

## ONLINE SUPPLEMENTAL MATERIAL

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### SUPPLEMENTAL REFERENCES

<sup>1</sup> *ClustalW*: Larkin MA et al. (2007), "Clustal W and Clustal X version 2.0", *Bioinformatics*. 23:2947; BLOSUM62: Henikoff S and Henikoff JG (1993), "Performance evaluation of amino acid substitution matrices.", *Proteins*, 17:49.

<sup>2</sup> *Phosphosite*: [www.phosphosite.org](http://www.phosphosite.org)

<sup>3</sup> *Rat CBP90*: Ohoka Y and Takai Y (1998), "Isolation and characterization of cortactin isoforms and a novel cortactin-binding protein, CBP90", *Genes Cells*, 3: 603.

<sup>4</sup> *CDD reference*: Marchler-Bauer A et al. (2007), "CDD: a conserved domain database for interactive domain family analysis", *Nucleic Acids Res.* 35(D)237-240

<sup>5</sup> *Paircoil reference*: A.V. McDonnell, T. Jiang, A.E. Keating, B. Berger, "Paircoil2: Improved prediction of coiled coils from sequence", *Bioinformatics Vol.* 22(3) (2006).

## SUPPLEMENTAL TABLE S1. PROTEIN AND GENE NAMES.

| PROTEIN NAME <sup>1</sup> | GENE NAME <sup>2</sup> | FULL PROTEIN NAME   | ALIASES                             |
|---------------------------|------------------------|---|-------------------------------------|
| calcineurin               | PPP3CA                 | protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform | CALNA, CCN1, CNA1, PP2B             |
| CCT2                      | CCT2                   | chaperonin containing TCP1, subunit 2 (beta)                          | CCTB, PRO1633, TCPB                 |
| CCT3                      | CCT3                   | chaperonin containing TCP1, subunit 3 (gamma)                         | CCTG, PIG48, TCPG, TRIC5            |
| CCT4                      | CCT4                   | chaperonin containing TCP1, subunit 4                                 | CCTD, TCPD, SRB                     |
| CCT5                      | CCT5                   | chaperonin containing TCP1, subunit 5 (epsilon)                       | CCTE, KIAA0098, TCPE                |
| CCT6A                     | CCT6A                  | chaperonin containing TCP1, subunit 6A (zeta 1)                       | CCTZ1, MoDP-2, TCPZ                 |
| CCT7                      | CCT7                   | chaperonin containing TCP1, subunit 7 (eta)                           | CCTH, Nip7-1, TCPH                  |
| Cdc25C                    | CDC25C                 | cell division cycle 25 homolog C                                      | CDC25                               |
| CTTNBP2                   | CTTNBP2                | Cortactin binding protein 2   | c7orf8, CORTBP2, KIAA1758           |
| CTTNBP2NL                 | CTTNBP2NL              | CTTNBP2 N-terminal like   | KIAA1433                            |
| dynein                    | DYNC1H1                | dynein, cytoplasmic 1, heavy chain 1                                  | DHC1; DNCL; DYHC                    |
| STRIP1                    | FAM40A                 | FAM40A  | KIAA1761                            |
| STRIP2                    | FAM40B                 | FAM40B  | KIAA1170                            |
| FGFR1OP2                  | FGFR1OP2               | FGFR1 oncogene partner 2  | HSPC123                             |
| Mob3                      | MOBK13                 | Mps one binder kinase activator-like 3                                | PREI3, phocein                      |
| MST4                      | MST4                   | serine/threonine protein kinase MST4                                  | MASK, EC 2.7.11.1                   |
| CCM3                      | PDCD10                 | Programmed cell death protein 10                                      | CCM3, TFAR15                        |
| PP1c                      | PPP1CA                 | protein phosphatase 1, catalytic subunit, alpha isoform               | PP-1A, PPP1A                        |
| PP2A $\alpha$             | PPP2CA                 | protein phosphatase 2 catalytic subunit, alpha isoform                | PP2A-alpha, EC 3.1.3.16             |
| PP2A $\beta$              | PPP2CB                 | protein phosphatase 2 catalytic subunit, beta isoform                 | PP2A-beta, EC 3.1.3.16              |
| PP2A $\alpha$             | PPP2R1A                | protein phosphatase 2 65kDa regulatory subunit A alpha isoform        | PP2A A, PR65 alpha                  |
| PP2A $\beta$              | PPP2R1B                | protein phosphatase 2 65kDa regulatory subunit A beta isoform         | PP2A A, PR65 beta                   |
| PP2AB $\alpha$            | PPP2R2A                | protein phosphatase 2, regulatory subunit B, alpha isoform            | B55A, PR52A, PR55A                  |
| PP2AB $\beta$             | PPP2R2B                | protein phosphatase 2, regulatory subunit B, gamma isoform            | B55G, IMYPNO, PR52, PR55G           |
| PP2AB $\delta$            | PPP2R2D                | protein phosphatase 2, regulatory subunit B, delta isoform            |                                     |
| PP2AB' $\alpha$           | PPP2R5A                | protein phosphatase 2, regulatory subunit B', alpha isoform           | B56A, PR61A                         |
| PP2AB' $\gamma$           | PPP2R5C                | protein phosphatase 2, regulatory subunit B', gamma isoform           | B56G, PR61G                         |
| PP2AB' $\delta$           | PPP2R5D                | protein phosphatase 2, regulatory subunit B', delta isoform           | B56D, PR61D                         |
| PP2AB' $\epsilon$         | PPP2R5E                | protein phosphatase 2, regulatory subunit B', epsilon isoform         | B56E, PR61E                         |
| PP4c                      | PPP4C                  | protein phosphatase 4 (formerly X), catalytic subunit                 | PP4, PPH3, PPX                      |
| PP6c                      | PPP6C                  | protein phosphatase 6, catalytic subunit                              |                                     |
| PP7                       | PPEF1                  | protein phosphatase, EF-hand calcium binding domain 1                 | PP7, PPEF, PPP7C                    |
| liprin A1                 | PPFIA1                 | PTPRF interacting protein (liprin) alpha 1                            | LIP.1, LIP1, LIPRIN                 |
| liprin A3                 | PPFIA3                 | PTPRF interacting protein (liprin) alpha 3                            | KIAA0654, LPNA3                     |
| SIKE                      | SIKE                   | Suppressor of IKK-epsilon   | FLJ21168                            |
| SLMAP                     | SLMAP                  | Sarcolemmal membrane-associated protein                               | SLAP, KIAA1601                      |
| STK24                     | STK24                  | serine/threonine protein kinase 24                                    | MST3, STK3                          |
| STK25                     | STK25                  | serine/threonine protein kinase 25                                    | SOK, YSK1                           |
| striatin                  | STRN                   | striatin  |                                     |
| striatin3                 | STRN3                  | striatin-3  | cell cycle autoantigen SG2NA, GS2NA |
| striatin4                 | STRN4                  | striatin-4  | zinedin, ZIN                        |
| TCP1                      | TCP1                   | t-complex 1   | CCTA, CCT1, D6S230E, TCPA           |
| TRAF3IP3                  | TRAF3IP3               | TRAF3-interacting JNK-activating modulator                            | T3JAM                               |

<sup>1</sup> Protein names used in this publication<sup>2</sup> Gene name as per HUGO (ncbi Gene)

## SUPPLEMENTAL TABLE S2: CONSTRUCTS USED IN THIS STUDY

| PROTEIN <sup>1</sup> | GENE NAME <sup>2</sup> | SPECIES | SOURCE <sup>3</sup> | ACCESSION | FLAG SITES <sup>4</sup> | FLAG PUB <sup>5</sup> | TAP SITES <sup>6</sup> | TAP PUB <sup>7</sup> |
|----------------------|------------------------|---------|---------------------|-----------|-------------------------|-----------------------|------------------------|----------------------|
| alpha4               | IGBP1                  | human   | Kim Arndt           | NM_001551 | BamHI/NotI              | Gingras 05            | PmeI/PacI              | Gingras 05           |
| CTTNBP2              | CTTNBP2                | human   | MGC                 | BC106000  | EcoRI/NotI              | this study            | N/A                    | N/A                  |
| CTTNBP2NL            | CTTNBP2NL              | human   | MGC                 | BC016029  | EcoRI/NotI              | this study            | N/A                    | N/A                  |
| STRIP1               | FAM40A                 | mouse   | MGC                 | BC023952  | EcoRV/NotI              | this study            | N/A                    | N/A                  |
| TIP41                | TIP41RL                | human   | Hela library        | NM_152902 | N/A                     | N/A                   | PmeI/PacI              | Gingras 05           |
| Mob3                 | MOBK3                  | human   | MGC                 | BC005237  | EcoRI/NotI              | this study            | PmeI/PacI              | this study           |
| MST4                 | MST4                   | mouse   | MGC                 | BC005708  | AscI/NotI               | this study            | N/A                    | N/A                  |
| CCM3                 | PDCD10                 | human   | MGC                 | BC002506  | AscI/NotI               | this study            | N/A                    | N/A                  |
| PP2A $\alpha$        | PPP2CA                 | human   | Hela library        | NM_002715 | EcoRI/NotI              | Gingras 05            | PmeI/PacI              | this study           |
| PP2A $\beta$         | PPP2CB                 | human   | Hela library        | NM_004156 | EcoRI/NotI              | Gingras 05            | PmeI/PacI              | this study           |
| PP2A $\alpha$        | PPP2R1A                | human   | MGC                 | BC001537  | AscI/NotI               | this study            | PmeI/PacI              | Chen 08              |
| SIKE                 | SIKE                   | human   | MGC                 | BC005934  | EcoRI/XhoI              | this study            | N/A                    | N/A                  |
| STK24                | STK24                  | human   | MGC                 | BC035578  | AscI/NotI               | this study            | N/A                    | N/A                  |
| STK25                | STK25                  | human   | MGC                 | BC007852  | EcoRI/NotI              | this study            | N/A                    | N/A                  |
| striatin             | STRN                   | mouse   | MGC                 | BC090968  | AscI/NotI               | this study            | N/A                    | N/A                  |
| striatin3            | STRN3                  | human   | MGC                 | BC126221  | EcoRI/NotI              | this study            | N/A                    | N/A                  |
| striatin4            | STRN4                  | human   | Origene             | NM_013403 | N/A                     | N/A                   | PmeI/PacI              | this study           |
| TRAF3IP3             | TRAF3IP3               | human   | MGC                 | BC110302  | EcoRI/NotI              | this study            | NA                     | N/A                  |

<sup>1</sup> Protein name as used in this publication

<sup>2</sup> Gene name as per HUGO (ncbi Gene)

<sup>3</sup> Source of the original cDNAs used for cloning (MGC: mammalian gene collection)

<sup>4</sup> Restriction sites used to clone into pcDNA3-flag or pcDNA3-3HA

<sup>5</sup> Original reference for the pcDNA3-flag construct: (Gingras 05: Gingras, AC *et al*, Mol Cell Proteomics, 2005, **4**: 1725-40)

<sup>6</sup> Restriction sites used to clone into pcDNA3-NTAP

<sup>7</sup> Original reference for the pcDNA3-NTAP construct (Chen 08: Chen, GI *et al*, 2008, submitted)

## SUPPLEMENTAL TABLE S3. PARALOGY GROUPS

| NODE NAME <sup>1</sup> | PROT 1 <sup>2</sup> | PROT 2            | PROT 3           | PROT 4           | PROT 5             | PROT 6 | PROT 7 | PROT 8 | MIN ID <sup>3</sup> |
|------------------------|---------------------|-------------------|------------------|------------------|--------------------|--------|--------|--------|---------------------|
| CCT                    | TCP1                | CCT2              | CCT3             | CCT4             | CCT5               | CCT6A  | CCT7   | CCT7   | 23%                 |
| CTTNBP2/NL             | CTTNBP2             | CTNBP2NL          |                  |                  |                    |        |        |        | 36%                 |
| STRIP1/2               | STRIP1/<br>FAM40A   | STRIP2/<br>FAM40B |                  |                  |                    |        |        |        | 68%                 |
| liprin                 | liprin A1           | liprin A3         |                  |                  |                    |        |        |        | 61%                 |
| PP2A A                 | PP2A A $\alpha$     | PP2A A $\beta$    |                  |                  |                    |        |        |        | 85%                 |
| PP2A B                 | PP2A B $\alpha$     | PP2A B $\beta$    | PP2A B $\gamma$  | PP2A B $\delta$  |                    |        |        |        | 80%                 |
| PP2A B'                | PP2A B' $\alpha$    | PP2A B' $\beta$   | PP2A B' $\gamma$ | PP2A B' $\delta$ | PP2A B' $\epsilon$ |        |        |        | 57%                 |
| PP2Ac                  | PP2Ac $\alpha$      | PP2Ac $\beta$     |                  |                  |                    |        |        |        | 97%                 |
| SIKE/<br>FGFR1OP2      | SIKE                | FGFR1OP2          |                  |                  |                    |        |        |        | 47%                 |
| SLMAP/<br>TRAF3IP3     | SLMAP               | TRAF3IP3          |                  |                  |                    |        |        |        | 20%                 |
| striatins              | striatin            | striatin3         | striatin4        |                  |                    |        |        |        | 46%                 |
| GCK-III                | STK24               | STK25             | MST4             |                  |                    |        |        |        | 66%                 |

<sup>1</sup> Name used on Figures 1, 3 and 4 to represent the paralogous protein families.

<sup>2</sup> Members of the paralogy group

<sup>3</sup> Lowest percentage of identity (amino acid sequence) amongst components of the paralogy group.  
Percentage ID calculated from Clustal alignments with BLOSUM 62 matrix, using the longest protein isoform deposited in RefSeq.

## SUPPLEMENTAL TABLE S4

Detailed mass spectrometry data for TAP interactions. "Prophet" indicates the ProteinProphet p value, "%cover" is the coverage of each of the proteins, "npeps" is the number of unique peptides, "nspecs" is the total number of spectra assigned to the protein, "Ratio cover" is the percentage coverage of the interactor relative to the bait. **Red** denotes components of the PP2Ac•PP2AA core phosphatase, **green** represents the known PP2A B regulatory subunits (including the striatins), and **blue** indicates the detection of STRIP1/2 and CTTNBP2/NL in the pull-downs. The highlighted numbers are for proteins identified on the basis of a single unique peptide: the corresponding peptide annotation and annotated spectra are presented in Sup Table S6 and Sup Fig S7.

| Bait name          | Gene name | Protein name         | RefSeq               | Prophet | %cover | npeps | nspecs | Ratio cover |
|--------------------|-----------|----------------------|----------------------|---------|--------|-------|--------|-------------|
| TAP-PP2AA $\alpha$ | PPP2R1A   | PP2A A $\alpha$      | NP_055040            | 1       | 55     | 54    | 124    | 1.00        |
| TAP-PP2AA $\alpha$ | PPP2R5D   | PP2A B' $\delta$     | NP_006236            | 1       | 45.5   | 23    | 39     | 0.83        |
| TAP-PP2AA $\alpha$ | PPP2CA/B  | PP2Ac $\alpha/\beta$ | NP_002706, NP_004147 | 1       | 42.7   | 15    | 36     | 0.78        |
| TAP-PP2AA $\alpha$ | PPP2R2A   | PP2A B $\alpha$      | NP_002708            | 1       | 44.9   | 16    | 33     | 0.82        |
| TAP-PP2AA $\alpha$ | PPFIA1    | liprin A1            | NP_003617            | 1       | 14.7   | 13    | 24     | 0.27        |
| TAP-PP2AA $\alpha$ | FAM40A    | STRIP1               | XP_042708            | 1       | 15.5   | 7     | 13     | 0.28        |
| TAP-PP2AA $\alpha$ | STRN      | striatin             | NP_003153            | 1       | 9.9    | 5     | 9      | 0.18        |
| TAP-PP2AA $\alpha$ | STRN3     | striatin 3           | NP_001077362         | 1       | 31.9   | 5     | 9      | 0.58        |
| TAP-PP2AA $\alpha$ | STRN4     | striatin 4           | NP_037535            | 1       | 14.2   | 5     | 8      | 0.26        |
| TAP-PP2AA $\alpha$ | PPP2R2D   | PP2A B $\delta$      | NP_006236            | 1       | 20.1   | 4     | 7      | 0.37        |
| TAP-PP2AA $\alpha$ | PPP2R5C   | PP2A B' $\gamma$     | NP_002710            | 1       | 27.2   | 6     | 7      | 0.49        |
| TAP-PP2AA $\alpha$ | MOBKL3    | Mob3                 | NP_056202            | 1       | 22.8   | 2     | 6      | 0.41        |
| TAP-PP2AA $\alpha$ | CTTNBP2NL | CTTNBP2NL            | NP_061174            | 1       | 8.4    | 4     | 5      | 0.15        |
| TAP-PP2A $\alpha$  | PPP2R1A   | PP2A A $\alpha$      | NP_055040            | 1       | 63.2   | 41    | 112    | 1.14        |
| TAP-PP2A $\alpha$  | PPP2CA/B  | PP2Ac $\alpha/\beta$ | NP_002706, NP_004147 | 1       | 55.3   | 23    | 77     | 1.00        |
| TAP-PP2A $\alpha$  | PPP2R2A   | PP2A B $\alpha$      | NP_002708            | 1       | 55.1   | 27    | 64     | 1.00        |
| TAP-PP2A $\alpha$  | IGBP1     | alpha4               | NP_001542            | 1       | 51.3   | 20    | 37     | 0.93        |
| TAP-PP2A $\alpha$  | PPP2R5D   | PP2A B' $\delta$     | NP_006236            | 1       | 37     | 15    | 29     | 0.67        |
| TAP-PP2A $\alpha$  | PPP2R1B   | PP2A A $\beta$       | NP_002707            | 1       | 14.4   | 5     | 11     | 0.26        |
| TAP-PP2A $\alpha$  | PPP2R2D   | PP2A B $\delta$      | NP_006236            | 1       | 27.5   | 5     | 11     | 0.50        |
| TAP-PP2A $\alpha$  | PPP2R5E   | PP2A B' $\epsilon$   | NP_006237            | 1       | 14.6   | 4     | 10     | 0.26        |
| TAP-PP2A $\alpha$  | STRN3     | striatin 3           | NP_055389            | 1       | 15.8   | 7     | 9      | 0.29        |
| TAP-PP2A $\alpha$  | FAM40A    | STRIP1               | NP_149079            | 1       | 12.3   | 4     | 4      | 0.22        |
| TAP-PP2A $\alpha$  | MOBKL3    | Mob3                 | NP_056202            | 1       | 22.8   | 2     | 4      | 0.41        |
| TAP-PP2A $\alpha$  | PPP2R5C   | PP2A B' $\gamma$     | NP_002710            | 1       | 12.2   | 2     | 4      | 0.22        |
| TAP-PP2A $\alpha$  | STRN      | striatin             | NP_003153            | 1       | 4.5    | 2     | 2      | 0.08        |
| TAP-PP2A $\alpha$  | CCT2      | CCT2                 | NP_006422            | 1       | 7.9    | 2     | 2      | 0.14        |
| TAP-PP2A $\alpha$  | TCP1      | TCP1                 | NP_110379            | 1       | 5.6    | 2     | 2      | 0.10        |
| TAP-PP2A $\alpha$  | STRN4     | striatin 4           | NP_037535            | 1       | 3.2    | 2     | 2      | 0.06        |
| TAP-PP2A $\alpha$  | PPFIA3    | liprin A3            | NP_003651            | 0.99    | 2.4    | 1     | 1      | 0.04        |
| TAP-PP2A $\alpha$  | PPFIA1    | liprin A1            | NP_003617            | 0.99    | 2.5    | 1     | 1      | 0.05        |
| TAP-PP2A $\alpha$  | CTTNBP2NL | CTTNBP2NL            | NP_061174            | 0.92    | 2.8    | 1     | 1      | 0.05        |
| TAP-PP2A $\alpha$  | PPP2R1A   | PP2A A $\alpha$      | NP_055040            | 1       | 46.3   | 33    | 69     | 1.02        |
| TAP-PP2A $\alpha$  | PPP2CB    | PP2Ac $\beta$        | NP_004147            | 1       | 45.6   | 19    | 60     | 1.00        |
| TAP-PP2A $\alpha$  | STRN      | striatin             | NP_003153            | 1       | 39.7   | 29    | 55     | 0.87        |
| TAP-PP2A $\alpha$  | FAM40A    | STRIP1               | XP_042708            | 1       | 38.8   | 22    | 41     | 0.85        |
| TAP-PP2A $\alpha$  | STRN4     | striatin 4           | NP_037535            | 1       | 33.9   | 14    | 30     | 0.74        |
| TAP-PP2A $\alpha$  | STRN3     | striatin 3           | NP_001077362         | 1       | 37.5   | 10    | 27     | 0.82        |
| TAP-PP2A $\alpha$  | TCP1      | TCP1                 | NP_110379            | 1       | 31.1   | 14    | 22     | 0.68        |
| TAP-PP2A $\alpha$  | CCT2      | CCT2                 | NP_006422            | 1       | 30.5   | 10    | 20     | 0.67        |
| TAP-PP2A $\alpha$  | CCT6A     | CCT6A                | NP_001753            | 1       | 19.8   | 7     | 14     | 0.43        |
| TAP-PP2A $\alpha$  | CTTNBP2NL | CTTNBP2NL            | NP_061174            | 1       | 15.2   | 8     | 14     | 0.33        |
| TAP-PP2A $\alpha$  | MOBKL3    | Mob3                 | NP_056202            | 1       | 22.8   | 4     | 12     | 0.50        |
| TAP-PP2A $\alpha$  | CCT3      | CCT3                 | NP_005989            | 1       | 21.3   | 9     | 12     | 0.47        |
| TAP-PP2A $\alpha$  | CCT5      | CCT5                 | NP_036205            | 1       | 19.6   | 9     | 12     | 0.43        |
| TAP-PP2A $\alpha$  | IGBP1     | alpha4               | NP_001542            | 1       | 28.6   | 8     | 12     | 0.63        |
| TAP-PP2A $\alpha$  | PPP2R2A   | PP2A B $\alpha$      | NP_002708            | 1       | 26.7   | 8     | 10     | 0.59        |
| TAP-PP2A $\alpha$  | CCT8      | CCT8                 | NP_006576            | 1       | 16.6   | 8     | 9      | 0.36        |
| TAP-PP2A $\alpha$  | CCT7      | CCT7                 | NP_006420            | 1       | 14     | 5     | 8      | 0.31        |
| TAP-PP2A $\alpha$  | CCT4      | CCT4                 | NP_006421            | 1       | 22.6   | 7     | 8      | 0.50        |
| TAP-PP2A $\alpha$  | FGFR1OP   | FOP                  | NP_008976,           | 1       | 14.2   | 3     | 3      | 0.31        |

