.45 | 2315.76 | 1.28 | 0.00916 |
| Q7L1I2 | Synaptic vesicle glycoprotein 2B OS=Homo sapiens OX=9606 GN=SV2B PE=1 SV=1 | 1878.96 | 2413.81 | 1.28 | 0.00957 |
| Q9Y2Q5 | Isoform 2 of Ragulator complex protein LAMTOR2 OS=Homo sapiens OX=9606 GN=LAMTOR2 | 118.52 | 156.14 | 1.32 | 0.00957 |
| Q9NZ01 | Very-long-chain enoyl-CoA reductase OS=Homo sapiens OX=9606 GN=TECR PE=1 SV=1 | 495.10 | 1013.58 | 2.05 | 0.01001 |
| P08247 | Synaptophysin OS=Homo sapiens OX=9606 GN=SYP PE=1 SV=3 | 2118.06 | 2832.64 | 1.34 | 0.01005 |
| Q99643 | Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=Homo sapiens OX=9606 GN=SDHC PE=1 SV=1 | 43.79 | 119.01 | 2.72 | 0.01007 |
| Q9UNZ2 | Isoform 2 of NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C | 193.21 | 242.88 | 1.26 | 0.01013 |
| A6NCE7 | Microtubule-associated proteins 1A/1B light chain 3 beta 2 OS=Homo sapiens OX=9606 GN=MAP1LC3B2 PE=2 SV=1 | 251.59 | 336.37 | 1.34 | 0.01024 |
| O75964 | ATP synthase subunit g, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5MG PE=1 SV=3 | 755.61 | 949.07 | 1.26 | 0.01025 |
| Q9Y342 | Plasmolipin OS=Homo sapiens OX=9606 GN=PLLP PE=1 SV=1 | 503.23 | 746.06 | 1.48 | 0.01027 |

| | | | | | |
|---|---|---|---|---|---|
| Q53GQ0 | Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens OX=9606 GN=HSD17B12 PE=1 SV=2 | 420.16 | 594.62 | 1.42 | 0.01061 |
| Q6IA86 | Isoform 6 of Elongator complex protein 2 OS=Homo sapiens OX=9606 GN=ELP2 | 29.02 | 47.17 | 1.63 | 0.01071 |
| P52306 | Isoform 5 of Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens OX=9606 GN=RAP1GDS1 | 1657.36 | 2515.77 | 1.52 | 0.01104 |
| Q8N414 | PiggyBac transposable element-derived protein 5 OS=Homo sapiens OX=9606 GN=PGBD5 PE=1 SV=4 | 188.72 | 240.35 | 1.27 | 0.01139 |
| Q96DZ9 | CKLF-like MARVEL transmembrane domain-containing protein 5 OS=Homo sapiens OX=9606 GN=CMTM5 PE=1 SV=2 | 83.78 | 131.69 | 1.57 | 0.01153 |
| O14656 | Torsin-1A OS=Homo sapiens OX=9606 GN=TOR1A PE=1 SV=1 | 126.66 | 173.14 | 1.37 | 0.01157 |
| A0A0A0MR60 | Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens OX=9606 GN=PTPRS PE=1 SV=1 | 150.33 | 239.92 | 1.60 | 0.01174 |
| Q9P2U7 | Vesicular glutamate transporter 1 OS=Homo sapiens OX=9606 GN=SLC17A7 PE=2 SV=1 | 1505.96 | 1936.15 | 1.29 | 0.01175 |
| Q6PI78 | Transmembrane protein 65 OS=Homo sapiens OX=9606 GN=TMEM65 PE=1 SV=2 | 396.94 | 524.99 | 1.32 | 0.01192 |
| Q7Z4H8 | KDEL motif-containing protein 2 OS=Homo sapiens OX=9606 GN=KDELC2 PE=1 SV=2 | 13.91 | 19.36 | 1.39 | 0.01219 |
| Q0VDG4 | Secernin-3 OS=Homo sapiens OX=9606 GN=SCRN3 PE=1 SV=1 | 299.83 | 390.26 | 1.30 | 0.01244 |
| J9JIE6 | Calcium load-activated calcium channel OS=Homo sapiens OX=9606 GN=TMCO1 PE=1 SV=1 | 142.68 | 181.48 | 1.27 | 0.01248 |
| P62068 | Ubiquitin carboxyl-terminal hydrolase 46 OS=Homo sapiens OX=9606 GN=USP46 PE=1 SV=1 | 72.79 | 93.27 | 1.28 | 0.01261 |
| P43007 | Neutral amino acid transporter A OS=Homo sapiens OX=9606 GN=SLC1A4 PE=1 SV=1 | 458.06 | 582.91 | 1.27 | 0.01268 |
| O15258 | Protein RER1 OS=Homo sapiens OX=9606 GN=RER1 PE=1 SV=1 | 227.66 | 312.78 | 1.37 | 0.01299 |
| A8MWY0 | UPF0577 protein KIAA1324-like OS=Homo sapiens OX=9606 GN=KIAA1324L PE=1 SV=2 | 79.83 | 115.75 | 1.45 | 0.01322 |
| Q9P035 | Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=2 | 728.56 | 1039.95 | 1.43 | 0.01344 |
| Q9NRZ7 | Isoform 3 of 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma OS=Homo sapiens OX=9606 GN=AGPAT3 | 645.42 | 814.66 | 1.26 | 0.01366 |
| P61313 | 60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2 | 384.18 | 486.48 | 1.27 | 0.01387 |
| Q8IYU2 | E3 ubiquitin-protein ligase HACE1 OS=Homo sapiens OX=9606 GN=HACE1 PE=1 SV=2 | 39.66 | 75.53 | 1.90 | 0.01391 |
| Q8N1A0 | Keratin-like protein KRT222 OS=Homo sapiens OX=9606 GN=KRT222 PE=2 SV=1 | 79.23 | 99.07 | 1.25 | 0.01405 |
| P61626 | Lysozyme C OS=Homo sapiens OX=9606 GN=LYZ PE=1 SV=1 | 236.28 | 303.67 | 1.29 | 0.01417 |
| Q7L5D6 | Golgi to ER traffic protein 4 homolog OS=Homo sapiens OX=9606 GN=GET4 PE=1 SV=1 | 231.38 | 314.12 | 1.36 | 0.01425 |
| E9PK54 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=8 | 62.82 | 95.93 | 1.53 | 0.01445 |
| Q8IVF5 | Isoform 2 of T-lymphoma invasion and metastasis-inducing protein 2 OS=Homo sapiens OX=9606 GN=TIAM2 | 135.06 | 170.50 | 1.26 | 0.01446 |
| Q9UHG3 | Prenylcysteine oxidase 1 OS=Homo sapiens OX=9606 GN=PCYOX1 PE=1 SV=3 | 1250.40 | 1708.44 | 1.37 | 0.01458 |

| | | | | | |
|---|---|---|---|---|---|
| Q8TB96 | T-cell immunomodulatory protein OS=Homo sapiens OX=9606 GN=ITFG1 PE=1 SV=1 | 139.41 | 220.20 | 1.58 | 0.01481 |
| Q15759 | Mitogen-activated protein kinase 11 OS=Homo sapiens OX=9606 GN=MAPK11 PE=1 SV=2 | 27.49 | 34.87 | 1.27 | 0.01489 |
| O75508 | Claudin-11 OS=Homo sapiens OX=9606 GN=CLDN11 PE=1 SV=2 | 931.95 | 1755.88 | 1.88 | 0.01519 |
| O43592 | Exportin-T OS=Homo sapiens OX=9606 GN=XPOT PE=1 SV=2 | 418.12 | 625.84 | 1.50 | 0.01534 |
| Q9BVC4 | Target of rapamycin complex subunit LST8 OS=Homo sapiens OX=9606 GN=MLST8 PE=1 SV=1 | 115.07 | 174.32 | 1.51 | 0.01537 |
| Q5HYK3 | 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial OS=Homo sapiens OX=9606 GN=COQ5 PE=1 SV=2 | 183.50 | 231.56 | 1.26 | 0.01549 |
| P52434 | Isoform 4 of DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H | 25.33 | 38.08 | 1.50 | 0.01557 |
| P62495 | Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens OX=9606 GN=ETF1 PE=1 SV=3 | 428.22 | 546.80 | 1.28 | 0.01593 |
| P47870 | Gamma-aminobutyric acid receptor subunit beta-2 OS=Homo sapiens OX=9606 GN=GABRB2 PE=1 SV=2 | 650.31 | 835.04 | 1.28 | 0.01610 |
| Q9NS86 | LanC-like protein 2 OS=Homo sapiens OX=9606 GN=LANCL2 PE=1 SV=1 | 1029.17 | 1405.93 | 1.37 | 0.01626 |
| O43414 | ERI1 exoribonuclease 3 OS=Homo sapiens OX=9606 GN=ERI3 PE=1 SV=2 | 157.60 | 241.55 | 1.53 | 0.01651 |
| A0A0D9SF30 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 | 2289.56 | 2941.53 | 1.28 | 0.01659 |
| O00410 | Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4 | 1458.50 | 1869.17 | 1.28 | 0.01682 |
| O43760 | Isoform 2 of Synaptogyrin-2 OS=Homo sapiens OX=9606 GN=SYNGR2 | 81.74 | 122.19 | 1.49 | 0.01763 |
| A0A087WVA1 | Selenoprotein T OS=Homo sapiens OX=9606 GN=SELENOT PE=1 SV=1 | 30.43 | 46.11 | 1.52 | 0.01770 |
| Q969M1 | Mitochondrial import receptor subunit TOM40B OS=Homo sapiens OX=9606 GN=TOMM40L PE=1 SV=1 | 250.31 | 364.08 | 1.45 | 0.01785 |
| E9PCN2 | Guanylate cyclase soluble subunit beta-1 OS=Homo sapiens OX=9606 GN=GUCY1B1 PE=1 SV=1 | 464.20 | 587.32 | 1.27 | 0.01789 |
| H0UI06 | Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens OX=9606 GN=COX7A2 PE=1 SV=1 | 578.47 | 796.18 | 1.38 | 0.01793 |
| B4DJ07 | Exocyst complex component 7 OS=Homo sapiens OX=9606 GN=EXOC7 PE=1 SV=1 | 32.24 | 45.20 | 1.40 | 0.01806 |
| P49720 | Proteasome subunit beta type-3 OS=Homo sapiens OX=9606 GN=PSMB3 PE=1 SV=2 | 201.54 | 301.01 | 1.49 | 0.01821 |
| Q8TDQ7 | Glucosamine-6-phosphate isomerase 2 OS=Homo sapiens OX=9606 GN=GNPDA2 PE=1 SV=1 | 463.68 | 686.17 | 1.48 | 0.01843 |
| P07099 | Epoxide hydrolase 1 OS=Homo sapiens OX=9606 GN=EPHX1 PE=1 SV=1 | 956.55 | 1258.94 | 1.32 | 0.01850 |
| Q9NR22 | Protein arginine N-methyltransferase 8 OS=Homo sapiens OX=9606 GN=PRMT8 PE=1 SV=2 | 57.08 | 115.68 | 2.03 | 0.01875 |
| A0A2Y9D025 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens OX=9606 GN=NDUFA6 PE=4 SV=1 | 153.59 | 210.99 | 1.37 | 0.01926 |
| P60981 | Destrin OS=Homo sapiens OX=9606 GN=DSTN PE=1 SV=3 | 1122.96 | 1409.92 | 1.26 | 0.01955 |

