Supporting Information

Ivarsson et al. 10.1073/pnas.1312296111

SI Methods

Protein Purifications. Overnight cultures of GST and GST-PDZ (protein-95/disks large/zonula occludens-1) fusion proteins were used to inoculate 50 mL autoinducing MagicMedia (Invitrogen) supplemented with 25 μ g/mL kanamycin and were grown for 24 h at 37 °C with shaking. The bacteria were pelleted (8,000 rpm, 10 min), stored overnight at 20 °C, and purified using glutathione affinity resin (GE Healthcare). The coding regions were as described in Tonikian et al. (1).

Phage Selections. In brief, proteins were coated in 96-well Maxisorp microtiter plates (NUNC) overnight (15 µg/mL protein in 100 µL PBS per well). For the first two rounds of selection, three wells were used for each library, whereas a single well was used for the following rounds. Parallel plates were coated with GST alone to remove nonspecific binders by preselection. The next day, wells were blocked with BSA for 2 h with blocking buffer (PBS, 0.2% BSA). Phage pools representing the naïve peptide library were diluted 10-fold in PBS, precipitated with polyethylene glycol-NaCl [4% PEG-800 (wt/vol) and 0.5 M NaCl] and resuspended to a final concentration of 10^{12} cfu/mL in PBT. In the first selection round, 100 µL of the phage pool representing the naïve peptide library was added to each well of the preselection plate, incubated for 1 h, transferred to the target plate, and incubated for an additional 2 h. The plate was washed four times with cold wash buffer (PBS, 0.5% Tween-20) and bound phage was eluted by direct infection into bacteria by the addition of 100 μ L of log-phase Escherichia coli SS230 (A_{600} = 0.8) in 2YT to each well and incubation for 30 min at 37 °C with shaking. M13K07 helper phage (New England Biolabs) was added to a final concentration of 10^{10} phage per milliliter to enable phage production, and the cultures were incubated for 45 min at 37 °C with shaking. The cultures were transferred to 20 mL of 2YT supplemented with kanamycin (25 µg/mL), carbenicillin (100 µg/mL), and isfopropyl-β-D-thiogalactopyranoside (IPTG; 0.4 mM), and shaken overnight at 37 °C. The bacteria was pelleted by centrifugation (10 min, $17,090 \times g$), the supernatant transferred to a new tube, and phage particles were precipitated by addition of one-fifth volume of polyethylene glycol NaCl, incubated at 4 °C for 5 min, and centrifuged at $28,880 \times g$ for 20 min. The supernatant was removed and the phage pellet was resuspended in 2 mL of PBT and then used for the next round of selection. The selections were carried out for five rounds and the progress followed by analyzing aliquots of phage supernatants in a phage ELISA (2).

The phage pools of rounds three to five and the naïve phage libraries were barcoded for Illumina sequencing as outlined by McLaughlin and Sidhu (3). Briefly, undiluted amplified phage pools (5 μ L) were used as templates for 24 cycles of 50 μ L PCR reactions using unique combinations of barcoded primers for each reaction (0.5 μ M each; for sequences of amplicon and barcodes see ref. 3) and using Phusion High Fidelity DNA polymerase (New England Biolabs) using maximum polymerase and primer concentrations. The PCR products were confirmed by gel electrophoresis (2% agarose gel) of 1 μ L of PCR products.

The amount of the DNA amplicons was normalized by PEG/ NaCl precipitation in a 96-well plate using a limiting amount of Ampure XP magnetic beads (Beckman Coulter). The magnetic beads were diluted 16-fold in PEG/NaCl and 100 μ L of this solution was mixed by pipetting with 40 μ L PCR product, incubated at room temperature for 20 min and then on a magnetic plate for 5 min to collect the beads. The supernatant was removed and the beads were washed twice with 70% EtOH, dried for 20 min at room temperature, and eluted by addition of 20 µL TE buffer (10 mM Tris, pH 8.0, and 0.1 mM EDTA). The normalized PCR amplicons were pooled (15 µL per reaction) and concentrated using two columns of a QIAquick PCR purification kit. The pooled amplicons were run on 2% agarose gel (80 V for 30 min), excised, and purified on a column of a QIAquick gel extraction kit using a modified protocol that uses extended incubation at room temperature instead of heating in Buffer QG (4). The bound DNA was eluted with 30 µL TE buffer. The concentration of the DNA was estimated picogreen dye as previously described. The PCR amplicons (~3 mg) were sent to Cofactor Genomics (Saint Louis, MO) for deep sequencing (Illumina Miseq; paired end 150 base reads, 20% PhiX). The obtained sequencing reads were filtered by discarding reads with an average PHRED quality score <35 (99.95% sequencing accuracy) or having a minimal nucleotide position score lower than 26.