|                     |           |                      |                     |      |      |    |     |      |
|---------------------|-----------|----------------------|---------------------|------|------|----|-----|------|
| TAP-PP2Ac $\beta$   | PPP2R5D   | PP2A B' $\delta$     | NP_006236,          | 1    | 9.1  | 2  | 2   | 0.20 |
| TAP-PP2Ac $\beta$   | CTTNBP2   | CTTNBP2              | NP_219499           | 0.94 | 3.8  | 1  | 1   | 0.08 |
| TAP-PP2AB $\gamma$  | TCP1      | TCP1                 | NP_110379           | 1    | 54.1 | 32 | 56  | 1.21 |
| TAP-PP2AB $\gamma$  | PPP2R2C   | PP2A B $\gamma$      | NP_065149           | 1    | 44.7 | 5  | 51  | 1.00 |
| TAP-PP2AB $\gamma$  | CCT2      | CCT2                 | NP_006422           | 1    | 56.4 | 31 | 49  | 1.26 |
| TAP-PP2AB $\gamma$  | PPP2R1A   | PP2A A $\alpha$      | NP_055040           | 1    | 43.5 | 27 | 49  | 0.97 |
| TAP-PP2AB $\gamma$  | CCT6A     | CCT6A                | NP_001753           | 1    | 37.3 | 25 | 42  | 0.83 |
| TAP-PP2AB $\gamma$  | CCT5      | CCT5                 | NP_036205           | 1    | 46   | 26 | 41  | 1.03 |
| TAP-PP2AB $\gamma$  | CCT7      | CCT7                 | NP_006420           | 1    | 53.8 | 25 | 39  | 1.20 |
| TAP-PP2AB $\gamma$  | CCT4      | CCT4                 | NP_006421           | 1    | 47.4 | 20 | 35  | 1.06 |
| TAP-PP2AB $\gamma$  | CCT8      | CCT8                 | NP_006576           | 1    | 39.4 | 23 | 33  | 0.88 |
| TAP-PP2AB $\gamma$  | CCT3      | CCT3                 | NP_005989           | 1    | 47.1 | 23 | 32  | 1.05 |
| TAP-PP2AB $\gamma$  | PPP2CA/B  | PP2Ac $\alpha/\beta$ | NP_002706,NP_004147 | 1    | 28.8 | 9  | 16  | 0.64 |
| TAP-PP2AB $\gamma$  | PPP2R1B   | PP2A A $\beta$       | NP_002707           | 1    | 9.1  | 3  | 10  | 0.20 |
| TAP-PP2AB' $\alpha$ | PPP2R1A   | PP2A A $\alpha$      | NP_055040           | 1    | 28.2 | 18 | 36  | 0.95 |
| TAP-PP2AB' $\alpha$ | PPP2R5A   | PP2A B' $\alpha$     | NP_006234           | 1    | 29.6 | 14 | 20  | 1.00 |
| TAP-PP2AB' $\alpha$ | PPP2CA/B  | PP2Ac $\alpha/\beta$ | NP_002706,NP_004147 | 1    | 38.8 | 10 | 18  | 1.31 |
| TAP-PP2AB' $\alpha$ | PPP2R1B   | PP2A A $\beta$       | NP_002707           | 0.99 | 4.9  | 1  | 3   | 0.17 |
| TAP-striatin4       | STRN4     | striatin 4           | NP_037535           | 1    | 58.8 | 50 | 175 | 1.00 |
| TAP-striatin4       | STRN3     | striatin 3           | NP_001077362        | 1    | 47.8 | 28 | 107 | 0.81 |
| TAP-striatin4       | PPP2R1A   | PP2A A $\alpha$      | NP_055040           | 1    | 43   | 27 | 80  | 0.73 |
| TAP-striatin4       | STRN      | striatin             | NP_003153           | 1    | 36.3 | 26 | 70  | 0.62 |
| TAP-striatin4       | FAM40A    | STRIP1               | NP_149079           | 1    | 28.7 | 20 | 57  | 0.49 |
| TAP-striatin4       | MOBKL3    | Mob3                 | NP_056202           | 1    | 53.8 | 11 | 53  | 0.91 |
| TAP-striatin4       | CTTNBP2NL | CTTNBP2NL            | NP_061174,          | 1    | 31   | 17 | 49  | 0.53 |
| TAP-striatin4       | CCT3      | CCT3                 | NP_005989           | 1    | 46   | 17 | 30  | 0.78 |
| TAP-striatin4       | CCT6A     | CCT6A                | NP_001753           | 1    | 18.5 | 9  | 30  | 0.31 |
| TAP-striatin4       | CCT2      | CCT2                 | NP_006422           | 1    | 19.5 | 8  | 27  | 0.33 |
| TAP-striatin4       | CCT5      | CCT5                 | NP_006576           | 1    | 31.2 | 15 | 26  | 0.53 |
| TAP-striatin4       | CCT7      | CCT7                 | NP_006420           | 1    | 24.3 | 10 | 25  | 0.41 |
| TAP-striatin4       | CCT4      | CCT4                 | NP_006421           | 1    | 29.8 | 11 | 24  | 0.51 |
| TAP-striatin4       | TCP1      | TCP1                 | NP_110379           | 1    | 30   | 11 | 22  | 0.51 |
| TAP-striatin4       | PPP2CA/B  | PP2Ac $\alpha/\beta$ | NP_002706,NP_004147 | 1    | 27.8 | 5  | 18  | 0.47 |
| TAP-striatin4       | CCT5      | CCT5                 | NP_036205           | 1    | 23.8 | 8  | 13  | 0.40 |
| TAP-striatin4       | DNCL      | dynein               | NP_003737,NP_542408 | 0.97 | 12.4 | 1  | 6   | 0.21 |
| TAP-striatin4       | SIKE      | SIKE                 | NP_079349           | 0.99 | 13.5 | 2  | 2   | 0.23 |
| TAP-striatin4       | PPP2R1B   | PP2A A $\beta$       | NP_002707,NP_859050 | 0.99 | 11.3 | 1  | 2   | 0.19 |
| TAP-Mob3            | STRN3     | striatin 3           | NP_001077362        | 1    | 58.5 | 18 | 78  | 1.16 |
| TAP-Mob3            | STRN      | striatin             | NP_003153           | 1    | 46.4 | 34 | 63  | 0.92 |
| TAP-Mob3            | FAM40A    | STRIP1               | NP_149079           | 1    | 45   | 34 | 55  | 0.89 |
| TAP-Mob3            | CTTNBP2NL | CTTNBP2NL            | NP_061174           | 1    | 44.5 | 32 | 45  | 0.88 |
| TAP-Mob3            | STRN4     | striatin 4           | NP_037535           | 1    | 42.2 | 23 | 44  | 0.84 |
| TAP-Mob3            | PPP2R1A   | PP2A A $\alpha$      | NP_055040           | 1    | 44.3 | 20 | 37  | 0.88 |
| TAP-Mob3            | MOBKL3    | Mob3                 | NP_056202           | 1    | 50.3 | 13 | 27  | 1.00 |
| TAP-Mob3            | PPP2CA/B  | PP2Ac a/b            | NP_002706,NP_004147 | 1    | 44.3 | 10 | 15  | 0.88 |
| TAP-Mob3            | PPP2R1B   | PP2A A $\beta$       | NP_002707           | 1    | 10.9 | 3  | 12  | 0.22 |
| TAP-Mob3            | FAM40B    | STRIP1               | NP_065755           | 1    | 7.2  | 6  | 12  | 0.14 |
| TAP-Mob3            | DNCL      | dynein               | NP_003737           | 1    | 62.9 | 4  | 6   | 1.25 |
| TAP-Mob3            | SLMAP     | SLMAP                | NP_009090           | 1    | 9.1  | 4  | 5   | 0.18 |
| TAP-Mob3            | SIKE      | SIKE                 | NP_079349           | 1    | 15   | 2  | 2   | 0.30 |
| TAP-Mob3            | CTTNBP2   | CTTNBP2              | NP_219499           | 1    | 1.3  | 2  | 2   | 0.03 |

## SUPPLEMENTAL TABLE S5.

**Detailed mass spectrometric data for flag interactions.** The gene name for each prey (or "hit") is indicated; for protein names, refer to Sup Table S1. The accession numbers (protid) are from the International Protein Index (IPI). ProtLen is the length of the protein in amino acids and the GeneSymbol is from HUGO. Pw is the ProteinProphet probability, taking into account all peptides, regardless of the weight (based on shared peptides); Pfull is the ProteinProphet probability calculated without taking the weight into account. Npeps is the number of unique peptide ions; Nspecs is the number of matched spectra; Nspecswt95 is the number of spectra assigned with a weight of 0.95 or more to a given protein. Npepswt95 is the number of peptides with a weight >0.95. Ewing score is the interaction probability value reported by Ewing et al. (2007) Mol. Syst Biol. 3:89, when applicable (STK24 as a bait). Only proteins absent from flag alone purifications and detected with >20 spectra in at least two different AP-MS are reported. The exception to the 20 peptide rule consists in previously-reported interactions, such as those involving PP2Ac, PP2A A and PP2A B subunits; in this case, all hits are reported. Note that STRN3, SIKE and SLMAP are represented by two entries; the highest spectral count is used in Table II. The highlighted numbers are proteins identified on the basis of a single peptide; the corresponding peptide annotation and annotated spectra are presented in Sup Table S6 and Sup Fig S7. **Red** denotes components of the PP2Ac-PP2A core phosphatase, **green** represents the known PP2A B regulatory subunits (including the striatins), and **blue** indicates the detection of STRIP1/2 and CTTNBP2/NL in the pull-downs

| BAIT            | protid      | protLen | GeneSymbol       | Protein name       | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
|-----------------|-------------|---------|------------------|--------------------|--------|--------|-------|--------|------------|-----------|-------------|
| PP2A A $\alpha$ | IPI00554737 | 589     | PPP2R1A          | PP2A A $\alpha$    | 1      | 1      | 126   | 548    | 548        | 134       |             |
|                 | IPI00008380 | 309     | PPP2CA           | PP2A C $\alpha$    | 1      | 1      | 36    | 121    | 4          | 1         |             |
|                 | IPI00332511 | 447     | PPP2R2A          | PP2A B $\alpha$    | 1      | 1      | 37    | 108    | 50         | 18        |             |
|                 | IPI00014456 | 780     | STRN             | striatin           | 1      | 1      | 4     | 9      | 9          | 4         |             |
|                 | IPI00549766 | 837     | FAM40A           | STRIP1             | 1      | 1      | 6     | 8      | 8          | 6         |             |
|                 | IPI00879459 | 797     | STRN3            | striatin 3         | 1      | 1      | 14    | 27     | 4          | 3         |             |
|                 | IPI00477001 | 713     | STRN3            | striatin 3         | 1      | 1      | 13    | 25     | 2          | 1         |             |
|                 | IPI00000030 | 602     | PPP2R5D          | PP2A B' $\delta$   | 1      | 1      | 33    | 73     | 58         | 28        |             |
|                 | IPI00294178 | 601     | PPP2R1B          | PP2A A $\beta$     | 0      | 1      | 36    | 208    | 2          | 1         |             |
|                 | IPI00003016 | 753     | STRN4            | striatin 4         | 1      | 1      | 7     | 10     | 10         | 7         |             |
|                 | IPI00012834 | 524     | PPP2R5C          | PP2A B' $\gamma$   | 1      | 1      | 23    | 47     | 25         | 12        |             |
|                 | IPI00470920 | 453     | PPP2R2D;ACTG1    | PP2A B $\delta$    | 1      | 1      | 29    | 75     | 17         | 8         |             |
|                 | IPI00442098 | 540     | PPP2R5C          | PP2A B' $\gamma$   | 0      | 1      | 22    | 44     | 0          | 0         |             |
|                 | IPI00007694 | 386     | PPME1            | PME1               | 1      | 1      | 14    | 27     | 27         | 14        |             |
|                 | IPI00514311 | 639     | CTTNBP2NL        | CTTNBP2NL          | 0.9999 | 0.9999 | 2     | 3      | 3          | 4         |             |
|                 | IPI00002853 | 467     | PPP2R5E          | PP2A B' $\epsilon$ | 1      | 1      | 17    | 31     | 24         | 13        |             |
|                 | IPI00163496 | 1202    | PPFIA1           | liprin A1          | 1      | 1      | 15    | 24     | 24         | 16        |             |
|                 | IPI00793853 | 433     | SLMAP            | SLMAP              | 0.809  | 0.809  | 1     | 2      | 2          | 1         |             |
| IPI00014978     | 486         | PPP2R5A | PP2A B' $\alpha$ | 1                  | 1      | 7      | 11    | 10     | 6          |           |             |
| IPI00845329     | 575         | PPP2R3B | PP2A B'' $\beta$ | 1                  | 1      | 2      | 3     | 3      | 2          |           |             |
| IPI00289271     | 1259        | PPFIA2  | liprin A2        | 0                  | 0.9959 | 4      | 6     | 0      | 0          |           |             |
| IPI00014980     | 497         | PPP2R5B | PP2A B' $\beta$  | 0                  | 0.7772 | 2      | 2     | 0      | 0          |           |             |
| PP2A C $\alpha$ | IPI00554737 | 589     | PPP2R1A          | PP2A A $\alpha$    | 1      | 1      | 58    | 345    | 310        | 56        |             |
|                 | IPI00008380 | 309     | PPP2CA           | PP2A C $\alpha$    | 1      | 1      | 32    | 124    | 124        | 40        |             |
|                 | IPI00332511 | 447     | PPP2R2A          | PP2A B $\alpha$    | 1      | 1      | 35    | 162    | 96         | 23        |             |
|                 | IPI00014456 | 780     | STRN             | striatin           | 1      | 1      | 14    | 34     | 32         | 14        |             |
|                 | IPI00549766 | 837     | FAM40A           | STRIP1             | 1      | 1      | 7     | 13     | 13         | 8         |             |
|                 | IPI00879459 | 797     | STRN3            | striatin 3         | 1      | 1      | 14    | 33     | 1          | 1         |             |
|                 | IPI00477001 | 713     | STRN3            | striatin 3         | 1      | 1      | 14    | 37     | 5          | 1         |             |
|                 | IPI00000030 | 602     | PPP2R5D          | PP2A B' $\delta$   | 1      | 1      | 39    | 144    | 100        | 33        |             |
|                 | IPI00294178 | 601     | PPP2R1B          | PP2A A $\beta$     | 1      | 1      | 20    | 57     | 22         | 12        |             |
|                 | IPI00003016 | 753     | STRN4            | striatin 4         | 1      | 1      | 8     | 10     | 10         | 9         |             |
|                 | IPI00012834 | 524     | PPP2R5C          | PP2A B' $\gamma$   | 0      | 1      | 13    | 42     | 0          | 0         |             |
|                 | IPI00470920 | 453     | PPP2R2D;ACTG1    | PP2A B $\delta$    | 1      | 1      | 27    | 88     | 22         | 14        |             |
|                 | IPI00442098 | 540     | PPP2R5C          | PP2A B' $\gamma$   | 1      | 1      | 17    | 48     | 12         | 6         |             |
|                 | IPI00386122 | 225     | MOBK3            | Mob3               | 1      | 1      | 4     | 10     | 10         | 4         |             |
|                 | IPI00007694 | 386     | PPME1            | Pme1               | 1      | 1      | 18    | 51     | 51         | 19        |             |
|                 | IPI00514311 | 639     | CTTNBP2NL        | CTTNBP2NL          | 1      | 1      | 8     | 13     | 13         | 9         |             |
|                 | IPI00002853 | 467     | PPP2R5E          | PP2A B' $\epsilon$ | 1      | 1      | 9     | 26     | 24         | 10        |             |
|                 | IPI00163496 | 1202    | PPFIA1           | liprin A1          | 1      | 1      | 32    | 79     | 72         | 28        |             |
|                 | IPI00019148 | 339     | IGBP1            | alpha4             | 1      | 1      | 11    | 39     | 39         | 11        |             |
|                 | IPI00793853 | 433     | SLMAP            | SLMAP              | 0.2292 | 0.2292 | 1     | 1      | 1          | 1         |             |
|                 | IPI00297779 | 535     | CCT2             | CCT2               | 1      | 1      | 8     | 18     | 18         | 8         |             |
|                 | IPI00784090 | 548     | CCT8             | CCT8               | 1      | 1      | 17    | 35     | 35         | 18        |             |
|                 | IPI00103869 | 1663    | CTTNBP2          | CTTNBP2            | 0.9627 | 0.9627 | 1     | 1      | 1          | 1         |             |
|                 | IPI00553185 | 545     | CCT3             | CCT3               | 1      | 1      | 11    | 20     | 20         | 12        |             |
|                 | IPI00290566 | 556     | TCP1             | TCP1               | 1      | 1      | 17    | 30     | 29         | 17        |             |
|                 | IPI00010720 | 541     | CCT5             | CCT5               | 1      | 1      | 5     | 11     | 11         | 6         |             |
|                 | IPI00027626 | 531     | CCT6A            | CCT6A              | 1      | 1      | 7     | 11     | 11         | 7         |             |
|                 | IPI00018465 | 543     | CCT7             | CCT7               | 1      | 1      | 7     | 19     | 19         | 7         |             |
| IPI00398364     | 1194        | PPFIA3  | liprin A3        | 1                  | 1      | 21     | 35    | 28     | 18         |           |             |
| IPI00014978     | 486         | PPP2R5A | PP2A B' $\alpha$ | 1                  | 1      | 7      | 20    | 20     | 7          |           |             |
| IPI00302927     | 539         | CCT4    | CCT4             | 1                  | 1      | 8      | 18    | 17     | 7          |           |             |
| IPI00845329     | 575         | PPP2R3B | PP2A B'' $\beta$ | 1                  | 1      | 10     | 19    | 19     | 10         |           |             |
| IPI00289271     | 1259        | PPFIA2  | liprin A2        | 0                  | 1      | 10     | 21    | 0      | 0          |           |             |
| IPI00013076     | 399         | FGFR1OP | FOP              | 1                  | 1      | 4      | 6     | 6      | 4          |           |             |
| IPI00014980     | 497         | PPP2R5B | PP2A B' $\beta$  | 0                  | 0.9996 | 2      | 3     | 1      | 1          |           |             |
| striatin        | IPI00554737 | 589     | PPP2R1A          | PP2A A $\alpha$    | 1      | 1      | 29    | 76     | 62         | 25        |             |
|                 | IPI00008380 | 309     | PPP2CA           | PP2A C $\alpha$    | 1      | 1      | 7     | 29     | 29         | 7         |             |
|                 | IPI00014456 | 780     | STRN             | striatin           | 1      | 1      | 68    | 845    | 844        | 70        |             |
|                 | IPI00549766 | 837     | FAM40A           | STRIP1             | 1      | 1      | 34    | 93     | 90         | 33        |             |
|                 | IPI00879459 | 797     | STRN3            | striatin 3         | 1      | 1      | 24    | 51     | 5          | 3         |             |
|                 | IPI00477001 | 713     | STRN3            | striatin 3         | 0.9997 | 1      | 22    | 47     | 1          | 1         |             |
|                 | IPI00292827 | 416     | RP6-213H19.1     | MST4               | 1      | 1      | 14    | 37     | 14         | 8         |             |
|                 | IPI00294178 | 601     | PPP2R1B          | PP2A A $\beta$     | 0.9998 | 1      | 7     | 16     | 2          | 2         |             |