| | | | | | |
|---|---|---|---|---|---|
| Q5T653 | 39S ribosomal protein L2, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL2 PE=1 SV=2 | 10.16 | 15.94 | 1.57 | 0.01958 |
| Q9H8T0 | Isoform 2 of AKT-interacting protein OS=Homo sapiens OX=9606 GN=AKTIP | 42.61 | 58.39 | 1.37 | 0.01995 |
| Q9H3K2 | Growth hormone-inducible transmembrane protein OS=Homo sapiens OX=9606 GN=GHITM PE=1 SV=2 | 368.06 | 482.18 | 1.31 | 0.02028 |
| Q9BZL1 | Ubiquitin-like protein 5 OS=Homo sapiens OX=9606 GN=UBL5 PE=1 SV=1 | 102.03 | 146.85 | 1.44 | 0.02042 |
| Q8NE35 | Cytoplasmic polyadenylation element-binding protein 3 OS=Homo sapiens OX=9606 GN=CPEB3 PE=1 SV=2 | 141.69 | 180.83 | 1.28 | 0.02050 |
| Q15363 | Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=TMED2 PE=1 SV=1 | 161.50 | 213.96 | 1.32 | 0.02053 |
| P47972 | Neuronal pentraxin-2 OS=Homo sapiens OX=9606 GN=NPTX2 PE=1 SV=2 | 249.23 | 493.62 | 1.98 | 0.02064 |
| K7EQD6 | Vesicle-fusing ATPase (Fragment) OS=Homo sapiens OX=9606 GN=NSF PE=1 SV=1 | 88.07 | 203.20 | 2.31 | 0.02143 |
| A0A0A0MRR7 | U1 small nuclear ribonucleoprotein C OS=Homo sapiens OX=9606 GN=SNRPC PE=1 SV=1 | 95.53 | 129.32 | 1.35 | 0.02149 |
| O00487 | 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens OX=9606 GN=PSMD14 PE=1 SV=1 | 533.79 | 668.57 | 1.25 | 0.02159 |
| Q6PI48 | Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1 | 253.47 | 320.39 | 1.26 | 0.02164 |
| P30536 | Translocator protein OS=Homo sapiens OX=9606 GN=TSPO PE=1 SV=3 | 222.42 | 369.50 | 1.66 | 0.02181 |
| Q9H4L5 | Oxysterol-binding protein-related protein 3 OS=Homo sapiens OX=9606 GN=OSBPL3 PE=1 SV=1 | 4.51 | 8.23 | 1.82 | 0.02204 |
| Q9BR01 | Sulfotransferase 4A1 OS=Homo sapiens OX=9606 GN=SULT4A1 PE=1 SV=2 | 131.92 | 164.95 | 1.25 | 0.02230 |
| A0A0A0MQU3 | Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens OX=9606 GN=UBE2D2 PE=1 SV=1 | 282.30 | 398.02 | 1.41 | 0.02239 |
| P60228 | Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens OX=9606 GN=EIF3E PE=1 SV=1 | 551.09 | 694.21 | 1.26 | 0.02245 |
| J3KNI1 | Conserved oligomeric Golgi complex subunit 4 OS=Homo sapiens OX=9606 GN=COG4 PE=1 SV=1 | 19.00 | 28.44 | 1.50 | 0.02278 |
| J3KNF5 | Centrosomal protein of 290 kDa OS=Homo sapiens OX=9606 GN=CEP290 PE=1 SV=1 | 99.97 | 169.63 | 1.70 | 0.02345 |
| J3KTA1 | F-box and leucine-rich repeat protein 20, isoform CRA_a OS=Homo sapiens OX=9606 GN=FBXL20 PE=1 SV=1 | 96.27 | 120.86 | 1.26 | 0.02442 |
| P17677 | Isoform 2 of Neuromodulin OS=Homo sapiens OX=9606 GN=GAP43 | 7618.54 | 10551.77 | 1.39 | 0.02447 |
| P42658 | Dipeptidyl aminopeptidase-like protein 6 OS=Homo sapiens OX=9606 GN=DPP6 PE=1 SV=2 | 4638.72 | 6420.29 | 1.38 | 0.02502 |
| Q9BQG1 | Synaptotagmin-3 OS=Homo sapiens OX=9606 GN=SYT3 PE=2 SV=1 | 226.08 | 287.14 | 1.27 | 0.02516 |
| Q9Y296 | Trafficking protein particle complex subunit 4 OS=Homo sapiens OX=9606 GN=TRAPPC4 PE=1 SV=1 | 88.93 | 127.17 | 1.43 | 0.02519 |
| O95847 | Mitochondrial uncoupling protein 4 OS=Homo sapiens OX=9606 GN=SLC25A27 PE=2 SV=1 | 84.23 | 114.89 | 1.36 | 0.02695 |

| | | | | | |
|---|---|---|---|---|---|
| Q6YP21 | Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens OX=9606 GN=KYAT3 PE=1 SV=1 | 979.50 | 1309.13 | 1.34 | 0.02707 |
| F8VYN9 | ADP-ribosylation factor-like protein 1 OS=Homo sapiens OX=9606 GN=ARL1 PE=1 SV=1 | 65.35 | 108.38 | 1.66 | 0.02764 |
| Q8TEA7 | TBC domain-containing protein kinase-like protein OS=Homo sapiens OX=9606 GN=TBCK PE=1 SV=4 | 70.76 | 88.81 | 1.26 | 0.02804 |
| Q9Y2J0 | Isoform 2 of Rabphilin-3A OS=Homo sapiens OX=9606 GN=RPH3A | 2222.47 | 2952.95 | 1.33 | 0.02919 |
| Q5JTD7 | Leucine-rich repeat-containing protein 73 OS=Homo sapiens OX=9606 GN=LRRC73 PE=2 SV=1 | 29.68 | 38.02 | 1.28 | 0.02979 |
| Q8NBI5 | Isoform 2 of Solute carrier family 43 member 3 OS=Homo sapiens OX=9606 GN=SLC43A3 | 74.82 | 124.45 | 1.66 | 0.03018 |
| Q9NRX5 | Serine incorporator 1 OS=Homo sapiens OX=9606 GN=SERINC1 PE=1 SV=1 | 86.64 | 187.03 | 2.16 | 0.03044 |
| Q9NVV5 | Androgen-induced gene 1 protein OS=Homo sapiens OX=9606 GN=AIG1 PE=1 SV=2 | 20.89 | 34.51 | 1.65 | 0.03065 |
| Q9Y2T3 | Isoform 3 of Guanine deaminase OS=Homo sapiens OX=9606 GN=GDA | 3827.96 | 5024.03 | 1.31 | 0.03069 |
| Q9C0H2 | Isoform 4 of Protein tweety homolog 3 OS=Homo sapiens OX=9606 GN=TTYH3 | 101.45 | 132.61 | 1.31 | 0.03077 |
| Q7KZN9 | Cytochrome c oxidase assembly protein COX15 homolog OS=Homo sapiens OX=9606 GN=COX15 PE=1 SV=1 | 117.01 | 147.10 | 1.26 | 0.03087 |
| P62330 | ADP-ribosylation factor 6 OS=Homo sapiens OX=9606 GN=ARF6 PE=1 SV=2 | 279.67 | 373.50 | 1.34 | 0.03125 |
| P26992 | Ciliary neurotrophic factor receptor subunit alpha OS=Homo sapiens OX=9606 GN=CNTFR PE=1 SV=2 | 197.06 | 259.76 | 1.32 | 0.03147 |
| P42261 | Isoform 6 of Glutamate receptor 1 OS=Homo sapiens OX=9606 GN=GRIA1 | 876.91 | 1205.72 | 1.37 | 0.03164 |
| O43759 | Synaptogyrin-1 OS=Homo sapiens OX=9606 GN=SYNGR1 PE=1 SV=2 | 577.59 | 726.74 | 1.26 | 0.03164 |
| M0QYZ2 | AP complex subunit sigma OS=Homo sapiens OX=9606 GN=AP2S1 PE=1 SV=1 | 311.04 | 429.95 | 1.38 | 0.03174 |
| A0A087WTF6 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 | 37.17 | 46.47 | 1.25 | 0.03366 |
| Q96GZ6 | Isoform 9 of Solute carrier family 41 member 3 OS=Homo sapiens OX=9606 GN=SLC41A3 | 24.68 | 34.82 | 1.41 | 0.03412 |
| P46199 | Translation initiation factor IF-2, mitochondrial OS=Homo sapiens OX=9606 GN=MTIF2 PE=1 SV=2 | 17.22 | 22.50 | 1.31 | 0.03511 |
| O95470 | Sphingosine-1-phosphate lyase 1 OS=Homo sapiens OX=9606 GN=SGPL1 PE=1 SV=3 | 91.84 | 151.01 | 1.64 | 0.03571 |
| A0A0C4DFZ2 | Arylsulfatase A OS=Homo sapiens OX=9606 GN=ARSA PE=1 SV=1 | 61.63 | 77.25 | 1.25 | 0.03590 |
| Q2M3C7 | A-kinase anchor protein SPHKAP OS=Homo sapiens OX=9606 GN=SPHKAP PE=1 SV=1 | 25.23 | 33.22 | 1.32 | 0.03595 |
| P41217 | Isoform 3 of OX-2 membrane glycoprotein OS=Homo sapiens OX=9606 GN=CD200 | 359.69 | 481.97 | 1.34 | 0.03607 |
| Q75T13 | GPI inositol-deacylase OS=Homo sapiens OX=9606 GN=PGAP1 PE=1 SV=1 | 242.43 | 345.54 | 1.43 | 0.03688 |
| P03915 | NADH-ubiquinone oxidoreductase chain 5 OS=Homo sapiens OX=9606 GN=MT-ND5 PE=1 SV=2 | 283.09 | 397.29 | 1.40 | 0.03701 |
| P63244 | Receptor of activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=3 | 984.54 | 1264.63 | 1.28 | 0.03710 |
| O15240 | Neurosecretory protein VGF OS=Homo sapiens OX=9606 GN=VGF PE=1 SV=2 | 1011.80 | 1395.75 | 1.38 | 0.03719 |

| | | | | | |
|---|---|---|---|---|---|
| Q96DD7 | Protein shisa-4 OS=Homo sapiens OX=9606 GN=SHISA4 PE=2 SV=3 | 148.17 | 195.11 | 1.32 | 0.03807 |
| P61764 | Syntaxin-binding protein 1 OS=Homo sapiens OX=9606 GN=STXBP1 PE=1 SV=1 | 4976.28 | 6254.46 | 1.26 | 0.03904 |
| P00403 | Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1 | 1863.43 | 2369.33 | 1.27 | 0.03942 |
| O43747 | Isoform 2 of AP-1 complex subunit gamma-1 OS=Homo sapiens OX=9606 GN=AP1G1 | 331.63 | 433.89 | 1.31 | 0.04046 |
| A0A1C7CYV9 | Solute carrier family 22 member 17 OS=Homo sapiens OX=9606 GN=SLC22A17 PE=1 SV=1 | 47.36 | 63.46 | 1.34 | 0.04072 |
| Q5SQH8 | Isoform 4 of Uncharacterized protein C6orf136 OS=Homo sapiens OX=9606 GN=C6orf136 | 62.98 | 87.02 | 1.38 | 0.04158 |
| Q9Y2H6 | Fibronectin type-III domain-containing protein 3A OS=Homo sapiens OX=9606 GN=FNDC3A PE=1 SV=4 | 68.78 | 88.06 | 1.28 | 0.04188 |
| P50583 | Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] OS=Homo sapiens OX=9606 GN=NUDT2 PE=1 SV=3 | 70.54 | 94.65 | 1.34 | 0.04205 |
| P51674 | Neuronal membrane glycoprotein M6-a OS=Homo sapiens OX=9606 GN=GPM6A PE=1 SV=2 | 1952.66 | 2523.72 | 1.29 | 0.04272 |
| Q9NWU2 | Glucose-induced degradation protein 8 homolog OS=Homo sapiens OX=9606 GN=GID8 PE=1 SV=1 | 4.39 | 8.46 | 1.93 | 0.04432 |
| Q8ND04 | Isoform 2 of Protein SMG8 OS=Homo sapiens OX=9606 GN=SMG8 | 43.98 | 63.32 | 1.44 | 0.04453 |
| Q13530 | Serine incorporator 3 OS=Homo sapiens OX=9606 GN=SERINC3 PE=2 SV=2 | 116.36 | 162.03 | 1.39 | 0.04468 |
| A0A0A0MSJ9 | Ras GTPase-activating protein 2 OS=Homo sapiens OX=9606 GN=RASA2 PE=1 SV=1 | 106.64 | 136.36 | 1.28 | 0.04531 |
| Q8N2U0 | Transmembrane protein 256 OS=Homo sapiens OX=9606 GN=TMEM256 PE=3 SV=1 | 24.16 | 38.70 | 1.60 | 0.04538 |
| O14787 | Isoform 2 of Transportin-2 OS=Homo sapiens OX=9606 GN=TNPO2 | 126.37 | 189.28 | 1.50 | 0.04554 |
| P11172 | Uridine 5'-monophosphate synthase OS=Homo sapiens OX=9606 GN=UMPS PE=1 SV=1 | 92.54 | 122.05 | 1.32 | 0.04556 |
| Q86TX2 | Acyl-coenzyme A thioesterase 1 OS=Homo sapiens OX=9606 GN=ACOT1 PE=1 SV=1 | 1185.78 | 1561.84 | 1.32 | 0.04742 |
| Q8NEZ5 | F-box only protein 22 OS=Homo sapiens OX=9606 GN=FBXO22 PE=1 SV=1 | 29.24 | 38.81 | 1.33 | 0.04765 |
| Q13304 | Uracil nucleotide/cysteinyl leukotriene receptor OS=Homo sapiens OX=9606 GN=GPR17 PE=2 SV=2 | 8.60 | 15.11 | 1.76 | 0.04815 |
| Q9H074 | Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens OX=9606 GN=PAIP1 PE=1 SV=1 | 362.63 | 470.83 | 1.30 | 0.04875 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; *P*<0.05