Analysis of the Naïve Libraries. The quality of the proteomic peptide-phage display (ProP-PD) libraries were assessed from the deep-sequencing data by estimating the percent of starting templates, point mutations, and frame-shift mutations. The frequency of point mutations was estimated by assigning for each mutated sequence the most similar peptide sequence in the library design (denoted as parental sequence) and counting the amount of mutations as differences between the parental and mutated sequences on the DNA level. Frame-shifts were detected by aligning the DNA sequence of each mutated sequence to all sequences in the library design on DNA level using the Smith Waterman implementation provided by JAligner (parameters: identity matrix, gap opening penalty -5, gap extension -1).

Processing of Data from the Selections. The sequencing data contains selected wild-type parental peptides as well as mutant versions thereof (Fig. S6). To retrieve relevant peptides, we filtered the data for peptides occurring in the original library designs. To remove the noise we plotted histograms of the peptide frequencies (after matching to the actual library design) and manually assigned cut-off values after the prominent peak representing spurious binders after visual inspection. To focus on relevant peptides from the human ProP-PD, we subdivided the library entries into three groups based on the data available in April 2013 into a "high interest" set of true C termini comprising sequences that are in addition to either RefSeq from 2010 or Ensembl62 [also contained in one of either RefSeq or Uniprot in their 2013 versions (excluding sequences annotated as fragmentary)], a "proteolytic set" with an experimental support for a cleavage event listed in the TopFind database, and a "low interest" set with Ensembl62 entries not matching the two other sets. We filtered for peptides found in the high interest set (Table S1) and list identified targets from the low and medium interest sets in Table S3. To obtain viral targets of interest from the deep-sequencing data (Table S2) we assigned cut-off values to remove nonspecific peptides and filtered the data by removing three hits that did not originate from viruses targeting higher eukarvotes.

Comparison with Conventional Phage Display. Position weight matrices (PWMs) were generated using the MUSI software (5) with standard settings and without realignment of the C termini. For comparison between human targets predicted using conventional

phage display, a set of 7mer and of 10mer PWMs were calculated from the Tonikian et al. (1) data using MUSI. To compare the hydrophobicity of the retrieved ligands we calculated for the heptamer PWMs (from ProP-PD and randomized phage display, respectively), an accumulated hydrophobicity value as the sum of each amino acid hydrophobicity weight multiplied by each amino acid normalized frequency in the PWM matrix over each position (6) (Fig. S2). To compare if ProP-PD ligands would have been predicted by conventional methods, we used the 10mer PWMs based on Tonikian's data to scan a human library equivalent to the high interest set of our design using MOTIPs (7) and ranked the target peptides from 1 and up. Sequences with identical scores were ranked equally.

Peptide Synthesis. Peptides (Table 1) were synthesized using a Multipep synthesizer (Intavis AG Bioanalytical Instruments) on Wang resins (p-benzyloxybenzyl alcohol resin; AnaSpec) using 9-Fluorenyl methoxycarbonyl chemistry, with longer incubation or multiple cycles to conjugate the first C-terminal amino acid in the presence of 4-Dimethylaminopyridine (Sigma Aldrich). N-hydroxysuccinimide fluorescein (Pierce) was used to tag the N termini of the peptides with a fluorescent label. A 6-aminohexanoic acid moiety (AnaSpec) was used as a linker to separate the peptide from the fluorescein label to mitigate potential steric hinderance of protein-peptide interactions.

Fluorescence Polarization Assays. Binding affinities of PDZ domains for fluorescein-labeled peptides were determined using a 2103 Multilabel Reader (PerkinElmer). Briefly, fluorescein-labeled peptides were diluted to a final concentration of 2-5 nM and incubated with increasing concentrations of hexaHis-tagged-PDZ domains (0-100 µM; 12 datapoints), using duplicate protein titrations in 384-well Corning plates. After mixing on a shaking platform for 2 min at 500 rpm and centrifuging for 2 min at $1,000 \times g$, the fluorescence polarization signals from the wells were measured. The data were analyzed using the Graphpad Prism software and $K_{\rm D}$ values were determined by curve fitting the data to a single bindingsite model.