|           |             |         |              |                 |        |        |       |        |            |           |             |
|-----------|-------------|---------|--------------|-----------------|--------|--------|-------|--------|------------|-----------|-------------|
|           | IPI00003016 | 753     | STRN4        | striatin 4      | 1      | 1      | 26    | 123    | 122        | 25        |             |
|           | IPI00012093 | 426     | STK25        | STK25           | 0      | 1      | 4     | 9      | 0          | 0         |             |
|           | IPI00872754 | 484     | STK24        | STK24           | 0      | 1      | 16    | 47     | 0          | 0         |             |
|           | IPI00386122 | 225     | MOBK3        | Mob3            | 1      | 1      | 10    | 59     | 59         | 11        |             |
|           | IPI00298558 | 212     | PDCD10       | CCM3            | 1      | 1      | 16    | 25     | 25         | 16        |             |
|           | IPI00514311 | 639     | CTTNBP2NL    | CTTNBP2NL       | 1      | 1      | 18    | 28     | 28         | 18        |             |
|           | IPI00640464 | 207     | SIKE         | SIKE            | 1      | 1      | 9     | 12     | 12         | 9         |             |
|           | IPI00305186 | 211     | SIKE         | SIKE            | 0      | 1      | 8     | 10     | 0          | 0         |             |
|           | IPI00607651 | 893     | FAM40B       | STRIP2          | 1      | 1      | 8     | 13     | 10         | 7         |             |
|           | IPI00793853 | 433     | SLMAP        | SLMAP           | 0      | 1      | 24    | 59     | 0          | 0         |             |
|           | IPI00297779 | 535     | CCT2         | CCT2            | 1      | 1      | 8     | 14     | 14         | 8         |             |
|           | IPI00784090 | 548     | CCT8         | CCT8            | 1      | 1      | 7     | 11     | 11         | 7         |             |
|           | IPI00103869 | 1663    | CTTNBP2      | CTTNBP2         | 1      | 1      | 3     | 7      | 7          | 3         |             |
|           | IPI00553185 | 545     | CCT3         | CCT3            | 1      | 1      | 8     | 11     | 11         | 8         |             |
|           | IPI00290566 | 556     | TCP1         | TCP1            | 1      | 1      | 10    | 13     | 13         | 10        |             |
|           | IPI00010720 | 541     | CCT5         | CCT5            | 1      | 1      | 13    | 23     | 23         | 13        |             |
|           | IPI00014903 | 253     | FGFR1OP2     | FGFR1OP2        | 1      | 1      | 8     | 30     | 30         | 8         |             |
|           | IPI00027626 | 531     | CCT6A        | CCT6A           | 1      | 1      | 7     | 12     | 12         | 7         |             |
|           | IPI00018465 | 543     | CCT7         | CCT7            | 1      | 1      | 9     | 15     | 15         | 9         |             |
|           | IPI00302927 | 539     | CCT4         | CCT4            | 1      | 1      | 7     | 9      | 9          | 7         |             |
|           | IPI00788882 | 94      | SLMAP        | SLMAP           | 0.8869 | 1      | 4     | 19     | 1          | 1         |             |
|           | IPI00220656 | 530     | CCT6B        | CCT6B           | 0      | 0.9887 | 2     | 2      | 0          | 0         |             |
| BAIT      | protid      | protLen | GeneSymbol   | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| striatin3 | IPI00554737 | 589     | PPP2R1A      | PP2A A $\alpha$ | 1      | 1      | 34    | 52     | 52         | 37        |             |
|           | IPI00008380 | 309     | PPP2CA       | PP2A $\alpha$   | 1      | 1      | 12    | 32     | 32         | 12        |             |
|           | IPI00014456 | 780     | STRN         | striatin        | 1      | 1      | 34    | 56     | 52         | 32        |             |
|           | IPI00549766 | 837     | FAM40A       | STRIP1          | 1      | 1      | 45    | 99     | 91         | 47        |             |
|           | IPI00879459 | 797     | STRN3        | striatin 3      | 1      | 1      | 72    | 212    | 11         | 9         |             |
|           | IPI00477001 | 713     | STRN3        | striatin 3      | 0.9998 | 1      | 64    | 203    | 2          | 1         |             |
|           | IPI00292827 | 416     | RP6-213H19.1 | MST4            | 1      | 1      | 8     | 8      | 4          | 4         |             |
|           | IPI00294178 | 601     | PPP2R1B      | PP2A A $\beta$  | 0      | 1      | 6     | 10     | 0          | 0         |             |
|           | IPI00003016 | 753     | STRN4        | striatin 4      | 1      | 1      | 39    | 69     | 65         | 36        |             |
|           | IPI00012093 | 426     | STK25        | STK25           | 0      | 1      | 5     | 5      | 0          | 0         |             |
|           | IPI00872754 | 484     | STK24        | STK24           | 0      | 1      | 7     | 7      | 0          | 0         |             |
|           | IPI00386122 | 225     | MOBK3        | Mob3            | 1      | 1      | 10    | 52     | 52         | 12        |             |
|           | IPI00298558 | 212     | PDCD10       | CCM3            | 1      | 1      | 5     | 6      | 6          | 5         |             |
|           | IPI00514311 | 639     | CTTNBP2NL    | CTTNBP2NL       | 1      | 1      | 35    | 52     | 52         | 36        |             |
|           | IPI00640464 | 207     | SIKE         | SIKE            | 1      | 1      | 18    | 20     | 20         | 19        |             |
|           | IPI00305186 | 211     | SIKE         | SIKE            | 0      | 1      | 16    | 18     | 0          | 0         |             |
|           | IPI00607651 | 893     | FAM40B       | STRIP2          | 1      | 1      | 12    | 18     | 10         | 9         |             |
|           | IPI00793853 | 433     | SLMAP        | SLMAP           | 1      | 1      | 37    | 51     | 1          | 1         |             |
|           | IPI00297779 | 535     | CCT2         | CCT2            | 1      | 1      | 17    | 18     | 18         | 17        |             |
|           | IPI00784090 | 548     | CCT8         | CCT8            | 1      | 1      | 10    | 10     | 10         | 10        |             |
|           | IPI00103869 | 1663    | CTTNBP2      | CTTNBP2         | 1      | 1      | 21    | 24     | 24         | 21        |             |
|           | IPI00553185 | 545     | CCT3         | CCT3            | 1      | 1      | 16    | 19     | 19         | 18        |             |
|           | IPI00290566 | 556     | TCP1         | TCP1            | 1      | 1      | 16    | 16     | 15         | 15        |             |
|           | IPI00010720 | 541     | CCT5         | CCT5            | 1      | 1      | 14    | 14     | 14         | 14        |             |
|           | IPI00014903 | 253     | FGFR1OP2     | FGFR1OP2        | 1      | 1      | 14    | 17     | 17         | 14        |             |
|           | IPI00027626 | 531     | CCT6A        | CCT6A           | 1      | 1      | 11    | 12     | 12         | 11        |             |
|           | IPI00018465 | 543     | CCT7         | CCT7            | 1      | 1      | 8     | 8      | 8          | 8         |             |
|           | IPI00302927 | 539     | CCT4         | CCT4            | 1      | 1      | 8     | 8      | 7          | 7         |             |
|           | IPI00788882 | 94      | SLMAP        | SLMAP           | 0      | 0.9998 | 3     | 4      | 0          | 0         |             |
| BAIT      | protid      | protLen | GeneSymbol   | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| Mob3      | IPI00554737 | 589     | PPP2R1A      | PP2A A $\alpha$ | 1      | 1      | 45    | 111    | 89         | 38        |             |
|           | IPI00008380 | 309     | PPP2CA       | PP2A $\alpha$   | 1      | 1      | 11    | 28     | 28         | 11        |             |
|           | IPI00014456 | 780     | STRN         | striatin        | 1      | 1      | 72    | 308    | 302        | 72        |             |
|           | IPI00549766 | 837     | FAM40A       | STRIP1          | 1      | 1      | 54    | 164    | 157        | 51        |             |
|           | IPI00879459 | 797     | STRN3        | striatin 3      | 1      | 1      | 65    | 260    | 30         | 13        |             |
|           | IPI00477001 | 713     | STRN3        | striatin 3      | 0.9997 | 1      | 53    | 232    | 2          | 1         |             |
|           | IPI00292827 | 416     | RP6-213H19.1 | MST4            | 1      | 1      | 15    | 36     | 19         | 5         |             |
|           | IPI00294178 | 601     | PPP2R1B      | PP2A A $\beta$  | 1      | 1      | 15    | 32     | 10         | 8         |             |
|           | IPI00003016 | 753     | STRN4        | striatin 4      | 1      | 1      | 56    | 396    | 393        | 56        |             |
|           | IPI00012093 | 426     | STK25        | STK25           | 0.9705 | 1      | 6     | 10     | 1          | 1         |             |
|           | IPI00872754 | 484     | STK24        | STK24           | 0      | 1      | 25    | 59     | 0          | 0         |             |
|           | IPI00386122 | 225     | MOBK3        | Mob3            | 1      | 1      | 16    | 179    | 179        | 17        |             |
|           | IPI00298558 | 212     | PDCD10       | CCM3            | 1      | 1      | 19    | 33     | 33         | 19        |             |
|           | IPI00514311 | 639     | CTTNBP2NL    | CTTNBP2NL       | 1      | 1      | 39    | 107    | 107        | 39        |             |
|           | IPI00640464 | 207     | SIKE         | SIKE            | 1      | 1      | 18    | 50     | 50         | 20        |             |
|           | IPI00305186 | 211     | SIKE         | SIKE            | 0      | 1      | 17    | 48     | 0          | 0         |             |
|           | IPI00607651 | 893     | FAM40B       | STRIP2          | 1      | 1      | 20    | 28     | 21         | 16        |             |
|           | IPI00793853 | 433     | SLMAP        | SLMAP           | 1      | 1      | 49    | 104    | 0          | 0         |             |
|           | IPI00297779 | 535     | CCT2         | CCT2            | 1      | 1      | 6     | 7      | 7          | 6         |             |
|           | IPI00784090 | 548     | CCT8         | CCT8            | 1      | 1      | 10    | 16     | 16         | 10        |             |
|           | IPI00103869 | 1663    | CTTNBP2      | CTTNBP2         | 1      | 1      | 33    | 51     | 51         | 33        |             |
|           | IPI00553185 | 545     | CCT3         | CCT3            | 1      | 1      | 7     | 8      | 8          | 7         |             |
|           | IPI00290566 | 556     | TCP1         | TCP1            | 1      | 1      | 9     | 9      | 9          | 9         |             |
|           | IPI00010720 | 541     | CCT5         | CCT5            | 1      | 1      | 5     | 7      | 7          | 5         |             |
|           | IPI00014903 | 253     | FGFR1OP2     | FGFR1OP2        | 1      | 1      | 17    | 29     | 29         | 17        |             |
|           | IPI00027626 | 531     | CCT6A        | CCT6A           | 1      | 1      | 6     | 8      | 8          | 6         |             |
|           | IPI00018465 | 543     | CCT7         | CCT7            | 1      | 1      | 5     | 7      | 7          | 5         |             |
|           | IPI00220656 | 530     | CCT6B        | CCT6B           | 0      | 0.6419 | 2     | 2      | 0          | 0         |             |
| BAIT      | protid      | protLen | GeneSymbol   | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| STRIP1    | IPI00554737 | 589     | PPP2R1A      | PP2A A $\alpha$ | 1      | 1      | 14    | 25     | 25         | 15        |             |
|           | IPI00008380 | 309     | PPP2CA       | PP2A $\alpha$   | 1      | 1      | 9     | 17     | 17         | 9         |             |



|             |             |              |                |                 |        |        |       |        |            |           |             |
|-------------|-------------|--------------|----------------|-----------------|--------|--------|-------|--------|------------|-----------|-------------|
| IPI00014456 | 780         | STRN         | striatin       | 1               | 1      | 36     | 104   | 92     | 37         |           |             |
| IPI00549766 | 837         | FAM40A       | STRIP1         | 1               | 1      | 78     | 424   | 393    | 80         |           |             |
| IPI00879459 | 797         | STRN3        | striatin 3     | 1               | 1      | 38     | 143   | 19     | 7          |           |             |
| IPI00477001 | 713         | STRN3        | striatin 3     | 0.9998          | 1      | 32     | 126   | 2      | 1          |           |             |
| IPI00292827 | 416         | RP6-213H19.1 | MST4           | 1               | 1      | 13     | 26    | 14     | 8          |           |             |
| IPI00294178 | 601         | PPP2R1B      | PP2A A $\beta$ | 0               | 1      | 4      | 8     | 0      | 0          |           |             |
| IPI00003016 | 753         | STRN4        | striatin 4     | 1               | 1      | 24     | 100   | 100    | 26         |           |             |
| IPI00012093 | 426         | STK25        | STK25          | 0               | 1      | 3      | 5     | 0      | 0          |           |             |
| IPI00872754 | 484         | STK24        | STK24          | 0               | 1      | 8      | 17    | 0      | 0          |           |             |
| IPI00386122 | 225         | MOBK13       | Mob3           | 1               | 1      | 13     | 42    | 42     | 13         |           |             |
| IPI00298558 | 212         | PDCD10       | CCM3           | 1               | 1      | 9      | 20    | 20     | 9          |           |             |
| IPI00514311 | 639         | CTTNBP2NL    | CTTNBP2NL      | 1               | 1      | 10     | 19    | 19     | 10         |           |             |
| IPI00640464 | 207         | SIKE         | SIKE           | 1               | 1      | 3      | 5     | 5      | 3          |           |             |
| IPI00305186 | 211         | SIKE         | SIKE           | 1               | 1      | 3      | 5     | 5      | 3          |           |             |
| IPI00607651 | 893         | FAM40B       | STRIP2         | 0.9995          | 1      | 7      | 34    | 3      | 1          |           |             |
| IPI00793853 | 433         | SLMAP        | SLMAP          | 1               | 1      | 8      | 17    | 0      | 0          |           |             |
| IPI00014903 | 253         | FGFR1OP2     | FGFR1OP2       | 1               | 1      | 6      | 11    | 11     | 6          |           |             |
| BAIT        | protid      | protLen      | GeneSymbol     | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| CTTNBP2NL   | IPI00554737 | 589          | PPP2R1A        | PP2A A $\alpha$ | 1      | 1      | 20    | 43     | 43         | 20        |             |
|             | IPI00008380 | 309          | PPP2CA         | PP2A $\alpha$   | 1      | 1      | 10    | 22     | 22         | 10        |             |
|             | IPI00014456 | 780          | STRN           | striatin        | 1      | 1      | 34    | 88     | 82         | 37        |             |
|             | IPI00549766 | 837          | FAM40A         | STRIP1          | 1      | 1      | 23    | 62     | 41         | 25        |             |
|             | IPI00879459 | 797          | STRN3          | striatin 3      | 1      | 1      | 27    | 107    | 16         | 6         |             |
|             | IPI00477001 | 713          | STRN3          | striatin 3      | 0.9998 | 1      | 22    | 95     | 4          | 1         |             |
|             | IPI00292827 | 416          | RP6-213H19.1   | MST4            | 0      | 1      | 8     | 16     | 0          | 0         |             |
|             | IPI00294178 | 601          | PPP2R1B        | PP2A A $\beta$  | 0      | 1      | 4     | 8      | 0          | 0         |             |
|             | IPI00003016 | 753          | STRN4          | striatin 4      | 1      | 1      | 21    | 75     | 75         | 22        |             |
|             | IPI00012093 | 426          | STK25          | STK25           | 0      | 1      | 5     | 10     | 1          | 1         |             |
|             | IPI00872754 | 484          | STK24          | STK24           | 0      | 1      | 5     | 9      | 0          | 0         |             |
|             | IPI00386122 | 225          | MOBK13         | Mob3            | 1      | 1      | 10    | 69     | 69         | 12        |             |
|             | IPI00298558 | 212          | PDCD10         | CCM3            | 1      | 1      | 7     | 15     | 15         | 7         |             |
|             | IPI00514311 | 639          | CTTNBP2NL      | CTTNBP2NL       | 1      | 1      | 26    | 108    | 108        | 26        |             |
|             | IPI00607651 | 893          | FAM40B         | STRIP2          | 1      | 1      | 4     | 26     | 5          | 3         |             |
| BAIT        | protid      | protLen      | GeneSymbol     | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| CTTNBP2     | IPI00554737 | 589          | PPP2R1A        | PP2A A $\alpha$ | 1      | 1      | 30    | 43     | 43         | 30        |             |
|             | IPI00008380 | 309          | PPP2CA         | PP2A $\alpha$   | 1      | 1      | 10    | 15     | 15         | 11        |             |
|             | IPI00014456 | 780          | STRN           | striatin        | 1      | 1      | 35    | 52     | 50         | 35        |             |
|             | IPI00549766 | 837          | FAM40A         | STRIP1          | 1      | 1      | 45    | 71     | 65         | 44        |             |
|             | IPI00879459 | 797          | STRN3          | striatin 3      | 1      | 1      | 44    | 96     | 9          | 7         |             |
|             | IPI00477001 | 713          | STRN3          | striatin 3      | 0.9998 | 1      | 38    | 90     | 3          | 1         |             |
|             | IPI00292827 | 416          | RP6-213H19.1   | MST4            | 0      | 1      | 3     | 3      | 1          | 1         |             |
|             | IPI00294178 | 601          | PPP2R1B        | PP2A A $\beta$  | 0      | 1      | 4     | 4      | 0          | 0         |             |
|             | IPI00003016 | 753          | STRN4          | striatin 4      | 1      | 1      | 32    | 66     | 66         | 34        |             |
|             | IPI00012093 | 426          | STK25          | STK25           | 0      | 0.9602 | 2     | 2      | 0          | 0         |             |
|             | IPI00872754 | 484          | STK24          | STK24           | 0      | 0.9948 | 4     | 4      | 0          | 0         |             |
|             | IPI00386122 | 225          | MOBK13         | Mob3            | 1      | 1      | 12    | 26     | 26         | 12        |             |
|             | IPI00298558 | 212          | PDCD10         | CCM3            | 1      | 1      | 4     | 4      | 4          | 4         |             |
|             | IPI00514311 | 639          | CTTNBP2NL      | CTTNBP2NL       | 1      | 1      | 7     | 7      | 7          | 8         |             |
|             | IPI00607651 | 893          | FAM40B         | STRIP2          | 1      | 1      | 14    | 18     | 12         | 10        |             |
|             | IPI00297779 | 535          | CCT2           | CCT2            | 0.9998 | 0.9998 | 2     | 2      | 2          | 2         |             |
|             | IPI00784090 | 548          | CCT8           | CCT8            | 0.9998 | 1      | 2     | 2      | 2          | 2         |             |
|             | IPI00103869 | 1663         | CTTNBP2        | CTTNBP2         | 1      | 1      | 42    | 122    | 122        | 47        |             |
|             | IPI00553185 | 545          | CCT3           | CCT3            | 1      | 1      | 3     | 5      | 5          | 4         |             |
|             | IPI00290566 | 556          | TCP1           | TCP1            | 1      | 1      | 3     | 4      | 4          | 3         |             |
|             | IPI00010720 | 541          | CCT5           | CCT5            | 1      | 1      | 2     | 2      | 2          | 2         |             |
|             | IPI00027626 | 531          | CCT6A          | CCT6A           | 0.9999 | 0.9999 | 2     | 2      | 2          | 2         |             |
| BAIT        | protid      | protLen      | GeneSymbol     | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| CCM3        | IPI00554737 | 589          | PPP2R1A        | PP2A A $\alpha$ | 1      | 1      | 18    | 19     | 19         | 18        |             |
|             | IPI00008380 | 309          | PPP2CA         | PP2A $\alpha$   | 1      | 1      | 6     | 6      | 6          | 6         |             |
|             | IPI00014456 | 780          | STRN           | striatin        | 1      | 1      | 31    | 31     | 31         | 33        |             |
|             | IPI00549766 | 837          | FAM40A         | STRIP1          | 1      | 1      | 13    | 13     | 13         | 15        |             |
|             | IPI00879459 | 797          | STRN3          | striatin 3      | 1      | 1      | 20    | 23     | 1          | 1         |             |
|             | IPI00477001 | 713          | STRN3          | striatin 3      | 1      | 1      | 20    | 23     | 1          | 1         |             |
|             | IPI00292827 | 416          | RP6-213H19.1   | MST4            | 1      | 1      | 79    | 294    | 104        | 54        |             |
|             | IPI00294178 | 601          | PPP2R1B        | PP2A A $\beta$  | 0      | 0.9933 | 2     | 2      | 0          | 0         |             |
|             | IPI00003016 | 753          | STRN4          | striatin 4      | 1      | 1      | 9     | 10     | 10         | 9         |             |
|             | IPI00012093 | 426          | STK25          | STK25           | 1      | 1      | 37    | 195    | 28         | 24        |             |
|             | IPI00872754 | 484          | STK24          | STK24           | 1      | 1      | 56    | 209    | 120        | 36        |             |
|             | IPI00386122 | 225          | MOBK13         | Mob3            | 1      | 1      | 7     | 9      | 9          | 7         |             |
|             | IPI00298558 | 212          | PDCD10         | CCM3            | 1      | 1      | 89    | 218    | 218        | 96        |             |
|             | IPI00514311 | 639          | CTTNBP2NL      | CTTNBP2NL       | 1      | 1      | 10    | 10     | 10         | 10        |             |
|             | IPI00640464 | 207          | SIKE           | SIKE            | 1      | 1      | 5     | 5      | 5          | 5         |             |
|             | IPI00305186 | 211          | SIKE           | SIKE            | 1      | 1      | 5     | 5      | 5          | 5         |             |
|             | IPI00793853 | 433          | SLMAP          | SLMAP           | 1      | 1      | 16    | 17     | 0          | 0         |             |
|             | IPI00103869 | 1663         | CTTNBP2        | CTTNBP2         | 0.9865 | 0.9865 | 1     | 1      | 1          | 1         |             |
|             | IPI00014903 | 253          | FGFR1OP2       | FGFR1OP2        | 1      | 1      | 8     | 8      | 8          | 8         |             |
|             | IPI00788882 | 94           | SLMAP          | SLMAP           | 1      | 1      | 2     | 2      | 0          | 0         |             |
| BAIT        | protid      | protLen      | GeneSymbol     | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| MST4        | IPI00554737 | 589          | PPP2R1A        | PP2A A $\alpha$ | 1      | 1      | 29    | 39     | 39         | 29        |             |
|             | IPI00008380 | 309          | PPP2CA         | PP2A $\alpha$   | 1      | 1      | 8     | 14     | 14         | 8         |             |
|             | IPI00014456 | 780          | STRN           | striatin        | 1      | 1      | 39    | 89     | 87         | 42        |             |
|             | IPI00549766 | 837          | FAM40A         | STRIP1          | 1      | 1      | 33    | 52     | 49         | 30        |             |
|             | IPI00879459 | 797          | STRN3          | striatin 3      | 1      | 1      | 31    | 68     | 8          | 5         |             |
|             | IPI00477001 | 713          | STRN3          | striatin 3      | 0.9998 | 1      | 27    | 63     | 3          | 1         |             |