**Supplementary Table 8.** Extended mass spectrometry data on significantly up-regulated proteins in the hippocampus of Alzheimer's patients compared to cognitively normal controls.

| **Accession** | **Description** | **AD (Means)** | **NC (Means)** | **FC** | ***P*** |
|---|---|---|---|---|---|
| Q9HBT6 | Cadherin-20 OS=Homo sapiens OX=9606 GN=CDH20 PE=2 SV=2 | 222.82 | 182.75 | 1.22 | 7.834E-05 |
| P35414 | Apelin receptor OS=Homo sapiens OX=9606 GN=APLNR PE=1 SV=1 | 320.10 | 225.15 | 1.42 | 0.00010 |
| Q7L266 | Isoaspartyl peptidase/L-asparaginase OS=Homo sapiens OX=9606 GN=ASRGL1 PE=1 SV=2 | 1035.82 | 842.48 | 1.23 | 0.00028 |
| Q9H4F8 | Isoform 2 of SPARC-related modular calcium-binding protein 1 OS=Homo sapiens OX=9606 GN=SMOC1 | 151.10 | 118.73 | 1.27 | 0.00068 |
| P04908 | Histone H2A type 1-B/E OS=Homo sapiens OX=9606 GN=HIST1H2AB PE=1 SV=2 | 719.93 | 448.08 | 1.61 | 0.00121 |
| P02795 | Metallothionein-2 OS=Homo sapiens OX=9606 GN=MT2A PE=1 SV=1 | 839.80 | 644.50 | 1.30 | 0.00128 |
| O14939 | Phospholipase D2 OS=Homo sapiens OX=9606 GN=PLD2 PE=1 SV=2 | 55.18 | 38.29 | 1.44 | 0.00137 |
| Q9BWL3 | Uncharacterized protein C1orf43 OS=Homo sapiens OX=9606 GN=C1orf43 PE=2 SV=1 | 43.42 | 34.07 | 1.27 | 0.00146 |
| P10636 | Isoform Tau-B of Microtubule-associated protein tau OS=Homo sapiens OX=9606 GN=MAPT | 1754.58 | 1019.13 | 1.72 | 0.00152 |
| Q7Z2Z2 | Elongation factor-like GTPase 1 OS=Homo sapiens OX=9606 GN=EFL1 PE=1 SV=2 | 66.41 | 52.01 | 1.28 | 0.00176 |
| A6NCE7 | Microtubule-associated proteins 1A/1B light chain 3 beta 2 OS=Homo sapiens OX=9606 GN=MAP1LC3B2 PE=2 SV=1 | 373.98 | 279.55 | 1.34 | 0.00189 |
| Q504Y0 | Zinc transporter ZIP12 OS=Homo sapiens OX=9606 GN=SLC39A12 PE=2 SV=3 | 53.32 | 43.24 | 1.23 | 0.00198 |
| A5D8V7 | Coiled-coil domain-containing protein 151 OS=Homo sapiens OX=9606 GN=CCDC151 PE=1 SV=1 | 31.35 | 14.65 | 2.14 | 0.00288 |
| Q5T447 | E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens OX=9606 GN=HECTD3 PE=1 SV=1 | 218.58 | 171.24 | 1.28 | 0.00375 |
| A0A087WZ40 | Ensconsin OS=Homo sapiens OX=9606 GN=MAP7 PE=1 SV=1 | 276.37 | 225.75 | 1.22 | 0.00385 |
| Q6SZW1 | Sterile alpha and TIR motif-containing protein 1 OS=Homo sapiens OX=9606 GN=SARM1 PE=1 SV=1 | 35.75 | 28.48 | 1.26 | 0.00400 |
| P48058 | Glutamate receptor 4 OS=Homo sapiens OX=9606 GN=GRIA4 PE=2 SV=2 | 172.33 | 141.53 | 1.22 | 0.00406 |
| Q02127 | Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Homo sapiens OX=9606 GN=DHODH PE=1 SV=3 | 73.57 | 59.76 | 1.23 | 0.00447 |
| Q5EBM0 | UMP-CMP kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=CMPK2 PE=1 SV=3 | 90.69 | 71.83 | 1.26 | 0.00448 |
| P05067 | Amyloid-beta A4 protein OS=Homo sapiens OX=9606 GN=APP PE=1 SV=3 | 1830.21 | 1388.08 | 1.32 | 0.00469 |
| Q9HBI6 | Phylloquinone omega-hydroxylase CYP4F11 OS=Homo sapiens OX=9606 GN=CYP4F11 PE=1 SV=3 | 195.21 | 160.20 | 1.22 | 0.00481 |
| Q7L311 | Armadillo repeat-containing X-linked protein 2 OS=Homo sapiens OX=9606 GN=ARMCX2 PE=2 SV=1 | 28.40 | 20.81 | 1.36 | 0.00493 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| P61960 | Ubiquitin-fold modifier 1 OS=Homo sapiens OX=9606 GN=UFM1 PE=1 SV=1 | 68.87 | 49.62 | 1.39 | 0.00614 |
| Q9BUT1 | 3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens OX=9606 GN=BDH2 PE=1 SV=2 | 1110.66 | 913.03 | 1.22 | 0.00770 |
| Q96HD9 | N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming) OS=Homo sapiens OX=9606 GN=ACY3 PE=1 SV=1 | 66.95 | 53.65 | 1.25 | 0.00790 |
| P55283 | Cadherin-4 OS=Homo sapiens OX=9606 GN=CDH4 PE=2 SV=2 | 31.41 | 23.96 | 1.31 | 0.00855 |
| Q9HCS7 | Pre-mRNA-splicing factor SYF1 OS=Homo sapiens OX=9606 GN=XAB2 PE=1 SV=2 | 20.12 | 15.26 | 1.32 | 0.00880 |
| P82914 | 28S ribosomal protein S15, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS15 PE=1 SV=1 | 141.06 | 116.02 | 1.22 | 0.00904 |
| O00625 | Pirin OS=Homo sapiens OX=9606 GN=PIR PE=1 SV=1 | 139.12 | 96.97 | 1.43 | 0.00933 |
| Q86SK9 | Stearoyl-CoA desaturase 5 OS=Homo sapiens OX=9606 GN=SCD5 PE=1 SV=2 | 114.32 | 95.01 | 1.20 | 0.00974 |
| A0A087WY08 | Thrombospondin type-1 domain-containing protein 7A OS=Homo sapiens OX=9606 GN=THSD7A PE=1 SV=1 | 49.29 | 37.98 | 1.30 | 0.00975 |
| Q9H4G0 | Isoform 2 of Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=EPB41L1 | 186.32 | 139.24 | 1.34 | 0.01174 |
| Q9UJ14 | Glutathione hydrolase 7 OS=Homo sapiens OX=9606 GN=GGT7 PE=1 SV=2 | 223.98 | 178.08 | 1.26 | 0.01183 |
| Q56VL3 | OCIA domain-containing protein 2 OS=Homo sapiens OX=9606 GN=OCIAD2 PE=1 SV=1 | 145.16 | 104.60 | 1.39 | 0.01260 |
| E9PLM6 | Midkine OS=Homo sapiens OX=9606 GN=MDK PE=1 SV=1 | 183.42 | 107.87 | 1.70 | 0.01307 |
| Q13905 | Isoform 3 of Rap guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=RAPGEF1 | 86.93 | 71.75 | 1.21 | 0.01348 |
| Q7Z7K0 | COX assembly mitochondrial protein homolog OS=Homo sapiens OX=9606 GN=CMC1 PE=1 SV=1 | 40.58 | 25.95 | 1.56 | 0.01349 |
| Q6S8J3 | POTE ankyrin domain family member E OS=Homo sapiens OX=9606 GN=POTEE PE=2 SV=3 | 44.09 | 34.79 | 1.27 | 0.01468 |
| Q14657 | EKC/KEOPS complex subunit LAGE3 OS=Homo sapiens OX=9606 GN=LAGE3 PE=1 SV=2 | 9.29 | 4.75 | 1.96 | 0.01549 |
| B1AKJ5 | Nardilysin (N-arginine dibasic convertase), isoform CRA_d OS=Homo sapiens OX=9606 GN=NRDC PE=1 SV=1 | 15.06 | 11.16 | 1.35 | 0.01617 |
| E7EQY1 | Protein FAM136A OS=Homo sapiens OX=9606 GN=FAM136A PE=1 SV=1 | 148.60 | 123.10 | 1.21 | 0.01757 |
| A0A2R8YFG2 | Nicotinamide-nucleotide adenylyltransferase OS=Homo sapiens OX=9606 GN=NMNAT3 PE=1 SV=1 | 145.78 | 117.03 | 1.25 | 0.01787 |
| Q13642 | Isoform 4 of Four and a half LIM domains protein 1 OS=Homo sapiens OX=9606 GN=FHL1 | 1744.47 | 1336.11 | 1.31 | 0.01813 |
| P46100 | Transcriptional regulator ATRX OS=Homo sapiens OX=9606 GN=ATRX PE=1 SV=5 | 26.16 | 20.26 | 1.29 | 0.01964 |
| Q9BPY8 | Isoform 3 of Homeodomain-only protein OS=Homo sapiens OX=9606 GN=HOPX | 95.27 | 77.20 | 1.23 | 0.02008 |
| Q92982 | Ninjurin-1 OS=Homo sapiens OX=9606 GN=NINJ1 PE=1 SV=2 | 66.20 | 43.84 | 1.51 | 0.02175 |
| Q3B8N2 | Galectin-9B OS=Homo sapiens OX=9606 GN=LGALS9B PE=1 SV=3 | 152.59 | 120.51 | 1.27 | 0.02352 |
| A0A0G2JH68 | Protein diaphanous homolog 1 OS=Homo sapiens OX=9606 GN=DIAPH1 PE=1 SV=1 | 55.73 | 43.74 | 1.27 | 0.02624 |

| | | | | | |
|---|---|---|---|---|---|
| Q8N339 | Metallothionein-1M OS=Homo sapiens OX=9606 GN=MT1M PE=3 SV=2 | 22.46 | 13.67 | 1.64 | 0.02734 |
| Q8NHP8 | Putative phospholipase B-like 2 OS=Homo sapiens OX=9606 GN=PLBD2 PE=1 SV=2 | 117.64 | 96.94 | 1.21 | 0.02778 |
| P04733 | Metallothionein-1F OS=Homo sapiens OX=9606 GN=MT1F PE=1 SV=1 | 356.64 | 269.30 | 1.32 | 0.02931 |
| Q8NF37 | Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens OX=9606 GN=LPCAT1 PE=1 SV=2 | 70.92 | 42.18 | 1.68 | 0.03070 |
| Q14956 | Transmembrane glycoprotein NMB OS=Homo sapiens OX=9606 GN=GPNMB PE=1 SV=2 | 182.47 | 136.61 | 1.34 | 0.03151 |
| P31431 | Syndecan-4 OS=Homo sapiens OX=9606 GN=SDC4 PE=1 SV=2 | 53.32 | 43.88 | 1.22 | 0.03279 |
| H3BM91 | COMM domain-containing protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=COMMD4 PE=1 SV=1 | 33.88 | 27.22 | 1.24 | 0.03327 |
| Q14005 | Pro-interleukin-16 OS=Homo sapiens OX=9606 GN=IL16 PE=1 SV=4 | 271.98 | 188.05 | 1.45 | 0.03369 |
| Q13255 | Metabotropic glutamate receptor 1 OS=Homo sapiens OX=9606 GN=GRM1 PE=1 SV=3 | 223.76 | 184.32 | 1.21 | 0.03552 |
| A0A1X7SBR3 | Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 | 174675.95 | 131497.94 | 1.33 | 0.03597 |
| P98179 | RNA-binding protein 3 OS=Homo sapiens OX=9606 GN=RBM3 PE=1 SV=1 | 67.72 | 47.17 | 1.44 | 0.03905 |
| Q9NRX2 | 39S ribosomal protein L17, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL17 PE=1 SV=1 | 48.53 | 39.53 | 1.23 | 0.04165 |
| P34981 | Thyrotropin-releasing hormone receptor OS=Homo sapiens OX=9606 GN=TRHR PE=1 SV=1 | 11.39 | 6.25 | 1.82 | 0.04225 |
| O95470 | Sphingosine-1-phosphate lyase 1 OS=Homo sapiens OX=9606 GN=SGPL1 PE=1 SV=3 | 54.38 | 43.88 | 1.24 | 0.04264 |
| A8K727 | Pleckstrin homology domain-containing family A member 2 OS=Homo sapiens OX=9606 GN=PLEKHA2 PE=1 SV=1 | 64.87 | 53.00 | 1.22 | 0.04265 |
| Q14789 | Isoform 2 of Golgin subfamily B member 1 OS=Homo sapiens OX=9606 GN=GOLGB1 | 22.82 | 15.76 | 1.45 | 0.04303 |
| Q9UL42 | Paraneoplastic antigen Ma2 OS=Homo sapiens OX=9606 GN=PNMA2 PE=1 SV=2 | 46.59 | 33.02 | 1.41 | 0.04338 |
| Q9Y6N7 | Isoform 2 of Roundabout homolog 1 OS=Homo sapiens OX=9606 GN=ROBO1 | 248.50 | 206.04 | 1.21 | 0.04568 |
| Q9H3G5 | Probable serine carboxypeptidase CPVL OS=Homo sapiens OX=9606 GN=CPVL PE=1 SV=2 | 120.54 | 88.45 | 1.36 | 0.04755 |
| Q8IXM3 | 39S ribosomal protein L41, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL41 PE=1 SV=1 | 45.67 | 34.79 | 1.31 | 0.04776 |
| Q9BWH6 | RNA polymerase II-associated protein 1 OS=Homo sapiens OX=9606 GN=RPAP1 PE=1 SV=3 | 43.05 | 34.16 | 1.26 | 0.04831 |
| Q8N468 | Major facilitator superfamily domain-containing protein 4A OS=Homo sapiens OX=9606 GN=MFSD4A PE=2 SV=3 | 37.21 | 30.08 | 1.24 | 0.04904 |
| Q8IXT5 | RNA-binding protein 12B OS=Homo sapiens OX=9606 GN=RBM12B PE=1 SV=2 | 115.27 | 86.40 | 1.33 | 0.04929 |
| Q9NZR2 | Low-density lipoprotein receptor-related protein 1B OS=Homo sapiens OX=9606 GN=LRP1B PE=1 SV=2 | 69.69 | 54.32 | 1.28 | 0.04967 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; *P*<0.05

**Supplementary Table 9.** Extended mass spectrometry data on significantly down-regulated proteins in the hippocampus of Alzheimer's patients compared to cognitively normal controls.

| **Accession** | **Description** | **AD (Means)** | **NC (Means)** | **FC (*-1)** | ***P*** |
|---|---|---|---|---|---|
| A0A087WX97 | Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1 | 202.70 | 267.92 | 1.32 | 0.00022 |
| P01009 | Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3 | 305.17 | 447.14 | 1.47 | 0.00145 |
| O15069 | NAC-alpha domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NACAD PE=1 SV=3 | 73.60 | 99.55 | 1.35 | 0.00214 |
| O60216 | Double-strand-break repair protein rad21 homolog OS=Homo sapiens OX=9606 GN=RAD21 PE=1 SV=2 | 26.78 | 34.90 | 1.30 | 0.00803 |
| P04921 | Glycophorin-C OS=Homo sapiens OX=9606 GN=GYPC PE=1 SV=1 | 7.88 | 13.01 | 1.65 | 0.00844 |
| O75508 | Claudin-11 OS=Homo sapiens OX=9606 GN=CLDN11 PE=1 SV=2 | 1483.96 | 2165.23 | 1.46 | 0.01040 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6 | 2539.06 | 4513.88 | 1.78 | 0.01402 |
| Q13595 | Transformer-2 protein homolog alpha OS=Homo sapiens OX=9606 GN=TRA2A PE=1 SV=1 | 115.71 | 147.30 | 1.27 | 0.01623 |
| P59768 | Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2 OS=Homo sapiens OX=9606 GN=GNG2 PE=1 SV=2 | 22.99 | 29.51 | 1.28 | 0.01759 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2 | 1529.15 | 2592.87 | 1.70 | 0.02018 |
| A0A0J9YY99 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 | 65.44 | 118.69 | 1.81 | 0.02178 |
| Q8NHP6 | Motile sperm domain-containing protein 2 OS=Homo sapiens OX=9606 GN=MOSPD2 PE=1 SV=1 | 160.84 | 202.93 | 1.26 | 0.02669 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4 | 397.86 | 710.05 | 1.78 | 0.02903 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3 | 536.14 | 855.82 | 1.60 | 0.03219 |
| P02671 | Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA PE=1 SV=2 | 2809.87 | 3929.11 | 1.40 | 0.03320 |
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6 | 7426.96 | 13057.02 | 1.76 | 0.03422 |
| P01780 | Immunoglobulin heavy variable 3-7 OS=Homo sapiens OX=9606 GN=IGHV3-7 PE=1 SV=2 | 34.45 | 52.87 | 1.53 | 0.03453 |
| Q9UF11 | Isoform 2 of Pleckstrin homology domain-containing family B member 1 OS=Homo sapiens OX=9606 GN=PLEKHB1 | 511.09 | 642.93 | 1.26 | 0.03473 |
| J3KQ48 | Peptidyl-tRNA hydrolase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PTRH2 PE=1 SV=1 | 15.74 | 20.97 | 1.33 | 0.03484 |
| Q96DZ9 | CKLF-like MARVEL transmembrane domain-containing protein 5 OS=Homo sapiens OX=9606 GN=CMTM5 PE=1 SV=2 | 244.82 | 307.59 | 1.26 | 0.03510 |
| P14923 | Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3 | 73.89 | 98.42 | 1.33 | 0.04179 |
| P02675 | Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2 | 1249.34 | 1699.98 | 1.36 | 0.04360 |
| Q96A33 | Coiled-coil domain-containing protein 47 OS=Homo sapiens OX=9606 GN=CCDC47 PE=1 SV=1 | 240.72 | 305.31 | 1.27 | 0.04513 |
| Q8N1N4 | Keratin, type II cytoskeletal 78 OS=Homo sapiens OX=9606 GN=KRT78 PE=1 SV=2 | 66.42 | 98.91 | 1.49 | 0.04869 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; *P*<0.05

**Supplementary Table 10.** Extended mass spectrometry data on significantly up-regulated proteins in the cerebellum of Alzheimer's patients compared to cognitively normal controls.

| Accession | Description | AD (Means) | NC (Means) | FC | *P* |
|---|---|---|---|---|---|
| P02792 | Ferritin light chain OS=Homo sapiens OX=9606 GN=FTL PE=1 SV=2 | 3676.15 | 2824.18 | 1.30 | 0.00036 |
| Q01484 | Isoform 2 of Ankyrin-2 OS=Homo sapiens OX=9606 GN=ANK2 | 90.25 | 74.93 | 1.20 | 0.00063 |
| H3BNK4 | Protein NDRG4 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG4 PE=1 SV=8 | 138.98 | 111.94 | 1.24 | 0.00079 |
| Q8WWI1 | LIM domain only protein 7 OS=Homo sapiens OX=9606 GN=LMO7 PE=1 SV=3 | 117.66 | 97.99 | 1.20 | 0.00090 |
| P15531 | Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 | 141.43 | 103.32 | 1.37 | 0.00200 |
| Q6ZTA4 | Tripartite motif-containing protein 67 OS=Homo sapiens OX=9606 GN=TRIM67 PE=2 SV=3 | 44.19 | 32.24 | 1.37 | 0.00249 |
| Q9Y2T3 | Isoform 3 of Guanine deaminase OS=Homo sapiens OX=9606 GN=GDA | 7.74 | 4.38 | 1.77 | 0.00274 |
| P45984 | Isoform Alpha-1 of Mitogen-activated protein kinase 9 OS=Homo sapiens OX=9606 GN=MAPK9 | 94.83 | 77.16 | 1.23 | 0.00302 |
| A8MVW0 | Protein FAM171A2 OS=Homo sapiens OX=9606 GN=FAM171A2 PE=1 SV=1 | 301.93 | 249.63 | 1.21 | 0.00330 |
| Q9BWJ5 | Splicing factor 3B subunit 5 OS=Homo sapiens OX=9606 GN=SF3B5 PE=1 SV=1 | 116.41 | 95.75 | 1.22 | 0.00331 |
| P18084 | Integrin beta-5 OS=Homo sapiens OX=9606 GN=ITGB5 PE=1 SV=1 | 252.02 | 180.03 | 1.40 | 0.00383 |
| Q8NBL3 | Transmembrane protein 178A OS=Homo sapiens OX=9606 GN=TMEM178A PE=2 SV=1 | 43.34 | 31.51 | 1.38 | 0.00438 |
| P17677 | Isoform 2 of Neuromodulin OS=Homo sapiens OX=9606 GN=GAP43 | 6307.28 | 4933.66 | 1.28 | 0.00445 |
| Q53TN4 | Cytochrome b reductase 1 OS=Homo sapiens OX=9606 GN=CYBRD1 PE=1 SV=1 | 90.34 | 73.18 | 1.23 | 0.00480 |
| E9PGV9 | ATP-binding cassette sub-family G member 1 OS=Homo sapiens OX=9606 GN=ABCG1 PE=1 SV=1 | 179.00 | 135.22 | 1.32 | 0.00492 |
| Q96PK6 | Isoform 5 of RNA-binding protein 14 OS=Homo sapiens OX=9606 GN=RBM14 | 81.36 | 60.28 | 1.35 | 0.00529 |
| Q9NY47 | Voltage-dependent calcium channel subunit alpha-2/delta-2 OS=Homo sapiens OX=9606 GN=CACNA2D2 PE=1 SV=2 | 1742.32 | 1441.09 | 1.21 | 0.00552 |
| Q10589 | Bone marrow stromal antigen 2 OS=Homo sapiens OX=9606 GN=BST2 PE=1 SV=1 | 59.92 | 43.72 | 1.37 | 0.00663 |
| Q3ZAQ7 | Isoform 2 of Vacuolar ATPase assembly integral membrane protein VMA21 OS=Homo sapiens OX=9606 GN=VMA21 | 153.03 | 118.64 | 1.29 | 0.00751 |
| Q96PP8 | Guanylate-binding protein 5 OS=Homo sapiens OX=9606 GN=GBP5 PE=1 SV=1 | 214.69 | 160.06 | 1.34 | 0.00793 |
| O00625 | Pirin OS=Homo sapiens OX=9606 GN=PIR PE=1 SV=1 | 76.75 | 63.22 | 1.21 | 0.00805 |
| O75914 | Isoform 3 of Serine/threonine-protein kinase PAK 3 OS=Homo sapiens OX=9606 GN=PAK3 | 97.51 | 76.28 | 1.28 | 0.00940 |
| F6UJY1 | Putative hydroxypyruvate isomerase OS=Homo sapiens OX=9606 GN=HYI PE=1 SV=1 | 312.77 | 257.82 | 1.21 | 0.01084 |
| Q9NWQ8 | Phosphoprotein associated with glycosphingolipid-enriched microdomains 1 OS=Homo sapiens OX=9606 GN=PAG1 PE=1 SV=2 | 378.32 | 302.24 | 1.25 | 0.01190 |