|             |             |              |                |                 |        |        |       |        |            |           |             |
|-------------|-------------|--------------|----------------|-----------------|--------|--------|-------|--------|------------|-----------|-------------|
| IPI00292827 | 416         | RP6-213H19.1 | MST4           | 1               | 1      | 95     | 555   | 328    | 86         |           |             |
| IPI00294178 | 601         | PPP2R1B      | PP2A A $\beta$ | 0               | 1      | 6      | 10    | 0      | 0          |           |             |
| IPI00003016 | 753         | STRN4        | striatin 4     | 1               | 1      | 16     | 28    | 28     | 16         |           |             |
| IPI00012093 | 426         | STK25        | STK25          | 1               | 1      | 25     | 230   | 3      | 3          |           |             |
| IPI00872754 | 484         | STK24        | STK24          | 0               | 1      | 20     | 169   | 0      | 3          |           |             |
| IPI00386122 | 225         | MOBK3        | Mob3           | 1               | 1      | 10     | 29    | 29     | 10         |           |             |
| IPI00298558 | 212         | PDCD10       | CCM3           | 1               | 1      | 36     | 97    | 97     | 38         |           |             |
| IPI00514311 | 639         | CTTNBP2NL    | CTTNBP2NL      | 1               | 1      | 26     | 33    | 33     | 26         |           |             |
| IPI00640464 | 207         | SIKE         | SIKE           | 1               | 1      | 10     | 11    | 11     | 10         |           |             |
| IPI00305186 | 211         | SIKE         | SIKE           | 0               | 1      | 9      | 10    | 0      | 0          |           |             |
| IPI00607651 | 893         | FAM40B       | STRIP2         | 1               | 1      | 8      | 8     | 5      | 5          |           |             |
| IPI00793853 | 433         | SLMAP        | SLMAP          | 1               | 1      | 27     | 33    | 0      | 0          |           |             |
| IPI00103869 | 1663        | CTTNBP2      | CTTNBP2        | 1               | 1      | 3      | 3     | 3      | 3          |           |             |
| IPI00014903 | 253         | FGFR1OP2     | FGFR1OP2       | 1               | 1      | 10     | 13    | 13     | 10         |           |             |
| IPI00788882 | 94          | SLMAP        | SLMAP          | 0               | 0.9998 | 2      | 3     | 0      | 0          |           |             |
| BAIT        | protid      | protLen      | GeneSymbol     | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| STK24       | IPI00554737 | 589          | PPP2R1A        | PP2A A $\alpha$ | 1      | 1      | 33    | 63     | 47         | 26        | 0.51        |
|             | IPI00008380 | 309          | PPP2CA         | PP2A $\alpha$   | 0.9989 | 1      | 7     | 10     | 1          | 1         | 0.42        |
|             | IPI00014456 | 780          | STRN           | striatin        | 1      | 1      | 57    | 113    | 113        | 59        | 0.521       |
|             | IPI00549766 | 837          | FAM40A         | STRIP1          | 1      | 1      | 36    | 55     | 50         | 33        | 0.426       |
|             | IPI00879459 | 797          | STRN3          | striatin 3      | 1      | 1      | 41    | 84     | 12         | 5         | 0.559       |
|             | IPI00477001 | 713          | STRN3          | striatin 3      | 0.9997 | 1      | 37    | 74     | 2          | 1         |             |
|             | IPI00292827 | 416          | RP6-213H19.1   | MST4            | 0      | 1      | 13    | 79     | 0          | 0         |             |
|             | IPI00294178 | 601          | PPP2R1B        | PP2A A $\beta$  | 0.9868 | 1      | 8     | 17     | 1          | 1         |             |
|             | IPI00003016 | 753          | STRN4          | striatin 4      | 1      | 1      | 23    | 43     | 43         | 24        |             |
|             | IPI00012093 | 426          | STK25          | STK25           | 0      | 1      | 6     | 64     | 0          | 0         | 0.444       |
|             | IPI00872754 | 484          | STK24          | STK24           | 0      | 1      | 52    | 322    | 0          | 0         |             |
|             | IPI00386122 | 225          | MOBK3          | Mob3            | 1      | 1      | 11    | 22     | 22         | 11        | 0.446       |
|             | IPI00298558 | 212          | PDCD10         | CCM3            | 1      | 1      | 39    | 81     | 81         | 40        | 0.462       |
|             | IPI00514311 | 639          | CTTNBP2NL      | CTTNBP2NL       | 1      | 1      | 28    | 44     | 44         | 28        |             |
|             | IPI00640464 | 207          | SIKE           | SIKE            | 1      | 1      | 12    | 16     | 16         | 12        |             |
|             | IPI00305186 | 211          | SIKE           | SIKE            | 0      | 1      | 11    | 15     | 0          | 0         |             |
|             | IPI00607651 | 893          | FAM40B         | STRIP2          | 1      | 1      | 12    | 13     | 8          | 8         |             |
|             | IPI00793853 | 433          | SLMAP          | SLMAP           | 1      | 1      | 28    | 41     | 0          | 0         | 0.377       |
|             | IPI00297779 | 535          | CCT2           | CCT2            | 1      | 1      | 3     | 3      | 3          | 3         |             |
|             | IPI00784090 | 548          | CCT8           | CCT8            | 1      | 1      | 4     | 4      | 4          | 4         |             |
|             | IPI00103869 | 1663         | CTTNBP2        | CTTNBP2         | 1      | 1      | 6     | 7      | 7          | 6         |             |
|             | IPI00553185 | 545          | CCT3           | CCT3            | 1      | 1      | 7     | 11     | 11         | 7         |             |
|             | IPI00290566 | 556          | TCP1           | TCP1            | 1      | 1      | 6     | 6      | 6          | 6         |             |
|             | IPI00010720 | 541          | CCT5           | CCT5            | 1      | 1      | 3     | 3      | 3          | 3         |             |
|             | IPI00014903 | 253          | FGFR1OP2       | FGFR1OP2        | 1      | 1      | 8     | 9      | 9          | 8         |             |
|             | IPI00027626 | 531          | CCT6A          | CCT6A           | 1      | 1      | 3     | 4      | 4          | 3         |             |
|             | IPI00018465 | 543          | CCT7           | CCT7            | 1      | 1      | 4     | 5      | 5          | 4         |             |
|             | IPI00302927 | 539          | CCT4           | CCT4            | 1      | 1      | 3     | 4      | 4          | 3         |             |
|             | IPI00788882 | 94           | SLMAP          | SLMAP           | 1      | 1      | 3     | 5      | 0          | 0         |             |
| BAIT        | protid      | protLen      | GeneSymbol     | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| STK25       | IPI00554737 | 589          | PPP2R1A        | PP2A A $\alpha$ | 1      | 1      | 21    | 40     | 30         | 16        |             |
|             | IPI00008380 | 309          | PPP2CA         | PP2A $\alpha$   | 1      | 1      | 5     | 9      | 9          | 5         |             |
|             | IPI00014456 | 780          | STRN           | striatin        | 1      | 1      | 50    | 229    | 154        | 49        |             |
|             | IPI00549766 | 837          | FAM40A         | STRIP1          | 1      | 1      | 24    | 33     | 31         | 22        |             |
|             | IPI00879459 | 797          | STRN3          | striatin 3      | 1      | 1      | 34    | 153    | 13         | 8         |             |
|             | IPI00477001 | 713          | STRN3          | striatin 3      | 0.9998 | 1      | 27    | 142    | 2          | 1         |             |
|             | IPI00292827 | 416          | RP6-213H19.1   | MST4            | 1      | 1      | 22    | 387    | 16         | 11        |             |
|             | IPI00294178 | 601          | PPP2R1B        | PP2A A $\beta$  | 0.9998 | 1      | 6     | 11     | 1          | 1         |             |
|             | IPI00003016 | 753          | STRN4          | striatin 4      | 1      | 1      | 17    | 32     | 32         | 17        |             |
|             | IPI00012093 | 426          | STK25          | STK25           | 1      | 1      | 42    | 577    | 206        | 33        |             |
|             | IPI00872754 | 484          | STK24          | STK24           | 0      | 1      | 14    | 149    | 0          | 0         |             |
|             | IPI00386122 | 225          | MOBK3          | Mob3            | 1      | 1      | 9     | 33     | 33         | 9         |             |
|             | IPI00298558 | 212          | PDCD10         | CCM3            | 1      | 1      | 29    | 63     | 63         | 30        |             |
|             | IPI00514311 | 639          | CTTNBP2NL      | CTTNBP2NL       | 1      | 1      | 17    | 46     | 46         | 17        |             |
|             | IPI00640464 | 207          | SIKE           | SIKE            | 1      | 1      | 2     | 2      | 2          | 3         |             |
|             | IPI00305186 | 211          | SIKE           | SIKE            | 1      | 1      | 2     | 2      | 2          | 3         |             |
|             | IPI00607651 | 893          | FAM40B         | STRIP2          | 1      | 1      | 5     | 5      | 3          | 3         |             |
|             | IPI00793853 | 433          | SLMAP          | SLMAP           | 1      | 1      | 16    | 48     | 0          | 0         |             |
|             | IPI00103869 | 1663         | CTTNBP2        | CTTNBP2         | 0.992  | 0.992  | 1     | 1      | 1          | 1         |             |
|             | IPI00290566 | 556          | TCP1           | TCP1            | 1      | 1      | 3     | 3      | 3          | 3         |             |
|             | IPI00014903 | 253          | FGFR1OP2       | FGFR1OP2        | 1      | 1      | 9     | 12     | 12         | 9         |             |
|             | IPI00788882 | 94           | SLMAP          | SLMAP           | 1      | 1      | 3     | 4      | 0          | 0         |             |
| BAIT        | protid      | protLen      | GeneSymbol     | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| SIKE        | IPI00554737 | 589          | PPP2R1A        | PP2A A $\alpha$ | 1      | 1      | 16    | 30     | 30         | 17        |             |
|             | IPI00008380 | 309          | PPP2CA         | PP2A $\alpha$   | 1      | 1      | 6     | 11     | 11         | 6         |             |
|             | IPI00014456 | 780          | STRN           | striatin        | 1      | 1      | 30    | 69     | 69         | 35        |             |
|             | IPI00549766 | 837          | FAM40A         | STRIP1          | 1      | 1      | 25    | 40     | 40         | 25        |             |
|             | IPI00879459 | 797          | STRN3          | striatin 3      | 1      | 1      | 27    | 55     | 4          | 3         |             |
|             | IPI00477001 | 713          | STRN3          | striatin 3      | 0.9957 | 1      | 25    | 52     | 1          | 1         |             |
|             | IPI00294178 | 601          | PPP2R1B        | PP2A A $\beta$  | 0      | 0.9761 | 3     | 7      | 0          | 0         |             |
|             | IPI00003016 | 753          | STRN4          | striatin 4      | 1      | 1      | 15    | 33     | 32         | 16        |             |
|             | IPI00872754 | 484          | STK24          | STK24           | 0.9999 | 0.9999 | 2     | 4      | 4          | 2         |             |
|             | IPI00386122 | 225          | MOBK3          | Mob3            | 1      | 1      | 8     | 16     | 16         | 9         |             |
|             | IPI00298558 | 212          | PDCD10         | CCM3            | 1      | 1      | 4     | 6      | 6          | 4         |             |
|             | IPI00640464 | 207          | SIKE           | SIKE            | 1      | 1      | 35    | 218    | 218        | 41        |             |
|             | IPI00305186 | 211          | SIKE           | SIKE            | 0      | 1      | 32    | 209    | 0          | 0         |             |
|             | IPI00607651 | 893          | FAM40B         | STRIP2          | 0      | 0.9184 | 2     | 5      | 0          | 1         |             |
|             | IPI00793853 | 433          | SLMAP          | SLMAP           | 1      | 1      | 16    | 37     | 0          | 0         |             |

|          | IPI00014903 | 253     | FGFR1OP2     | FGFR1OP2        | 1      | 1      | 10    | 26     | 26         | 11        |             |
|----------|-------------|---------|--------------|-----------------|--------|--------|-------|--------|------------|-----------|-------------|
| BAIT     | protid      | protLen | GeneSymbol   | Protein name    | Pw     | Pfull  | Npeps | Nspecs | Nspecswt95 | Npepswt95 | Ewing score |
| TRAF3IP3 | IPI00554737 | 589     | PPP2R1A      | PP2A A $\alpha$ | 1      | 1      | 31    | 37     | 37         | 33        |             |
|          | IPI00008380 | 309     | PPP2CA       | PP2A C $\alpha$ | 1      | 1      | 10    | 15     | 15         | 10        |             |
|          | IPI00014456 | 780     | STRN         | striatin        | 1      | 1      | 42    | 85     | 84         | 45        |             |
|          | IPI00549766 | 837     | FAM40A       | STRIP1          | 1      | 1      | 38    | 62     | 55         | 34        |             |
|          | IPI00879459 | 797     | STRN3        | striatin 3      | 1      | 1      | 41    | 73     | 72         | 42        |             |
|          | IPI00477001 | 713     | STRN3        | striatin 3      | 0      | 1      | 34    | 63     | 0          | 0         |             |
|          | IPI00292827 | 416     | RP6-213H19.1 | MST4            | 0      | 1      | 3     | 3      | 0          | 0         |             |
|          | IPI00294178 | 601     | PPP2R1B      | PP2A A $\beta$  | 0      | 1      | 4     | 4      | 0          | 0         |             |
|          | IPI00003016 | 753     | STRN4        | striatin 4      | 1      | 1      | 33    | 64     | 64         | 35        |             |
|          | IPI00012093 | 426     | STK25        | STK25           | 0      | 0.997  | 2     | 2      | 0          | 1         |             |
|          | IPI00872754 | 484     | STK24        | STK24           | 1      | 1      | 6     | 8      | 8          | 6         |             |
|          | IPI00386122 | 225     | MOBK13       | Mob3            | 1      | 1      | 9     | 29     | 29         | 10        |             |
|          | IPI00298558 | 212     | PDCD10       | CCM3            | 1      | 1      | 7     | 7      | 7          | 7         |             |
|          | IPI00640464 | 207     | SIKE         | SIKE            | 1      | 1      | 21    | 39     | 4          | 2         |             |
|          | IPI00305186 | 211     | SIKE         | SIKE            | 0.9798 | 1      | 20    | 36     | 1          | 1         |             |
|          | IPI00607651 | 893     | FAM40B       | STRIP2          | 1      | 1      | 12    | 16     | 9          | 9         |             |
|          | IPI00784090 | 548     | CCT8         | CCT8            | 0.9995 | 0.9995 | 2     | 2      | 2          | 3         |             |
|          | IPI00553185 | 545     | CCT3         | CCT3            | 0.591  | 0.591  | 2     | 2      | 2          | 2         |             |
|          | IPI00290566 | 556     | TCP1         | TCP1            | 0.9999 | 0.9999 | 2     | 2      | 2          | 2         |             |
|          | IPI00010720 | 541     | CCT5         | CCT5            | 1      | 1      | 2     | 3      | 3          | 2         |             |
|          | IPI00014903 | 253     | FGFR1OP2     | FGFR1OP2        | 1      | 1      | 19    | 30     | 30         | 20        |             |
|          | IPI00719170 | 551     | TRAF3IP3     | TRAF3IP3        | 1      | 1      | 23    | 60     | 60         | 23        |             |
|          | IPI00019329 | 89      | DYNLL1       | DYNLL1          | 0.9997 | 0.9998 | 2     | 5      | 5          | 2         |             |

**SUPPLEMENTAL TABLE S6.**

List of proteins identified by a unique peptide. For the bait, F = flag-tag, T = TAP tag. The number of unique peptides (npeps) and spectra (nspecs) are indicated. The sequence of the identified peptide is shown. "Direct additional evidence" for the interaction indicates that the interaction was also detected between the same two proteins in an independent experiment (e.g. in the other tag system, or in a reciprocal AP-MS experiment in which the hit or prey is now tagged). "Indirect additional evidence" indicates that an interaction has been independently detected between paralogs of one or the two proteins.

| bait            | hit          | npeps | nspecs | peptide                    | direct additional evidence  | indirect additional evidence                           |
|-----------------|--------------|-------|--------|----------------------------|-----------------------------|--|
| F-PP2A $\alpha$ | SLMAP        | 1     | 2      | DEILLHQAAK                 |                             | reciprocal flag MS with paralog                        |
| F-PP2A $\alpha$ | SLMAP        | 1     | 1      | IEALQADNDFTNER             |                             | reciprocal flag MS with paralog                        |
| F-PP2A $\alpha$ | CTTNBP2      | 1     | 1      | APEDAAGAAEAAK              | TAP MS, reciprocal flag MS  | paralogy to CTTNBP2NL                                  |
| T-striatin4     | dynein       | 1     | 6      | NFGSYVTHETK                |                             | flag MS with paralogs                                  |
| T-striatin4     | PP2A $\beta$ | 1     | 2      | AAGGDGDDSLYIAVLIDELR       | published                   | flag MS with paralogs, reciprocal flag MS with paralog |
| T-PP2A $\alpha$ | liprin A3    | 1     | 1      | DSSSLAGTPSDETLATDPLGLAK    | flag MS                     |  |
| T-PP2A $\alpha$ | liprin A1    | 1     | 1      | TLTDGVLINHEQENTPSTSGK      | flag MS                     |  |
| T-PP2A $\alpha$ | CTTNBP2NL    | 1     | 1      | MTNTGLPGPATPAYSYAK         | flag MS, reciprocal flag MS | flag MS with paralog, reciprocal flag MS with paralog  |
| T-PP2A $\beta$  | CTTNBP2      | 1     | 1      | VAANTPSMYSQELFQLSQYLQEALHR | flag MS, reciprocal flag MS | flag MS with paralog, reciprocal flag MS with paralog  |
| T-PP2A $\beta$  | PP2A $\beta$ | 1     | 3      | AAGGDGDDSLYIAVLIDELR       | published                   |  |

**SUPPLEMENTAL TABLE S7.**

Peptide statistics for single peptide identifications. For the bait, F = flag-tag, T = TAP tag. The number of unique peptides (npeps) and spectra (nspecs) are indicated. The sequence of the identified peptide is shown. "ntt" is the number of tryptic termini, "missed" the number of missed cleavages, "charge" is the charge state of the parent ion, "parent mass" is the theoretical mass of the parent ion, "error" is the calculated error on the mass of the parent ion, "matched" is the proportion of match ions, and "PeptideProphet" is the statistical value assigned to the peptide by PeptideProphet. Software-specific scoring results (XITandem, SEQUEST) are indicated.