| | | | | | |
|---|---|---|---|---|---|
| Q9Y3B9 | RRP15-like protein OS=Homo sapiens OX=9606 GN=RRP15 PE=1 SV=2 | 26.65 | 18.63 | 1.43 | 0.01263 |
| A0A0A0MTC1 | E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens OX=9606 GN=RNF213 PE=1 SV=1 | 52.05 | 42.57 | 1.22 | 0.01334 |
| Q9P121 | Isoform 4 of Neurotrimin OS=Homo sapiens OX=9606 GN=NTM | 2674.45 | 2196.95 | 1.22 | 0.01343 |
| Q9BY67 | Isoform 3 of Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1 | 1215.62 | 935.75 | 1.30 | 0.01395 |
| Q8WWM9 | Cytoglobin OS=Homo sapiens OX=9606 GN=CYGB PE=1 SV=1 | 30.13 | 19.61 | 1.54 | 0.01637 |
| Q9P0R6 | GSK3B-interacting protein OS=Homo sapiens OX=9606 GN=GSKIP PE=1 SV=2 | 61.61 | 50.68 | 1.22 | 0.01666 |
| F6RH32 | Voltage-dependent N-type calcium channel subunit alpha OS=Homo sapiens OX=9606 GN=CACNA1B PE=1 SV=1 | 267.87 | 216.75 | 1.24 | 0.01781 |
| Q9H1U4 | Multiple epidermal growth factor-like domains protein 9 OS=Homo sapiens OX=9606 GN=MEGF9 PE=2 SV=3 | 153.67 | 112.63 | 1.36 | 0.01814 |
| Q7Z7G2 | Complexin-4 OS=Homo sapiens OX=9606 GN=CPLX4 PE=2 SV=1 | 185.54 | 149.72 | 1.24 | 0.01890 |
| K7EKU3 | FXYD domain-containing ion transport regulator OS=Homo sapiens OX=9606 GN=FXYD7 PE=1 SV=1 | 43.05 | 34.81 | 1.24 | 0.01893 |
| P42658 | Isoform DPPX-S of Dipeptidyl aminopeptidase-like protein 6 OS=Homo sapiens OX=9606 GN=DPP6 | 104.13 | 82.08 | 1.27 | 0.01969 |
| P80723 | Brain acid soluble protein 1 OS=Homo sapiens OX=9606 GN=BASP1 PE=1 SV=2 | 9285.55 | 7005.42 | 1.33 | 0.02061 |
| Q05519 | Serine/arginine-rich splicing factor 11 OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1 | 338.70 | 265.47 | 1.28 | 0.02113 |
| Q86X02 | Cerebellar degeneration-related protein 2-like OS=Homo sapiens OX=9606 GN=CDR2L PE=1 SV=2 | 258.16 | 213.60 | 1.21 | 0.02225 |
| O14492 | Isoform 2 of SH2B adapter protein 2 OS=Homo sapiens OX=9606 GN=SH2B2 | 29.74 | 18.78 | 1.58 | 0.02301 |
| A0A0A0MTH9 | TATA-binding protein-associated factor 172 OS=Homo sapiens OX=9606 GN=BTAF1 PE=1 SV=1 | 109.90 | 85.57 | 1.28 | 0.02402 |
| Q8NC67 | Neuropilin and tolloid-like protein 2 OS=Homo sapiens OX=9606 GN=NETO2 PE=1 SV=1 | 22.93 | 16.86 | 1.36 | 0.02529 |
| K7EQG4 | FXYD domain-containing ion transport regulator (Fragment) OS=Homo sapiens OX=9606 GN=FXYD1 PE=1 SV=2 | 230.84 | 189.31 | 1.22 | 0.02606 |
| S4R347 | Formin-binding protein 1-like OS=Homo sapiens OX=9606 GN=FNBP1L PE=1 SV=1 | 113.32 | 93.44 | 1.21 | 0.02761 |
| P13521 | Secretogranin-2 OS=Homo sapiens OX=9606 GN=SCG2 PE=1 SV=2 | 985.30 | 773.16 | 1.27 | 0.02806 |
| Q9Y4F5 | Isoform 2 of Centrosomal protein of 170 kDa protein B OS=Homo sapiens OX=9606 GN=CEP170B | 61.56 | 48.52 | 1.27 | 0.02817 |
| Q9Y333 | U6 snRNA-associated Sm-like protein LSm2 OS=Homo sapiens OX=9606 GN=LSM2 PE=1 SV=1 | 34.10 | 27.60 | 1.24 | 0.02830 |
| Q8WU79 | Stromal membrane-associated protein 2 OS=Homo sapiens OX=9606 GN=SMAP2 PE=1 SV=1 | 155.25 | 125.60 | 1.24 | 0.02945 |
| Q6ZVL6 | UPF0606 protein KIAA1549L OS=Homo sapiens OX=9606 GN=KIAA1549L PE=2 SV=2 | 167.56 | 126.82 | 1.32 | 0.02972 |
| Q96DF8 | Splicing factor ESS-2 homolog OS=Homo sapiens OX=9606 GN=ESS2 PE=1 SV=1 | 94.25 | 69.56 | 1.35 | 0.03000 |

| | | | | | |
|---|---|---|---|---|---|
| Q9H7P6 | Multivesicular body subunit 12B OS=Homo sapiens OX=9606 GN=MVB12B PE=1 SV=2 | 58.99 | 48.09 | 1.23 | 0.03048 |
| P56945 | Isoform 6 of Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens OX=9606 GN=BCAR1 | 429.04 | 355.86 | 1.21 | 0.03057 |
| P07998 | Ribonuclease pancreatic OS=Homo sapiens OX=9606 GN=RNASE1 PE=1 SV=4 | 7.02 | 4.44 | 1.58 | 0.03082 |
| O43597 | Protein sprouty homolog 2 OS=Homo sapiens OX=9606 GN=SPRY2 PE=1 SV=1 | 44.77 | 36.53 | 1.23 | 0.03087 |
| Q6DN14 | Multiple C2 and transmembrane domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MCTP1 PE=2 SV=2 | 338.52 | 277.37 | 1.22 | 0.03239 |
| B1AL88 | Transmembrane protein FAM155A OS=Homo sapiens OX=9606 GN=FAM155A PE=2 SV=1 | 18.77 | 11.98 | 1.57 | 0.03266 |
| O15357 | Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Homo sapiens OX=9606 GN=INPPL1 PE=1 SV=2 | 60.38 | 47.74 | 1.26 | 0.03302 |
| Q9H4X1 | Regulator of cell cycle RGCC OS=Homo sapiens OX=9606 GN=RGCC PE=1 SV=1 | 31.37 | 22.20 | 1.41 | 0.03371 |
| Q15560 | Transcription elongation factor A protein 2 OS=Homo sapiens OX=9606 GN=TCEA2 PE=1 SV=1 | 59.24 | 47.00 | 1.26 | 0.03427 |
| Q13595 | Transformer-2 protein homolog alpha OS=Homo sapiens OX=9606 GN=TRA2A PE=1 SV=1 | 506.46 | 415.74 | 1.22 | 0.03498 |
| O15069 | NAC-alpha domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NACAD PE=1 SV=3 | 45.99 | 36.21 | 1.27 | 0.03515 |
| M0QYM7 | Tubulin beta-4A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=8 | 67.22 | 52.02 | 1.29 | 0.03602 |
| Q16849 | Receptor-type tyrosine-protein phosphatase-like N OS=Homo sapiens OX=9606 GN=PTPRN PE=1 SV=1 | 57.29 | 47.31 | 1.21 | 0.03790 |
| P52824 | Diacylglycerol kinase theta OS=Homo sapiens OX=9606 GN=DGKQ PE=1 SV=2 | 19.68 | 15.54 | 1.27 | 0.03881 |
| Q9P266 | Junctional protein associated with coronary artery disease OS=Homo sapiens OX=9606 GN=JCAD PE=1 SV=3 | 26.17 | 18.62 | 1.41 | 0.04153 |
| Q9BZJ0 | Crooked neck-like protein 1 OS=Homo sapiens OX=9606 GN=CRNKL1 PE=1 SV=4 | 54.50 | 40.14 | 1.36 | 0.04167 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3 | 74.91 | 39.21 | 1.91 | 0.04254 |
| O75391 | Sperm-associated antigen 7 OS=Homo sapiens OX=9606 GN=SPAG7 PE=1 SV=2 | 81.55 | 52.93 | 1.54 | 0.04353 |
| Q5EBL4 | RILP-like protein 1 OS=Homo sapiens OX=9606 GN=RILPL1 PE=1 SV=1 | 112.30 | 91.73 | 1.22 | 0.04382 |
| P82914 | 28S ribosomal protein S15, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS15 PE=1 SV=1 | 278.90 | 214.57 | 1.30 | 0.04509 |
| Q8TB61 | Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Homo sapiens OX=9606 GN=SLC35B2 PE=1 SV=1 | 30.22 | 24.06 | 1.26 | 0.04595 |
| Q8NI22 | Multiple coagulation factor deficiency protein 2 OS=Homo sapiens OX=9606 GN=MCFD2 PE=1 SV=1 | 59.54 | 34.99 | 1.70 | 0.04720 |
| Q5T8D3 | Isoform 3 of Acyl-CoA-binding domain-containing protein 5 OS=Homo sapiens OX=9606 GN=ACBD5 | 194.83 | 160.83 | 1.21 | 0.04759 |
| Q2NKQ1 | Small G protein signaling modulator 1 OS=Homo sapiens OX=9606 GN=SGSM1 PE=1 SV=2 | 169.53 | 136.66 | 1.24 | 0.04935 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; *P*<0.05

**Supplementary Table 11.** Extended mass spectrometry data on significantly down-regulated proteins in the cerebellum of Alzheimer's patients compared to cognitively normal controls.

| **Accession** | **Description** | **AD (Means)** | **NC (Means)** | **FC (*-1)** | ***P*** |
|---|---|---|---|---|---|
| A0A2R8YGD3 | Rap guanine nucleotide exchange factor 2 OS=Homo sapiens OX=9606 GN=RAPGEF2 PE=1 SV=1 | 256.60 | 371.95 | 1.45 | 0.00042 |
| P10643 | Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2 | 71.40 | 101.74 | 1.42 | 0.00249 |
| P11908 | Isoform 2 of Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens OX=9606 GN=PRPS2 | 31.71 | 40.25 | 1.27 | 0.00387 |
| A0A3B3ITJ4 | Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=1 | 50.33 | 63.23 | 1.26 | 0.00534 |
| Q92903 | Phosphatidate cytidylyltransferase 1 OS=Homo sapiens OX=9606 GN=CDS1 PE=2 SV=2 | 55.24 | 69.13 | 1.25 | 0.00728 |
| A0A2R8Y7X9 | GLOBIN domain-containing protein OS=Homo sapiens OX=9606 PE=3 SV=1 | 395.56 | 742.14 | 1.88 | 0.00782 |
| Q9BS92 | Protein NipSnap homolog 3B OS=Homo sapiens OX=9606 GN=NIPSNAP3B PE=2 SV=1 | 184.30 | 299.11 | 1.62 | 0.01036 |
| Q01814 | Isoform WA of Plasma membrane calcium-transporting ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2B2 | 149.15 | 192.35 | 1.29 | 0.01163 |
| A0A0G2JPD3 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 | 15.82 | 34.98 | 2.21 | 0.01184 |
| Q8WVD5 | RING finger protein 141 OS=Homo sapiens OX=9606 GN=RNF141 PE=1 SV=1 | 355.75 | 444.89 | 1.25 | 0.01409 |
| Q86VN1 | Vacuolar protein-sorting-associated protein 36 OS=Homo sapiens OX=9606 GN=VPS36 PE=1 SV=1 | 66.12 | 87.49 | 1.32 | 0.01713 |
| H3BP13 | Trafficking protein particle complex subunit 2-like protein OS=Homo sapiens OX=9606 GN=TRAPPC2L PE=1 SV=1 | 40.44 | 51.42 | 1.27 | 0.02071 |
| K7EQD6 | Vesicle-fusing ATPase (Fragment) OS=Homo sapiens OX=9606 GN=NSF PE=1 SV=1 | 157.55 | 207.26 | 1.32 | 0.02911 |
| P02679 | Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=3 | 1622.19 | 2447.99 | 1.51 | 0.03295 |
| S4R3E9 | NEDD8-MDP1 readthrough OS=Homo sapiens OX=9606 GN=NEDD8-MDP1 PE=4 SV=1 | 126.13 | 234.11 | 1.86 | 0.03462 |
| A0A0A0MRL7 | Caspase-7 OS=Homo sapiens OX=9606 GN=CASP7 PE=1 SV=1 | 23.66 | 34.42 | 1.45 | 0.03540 |
| Q14165 | Malectin OS=Homo sapiens OX=9606 GN=MLEC PE=1 SV=1 | 56.43 | 75.61 | 1.34 | 0.03599 |
| Q9Y4A5 | Transformation/transcription domain-associated protein OS=Homo sapiens OX=9606 GN=TRRAP PE=1 SV=3 | 26.60 | 34.09 | 1.28 | 0.03718 |
| Q7Z7A4 | PX domain-containing protein kinase-like protein OS=Homo sapiens OX=9606 GN=PXK PE=1 SV=1 | 15.09 | 25.69 | 1.70 | 0.04245 |
| A0A1W2PPJ5 | Protein cereblon OS=Homo sapiens OX=9606 GN=CRBN PE=1 SV=1 | 217.62 | 292.61 | 1.34 | 0.04359 |
| P60903 | Protein S100-A10 OS=Homo sapiens OX=9606 GN=S100A10 PE=1 SV=2 | 232.01 | 318.79 | 1.37 | 0.04415 |
| A0A087WZK0 | Deoxyhypusine synthase OS=Homo sapiens OX=9606 GN=DHPS PE=1 SV=1 | 19.34 | 24.75 | 1.28 | 0.04533 |

AD, Alzheimer's disease; FC, fold-change (FC>1.2 included); NC, cognitively normal controls; *P*<0.05

**Supplementary Table 12.** Common upregulated DEPs with previous brain datasets.

| | Gene Name | Dataset.1 | Dataset.2 | Dataset.3 | Dataset.4 | Dataset.5 | Dataset.6 | Dataset.7 |
|---|---|---|---|---|---|---|---|---|
| **1** | LSP1 | Up | Up | Up | Up | Up | Up | Up |
| **2** | BLVRB | Up | Up | Up | Up | Up | Up | Up |
| **3** | HSPB8 | Up | Up | Up | Up | Up | Up | Up |
| **4** | HSPB1 | Up | Up | Up | Up | Up | Up | Up |
| **5** | LZIC | No change | Up | Up | Up | Up | Up | Up |
| **6** | RSU1 | Up | No change | Up | Up | Up | Up | Up |
| **7** | PAFAH1B3 | Up | Up | Up | No change | Up | Up | Up |
| **8** | GCLM | No change | Up | Up | Up | Up | Up | Up |
| **9** | FBP1 | Up | Up | Up | Up | Up | Up | No change |
| **10** | FABP7 | Up | Up | Up | Up | Up | Up | No change |
| **11** | BDH2 | Up | Up | Up | Up | Up | Up | No change |
| **12** | BAG3 | Up | No change | Up | Up | Up | Up | Up |
| **13** | S100A1 | Up | Up | Up | No change | Up | Up | No change |
| **14** | ABHD14B | Up | Up | Up | Up | No change | No change | Up |
| **15** | HEBP2 | Up | Up | Up | No change | No change | Up | Up |
| **16** | FABP5 | No change | Up | Up | Up | Up | Up | No change |
| **17** | MAP2K6 | Up | Up | Up | No change | No change | Up | Up |
| **18** | CMBL | Up | No change | Up | Up | Up | Up | No change |
| **19** | PSMD9 | No change | Up | Up | Up | Up | Up | No change |
| **20** | PTRHD1 | Up | No change | Up | No change | Up | Up | Up |
| **21** | LAMA1 | Up | Up | Up | Up | No change | Up | No change |
| **22** | ALDH9A1 | No change | No change | Up | Up | Up | Up | No change |
| **23** | ANKRD45 | Up | Up | NA | Up | NA | Up | NA |
| **24** | THTPA | No change | No change | Up | No change | Up | Up | Up |
| **25** | TNS3 | No change | No change | Up | Up | Up | Up | No change |
| **26** | TAX1BP3 | No change | No change | Up | Up | Up | Up | No change |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **27** | SWAP70 | No change | Up | Up | No change | Up | Up | No change |
| **28** | SH3BGRL | Up | No change | Up | No change | Up | No change | Up |
| **29** | S100B | No change | No change | Up | Up | Up | Up | No change |
| **30** | FNTA | No change | Up | Up | Up | Up | No change | No change |
| **31** | TOMM34 | No change | Up | Up | Up | No change | No change | Up |
| **32** | GSTM2 | Up | No change | Up | No change | Up | Up | No change |
| **33** | GSN | No change | Up | NA | Up | Up | Up | No change |
| **34** | EIF4A1 | Up | Up | Up | No change | No change | No change | Up |
| **35** | DFFA | No change | No change | Up | Up | Up | Up | No change |
| **36** | CARHSP1 | No change | No change | Up | Up | Up | No change | Up |
| **37** | BOLA2 | No change | Up | Up | Up | No change | No change | Up |
| **38** | BLOC1S4 | Up | No change | Up | No change | NA | Up | Up |
| **39** | UBE2H | Up | No change | Up | Up | No change | No change | Up |
| **40** | RSRC1 | No change | No change | Up | Up | NA | Up | Up |
| **41** | DAG1 | Up | No change | Up | No change | Up | Up | No change |
| **42** | AKR1C1 | Up | Up | Up | Up | NA | No change | No change |
| **43** | NSFL1C | No change | No change | No change | No change | Up | Up | Up |
| **44** | JMJD6 | Up | Up | No change | No change | NA | No change | Up |
| **45** | GALK1 | No change | No change | Up | Up | No change | Up | No change |
| **46** | PEA15 | No change | No change | Up | No change | Up | Up | No change |
| **47** | TPD52L2 | No change | Up | NA | No change | Up | No change | Up |
| **48** | GALE | Up | Up | Up | No change | No change | No change | No change |
| **49** | UBA6 | No change | Up | Up | No change | No change | Up | No change |
| **50** | SOD1 | No change | Up | Up | No change | Up | No change | No change |
| **51** | PRKD1 | Up | No change | Up | No change | NA | Up | No change |
| **52** | RLBP1 | No change | No change | Up | Up | No change | Up | No change |
| **53** | UBR7 | No change | No change | No change | Up | No change | Up | Up |
| **54** | PARK7 | Up | No change | Up | No change | No change | No change | Up |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **55** | SUGT1 | No change | Up | NA | No change | No change | Up | Up |
| **56** | SLC7A6OS | No change | No change | NA | Up | NA | Up | Up |
| **57** | PPCS | No change | Up | Up | No change | No change | Up | No change |
| **58** | NUDCD2 | No change | No change | Up | No change | No change | Up | Up |
| **59** | ITGB2 | No change | Up | NA | NA | Up | Up | No change |
| **60** | HBD | Up | Up | No change | No change | No change | Up | No change |
| **61** | LAGE3 | Up | No change | No change | No change | No change | Up | Up |
| **62** | CRABP1 | Up | No change | Up | Up | No change | No change | No change |
| **63** | ASS1 | No change | No change | Up | Up | Up | No change | No change |
| **64** | AKR1C3 | No change | Up | Up | Up | No change | No change | No change |
| **65** | AKR7A3 | No change | No change | Up | No change | Up | Up | No change |
| **66** | PSMD10 | No change | No change | Up | No change | Up | Up | No change |
| **67** | PHPT1 | No change | No change | Up | No change | Up | Up | No change |
| **68** | C1orf198 | No change | No change | Up | No change | Up | Up | No change |
| **69** | TERF2IP | No change | No change | Up | Up | No change | No change | Up |
| **70** | CD58 | Up | NA | Up | No change | No change | Up | No change |
| **71** | FSTL1 | Up | No change | Up | Up | NA | No change | NA |
| **72** | FBXO2 | Up | No change | Up | No change | No change | Up | No change |
| **73** | DUSP23 | No change | No change | Up | No change | Up | No change | Up |
| **74** | COLEC12 | No change | Up | Up | Up | No change | No change | No change |
| **75** | CTSB | No change | Up | Up | Up | No change | No change | No change |
| **76** | AIF1 | No change | Up | Up | Up | No change | No change | No change |
| **77** | SELENBP1 | No change | No change | NA | No change | Up | Up | No change |
| **78** | VAV3 | No change | No change | Up | Up | NA | No change | No change |
| **79** | SHTN1 | No change | Up | Up | No change | NA | NA | No change |
| **80** | TYMP | No change | No change | Up | Up | No change | No change | No change |
| **81** | NAP1L4 | No change | No change | Up | No change | No change | Up | No change |
| **82** | TPM1 | No change | No change | NA | NA | No change | Up | Up |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **83** | TPM3 | No change | No change | NA | No change | Up | Up | No change |
| **84** | ITGAM | No change | No change | Up | No change | Up | No change | No change |
| **85** | ATG3 | No change | No change | Up | No change | No change | Up | No change |
| **86** | SPR | No change | No change | No change | No change | No change | Up | Up |
| **87** | ARHGDIB | No change | No change | Up | Up | No change | No change | No change |
| **88** | PSME1 | No change | No change | Up | No change | Up | No change | No change |
| **89** | PCNA | No change | No change | Up | No change | No change | Up | No change |
| **90** | PMVK | No change | No change | Up | No change | No change | Up | No change |
| **91** | IFT27 | No change | No change | Up | No change | No change | Up | No change |
| **92** | HBB | Up | Up | No change | No change | No change | No change | NA |
| **93** | HBA1 | Up | Up | No change | No change | No change | No change | NA |
| **94** | HEBP1 | No change | Up | Up | No change | No change | No change | No change |
| **95** | HCLS1 | No change | No change | Up | No change | Up | No change | No change |
| **96** | GCHFR | Up | No change | NA | Up | No change | No change | NA |
| **97** | GSTM3 | No change | No change | Up | No change | No change | Up | No change |
| **98** | FRMD8 | No change | No change | Up | No change | No change | No change | Up |
| **99** | FADD | Up | No change | Up | No change | No change | No change | No change |
| **100** | GSPT2 | Up | No change | Up | No change | No change | No change | No change |
| **101** | DUSP12 | Up | No change | Up | No change | NA | No change | No change |
| **102** | CCS | No change | No change | Up | No change | No change | No change | Up |
| **103** | CHKB | Up | No change | Up | No change | No change | No change | No change |
| **104** | CLIP1 | No change | No change | Up | No change | Up | No change | NA |
| **105** | BROX | No change | No change | Up | Up | No change | No change | No change |
| **106** | AIF1L | No change | Up | Up | No change | No change | No change | No change |
| **107** | NUDT1 | No change | No change | Up | Up | NA | No change | No change |
| **108** | TPM3 | No change | No change | NA | No change | Up | Up | No change |
| **109** | SLC16A2 | No change | No change | Up | No change | No change | No change | Up |
| **110** | MOB3B | No change | No change | Up | No change | No change | Up | No change |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **111** | EFNB1 | No change | No change | Up | No change | No change | Up | No change |
| **112** | CYP2U1 | No change | No change | Up | No change | NA | Up | No change |
| **113** | COMMD8 | No change | No change | Up | No change | No change | Up | No change |
| **114** | PCYT1B | Up | Up | No change | No change | No change | No change | No change |
| **115** | CDH4 | No change | No change | Up | No change | No change | Up | No change |
| **116** | C4BPA | Up | Up | No change | No change | No change | No change | No change |
| **117** | AIFM2 | Up | No change | Up | No change | NA | No change | No change |
| **118** | CAST | No change | No change | No change | No change | Up | No change | No change |
| **119** | TRAPPC2 | Up | No change | No change | No change | No change | No change | No change |
| **120** | EIF4A2 | No change | Up | No change | No change | No change | No change | No change |
| **121** | ERAP1 | No change | No change | Up | No change | No change | No change | No change |
| **122** | ACSS2 | No change | No change | No change | No change | No change | No change | Up |
| **123** | MEAF6 | No change | No change | NA | Up | NA | No change | No change |
| **124** | TCEAL4 | No change | No change | No change | No change | No change | No change | Up |
| **125** | UBE2L6 | No change | No change | Up | No change | No change | No change | No change |
| **126** | USP5 | No change | Up | No change | No change | No change | No change | No change |
| **127** | LSM8 | No change | No change | No change | No change | No change | Up | No change |
| **128** | LSM7 | No change | No change | No change | No change | No change | Up | No change |
| **129** | TXNL1 | Up | No change | No change | No change | No change | No change | No change |
| **130** | SAE1 | Up | No change | No change | No change | No change | No change | No change |
| **131** | SULT1A1 | No change | No change | Up | No change | No change | No change | No change |
| **132** | SKP1 | No change | No change | Up | No change | No change | No change | No change |
| **133** | SNX12 | No change | No change | No change | No change | No change | No change | Up |
| **134** | SH3BGRL3 | No change | No change | Up | No change | No change | No change | No change |
| **135** | STK4 | No change | No change | Up | No change | No change | No change | No change |
| **136** | AKT2 | No change | No change | Up | No change | No change | No change | NA |
| **137** | PDXK | No change | No change | No change | No change | No change | Up | No change |
| **138** | IMPACT | No change | No change | Up | No change | No change | No change | No change |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **139** | PDCL3 | No change | No change | No change | No change | No change | No change | Up |
| **140** | PPIL3 | No change | No change | No change | No change | No change | Up | No change |
| **141** | MIEN1 | No change | No change | No change | No change | No change | No change | Up |
| **142** | MIF4GD | No change | No change | Up | No change | No change | No change | No change |
| **143** | MDP1 | No change | No change | Up | No change | No change | No change | No change |
| **144** | INPP1 | No change | No change | No change | No change | No change | Up | No change |
| **145** | GLRX3 | No change | No change | No change | No change | No change | No change | Up |
| **146** | GLRX | No change | Up | No change | No change | No change | No change | No change |
| **147** | GSDMD | No change | No change | Up | No change | No change | No change | No change |
| **148** | EIF3G | No change | No change | Up | No change | No change | No change | No change |
| **149** | EIF1AX | No change | No change | Up | No change | No change | No change | No change |
| **150** | CRADD | No change | No change | Up | No change | NA | No change | No change |
| **151** | CTPS1 | No change | No change | No change | No change | No change | No change | Up |
| **152** | CA1 | No change | Up | No change | No change | No change | No change | No change |
| **153** | BPGM | No change | Up | No change | No change | No change | No change | No change |
| **154** | ATIC | No change | No change | Up | No change | No change | No change | No change |
| **155** | EPHX2 | No change | No change | Up | No change | No change | No change | No change |
| **156** | ATXN7L3B | No change | No change | No change | No change | No change | No change | Up |
| **157** | AHSA1 | No change | No change | No change | No change | No change | No change | Up |
| **158** | TBCEL | No change | No change | Up | No change | No change | No change | No change |
| **159** | TPM4 | No change | No change | Up | No change | No change | No change | No change |
| **160** | CTDP1 | No change | No change | Up | No change | No change | No change | No change |
| **161** | HEXIM2 | Up | No change | NA | No change | NA | No change | No change |
| **162** | CTSH | No change | No change | Up | No change | No change | No change | No change |
| **163** | PLLP | No change | No change | No change | No change | No change | No change | Up |
| **164** | PPL | No change | Up | No change | No change | No change | No change | No change |
| **165** | GCSH | Up | No change | No change | No change | No change | No change | No change |
| **166** | NCCRP1 | Up | NA | NA | NA | NA | NA | NA |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **167** | POLR2D | No change | No change | Up | No change | No change | No change | No change |
| **168** | DERL2 | Up | NA | NA | NA | NA | NA | NA |
| **169** | CSTA | Up | No change | NA | No change | NA | No change | NA |
| **170** | CRTC1 | No change | No change | No change | No change | No change | No change | Up |
| **171** | ARF6 | Up | No change | No change | No change | No change | No change | No change |