A) flag-tag experiments. Instrument: ThermoFinnigan LTQ. Searches performed with XITandem

| bait            | hit     | npeps | nspecs | peptide       | ntt | missed | charge | parent mass | error | matched | hyperscore | nextscore | expect | PeptideProphet |
|-----------------|---------|-------|--------|---------------|-----|--------|--------|-------------|-------|---------|------------|-----------|--------|----------------|
| F-PP2A $\alpha$ | SLMAP   | 1     | 2      | DEILLHQAAK    | 2   | 0      | 2      | 1321.7      | -0.2  | 19/22   | 491        | 353       | 0.046  | 0.9977         |
| F-PP2A $\alpha$ | SLMAP   | 1     | 1      | IEALQADNDFNER | 2   | 0      | 2      | 1635.8      | -0.1  | 21/26   | 351        | 312       | 1.4    | 0.9589         |
| F-PP2A $\alpha$ | CTTNBP2 | 1     | 1      | APEDAAGAAEAAK | 2   | 0      | 2      | 1242.6      | -0.3  | 20/26   | 357        | 287       | 0.11   | 0.9905         |

B) TAP-tag experiments. Instrument: ThermoFinnigan LCQ. Searches performed with SEQUEST

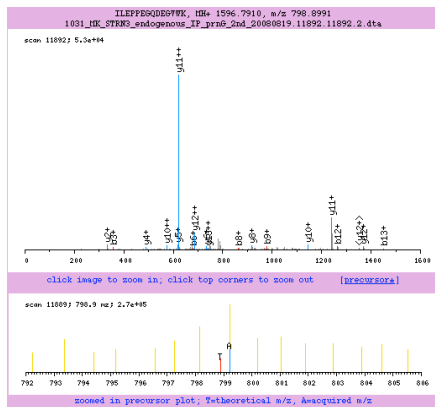
| bait            | hit           | npeps | nspecs | peptide                    | ntt | missed | charge | parent mass | error | matched | Xcorr  | delCN | Sp     | RSp | PeptideProphet |
|-----------------|---------------|-------|--------|----------------------------|-----|--------|--------|-------------|-------|---------|--------|-------|--------|-----|----------------|
| T-striatin4     | dynein        | 1     | 6      | NFGSYVTHETK                | 2   | 0      | 2      | 1283.4      | 0.1   | 15/20   | 3.16   | 0.357 | 798    | 1   | 1              |
| T-striatin4     | PP2A $\alpha$ | 1     | 2      | AAGGGDDSLYPIAVLIDELR       | 1   | 0      | 3      | 2161.4      | -1.2  | 36/80   | 4.89   | 0.196 | 1526.6 | 1   | 0.99           |
| T-PP2A $\alpha$ | liprin A3     | 1     | 1      | DSSSLAGTPSDETLATDPLGLAK    | 2   | 0      | 2      | 2247.4      | 0.9   | 23/44   | 4.31   | 0.4   | 864.9  | 1   | 0.99           |
| T-PP2A $\alpha$ | liprin A1     | 1     | 1      | TLTDGVLINHEQENTPSTSGK      | 2   | 0      | 2      | 2357.5      | -0.9  | 18/42   | 3.5426 | 0.421 | 734.2  | 1   | 1              |
| T-PP2A $\alpha$ | CTTNBP2NL     | 1     | 1      | MTNTGLPGPATPAYSAK          | 2   | 0      | 2      | 1841.1      | -0.1  | 15/34   | 2.0184 | 0.276 | 190.3  | 5   | 0.99           |
| T-PP2A $\alpha$ | CTTNBP2       | 1     | 1      | VAANTPSMYSQELFQLSQYLQEALHR | 2   | 0      | 3      | 3026.4      | 1.8   | 28/100  | 3.35   | 0.369 | 387.2  | 1   | 1              |
| T-PP2A $\alpha$ | PP2A $\alpha$ | 1     | 3      | AAGGGDDSLYPIAVLIDELR       | 1   | 0      | 3      | 2161.4      | -1.5  | 33/80   | 4.72   | 0.253 | 1197.8 | 1   | 1              |

SUPPLEMENTAL TABLE S7.

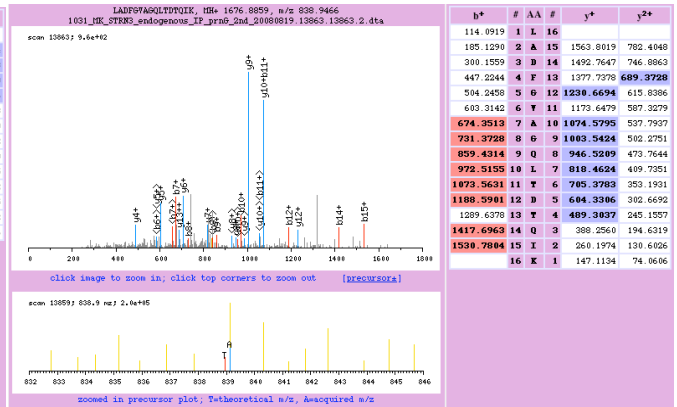
**Mass spectrometric data for interactions with endogenous MST4 and striatin 3.** Immunoprecipitation/mass spectrometry was performed as described in Experimental Procedures. The accession numbers (protid) for each of the identified proteins are from the International Protein Index (IPI). ProtLen is the length of the protein in amino acids and the GeneSymbol is from HUGO. The number of unique peptides in the MST4 and Striatin 3 IPs (MST4 Npeps, Striatin3 Npeps) is indicated, along with the total number of spectra in each IP (MST4 Nspecs, Striatin3 Nspecs). The ProteinProphet probability was >0.99 in all cases, excepted for Mob3 in the Striatin3 IP (0.9796) and MST4 in the Striatin3 IP (0.9790). The numbers highlighted in purple correspond to proteins identified on the basis of a single unique peptide: the corresponding annotated spectra are presented below. • indicates that peptides were detected, but that they fell below the ProteinProphet cutoff value (0.8), •• indicates that peptides were detected, but that they were all shared with different entries. Red denotes components of the PP2Ac•PP2A core phosphatase, green represents the known PP2A B regulatory subunits (including the striatins), and blue indicates the detection of STRIP1/2 and CTTNBP2/NL in the pull-downs

| protid      | protLen | GeneSymbol   | Protein name | MST4 Npeps | MST4 Nspecs | Striatin3 Npeps | striatin3 Nspecs |
|-------------|---------|--------------|--------------|------------|-------------|-----------------|------------------|
| IPI00298558 | 212     | PDCD10       | CCM3         | 25         | 97          | 3               | 3                |
| IPI00103869 | 1663    | CTTNBP2      | CTTNBP2      | 2          | 3           | ••              | ••               |
| IPI00514311 | 639     | CTTNBP2NL    | CTTNBP2NL    | 9          | 12          | 16              | 23               |
| IPI00386122 | 225     | MOBKL3       | Mob3         | 2          | 8           | 1               | 2                |
| IPI00292827 | 416     | RP6-213H19.1 | MST4         | 45         | 219         | 1               | 2                |
| IPI00554737 | 589     | PPP2R1A      | PP2A Aa      | 5          | 8           | 11              | 20               |
| IPI00008380 | 309     | PPP2CA/B     | PP2Aca/b     | 2          | 2           | 3               | 7                |
| IPI00793853 | 433     | SLMAP        | SLMAP        | 3          | 3           | •               | •                |
| IPI00014456 | 780     | STRN         | striatin     | 11         | 22          | ••              | ••               |
| IPI00879459 | 797     | STRN3        | striatin 3   | 11         | 20          | 16              | 31               |
| IPI00003016 | 753     | STRN4        | striatin 4   | 3          | 5           | 10              | 16               |
| IPI00549766 | 837     | FAM40A       | STRIP1       | •          | •           | 9               | 17               |
| IPI00607651 | 893     | FAM40B       | STRIP2       | ••         | ••          | •               | •                |

Detection of Mob3 in Striatin3 IP



Detection of MST4 in Striatin3 IP

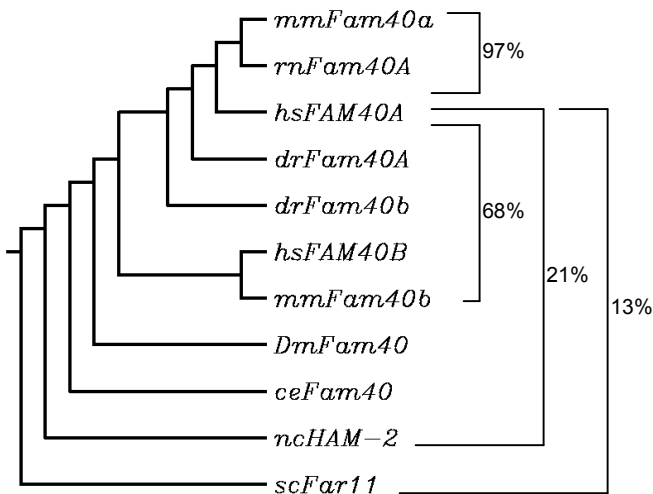


## SUPPLEMENTAL FIGURE S1

## A

hsSTRIP1 1 MEPAVGGPGLIVNNKQPQPPPPPPAAQPPPGAPRAAAGLLP GKKAREFNRNQRKDSEGYSESPDLEFEYADTKWAA  
 hsSTRIP2 1 -----MEDPAAPGTGCPPANGNGNGGKKGQAAPKGREAFRSORRESEGSVDCPTLEFEYGDADGHAA  
  
 hsSTRIP1 81 ELSELYSYTEGPEFLMNRKCFEEDFRHVTDKKMTLPTNQHTHAMRLLDGLEVTAREKRLKVARALYVAQGTFGES  
 hsSTRIP2 64 ELSELYSYTENLEFTNNRRCFEEDFRQVQGGKWELELEDAQRAYIMGLLDRLEVVSRERRLKVARALYLAQGTFGED  
  
 hsSTRIP1 161 SEAEVQSWMRYNIFLLELVGTENALVELLNMEIDNSAACSSARKPAISLADSTDLRVLLNIMYLIVETVHQECGDKAE  
 hsSTRIP2 144 SEVDVHLHWSRYNCFLLYQMGTFSTFLELLHMEIDNSAACSSARKPAVSIADSTELRVLLSVMYLMVENIRLERETDPCG  
  
 hsSTRIP1 241 WRTMRQTFRAETGSPYNNPEFALMLFGMVTKFCSGHAPHFPMKKVLLLWKTVLCTLGGFELQSMKAEKRSILGLPPL  
 hsSTRIP2 224 WRTARETFRTELFSFSHNEEPFALLLFSMVTKFCSGHAPHFPMKKVLLLWKVVMFTLGGFELQTLKVKRAELGLPPL  
  
 hsSTRIP1 321 PEDSIKVIIRNMRAASPPASASDLIEQQOK-----RGRREKALIKQDNLDAFNERDPYKADD SREEEEN---DDN  
 hsSTRIP2 304 AEDSIQVVKSMRAASPPSYTLDLIGESQLAPPPSKLGRGRGSRQQLITKQDSLDTYNERDLFKTEEPATEEEEEESAGDGR  
  
 hsSTRIP1 390 SLEGEFTPLERDEVMPPPLQHP--QTDRLTCPKGLPWAPKVRKDKDIEMFLESSRSKFIGYTLGSDTNTVGLPRPIHESI  
 hsSTRIP2 384 TLDGELDLLEQDPLVPPPPSQAPLSARVAFPKGLPWAPKVRKDKDIEMFLEMSRNKFIGFTLGDQDITLVGLPRPIHESV  
  
 hsSTRIP1 468 KTLKQHKYTSIAEVQAQMEEEYLRSPLSGGEEVEQVPAETLYQGLPSPLPQYMIALLKILLAAPTSKAKTDSINILAD  
 hsSTRIP2 464 KTLKQHKYTSIADVQIKNEEELKCPMSLGEVVPETPCEILYQGMLYSLPQYMIALLKILLAAPTSKAKTDSINILAD  
  
 hsSTRIP1 548 VLPEEMETIVLQSMKLGVDVNRHKEIVKAISSAVLLLLLKHFKLNHYQFEYVAQHLVFANCIPLILKFFNQNIISYITA  
 hsSTRIP2 544 VLPEEMETIVLQSMKLGVDVNRHKEIVKSISSAVLLLLLKHFKLNHYQFEYVSAQHLVFANCIPLILKFFNQNIISYITA  
  
 hsSTRIP1 628 KNSISVLDYPHGVVHLEPELTAESLEAGDSNQFCWRNLFSCINLLRLNKLTKWKHSRTMMLVVFKSAPILKRALKVKQA  
 hsSTRIP2 624 KNSISVLDYPCCTIQDLPELTAESLEAGDSNQFCWRNLFSCINLLRLNKLTKWKHSRTMMLVVFKSAPILKRALKVKQA  
  
 hsSTRIP1 708 MQLYVLKLLKIQTKYLGQRWRKSNMKTMSAIVQKVRHRINDDWAYGNLDARPWDFQAECCALRANIERFNARRYDRAH  
 hsSTRIP2 704 MQLYVLKLLKIQTKYLGQRWRKSNMKTMSAIVQKVRHRINDDWAYGNLDARPWDFQAEECTLRANIEAFNSRRYDRPQ  
  
 hsSTRIP1 788 SNPDLFLPVDNCLQSVLGQRVLDLPEDFQMNYDLWLEREVFSKPTISWEEELLQ--  
 hsSTRIP2 784 DS-EFSPVDNCLQSVLGQRVLDLPEDFHYSYELWLEREVFSQPTICWEEELLQNH

## B



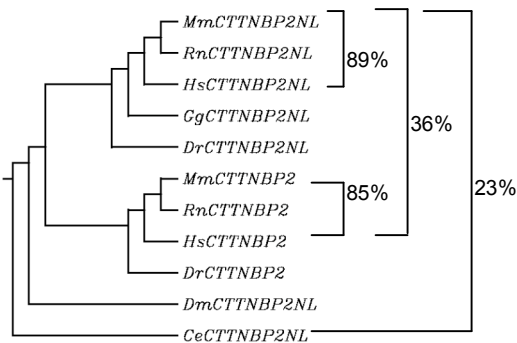
**A) Sequence alignment between human STRIP1 (FAM40A) and STRIP2 (FAM40B).** Alignment performed with BLOSUM62 (ClustalW<sup>1</sup>). Identical residues are highlighted in **BLACK**; conservative substitutions in **GREY**. Phosphorylation sites (in either the mouse or human protein; Phosphosite<sup>2</sup>) are in **orange**. **B) Phylogenetic tree of the STRIP (FAM40A/FAM40B) orthology groups.** Percentage identity between selected pairs of sequences is indicated on the right. Accession numbers used are hsFAM40A, NP\_149079.2; mmFam40a, NP\_705791.1; rnFam40A, XP\_342312.3; drFam40a, NP\_998686.1; dmFam40, NP\_647806.2; hsFAM40B, NP\_065755.1; mmFam40b, NP\_796178.2; drFam40b, XP\_684274.2; ceFam40, NP\_495467.1; scFar11, NP\_014272.1; ncHAM-2, XP\_961503.2. Species names are Hs, *Homo sapiens*; Mm, *Mus musculus*; Rn, *Rattus norvegicus*; Dr, *Danio rerio*; Dm, *Drosophila melanogaster*; Ce, *Caenorhabditis elegans*; Nc, *Neurospora crassa*; Sc, *Saccharomyces cerevisiae*.