**Ref**: Bai, B., Vanderwall, D., Li, Y. *et al.* Proteomic landscape of Alzheimer's Disease
Mol Neurodegeneration 16, 55 (2021). https://doi.org/10.1186/s13024-021-00474-z
Dataset 1-3; Bai et al. Neuron 2020, 105:975-991:
Dataset 2: individual case TMT analysis of Banner Sun cohort
Dataset 3: individual case TMT analysis of Mount Sinai cohort
Banner Sun cohort: Human postmortem brain tissue samples
Mount Sinai cohort: frontal pole (https://www.nature.com/articles/sdata2018185)
Dataset 4: Wang et al. Anal. Chem. 2020, 92:7162-7170 (16-plex TMT analysis of Banner Sun cohort)
Datasets 5-6: Higginbotham et al. Sci. Adv. 2020, 6:eaaz9360 (dataset5: Table S2C; dataset6: Table S2F)
Dataset 7: Sathe et al. J. Neurochem. 2021, 156:988-1002
*For the comparison of our retinal data against the literature brain cortex proteome data, proteins in each of the seven studies were regarded as DEP if the t-test p-value was less than 0.05, up or down regulated based on the log fold change AD/control (>0 up-regulated, <0 down-regulated).*
*Proteins p-values less than 0.05 were regarded as unchanged.*

**Supplementary Table 13.** Common downregulated DEPs with previous brain datasets.

| | *Gene Name* | *Dataset.1* | *Dataset.2* | *Dataset.3* | *Dataset.4* | *Dataset.5* | *Dataset.6* | *Dataset.7* |
|---|---|---|---|---|---|---|---|---|
| **1** | RTN4 | Down | Down | Down | Down | Down | Down | Down |
| **2** | NDUFB3 | Down | Down | Down | Down | Down | Down | Down |
| **3** | NDUFS1 | No change | Down | Down | Down | Down | Down | Down |
| **4** | STXBP1 | No change | Down | Down | Down | Down | Down | Down |
| **5** | AP2M1 | No change | Down | Down | Down | Down | Down | Down |
| **6** | ADCY1 | No change | Down | Down | Down | Down | Down | Down |
| **7** | SDHB | No change | Down | Down | Down | Down | Down | Down |
| **8** | SLC2A3 | No change | Down | Down | Down | Down | Down | Down |
| **9** | FAM210A | No change | Down | Down | Down | Down | Down | Down |
| **10** | NDUFS7 | No change | Down | Down | Down | Down | Down | Down |
| **11** | NDUFS2 | No change | Down | Down | Down | Down | Down | Down |
| **12** | NDUFV1 | No change | Down | Down | Down | Down | Down | Down |
| **13** | NDUFB7 | No change | Down | Down | Down | Down | Down | Down |
| **14** | NDUFB4 | No change | Down | Down | Down | Down | Down | Down |
| **15** | NDUFA7 | No change | Down | Down | Down | Down | Down | Down |
| **16** | NDUFA10 | No change | Down | Down | Down | Down | Down | Down |
| **17** | SLC25A22 | No change | Down | Down | Down | Down | Down | Down |
| **18** | MDH2 | No change | Down | Down | Down | Down | Down | Down |
| **19** | DBT | Down | Down | Down | No change | Down | Down | Down |
| **20** | AGK | No change | Down | Down | Down | Down | Down | Down |
| **21** | HK1 | No change | Down | Down | Down | Down | Down | No change |
| **22** | UNC13A | No change | Down | Down | Down | Down | No change | Down |
| **23** | GNB5 | No change | Down | NA | Down | Down | Down | Down |
| **24** | GLS | No change | No change | Down | Down | Down | Down | Down |
| **25** | NIPSNAP1 | No change | No change | Down | Down | Down | Down | Down |
| **26** | FAM162A | No change | No change | Down | Down | Down | Down | Down |
| **27** | NDUFS5 | No change | No change | Down | Down | Down | Down | Down |