SUPPLEMENTAL FIGURE S2

A

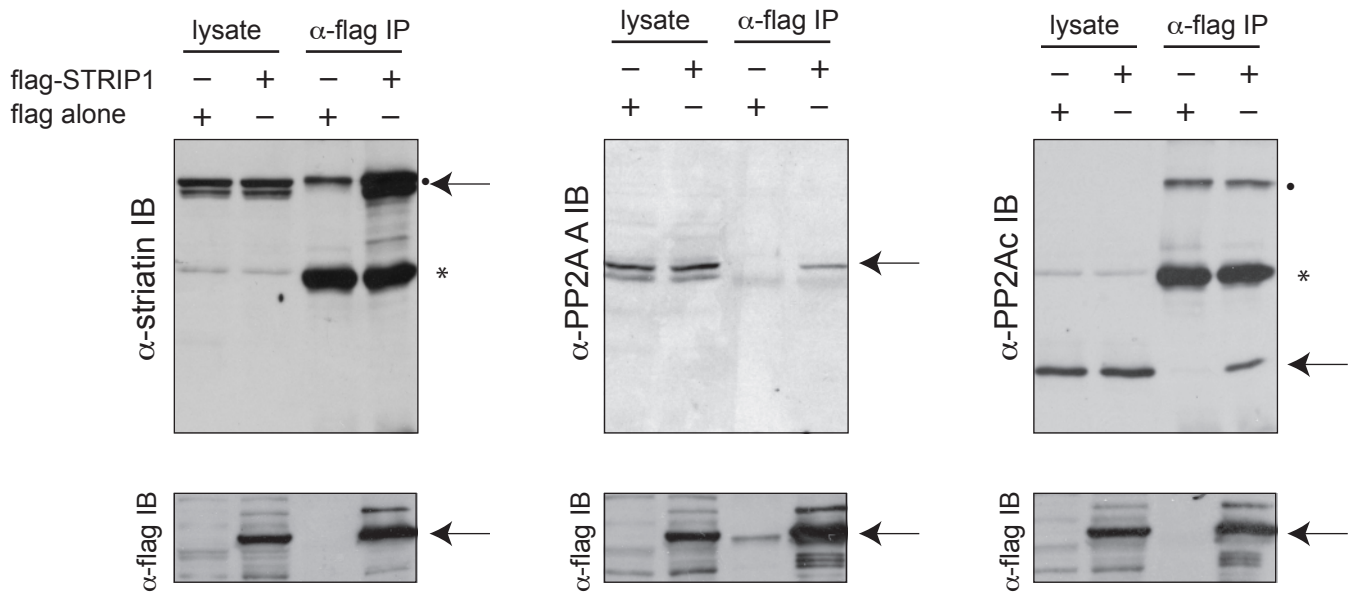
|             |      |                                   |           |              |        |                       |                    |                   |                                 |
|-------------|------|-----------------------------------|-----------|--------------|--------|-----------------------|--------------------|-------------------|---------------------------------|
| HsCTTNBP2   | 1    | MATDGASCEPDLSRAPEDAAGAAAEAAKKEFDV | TL        | SKS          | ELRMLL | LSVMEGELEARDLVIEALRAR | RKEVF              | IQ                | ERYGRFNI                        |
| RnCBP90     | 1    | MATDSASCEPDLSRAPGDAEGATAEAAKKEFDV | TL        | SKS          | ELRMLL | LSVMEGELEARDLVIEALRAR | RKEVF              | IQ                | ERYGRFNI                        |
| HsCTTNBP2NL | 1    | -----MNL                          | EL        | SKP          | ELLT   | LS                    | ILEGELEARDLVIEALKA | QR                | DTFIERYGKYNI                    |
| HsCTTNBP2   | 81   | NDE                               | FTALQ     | RDYEAG--AGD  | KEKK   | PVCTNPLSILEAVMAH      | CR                 | KMQERMSAQLAAAESRQ | -----                           |
| RnCBP90     | 81   | NDE                               | FTALQ     | RDYEAG--AGD  | KEK    | PVCTNPLSILEAVMAH      | CR                 | KMQERMSAQLAAAESRQ | -----                           |
| HsCTTNBP2NL | 51   | SD                                | FTALQ     | RDYEFTLKEKND | GEKQ   | PVCTNPLSILKVV         | MKQ                | CNNMQERMLS        | QLAAAESRHRKVILDLEEERQRHAQDTAEGD |
| HsCTTNBP2   | 137  | -----                             | KKLEMEK   | LQ           | QALE   | QEHKKLAARLEEB         | EG                 | KNQVLMV           | LKCEKQLGKRVIEE                  |
| RnCBP90     | 136  | -----                             | KKLEMEK   | LQ           | QALE   | QEHKKLAARLEEB         | EG                 | KNQVLMV           | LKCEKQLGKRVIEE                  |
| HsCTTNBP2NL | 131  | DVT                               | YMLEKERER | L            | TQ     | LEEK                  | SQ                 | KKFK              | EQ                              |
| HsCTTNBP2   | 203  | KK                                | TNELE     | EL           | LSA    | ERRRST                | EMEAQ              | MEKQL             | SE                              |
| RnCBP90     | 202  | KK                                | TSELE     | EL           | QLS    | AEK                   | QRS                | SAG               | MEAQ                            |
| HsCTTNBP2NL | 211  | KS                                | VSKLE     | EL           | LA     | AE                    | KK                 | GLQ               | TEA                             |
| HsCTTNBP2   | 283  | RKT                               | KDRRLV    | SISV         | TEGT   | TR                    | SVAC               | QTD               | -LVT                            |
| RnCBP90     | 282  | RKT                               | KDKRLA    | SISV         | TEGP   | TR                    | SVAC               | QTD               | -VVT                            |
| HsCTTNBP2NL | 288  | EQL                               | KKPVTV    | SKGT         | TEPL   | ML                    | MSV                | EC                | QTE                             |
| HsCTTNBP2   | 362  | Y                                 | DLIGASV   | PAFP         | PPS    | ANK                   | TE                 | ENG               | -----                           |
| RnCBP90     | 361  | H                                 | SLDG-PS   | PPTAL        | PSS    | SASR                  | TE                 | ENG               | -----                           |
| HsCTTNBP2NL | 368  | V                                 | ENQVPP    | PREKS        | V      | ALAE                  | QEK                | VEN               | GC                              |
| HsCTTNBP2   | 434  | NT                                | SLHPG     | IN           | PR     | IQ                    | AAR                | FR                | FQ                              |
| RnCBP90     | 433  | NT                                | --HP      | GIN          | PR     | IQ                    | AAR                | FR                | FQ                              |
| HsCTTNBP2NL | 448  | QS                                | SYQV      | GIN          | PR     | IF                    | AAR                | HK                | FQ                              |
| HsCTTNBP2   | 512  | -----                             | VP        | PTG          | DV     | GH                    | TP                 | VP                | GR                              |
| RnCBP90     | 509  | -----                             | AS        | PGD          | AG     | TC                    | FP                 | VG                | RT                              |
| HsCTTNBP2NL | 527  | S                                 | PF        | GD           | YR     | NL                    | AN                 | TAN               | PR                              |
| HsCTTNBP2   | 570  | S                                 | RASNTG    | AKVD         | NK     | TVAS                  | TP                 | SS                | LP                              |
| RnCBP90     | 565  | -----                             | AG        | AKVD         | NK     | IVAS                  | PP                 | ST                | LP                              |
| HsCTTNBP2NL | 605  | -----                             | Q         | AS           | L      | T                     | A                  | E                 | D                               |
| HsCTTNBP2   | 650  | AC                                | SDSS      | LV           | IP     | TTIA                  | FC                 | SS                | IN                              |
| HsCTTNBP2   | 730  | L                                 | NEEGLD    | IN           | Y      | S                     | C                  | E                 | D                               |
| HsCTTNBP2   | 810  | G                                 | QT        | PL           | YL     | ACK                   | NG                 | NK                | E                               |
| HsCTTNBP2   | 890  | E                                 | SE        | PE           | G      | I                     | S                  | K                 | P                               |
| HsCTTNBP2   | 970  | I                                 | PL        | R            | I      | S                     | V                  | G                 | E                               |
| HsCTTNBP2   | 1050 | R                                 | S         | I            | R      | S                     | I                  | T                 | L                               |
| HsCTTNBP2   | 1130 | G                                 | S         | L            | Q      | D                     | Y                  | I                 | V                               |
| HsCTTNBP2   | 1210 | R                                 | D         | F            | L      | A                     | P                  | L                 | E                               |
| HsCTTNBP2   | 1290 | V                                 | N         | K            | F      | K                     | Q                  | A                 | P                               |
| HsCTTNBP2   | 1370 | I                                 | L         | S            | R      | A                     | S                  | V                 | K                               |
| HsCTTNBP2   | 1450 | G                                 | E         | S            | G      | A                     | R                  | K                 | V                               |
| HsCTTNBP2   | 1530 | L                                 | V         | K            | E      | L                     | Q                  | S                 | M                               |
| HsCTTNBP2   | 1610 | K                                 | S         | F            | L      | P                     | V                  | P                 | R                               |

B



**A) Sequence alignment between human CTTNBP2, rat CBP90 and human CTTNBP2NL.** The published CBP90 rat protein (AF053768) is orthologous to human CTTNBP2, but represents a shorter variant<sup>3</sup>. Underlining indicates a CDD (Conserved domain database)<sup>4</sup>-predicted chromosome segregation ATPase region (1e-08 on CTTNBP2, 3e-07 on CTTNBP2NL); the region in blue corresponds to predicted ankyrin repeats (CDD 3e-31). Red on CBP90 indicates a proline-rich region, postulated to be required for binding to the cortactin SH3 domain. The residues in green are predicted to form coiled-coils (paircoil2, 0.03 p-score cut-off<sup>5</sup>). Orange indicates phosphorylation sites detected in mouse or human species (Phosphosite<sup>2</sup>). **B) Phylogeny of the CTTNBP2NL and CTTNBP2 families.** Percentage identity between the aligned regions of selected pairs is indicated on the right (Matrix BLOSUM62). hsCTTNBP2NL, NP\_061174.1; mmCttnbp2nl, NP\_084525.1; mCttnbp2nl, XP\_227556.2; drCttnbp2nl, NP\_001070839.1; dmCttnbp2nl (CG10915), NP\_611299.2; ceCttnbp2nl (C49H3.6a), NP\_501315.1; hsCTTNBP2, NP\_219499.1; mmCttnbp2, NP\_525024.1; mCttnbp2, XP\_347231.3; drCttnbp2, XP\_683573.2.





**Confirmation of the interaction between stably-expressed flag-STRIP1 and endogenous PP2A components.** Immunoprecipitation (IP) on  $\alpha$ -flag M2 agarose beads was conducted on lysate from HEK293 cells stably expressing flag-STRIP1 or flag alone. Immune complexes were resolved by SDS-PAGE, followed by transfer to nitrocellulose. Co-precipitation of endogenous striatin (top left), PP2A A (top middle) and PP2Ac (top right) was monitored using antibodies to the endogenous proteins. Arrows indicate the position of each protein. A contaminating band is visible in the flag alone lane on the  $\alpha$ -striatin IB and  $\alpha$ -PP2Ac blots (indicated by a dot); this band comigrates with the striatin protein. Note that a doublet corresponding to endogenous striatin is present in much higher amounts in the flag-STRIP1 sample. Asterisks denote the antibody heavy chain. The bottom panels show the reprobing of each membrane with  $\alpha$ -flag antibodies for detection of flag-STRIP1 protein.

## SUPPLEMENTAL FIGURE S4

A

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HsSIKE      1  MSCTTEKILTDAKTLEERLRHDDAAESLVDQSAAIHRRVVAAMREAGTALPDQVRQRYQEDASDMKDMSKYKPHLLSQQE
HsFGFR1OP2 1  MSCTTEKALADAKALWERLRHDDAAESLVDQSAAIHRRVVAAMREAGTALPDQVRQRYQEDASDMKDMSKYKPHLLSQQE

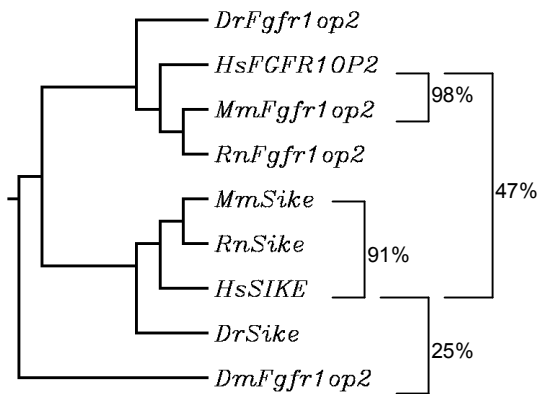
HsSIKE      81  NTQIRDLQOENRELWISLEEHQDALELIMSKYRKMQLQLMVAKKAVDAEPVIKAAHQSHS-----
HsFGFR1OP2  73  NRQIRELQOENRELRISLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMKLEQHSKIDMVHRNKSEGFFLDASRHI

HsSIKE      140 -----AESQIDRICEMCEVMRKAVQVDDDFCKIQEKLAAQLELENKELRELLSISSESLSQARMENS
HsFGFR1OP2  153 LEAPQHGLERRHLEANQNEIQAHNDQITEMAVMRKALEIDFQQGCKEQERTIFQLEQENKGLRELLQITRESFLNLKDD

HsSIKE      203 MDTASQAIK-----
HsFGFR1OP2  233 ASESLSALVTNSDLSLRKS

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B



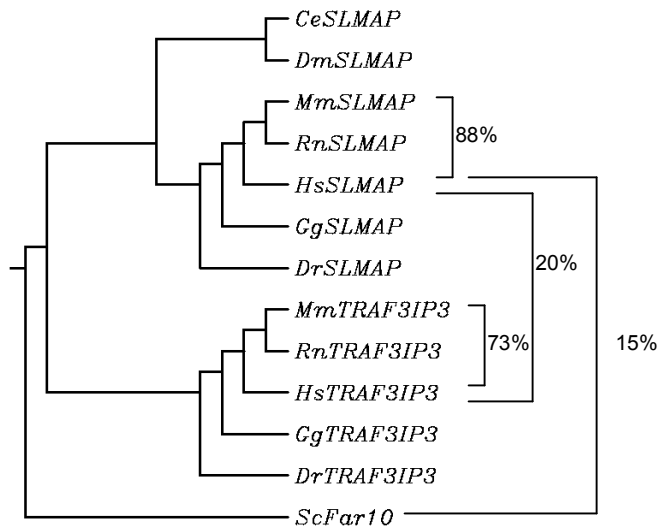
**A) Sequence alignment between human SIKE and human FGFR1OP2.** Alignment performed with BLOSUM62 (ClustalW<sup>1</sup>). Identical residues are highlighted in **BLACK**; conservative substitutions in **GREY**. Phosphorylation sites (detected in either the mouse or human protein; Phosphosite<sup>2</sup>) are in **orange**. The residues in **green** are predicted to form coiled-coils (paicoil<sup>5</sup>, 0.3 p-score cut-off). **B) Phylogenetic tree of the SIKE/FGFR1OP2 orthology groups.** Percentage identity between selected pairs of sequences is indicated on the right. Accession numbers used are HsSIKE, NP\_001095866.1; MmSike, NP\_079955.1; RnSike, NP\_001012182.1; DrSike, XP\_696578.2; HsFgfr1op2, NP\_056448.1; MmFgfr1op2, NP\_080494.1; RnFgfr1op2, NP\_958824.1; DrFgfr1op2, NP\_956249.1; DmFgfr1op2, NP\_609084.1.

## SUPPLEMENTAL FIGURE S5

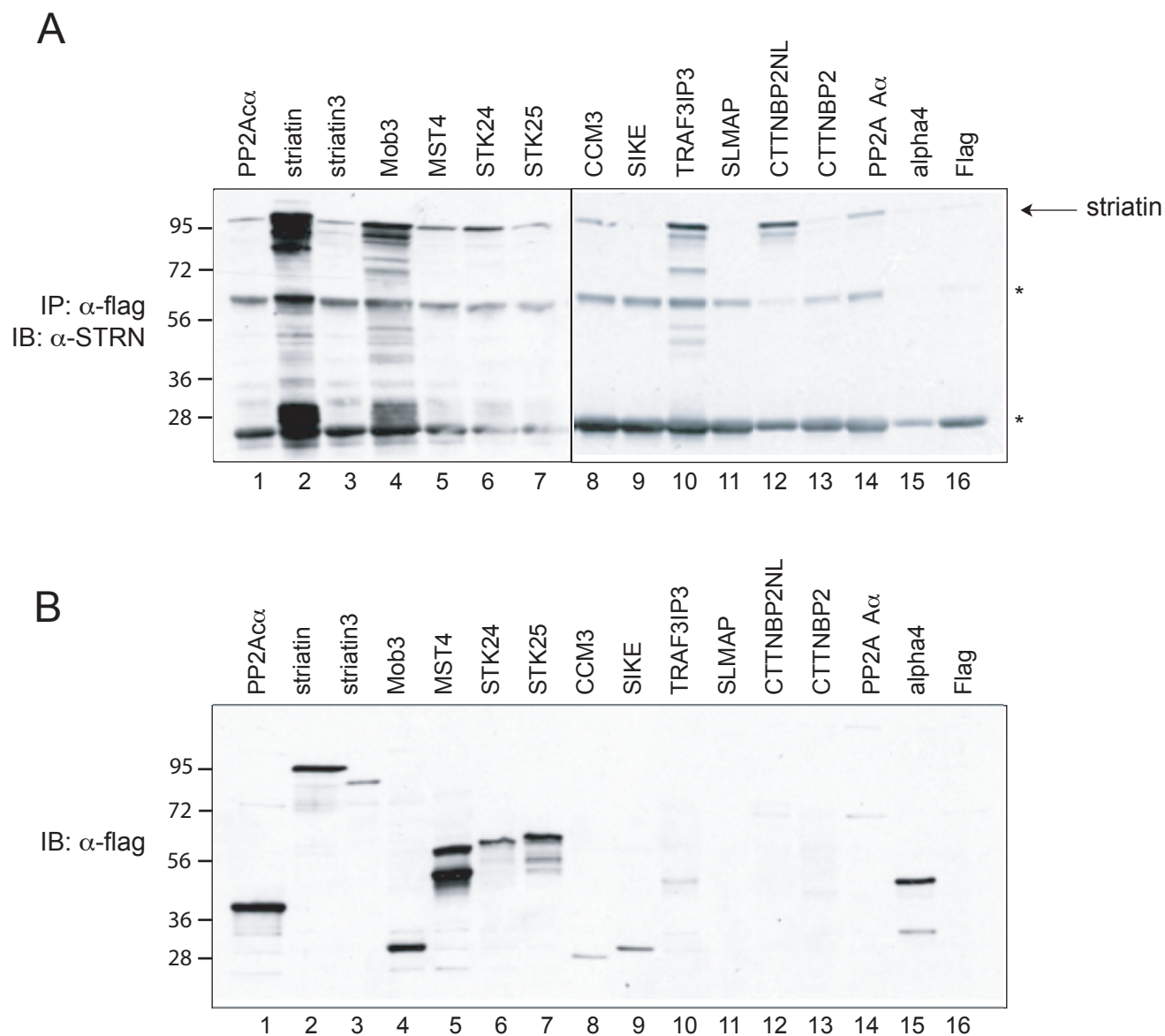
A

|            |     |   |
|------------|-----|---|
| HsSLMAP    | 1   | -----MPSALAIFTCRPNSHPFQERIVYLD <del>EP</del> IKIGRSVAFRCRPAQNNATFDCVLSRNHAI <del>VWF</del> DEKTKGKFLYQTKSS  |
| HsTRAF3IP3 | 1   | MISPDPRPSPGLARWAESYEAKCERRQ <del>ER</del> SRRCRPNVTT <del>CR</del> QVQKTLRIQQREQLQRARLQQ <del>FF</del> RRR-NLELEKGA   |
| HsSLMAP    | 76  | <del>NGTFINSQR</del> LSR--GSEESPPCE <del>LS</del> SDIIQFG---VDVTE <del>N</del> TRKVTHTGCIVSTIK <del>F</del> LPDGMEARLRS <del>SD</del> VIHAP <del>P</del> SPV  |
| HsTRAF3IP3 | 80  | QHPQAREQ <del>GP</del> SRRP <del>Q</del> VTGTSS <del>EV</del> FPAQHPPSGICR <del>DL</del> SDHLSSQAGGLPPQDTP <del>KK</del> PKHHRGTQTKAEGPT <del>KN</del> DA   |
| HsSLMAP    | 151 | DKVAANTPS <del>YS</del> Q <del>E</del> F <del>Q</del> LS <del>Q</del> YL <del>Q</del> EAL <del>H</del> R <del>E</del> Q <del>N</del> L <del>E</del> Q <del>K</del> L <del>A</del> T <del>L</del> Q <del>R</del> L <del>L</del> A <del>I</del> T <del>Q</del> E <del>A</del> S <del>D</del> T <del>S</del> W <del>Q</del> L <del>L</del> D <del>E</del> D <del>E</del> L <del>L</del> S <del>R</del> E <del>V</del> M <del>G</del> N <del>Q</del> L <del>Q</del> A <del>C</del> S <del>K</del> N   |
| HsTRAF3IP3 | 160 | SQQTNYGVAVLDKE <del>LI</del> Q <del>L</del> S <del>D</del> YL <del>K</del> EAL <del>Q</del> REL <del>V</del> L <del>K</del> Q <del>K</del> M <del>V</del> IL <del>Q</del> DL <del>L</del> ST <del>L</del> I <del>Q</del> A <del>S</del> D <del>S</del> SW <del>K</del> Q <del>L</del> N <del>E</del> D <del>K</del> L <del>K</del> G <del>K</del> L <del>R</del> S <del>L</del> E <del>N</del> Q <del>L</del> Y <del>T</del> C <del>H</del> Q <del>K</del>  |
| HsSLMAP    | 231 | <del>Q</del> T <del>E</del> D <del>S</del> L <del>R</del> R <del>E</del> L <del>L</del> I <del>A</del> L <del>Q</del> E <del>D</del> K <del>H</del> N <del>Y</del> E <del>T</del> T <del>A</del> K <del>E</del> S <del>L</del> R <del>R</del> V <del>L</del> C <del>E</del> K <del>L</del> E <del>V</del> V <del>R</del> R <del>L</del> S <del>E</del> V <del>E</del> R <del>S</del> L <del>S</del> N <del>T</del> E <del>D</del> E <del>C</del> H <del>L</del> R <del>E</del> M <del>N</del> E <del>R</del> T <del>Q</del> E <del>L</del> L <del>R</del> E <del>L</del> A <del>N</del> K <del>Y</del> N <del>G</del> A |
| HsTRAF3IP3 | 240 | <u>Y</u> SPWGMKKV <del>L</del> LE <del>M</del> E <del>D</del> Q <del>K</del> N <del>S</del> Y <del>E</del> Q <del>K</del> A <del>K</del> E <del>S</del> L <del>Q</del> K <del>V</del> L <del>E</del> E <del>K</del> N <del>A</del> E <del>Q</del> Q <del>L</del> Q <del>S</del> T <del>Q</del> R <del>S</del> L <del>A</del> L <del>A</del> E <del>Q</del> K <del>C</del> E <del>E</del> W <del>R</del> S <del>Q</del> Y <del>E</del> A <del>L</del> K <del>E</del> D <del>W</del> R <del>T</del> L <del>G</del> T <del>Q</del> H <del>R</del> E <del>L</del>   |
| HsSLMAP    | 311 | <del>V</del> N <del>E</del> I <del>T</del> A <del>L</del> L <del>S</del> D <del>R</del> T <del>K</del> V <del>A</del> L <del>G</del> R <del>Q</del> E <del>E</del> I <del>Q</del> Q <del>K</del> G <del>Q</del> A <del>E</del> K <del>K</del> E <del>L</del> C <del>H</del> K <del>L</del> D <del>E</del> V <del>E</del> E <del>K</del> E <del>C</del> E <del>L</del> Q <del>A</del> K <del>I</del> E <del>A</del> L <del>Q</del> A <del>L</del> N <del>I</del> F <del>T</del> N <del>E</del> R <del>L</del> T <del>A</del> L <del>Q</del> E <del>H</del> L <del>L</del> S <del>K</del> S <del>G</del> D <del>C</del> T |
| HsTRAF3IP3 | 320 | <u>E</u> S <del>Q</del> L <del>H</del> V <del>L</del> Q <del>S</del> K <del>L</del> Q <del>G</del> A <del>S</del> R <del>D</del> -----L <del>Q</del> M <del>N</del> Q <del>A</del> L <del>R</del> F <del>L</del> E <del>N</del> H <del>Q</del> Q <del>L</del> Q <del>A</del> K <del>I</del> E <del>C</del> L <del>O</del> G <del>D</del> R <del>D</del> L <del>C</del> S <del>L</del> D <del>T</del> Q <del>D</del> L <del>Q</del> D <del>L</del> K <del>R</del> S <del>E</del> E <del>K</del> L <del>T</del>   |
| HsSLMAP    | 391 | <del>F</del> I <del>H</del> Q <del>F</del> I <del>E</del> C <del>C</del> K <del>L</del> I <del>V</del> E <del>G</del> H <del>L</del> T <del>K</del> A <del>V</del> E <del>T</del> R <del>L</del> S <del>K</del> E <del>N</del> Q <del>T</del> R <del>A</del> K <del>E</del> S <del>D</del> F <del>S</del> D <del>T</del> L <del>S</del> P <del>S</del> K <del>E</del> K <del>S</del> S <del>D</del> D <del>T</del> T <del>D</del> A <del>Q</del> M <del>D</del> E <del>Q</del> D <del>L</del> N <del>E</del> P <del>L</del> A <del>K</del> V <del>S</del> L <del>L</del> K <del>D</del> D <del>L</del> Q                |
| HsTRAF3IP3 | 389 | L <del>V</del> T <del>R</del> V <del>Q</del> Q <del>L</del> G <del>L</del> I <del>Q</del> N <del>Q</del> S <del>L</del> Q <del>L</del> Q <del>E</del> Q <del>E</del> K <del>L</del> L <del>L</del> K <del>K</del> D-----  |
| HsSLMAP    | 471 | <del>G</del> A <del>Q</del> S <del>E</del> I <del>E</del> A <del>K</del> Q <del>E</del> I <del>Q</del> H <del>L</del> R <del>K</del> E <del>L</del> I <del>E</del> A <del>Q</del> E <del>L</del> A <del>R</del> T <del>S</del> K <del>Q</del> K <del>F</del> E <del>L</del> <u>Q</u> A <del>L</del> L <del>E</del> E <del>E</del> R <del>K</del> A <del>V</del> R <del>N</del> O <del>V</del> E <del>S</del> T <del>K</del> Q <del>I</del> Q <del>V</del> L <del>Q</del> A <del>Q</del> L <del>R</del> L <del>H</del> I <del>D</del> T <del>E</del> N <del>L</del> R <del>E</del> E <del>K</del> D                      |
| HsTRAF3IP3 | 419 | ----- <u>Q</u> A <del>L</del> P <del>V</del> W <del>S</del> P <del>K</del> S <del>E</del> P <del>N</del> E <del>V</del> E <del>P</del> -----  |
| HsSLMAP    | 551 | <del>S</del> E <del>I</del> T <del>S</del> T <del>R</del> D <del>E</del> L <del>L</del> S <del>A</del> R <del>D</del> E <del>I</del> L <del>L</del> L <del>H</del> Q <del>A</del> A <del>A</del> K <del>V</del> A <del>S</del> E <del>R</del> D <del>T</del> D <del>I</del> A <del>S</del> L <del>Q</del> E <del>E</del> L <del>K</del> K <del>V</del> R <del>A</del> E <del>L</del> E <del>R</del> R <del>W</del> R <del>K</del> A <del>A</del> S <del>E</del> Y <del>E</del> K <del>E</del> I <del>T</del> S <del>L</del> Q <del>N</del> S <del>F</del> Q <del>L</del> R <del>C</del> Q <del>Q</del> E <del>D</del> Q |
| HsTRAF3IP3 | 436 | ----- <u>E</u> G <del>T</del>   |
| HsSLMAP    | 631 | <del>Q</del> R <del>E</del> A <del>T</del> R <del>L</del> Q <del>G</del> E <del>L</del> E <del>R</del> L <del>R</del> K <del>E</del> N <del>A</del> L <del>E</del> T <del>E</del> C <del>H</del> S <del>L</del> R <del>E</del> N <del>V</del> L <del>S</del> S <del>E</del> L <del>Q</del> R <del>Q</del> E <del>K</del> E <del>L</del> H <del>N</del> S <del>Q</del> K <del>Q</del> S <del>L</del> E <del>L</del> T <del>S</del> D <del>L</del> S <del>I</del> L <del>Q</del> M <del>S</del> R <del>K</del> E <del>L</del> E <del>N</del> Q <del>V</del> G <del>S</del> L <del>K</del> E                               |
| HsTRAF3IP3 | 439 | G <del>K</del> E <del>K</del> D <del>W</del> D <del>L</del> R <del>Q</del> L <del>Q</del> K <del>T</del> L <del>Q</del> L <del>Q</del> A <del>K</del> E <del>K</del> E <del>C</del> R <del>E</del> L <del>S</del> E <del>L</del> D <del>N</del> L <del>S</del> D <del>E</del> Y <del>L</del> S <del>C</del> L <del>R</del> L <del>Q</del> H <del>C</del> R-----   |
| HsSLMAP    | 711 | <del>Q</del> H <del>L</del> R <del>D</del> S <del>A</del> D <del>L</del> K <del>T</del> L <del>L</del> S <del>K</del> A <del>E</del> N <del>Q</del> A <del>K</del> D <del>V</del> Q <del>E</del> Y <del>E</del> K <del>T</del> Q <del>T</del> V <del>S</del> E <del>L</del> K <del>L</del> K <del>F</del> E <del>M</del> T <del>E</del> Q <del>E</del> K <del>S</del> I <del>T</del> <u>D</u> E <del>L</del> K <del>Q</del> C <del>K</del> M <del>L</del> K <del>L</del> E <del>K</del> G <del>N</del> N <del>K</del> F <del>W</del> P <del>W</del> <u>P</u> M <del>L</del>   |
| HsTRAF3IP3 | 490 | ----- <u>E</u> L <del>N</del> Q <del>S</del> Q <del>L</del> I <del>P</del> P <del>R</del> Q <del>C</del> G-----R <del>W</del> L <del>P</del> V <del>L</del>   |
| HsSLMAP    | 791 | <u>A</u> A <del>L</del> A <del>V</del> T <del>A</del> I <del>V</del> L <del>V</del> P <del>L</del> A <del>R</del> A <del>S</del> P  |
| HsTRAF3IP3 | 512 | M <del>V</del> V <del>I</del> A <del>A</del> A <del>L</del> A <del>V</del> F <del>L</del> A <del>N</del> K <del>D</del> N <del>L</del> M <del>I</del> -   |

B



**A) Sequence alignment between human SLMAP and human TRAF3IP3.** Red lettering indicates potential leucine zippers and blue lettering represents potential hydrophobic membrane anchor (Wiggle 1997), in pink is an FHA domain (Conserved domain database, CDD; 4e-12); italics indicates a chromosome segregation ATPase region (5e-13). On TRAF3IP3, the underlined region corresponds to the CDD COG4372, myosin-like (5e-06). **B) Phylogenetic tree of the SLMAP and TRAF3IP3 families.** Percentage identity between the aligned regions of selected pairs is indicated on the right (Matrix BLOSUM62).

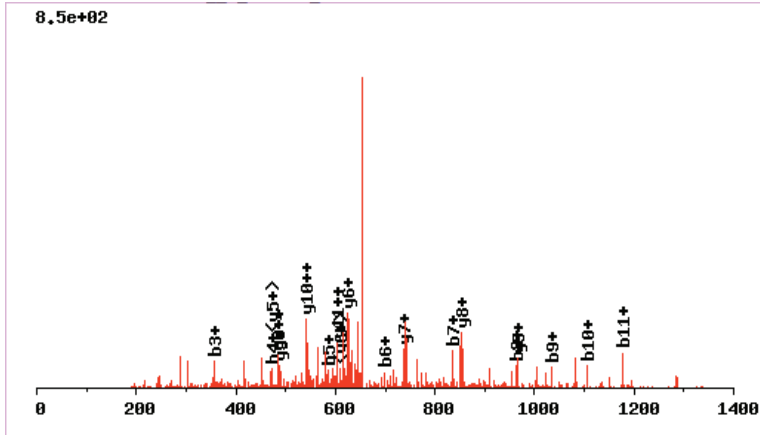


### Confirmation of the association between flag-tagged proteins and endogenous striatin.

(A) Immunoprecipitation (IP) on  $\alpha$ -flag M2 agarose beads was performed on lysate from HEK293 cells stably expressing the indicated flag-tagged constructs. To ensure specificity of the interactions, IPs were also performed from lysate of flag alone and flag-alpha4 stable cell lines. The immune complexes were resolved by SDS-PAGE, followed by transfer onto nitrocellulose. Co-precipitation of endogenous striatin was detected by immunoblotting ( $\alpha$ -STRN; position indicated by arrow). Upon prolonged exposure, striatin was also detected in the CTTNBP2 sample. (B) Recombinant protein expression detected in whole cell lysate from HEK293 cells stably expressing the indicated flag-tagged proteins. Upon prolonged exposure, TRAF3IP3, CTTNBP2NL, CTTNBP2, PP2AA $\alpha$  are visible. The antibody heavy and light chains are identified by asterisks (\*).

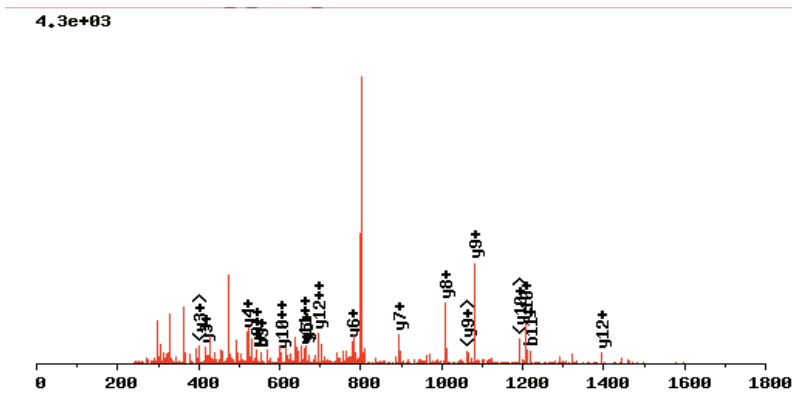
Annotated spectra for proteins identified on the basis of a single peptide.

| bait            | hit   | npeps | nspecs | peptide     |
|-----------------|-------|-------|--------|-------------|
| F-PP2A $\alpha$ | SLMAP | 1     | 2      | DEILLHQAALK |



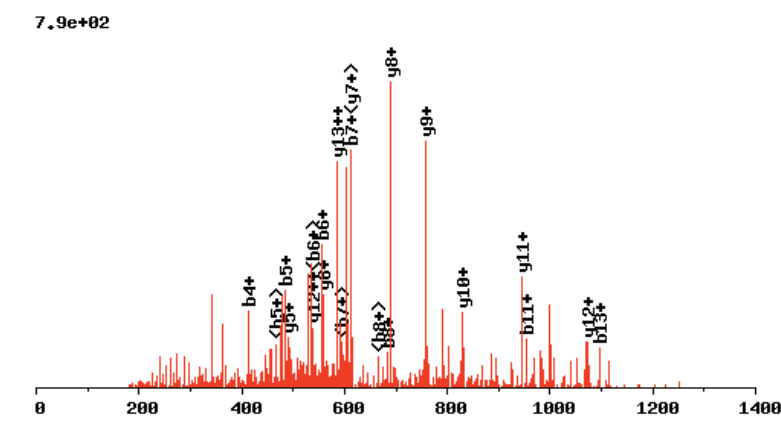
| b <sup>+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> |
|----------------|----|----|----|----------------|-----------------|
| 116.0348       | 1  | D  | 12 |                |                 |
| 245.0774       | 2  | E  | 11 | 1206.7210      | 603.8644        |
| 358.1614       | 3  | I  | 10 | 1077.6784      | 539.3431        |
| 471.2455       | 4  | L  | 9  | 964.5944       | 482.8011        |
| 584.3296       | 5  | L  | 8  | 851.5103       | 426.2591        |
| 697.4136       | 6  | L  | 7  | 738.4262       | 369.7170        |
| 834.4725       | 7  | H  | 6  | 625.3422       | 313.1750        |
| 962.5311       | 8  | Q  | 5  | 488.2833       | 244.6455        |
| 1033.5682      | 9  | A  | 4  | 360.2247       | 180.6163        |
| 1104.6053      | 10 | A  | 3  | 289.1876       | 145.0977        |
| 1175.6424      | 11 | A  | 2  | 218.1505       | 109.5791        |
|                | 12 | K  | 1  | 147.1134       | 74.0606         |

| bait            | hit   | npeps | nspecs | peptide      |
|-----------------|-------|-------|--------|--------------|
| F-PP2A $\alpha$ | SLMAP | 1     | 1      | IEALQADNDFTR |



| b <sup>+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> |
|----------------|----|----|----|----------------|-----------------|
| 114.0919       | 1  | I  | 14 |                |                 |
| 243.1345       | 2  | E  | 13 | 1522.6774      | 761.8426        |
| 314.1716       | 3  | A  | 12 | 1393.6348      | 697.3213        |
| 427.2557       | 4  | L  | 11 | 1322.5977      | 661.8028        |
| 555.3142       | 5  | Q  | 10 | 1209.5136      | 605.2607        |
| 626.3513       | 6  | A  | 9  | 1081.4550      | 541.2314        |
| 741.3783       | 7  | D  | 8  | 1010.4179      | 505.7129        |
| 855.4212       | 8  | N  | 7  | 895.3910       | 448.1994        |
| 970.4482       | 9  | D  | 6  | 781.3481       | 391.1779        |
| 1117.5166      | 10 | F  | 5  | 666.3211       | 333.6645        |
| 1218.5643      | 11 | T  | 4  | 519.2527       | 260.1303        |
| 1332.6072      | 12 | N  | 3  | 418.2050       | 209.6064        |
| 1461.6498      | 13 | E  | 2  | 304.1621       | 152.5850        |
|                | 14 | R  | 1  | 175.1195       | 88.0637         |

| bait            | hit     | npeps | nspecs | peptide       |
|-----------------|---------|-------|--------|---------------|
| F-PP2A $\alpha$ | CTTNBP2 | 1     | 1      | APEDAAGAAEAAK |

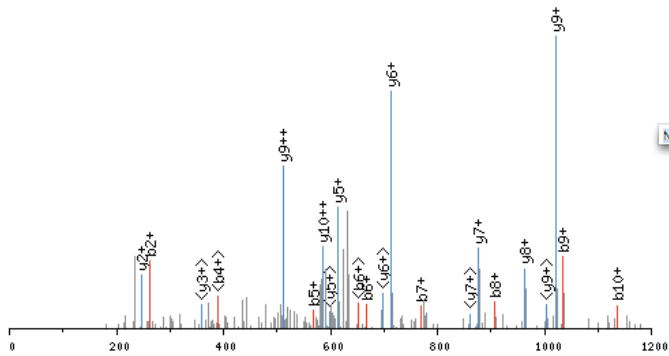


| b <sup>+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> |
|----------------|----|----|----|----------------|-----------------|
| 72.0449        | 1  | A  | 14 |                |                 |
| 169.0977       | 2  | P  | 13 | 1171.5595      | 586.2837        |
| 298.1403       | 3  | E  | 12 | 1074.5067      | 537.7573        |
| 413.1672       | 4  | D  | 11 | 945.4641       | 473.2360        |
| 484.2044       | 5  | A  | 10 | 830.4372       | 415.7225        |
| 555.2415       | 6  | A  | 9  | 759.4001       | 380.2040        |
| 612.2629       | 7  | G  | 8  | 688.3630       | 344.6854        |
| 683.3000       | 8  | A  | 7  | 631.3415       | 316.1747        |
| 754.3372       | 9  | A  | 6  | 560.3044       | 280.6561        |
| 825.3743       | 10 | A  | 5  | 489.2673       | 245.1376        |
| 954.4169       | 11 | E  | 4  | 418.2302       | 209.6190        |
| 1025.4540      | 12 | A  | 3  | 289.1876       | 145.0977        |
| 1096.4911      | 13 | A  | 2  | 218.1505       | 109.5791        |
|                | 14 | K  | 1  | 147.1134       | 74.0606         |

Annotated spectra for proteins identified on the basis of a single peptide.

| bait        | hit    | npeps | nspecs | peptide     |
|-------------|--------|-------|--------|-------------|
| T-striatin4 | dynein | 1     | 6      | NFGSYVTHETK |

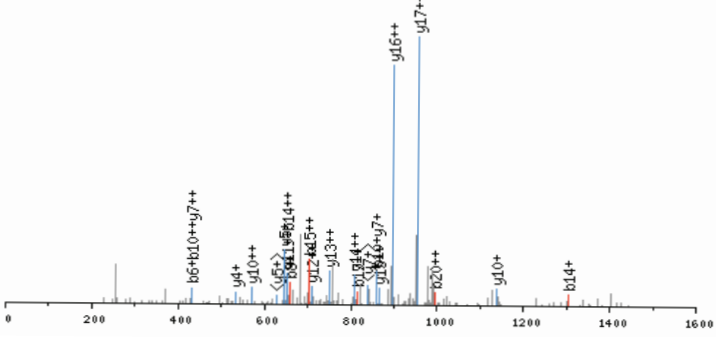
scan 13237: 1.3e+06



| b <sup>+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> |
|----------------|----|----|----|----------------|-----------------|
| 115.1118       | 1  | N  | 11 |                |                 |
| 262.2883       | 2  | F  | 10 | 1169.2792      | 585.1436        |
| 319.3403       | 3  | G  | 9  | 1022.1027      | 511.5553        |
| 406.4185       | 4  | S  | 8  | 965.0507       | 483.0293        |
| 569.5944       | 5  | Y  | 7  | 877.9725       | 439.4902        |
| 668.7270       | 6  | V  | 6  | 714.7966       | 357.9023        |
| 769.8321       | 7  | T  | 5  | 615.6640       | 308.3360        |
| 906.9731       | 8  | H  | 4  | 514.5589       | 257.7834        |
| 1036.0886      | 9  | E  | 3  | 377.4179       | 189.2129        |
| 1137.1937      | 10 | T  | 2  | 248.3024       | 124.6552        |
|                | 11 | K  | 1  | 147.1973       | 74.1026         |

| T-striatin4 | PP2A Aβ | 1 | 2 | AAGGDGDDSLYPIAVLIDELR | 2 |
|-------------|---------|---|---|-----------------------|---|
|-------------|---------|---|---|-----------------------|---|