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| **28** | NDUFS3 | No change | Down | Down | Down | Down | Down | No change |
| **29** | NDUFB9 | No change | Down | Down | Down | Down | Down | No change |
| **30** | NDUFB6 | No change | Down | Down | Down | Down | Down | No change |
| **31** | NDUFB5 | No change | No change | Down | Down | Down | Down | Down |
| **32** | NDUFB10 | No change | No change | Down | Down | Down | Down | Down |
| **33** | NDUFA9 | No change | No change | Down | Down | Down | Down | Down |
| **34** | NDUFA8 | No change | No change | Down | Down | Down | Down | Down |
| **35** | NDUFA6 | No change | Down | Down | Down | Down | Down | No change |
| **36** | NDUFA5 | No change | No change | Down | Down | Down | Down | Down |
| **37** | NDUFA12 | No change | No change | Down | Down | Down | Down | Down |
| **38** | MFN2 | No change | No change | Down | Down | Down | Down | Down |
| **39** | DNAJC19 | No change | No change | Down | Down | Down | Down | Down |
| **40** | IDH3G | No change | Down | Down | Down | Down | Down | No change |
| **41** | FBXO41 | No change | No change | Down | Down | Down | Down | Down |
| **42** | COX4I1 | No change | No change | Down | Down | Down | Down | Down |
| **43** | CKMT1A | No change | Down | Down | Down | Down | Down | NA |
| **44** | SLC25A5 | No change | No change | Down | Down | Down | Down | Down |
| **45** | SLC25A4 | No change | Down | Down | Down | Down | Down | No change |
| **46** | ACO2 | No change | No change | Down | Down | Down | Down | Down |
| **47** | KCNMA1 | No change | Down | NA | NA | Down | Down | Down |
| **48** | SCAMP5 | No change | No change | Down | Down | Down | No change | Down |
| **49** | VDAC2 | No change | No change | Down | Down | Down | Down | No change |
| **50** | KCNB1 | No change | Down | Down | Down | No change | Down | No change |
| **51** | RPS8 | No change | No change | Down | No change | Down | Down | Down |
| **52** | PDK1 | No change | Down | Down | Down | No change | No change | Down |
| **53** | OXCT1 | No change | No change | Down | Down | Down | No change | Down |
| **54** | SLC25A36 | Down | Down | No change | Down | NA | Down | No change |
| **55** | LMTK2 | No change | Down | Down | Down | No change | Down | No change |
| **56** | RAB18 | No change | No change | Down | No change | Down | Down | Down |
| **57** | OPA3 | No change | Down | No change | Down | No change | Down | Down |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **58** | CHCHD3 | No change | No change | Down | Down | Down | Down | No change |
| **59** | IDH3B | No change | Down | Down | No change | Down | Down | No change |
| **60** | IDH3A | No change | No change | Down | Down | Down | Down | No change |
| **61** | ABHD16A | No change | No change | Down | No change | Down | Down | Down |
| **62** | DNAJC11 | No change | No change | No change | Down | Down | Down | Down |
| **63** | CYC1 | No change | No change | Down | Down | Down | Down | No change |
| **64** | MRPL2 | No change | No change | Down | No change | Down | Down | Down |
| **65** | RAC1 | No change | No change | No change | Down | Down | No change | Down |
| **66** | PPP3CC | No change | No change | Down | Down | No change | No change | Down |
| **67** | CPNE4 | No change | No change | Down | No change | Down | No change | Down |
| **68** | SLC25A10 | No change | Down | No change | No change | Down | Down | No change |
| **69** | AP2A2 | No change | No change | Down | Down | Down | No change | No change |
| **70** | TRAPPC6B | No change | No change | Down | No change | Down | Down | No change |
| **71** | TARS2 | Down | No change | No change | No change | No change | Down | Down |
| **72** | PCM1 | Down | Down | No change | No change | No change | Down | No change |
| **73** | LONP1 | No change | No change | No change | Down | Down | No change | Down |
| **74** | KATNB1 | No change | No change | Down | No change | Down | Down | No change |
| **75** | TUFM | Down | No change | No change | No change | Down | Down | No change |
| **76** | NT5C3A | No change | No change | No change | No change | Down | Down | Down |
| **77** | COA1 | Down | No change | Down | No change | No change | Down | No change |
| **78** | CELF2 | No change | No change | NA | NA | Down | Down | Down |
| **79** | NECAP1 | No change | Down | Down | Down | No change | No change | No change |
| **80** | RPS9 | No change | No change | No change | No change | Down | Down | Down |
| **81** | RPS3A | No change | No change | Down | No change | Down | Down | No change |
| **82** | TMEM143 | No change | No change | No change | Down | Down | Down | No change |
| **83** | SLC25A44 | No change | No change | No change | Down | NA | Down | Down |
| **84** | SLC25A40 | No change | No change | No change | Down | No change | Down | Down |
| **85** | ATP1B2 | No change | No change | No change | No change | Down | Down | Down |
| **86** | SCCPDH | No change | No change | No change | No change | Down | Down | Down |
| **87** | RDH14 | No change | No change | Down | Down | No change | Down | No change |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **88** | SCO1 | No change | No change | Down | Down | No change | Down | No change |
| **89** | MPV17 | No change | No change | No change | No change | Down | Down | Down |
| **90** | PISD | No change | No change | No change | Down | No change | Down | Down |
| **91** | PTCD3 | No change | No change | Down | No change | No change | Down | Down |
| **92** | OAT | No change | No change | No change | No change | Down | Down | Down |
| **93** | OCIAD2 | No change | No change | No change | Down | No change | Down | Down |
| **94** | TIMM44 | No change | No change | Down | No change | Down | Down | No change |
| **95** | MCAT | No change | No change | No change | No change | Down | Down | Down |
| **96** | GDPD1 | No change | No change | Down | No change | Down | No change | Down |
| **97** | IARS2 | No change | No change | No change | No change | Down | Down | Down |
| **98** | TSFM | No change | No change | Down | No change | Down | No change | Down |
| **99** | COX6C | No change | No change | Down | Down | Down | No change | No change |
| **100** | TMEM63B | Down | No change | Down | No change | No change | Down | No change |
| **101** | CCDC51 | No change | Down | Down | Down | No change | No change | No change |
| **102** | AIFM1 | No change | No change | No change | Down | Down | Down | No change |
| **103** | RPL13 | Down | No change | No change | No change | Down | Down | No change |
| **104** | MRPL16 | Down | No change | No change | No change | NA | Down | Down |
| **105** | MRPS7 | Down | No change | No change | No change | No change | Down | Down |
| **106** | MRPS35 | No change | No change | Down | No change | No change | Down | Down |
| **107** | MRPS15 | Down | No change | No change | No change | Down | Down | No change |
| **108** | SLC4A7 | No change | Down | NA | Down | No change | No change | No change |
| **109** | SLC25A25 | No change | No change | NA | Down | No change | Down | No change |
| **110** | SSR3 | No change | NA | No change | No change | No change | Down | Down |
| **111** | ALDH5A1 | No change | No change | No change | No change | Down | No change | Down |
| **112** | COX20 | No change | No change | Down | Down | No change | No change | No change |
| **113** | IBA57 | No change | Down | No change | No change | No change | No change | Down |
| **114** | FAM126B | No change | No change | Down | Down | No change | No change | No change |
| **115** | PRPF19 | No change | No change | No change | No change | No change | Down | Down |
| **116** | ACOX1 | Down | No change | NA | No change | No change | No change | Down |
| **117** | MTHFD1L | No change | No change | NA | NA | Down | Down | No change |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **118** | MAP1LC3B2 | No change | No change | Down | No change | No change | Down | No change |
| **119** | IQSEC1 | Down | No change | NA | NA | Down | No change | No change |
| **120** | ELOVL4 | No change | No change | NA | No change | Down | Down | NA |
| **121** | RNF170 | No change | No change | No change | No change | No change | Down | Down |
| **122** | CAMK2A | No change | No change | NA | Down | Down | No change | No change |
| **123** | AGAP2 | No change | No change | NA | NA | Down | Down | No change |
| **124** | AARS2 | No change | Down | No change | No change | Down | No change | No change |
| **125** | SSX2IP | No change | No change | No change | No change | Down | Down | No change |
| **126** | RPL32 | No change | No change | No change | No change | Down | Down | No change |
| **127** | RPL26 | No change | No change | Down | No change | No change | Down | No change |
| **128** | RPL24 | No change | No change | No change | No change | Down | Down | No change |
| **129** | RPL23 | No change | No change | Down | No change | No change | Down | No change |
| **130** | RPL18A | No change | No change | No change | No change | Down | Down | No change |
| **131** | RPL10 | No change | No change | No change | No change | Down | Down | No change |
| **132** | RPS4X | No change | No change | No change | No change | Down | Down | No change |
| **133** | SLC24A2 | No change | No change | NA | No change | Down | Down | No change |
| **134** | SLC35A4 | No change | No change | NA | Down | No change | Down | NA |
| **135** | SPCS1 | No change | NA | No change | No change | No change | Down | Down |
| **136** | RDH13 | No change | No change | Down | No change | No change | No change | Down |
| **137** | RAI1 | Down | Down | No change | No change | NA | No change | No change |
| **138** | FAM3C | No change | No change | Down | No change | No change | Down | No change |
| **139** | FAM210B | No change | Down | No change | No change | Down | No change | NA |
| **140** | NDUFAF7 | No change | No change | No change | No change | Down | Down | No change |
| **141** | OCIAD1 | Down | No change | No change | No change | No change | Down | No change |
| **142** | CYB5R1 | No change | No change | No change | No change | No change | Down | Down |
| **143** | MPC2 | No change | No change | No change | Down | No change | Down | No change |
| **144** | TOMM70 | No change | No change | Down | Down | NA | NA | NA |
| **145** | TIMM21 | No change | No change | No change | No change | Down | Down | No change |
| **146** | ACSL3 | No change | No change | No change | No change | Down | Down | No change |
| **147** | LRRC59 | No change | No change | No change | No change | Down | Down | No change |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **148** | L2HGDH | No change | No change | No change | No change | Down | Down | No change |
| **149** | NUBPL | No change | No change | No change | No change | No change | Down | Down |
| **150** | EI24 | Down | No change | Down | No change | NA | No change | NA |
| **151** | DYNLL2 | No change | No change | No change | No change | Down | No change | Down |
| **152** | COX7A1 | No change | NA | Down | No change | No change | Down | No change |
| **153** | ALG1 | Down | No change | No change | No change | No change | No change | Down |
| **154** | ZW10 | No change | No change | No change | No change | No change | Down | Down |
| **155** | CA14 | No change | No change | Down | No change | No change | Down | No change |
| **156** | ATAD1 | No change | No change | No change | Down | Down | No change | No change |
| **157** | MT-ATP8 | No change | Down | Down | No change | No change | No change | NA |
| **158** | GOT2 | No change | No change | Down | Down | No change | No change | No change |
| **159** | RPL8 | No change | No change | No change | No change | Down | Down | No change |
| **160** | RPL34 | No change | No change | No change | No change | Down | Down | No change |
| **161** | RPL3 | No change | No change | No change | No change | Down | Down | No change |
| **162** | MRPS30 | No change | No change | No change | No change | No change | Down | Down |
| **163** | FAM161A | No change | Down | NA | NA | NA | NA | NA |
| **164** | SFSWAP | No change | Down | No change | No change | NA | No change | NA |
| **165** | MYT1 | No change | NA | NA | Down | NA | NA | NA |
| **166** | DHX30 | No change | No change | Down | No change | No change | No change | No change |
| **167** | EPHB2 | No change | No change | NA | No change | No change | No change | Down |
| **168** | FKBP8 | No change | No change | NA | No change | Down | No change | No change |
| **169** | YTHDF2 | No change | No change | No change | No change | No change | Down | No change |
| **170** | VWA8 | No change | No change | No change | No change | No change | No change | Down |
| **171** | HSD17B12 | No change | No change | No change | No change | No change | No change | Down |
| **172** | TEX10 | No change | No change | No change | Down | No change | No change | No change |
| **173** | RDH11 | No change | No change | No change | No change | No change | No change | Down |
| **174** | DDX5 | No change | No change | No change | No change | No change | No change | Down |
| **175** | ME2 | No change | No change | No change | No change | No change | No change | Down |
| **176** | ACSL6 | No change | No change | No change | No change | Down | No change | No change |
| **177** | LRIF1 | No change | NA | NA | NA | NA | Down | NA |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **178** | SETD1A | Down | No change | No change | No change | NA | No change | NA |
| **179** | FMN1 | No change | No change | Down | No change | No change | No change | No change |
| **180** | FAM3A | Down | No change | NA | No change | NA | NA | NA |
| **181** | SUPT16H | No change | Down | No change | No change | No change | No change | No change |
| **182** | EEF1E1 | No change | No change | No change | No change | No change | Down | No change |
| **183** | CCDC90B | No change | No change | No change | Down | No change | No change | No change |
| **184** | DDX3Y | No change | No change | No change | No change | No change | No change | Down |
| **185** | RPL14 | No change | No change | NA | NA | No change | No change | Down |
| **186** | RPL13A | No change | No change | No change | No change | No change | Down | No change |
| **187** | RPS27 | No change | No change | No change | No change | No change | Down | No change |
| **188** | RPS2 | No change | No change | No change | No change | No change | Down | No change |
| **189** | RPS15A | No change | No change | No change | No change | No change | Down | No change |
| **190** | MRPS14 | No change | NA | NA | No change | NA | No change | Down |
| **191** | SEC22A | No change | No change | NA | No change | NA | Down | No change |
| **192** | TMED4 | No change | No change | No change | No change | No change | No change | Down |
| **193** | SCFD1 | No change | No change | No change | No change | No change | No change | Down |
| **194** | RTN4IP1 | No change | No change | Down | No change | No change | No change | No change |
| **195** | RAB10 | No change | No change | No change | No change | No change | Down | No change |
| **196** | POLDIP2 | No change | No change | No change | No change | No change | Down | No change |
| **197** | WWP1 | No change | No change | No change | No change | NA | Down | No change |
| **198** | OXA1L | No change | No change | NA | NA | No change | Down | No change |
| **199** | SSRP1 | Down | No change | No change | No change | No change | No change | No change |
| **200** | STT3B | No change | No change | No change | No change | No change | Down | No change |
| **201** | DNAJA3 | No change | No change | No change | No change | No change | Down | No change |
| **202** | DNAJB12 | Down | No change | No change | No change | No change | No change | No change |
| **203** | TMEM126B | No change | Down | NA | No change | NA | No change | No change |
| **204** | CCDC127 | No change | No change | No change | No change | No change | Down | No change |
| **205** | CPT2 | No change | No change | No change | No change | No change | No change | Down |
| **206** | CPT1C | No change | No change | No change | Down | No change | No change | No change |
| **207** | SLC25A13 | No change | No change | No change | No change | No change | Down | No change |

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| **208** | TMCO1 | No change | No change | No change | No change | No change | No change | Down |
| **209** | ACOT13 | No change | No change | No change | No change | No change | Down | No change |
| **210** | RPL4 | No change | No change | No change | No change | No change | Down | No change |
| **211** | RPL35 | No change | No change | No change | No change | No change | Down | No change |
| **212** | RPL30 | No change | No change | No change | No change | Down | No change | No change |
| **213** | RPL18 | No change | No change | No change | No change | No change | Down | No change |
| **214** | RPL10A | No change | No change | No change | No change | Down | No change | No change |
| **215** | MRPS31 | No change | No change | Down | No change | No change | No change | No change |
| **216** | MRPS12 | No change | No change | Down | No change | No change | No change | No change |

**Ref*:*** Bai, B., Vanderwall, D., Li, Y. *et al.* Proteomic landscape of Alzheimer's Disease
Mol Neurodegeneration 16, 55 (2021). https://doi.org/10.1186/s13024-021-00474-z
Dataset 1-3; Bai et al. Neuron 2020, 105:975-991:
Dataset 1: pooled TMT analysis of Banner Sun cohort without cell type normalization
Dataset 2: individual case TMT analysis of Banner Sun cohort
Dataset 3: individual case TMT analysis of Mount Sinai cohort
Banner Sun cohort: Human postmortem brain tissue samples
Mount Sinai cohort: frontal pole (https://www.nature.com/articles/sdata2018185)
Dataset 4: Wang et al. Anal. Chem. 2020, 92:7162-7170 (16-plex TMT analysis of Banner Sun cohort)
Datasets 5-6: Higginbotham et al. Sci. Adv. 2020, 6:eaaz9360 (dataset5: Table S2C; dataset6: Table S2F)
Dataset 7: Sathe et al. J. Neurochem. 2021, 156:988-1002

*For the comparision of our retinal data against the literature brain cortex proteome data, proteins in each of the seven studies were regarded as DEP if the t-test p-value was less than 0.05, up or down regulated based on the log fold change AD/control (>0 up-regulated, <0 down-regulated).*
*Proteins p-values equal or higher than 0.05 were regarded as unchanged.*