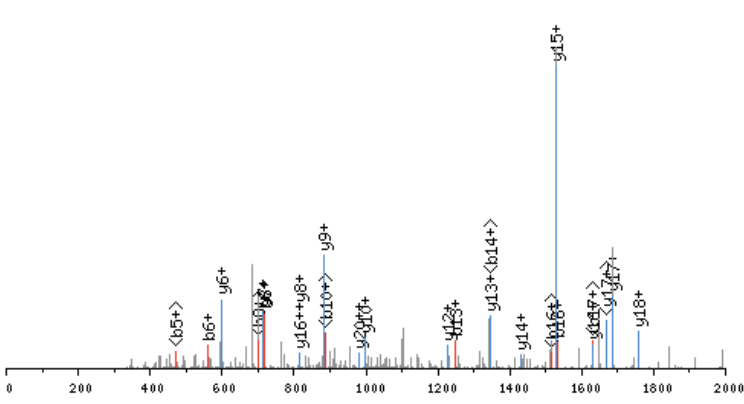
scan 23227: 1.5e+06



| b <sup>+</sup> | b <sup>2+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> | y <sup>3+</sup> |
|----------------|-----------------|----|----|----|----------------|-----------------|-----------------|
| 72.0867        | 36.5473         | 1  | A  | 21 |                |                 |                 |
| 143.1655       | 72.0867         | 2  | A  | 20 | 2090.2945      | 1045.6512       | 697.4368        |
| 200.2175       | 100.6127        | 3  | G  | 19 | 2019.2157      | 1010.1118       | 673.7439        |
| 257.2694       | 129.1387        | 4  | G  | 18 | 1962.1638      | 981.5859        | 654.7266        |
| 372.3580       | 186.6830        | 5  | D  | 17 | 1905.1119      | 953.0599        | 635.7093        |
| 429.4099       | 215.2089        | 6  | G  | 16 | 1790.0233      | 895.5156        | 597.3464        |
| 544.4985       | 272.7532        | 7  | D  | 15 | 1732.9714      | 866.9897        | 578.3291        |
| 659.5871       | 330.2975        | 8  | D  | 14 | 1617.8828      | 809.4454        | 539.9662        |
| 746.6653       | 373.8366        | 9  | S  | 13 | 1502.7942      | 751.9011        | 501.6034        |
| 859.8247       | 430.4163        | 10 | L  | 12 | 1415.7160      | 708.3620        | 472.5773        |
| 1023.0007      | 512.0043        | 11 | Y  | 11 | 1302.5565      | 651.7822        | 434.8575        |
| 1120.1174      | 560.5627        | 12 | P  | 10 | 1139.3806      | 570.1943        | 380.4655        |
| 1233.2768      | 617.1424        | 13 | I  | 9  | 1042.2639      | 521.6359        | 348.0933        |
| 1304.3556      | 652.6818        | 14 | A  | 8  | 929.1045       | 465.0562        | 310.3734        |
| 1403.4882      | 702.2481        | 15 | V  | 7  | 858.0257       | 429.5168        | 286.6805        |
| 1516.6476      | 758.8278        | 16 | L  | 6  | 758.8931       | 379.9505        | 253.6363        |
| 1629.8071      | 815.4075        | 17 | I  | 5  | 645.7337       | 323.3708        | 215.9165        |
| 1744.8957      | 872.9518        | 18 | D  | 4  | 532.5742       | 266.7911        | 178.1967        |
| 1874.0111      | 937.5095        | 19 | E  | 3  | 417.4856       | 209.2468        | 139.8338        |
| 1987.1706      | 994.0893        | 20 | L  | 2  | 288.3701       | 144.6890        | 96.7953         |
|                |                 | 21 | R  | 1  | 175.2107       | 88.1093         | 59.0755         |

| T-PP2Aα | liprin A3 | 1 | 1 | DSSSLAGTPSDETLATDPLGLAK |
|---------|-----------|---|---|-------------------------|
|---------|-----------|---|---|-------------------------|

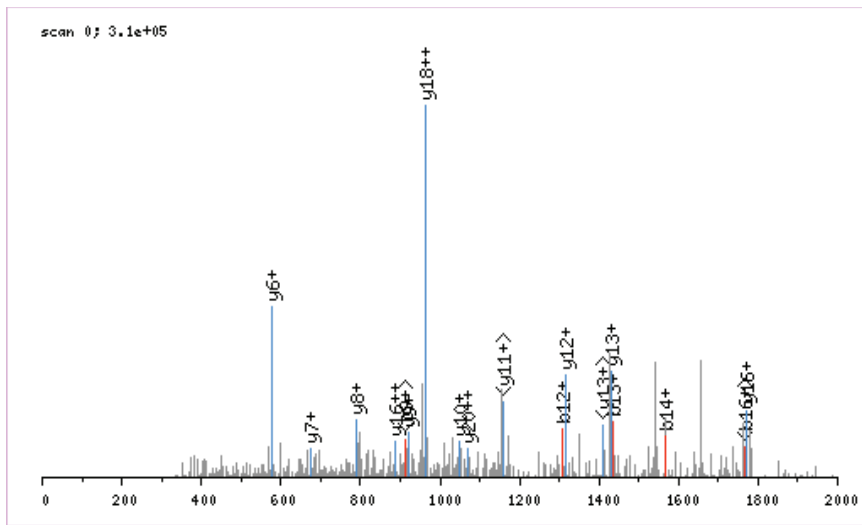
scan 0: 3.0e+05



| b <sup>+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> |
|----------------|----|----|----|----------------|-----------------|
| 116.0965       | 1  | D  | 23 |                |                 |
| 203.1747       | 2  | S  | 22 | 2132.3294      | 1066.6687       |
| 290.2529       | 3  | S  | 21 | 2045.2512      | 1023.1296       |
| 377.3311       | 4  | S  | 20 | 1958.1730      | 979.5905        |
| 490.4906       | 5  | L  | 19 | 1871.0948      | 936.0514        |
| 561.5694       | 6  | A  | 18 | 1757.9353      | 879.4716        |
| 618.6213       | 7  | G  | 17 | 1686.8565      | 843.9322        |
| 719.7264       | 8  | T  | 16 | 1629.8046      | 815.4063        |
| 816.8431       | 9  | P  | 15 | 1528.6995      | 764.8537        |
| 903.9213       | 10 | S  | 14 | 1431.5829      | 716.2954        |
| 1019.0099      | 11 | D  | 13 | 1344.5047      | 672.7563        |
| 1148.1253      | 12 | E  | 12 | 1229.4161      | 615.2120        |
| 1249.2304      | 13 | T  | 11 | 1100.3006      | 550.6543        |
| 1362.3899      | 14 | L  | 10 | 999.1955       | 500.1017        |
| 1433.4687      | 15 | A  | 9  | 886.0361       | 443.5220        |
| 1534.5737      | 16 | T  | 8  | 814.9573       | 407.9826        |
| 1649.6623      | 17 | D  | 7  | 713.8522       | 357.4301        |
| 1746.7790      | 18 | P  | 6  | 598.7636       | 299.8858        |
| 1859.9385      | 19 | L  | 5  | 501.6469       | 251.3274        |
| 1916.9904      | 20 | G  | 4  | 388.4875       | 194.7477        |
| 2030.1498      | 21 | L  | 3  | 331.4355       | 166.2217        |
| 2101.2286      | 22 | A  | 2  | 218.2761       | 109.6420        |
|                | 23 | K  | 1  | 147.1973       | 74.1026         |

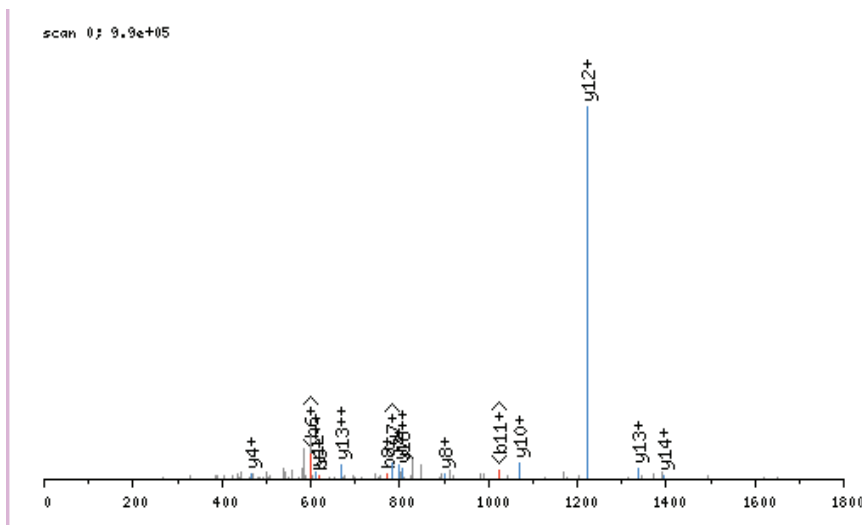
Annotated spectra for proteins identified on the basis of a single peptide.

| bait            | hit       | npeps | nspecs | peptide                |
|-----------------|-----------|-------|--------|------------------------|
| T-PP2A $\alpha$ | liprin A1 | 1     | 1      | TLTDGVLDINHEQENTPSTSGK |



| b <sup>+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> |
|----------------|----|----|----|----------------|-----------------|
| 102.1130       | 1  | T  | 22 |                |                 |
| 215.2725       | 2  | L  | 21 | 2256.3880      | 1128.6980       |
| 316.3775       | 3  | T  | 20 | 2143.2285      | 1072.1182       |
| 431.4661       | 4  | D  | 19 | 2042.1235      | 1021.5657       |
| 488.5181       | 5  | G  | 18 | 1927.0349      | 964.0214        |
| 587.6506       | 6  | V  | 17 | 1869.9829      | 935.4954        |
| 700.8101       | 7  | L  | 16 | 1770.8504      | 885.9292        |
| 815.8987       | 8  | D  | 15 | 1657.6909      | 829.3494        |
| 929.0581       | 9  | I  | 14 | 1542.6023      | 771.8051        |
| 1043.1619      | 10 | N  | 13 | 1429.4429      | 715.2254        |
| 1180.3030      | 11 | H  | 12 | 1315.3391      | 658.1735        |
| 1309.4185      | 12 | E  | 11 | 1178.1980      | 589.6030        |
| 1437.5492      | 13 | Q  | 10 | 1049.0825      | 525.0452        |
| 1566.6647      | 14 | E  | 9  | 920.9518       | 460.9799        |
| 1680.7685      | 15 | N  | 8  | 791.8363       | 396.4221        |
| 1781.8736      | 16 | T  | 7  | 677.7325       | 339.3702        |
| 1878.9903      | 17 | P  | 6  | 576.6274       | 288.8177        |
| 1966.0685      | 18 | S  | 5  | 479.5107       | 240.2593        |
| 2067.1736      | 19 | T  | 4  | 392.4325       | 196.7202        |
| 2154.2518      | 20 | S  | 3  | 291.3274       | 146.1677        |
| 2211.3037      | 21 | G  | 2  | 204.2492       | 102.6286        |
|                | 22 | K  | 1  | 147.1973       | 74.1026         |

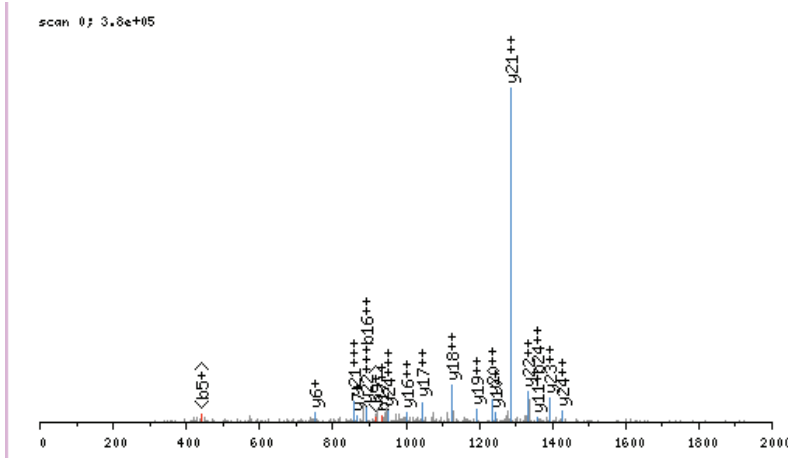
| bait            | hit       | npeps | nspecs | peptide            |
|-----------------|-----------|-------|--------|--------------------|
| T-PP2A $\alpha$ | CTTNBP2NL | 1     | 1      | MTNTGLPGPATPAYSYAK |



| b <sup>+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> |
|----------------|----|----|----|----------------|-----------------|
| 132.2005       | 1  | M  | 18 |                |                 |
| 233.3056       | 2  | T  | 17 | 1709.8962      | 855.4521        |
| 347.4094       | 3  | N  | 16 | 1608.7911      | 804.8995        |
| 448.5145       | 4  | T  | 15 | 1494.6873      | 747.8476        |
| 505.5664       | 5  | G  | 14 | 1393.5822      | 697.2951        |
| 618.7259       | 6  | L  | 13 | 1336.5303      | 668.7691        |
| 715.8425       | 7  | P  | 12 | 1223.3709      | 612.1894        |
| 772.8945       | 8  | G  | 11 | 1126.2542      | 563.6311        |
| 870.0111       | 9  | P  | 10 | 1069.2023      | 535.1051        |
| 941.0899       | 10 | A  | 9  | 972.0856       | 486.5468        |
| 1042.1950      | 11 | T  | 8  | 901.0068       | 451.0074        |
| 1139.3117      | 12 | P  | 7  | 799.9017       | 400.4548        |
| 1210.3905      | 13 | A  | 6  | 702.7850       | 351.8965        |
| 1373.5665      | 14 | Y  | 5  | 631.7062       | 316.3571        |
| 1460.6447      | 15 | S  | 4  | 468.5303       | 234.7691        |
| 1623.8206      | 16 | Y  | 3  | 381.4521       | 191.2300        |
| 1694.8994      | 17 | A  | 2  | 218.2761       | 109.6420        |
|                | 18 | K  | 1  | 147.1973       | 74.1026         |

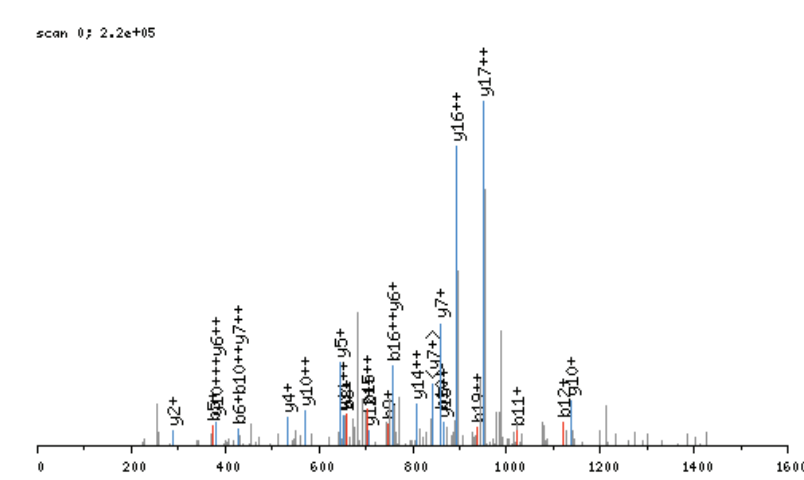
Annotated spectra for proteins identified on the basis of a single peptide.

| bait            | hit     | npeps | nspecs | peptide                    |
|-----------------|---------|-------|--------|----------------------------|
| T-PP2Ac $\beta$ | CTTNBP2 | 1     | 1      | VAANTPSMYSQELFQLSQYLQEALHR |



| b <sup>+</sup> | b <sup>2+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> | y <sup>3+</sup> |
|----------------|-----------------|----|----|----|----------------|-----------------|-----------------|
| 100.1405       | 50.5742         | 1  | V  | 26 |                |                 |                 |
| 171.2193       | 86.1136         | 2  | A  | 25 | 2927.2610      | 1464.1345       | 976.4256        |
| 242.2981       | 121.6530        | 3  | A  | 24 | 2856.1822      | 1428.5951       | 952.7327        |
| 356.4019       | 178.7049        | 4  | N  | 23 | 2785.1034      | 1393.0557       | 929.0398        |
| 457.5070       | 229.2575        | 5  | T  | 22 | 2670.9996      | 1336.0038       | 891.0052        |
| 554.6237       | 277.8158        | 6  | P  | 21 | 2569.8945      | 1285.4512       | 857.3035        |
| 641.7019       | 321.3549        | 7  | S  | 20 | 2472.7778      | 1236.8929       | 824.9312        |
| 772.8945       | 386.9512        | 8  | M  | 19 | 2385.6996      | 1193.3538       | 795.9052        |
| 936.0704       | 468.5392        | 9  | Y  | 18 | 2254.5071      | 1127.7575       | 752.1743        |
| 1023.1486      | 512.0783        | 10 | S  | 17 | 2091.3311      | 1046.1695       | 697.7823        |
| 1151.2793      | 576.1436        | 11 | Q  | 16 | 2004.2529      | 1002.6304       | 668.7563        |
| 1280.3948      | 640.7014        | 12 | E  | 15 | 1876.1222      | 938.5651        | 626.0460        |
| 1393.5543      | 697.2811        | 13 | L  | 14 | 1747.0067      | 874.0073        | 583.0075        |
| 1540.7308      | 770.8694        | 14 | F  | 13 | 1633.8473      | 817.4276        | 545.2877        |
| 1668.8615      | 834.9347        | 15 | Q  | 12 | 1486.6707      | 743.8393        | 496.2289        |
| 1782.0210      | 891.5145        | 16 | L  | 11 | 1358.5400      | 679.7740        | 453.5186        |
| 1869.0992      | 935.0536        | 17 | S  | 10 | 1245.3805      | 623.1942        | 415.7988        |
| 1997.2299      | 999.1189        | 18 | Q  | 9  | 1158.3023      | 579.6551        | 386.7727        |
| 2160.4059      | 1080.7069       | 19 | Y  | 8  | 1030.1716      | 515.5898        | 344.0625        |
| 2273.5653      | 1137.2866       | 20 | L  | 7  | 866.9957       | 434.0018        | 289.6705        |
| 2401.6960      | 1201.3520       | 21 | Q  | 6  | 753.8362       | 377.4221        | 251.9507        |
| 2530.8115      | 1265.9097       | 22 | E  | 5  | 625.7055       | 313.3567        | 209.2405        |
| 2601.8903      | 1301.4491       | 23 | A  | 4  | 496.5900       | 248.7990        | 166.2020        |
| 2715.0497      | 1358.0288       | 24 | L  | 3  | 425.5112       | 213.2596        | 142.5090        |
| 2852.1908      | 1426.5994       | 25 | H  | 2  | 312.3518       | 156.6799        | 104.7892        |
|                |                 | 26 | R  | 1  | 175.2107       | 88.1093         | 59.0755         |

| T-PP2AB' $\alpha$ | PP2A A $\beta$ | 1 | 3 | AAGDGDSDLYPIAVLIDELR |
|-------------------|----------------|---|---|----------------------|
|-------------------|----------------|---|---|----------------------|



| b <sup>+</sup> | b <sup>2+</sup> | #  | AA | #  | y <sup>+</sup> | y <sup>2+</sup> | y <sup>3+</sup> |
|----------------|-----------------|----|----|----|----------------|-----------------|-----------------|
| 72.0867        | 36.5473         | 1  | A  | 21 |                |                 |                 |
| 143.1655       | 72.0867         | 2  | A  | 20 | 2090.2945      | 1045.6512       | 697.4368        |
| 200.2175       | 100.6127        | 3  | G  | 19 | 2019.2157      | 1010.1118       | 673.7439        |
| 257.2694       | 129.1387        | 4  | G  | 18 | 1962.1638      | 981.5859        | 654.7266        |
| 372.3580       | 186.6830        | 5  | D  | 17 | 1905.1119      | 953.0599        | 635.7093        |
| 429.4099       | 215.2089        | 6  | G  | 16 | 1790.0233      | 895.5156        | 597.3464        |
| 544.4985       | 272.7532        | 7  | D  | 15 | 1732.9714      | 866.9897        | 578.3291        |
| 659.5871       | 330.2975        | 8  | D  | 14 | 1617.8828      | 809.4454        | 539.9662        |
| 746.6653       | 373.8366        | 9  | S  | 13 | 1502.7942      | 751.9011        | 501.6034        |
| 859.8247       | 430.4163        | 10 | L  | 12 | 1415.7160      | 708.3620        | 472.5773        |
| 1023.0007      | 512.0043        | 11 | Y  | 11 | 1302.5565      | 651.7822        | 434.8575        |
| 1120.1174      | 560.5627        | 12 | P  | 10 | 1139.3806      | 570.1943        | 380.4655        |
| 1233.2768      | 617.1424        | 13 | I  | 9  | 1042.2639      | 521.6359        | 348.0933        |
| 1304.3556      | 652.6818        | 14 | A  | 8  | 929.1045       | 465.0562        | 310.3734        |
| 1403.4882      | 702.2481        | 15 | V  | 7  | 858.0257       | 429.5168        | 286.6805        |
| 1516.6476      | 758.8278        | 16 | L  | 6  | 758.8931       | 379.9505        | 253.6363        |
| 1629.8071      | 815.4075        | 17 | I  | 5  | 645.7337       | 323.3708        | 215.9165        |
| 1744.8957      | 872.9518        | 18 | D  | 4  | 532.5742       | 266.7911        | 178.1967        |
| 1874.0111      | 937.5095        | 19 | E  | 3  | 417.4856       | 209.2468        | 139.8338        |
| 1987.1706      | 994.0893        | 20 | L  | 2  | 288.3701       | 144.6890        | 96.7953         |
|                |                 | 21 | R  | 1  | 175.2107       | 88.1093         | 59.0755         |