Cloning. Full-length Scribble, mitogen-activated kinase 12 (MK12), guanylate cyclase soluble subunit α -2 (GCAY2) constructs were generated by Gateway cloning (Invitrogen) from entry clones in pDONR223 and shuttled into pcDNA5 FRT/TO with either an N terminus GFP or 3xFlag tag. CTNB1 was PCR-amplified and cloned into pCMV2B (Stratagene) that contains a Flag-tag sequence at the N terminus. PKP4 was PCR-amplified and cloned into the Creator vector 3xFlag N terminus expression vector using the Creator recombination system (8).

Cell Line. HEK293T cells were maintained in DMEM (ATCC) supplemented with 10% FBS and 1% pen/strep/glutamine, and the appropriate selection antibiotics when required.

Coimmunoprecipitations. HEK293T cells were cotransfected with GFP-Scribble and Flag-tagged constructs (described above). Cells were lysed 48 h after transfections with radioimmune precipitation assay buffer [50 mM Tris HCl, pH 7.4, 1% Nonidet P-40, 150 mM NaCl, 1 mM EDTA, 10 mM Na₃VO₄, 10 mM sodium pyrophosphate, 25 mM NaF, 1x protease inhibitor mixture (Sigma)] for 30 min at 4 °C and and coimmunoprecipited with a GFP specific antibody (Abcam), as described previously (9). The resulting immunocomplexes and whole-cell lysates were analyzed by Western blot using the antibodies indicated in Fig. 4B. Protein samples were separated on a NuPage Bis-Tris 10% SDS/PAGE gel (Invitrogen) and transferred to nitrocellulose or PVDF membranes. Transferred samples were immunoblotted with primary anti-Flag antibodies, followed by incubation with horseradish peroxidase-conjugated goat antirabbit secondary antibodies (Santa Cruz Biotechnology) and detected using enhanced chemiluminescence (GE Healthcare).

Immunofluorescence. HEK293T cells were cotransfected with GFP-Scribble and Flag-tagged target constructs. Forty-eight hours after transfection, cells were fixed with 100% methanol for 20 min. Anti-Flag antibodies (1:400 Sigma) were incubated at room temperature for 1 h. Z-stack images were captured at room temperature by the Leica DMI6000B confocal microscope with a Leica 20×/0.40 NA objective lens and a Hamamatsu EM-CCD digital camera (C9100-13), and imported into Volocity software. The imaging medium was PBS.

Supplemental Network Analysis. We created a protein-protein interaction network of the four PDZ-containing proteins with their 78 putative binding using Cytoscape (10). The disk large homolog 1 (DLG1) part of the network contains previously known interactions with anion transporters, potassium channels, and G protein-coupled receptors. Consistent with the role of DLG1 in neuronal signaling, there are also known interactions with proteins involved in neuronal transmission, such as the motor protein KIF1 β (11) and the microtubule-binding protein CRIPT (12). Among the new ligands we predict for DLG1, we highlight the Ras association domain-containing protein 6 (RASSF6), which interacts with the mammalian Ste20-like kinases (MST1/2), which are core kinases of the Hippo pathway (13). The suggested interaction between DLG1 and RASSF6 may add to the growing list of links between the cell polarity proteins and the Hippo signaling pathway (14). In addition, our predicted interactions between DLG1 and the E3 ubiquitin ligases DCNL1, RNF12, and MARCH3 may suggest unexplored connections between the ubiquitin system and the DLGs. Overall, the putative ligands appear relevant to the functions of DLG1.

Consistent with previous studies and roles in cell polarity and adhesion, the network of the LAP proteins Densin-180, Erbin, and Scribble contains interactions with the catenin family members PKP4, δ-catenin, and ARVCF, proteins that are found at the adherens junctions where they are involved in cell polarity and motility, but are also found in the nucleus where they are involved in transcriptional regulation (15-17). We also confirmed the interaction between Scribble and ARGH7, which is involved in cell migration, attachment, and cell spreading (18), and suggest novel interactions with a set of organic anion transporters and potassium channels as well as some nuclear proteins involved in transcriptional regulation, such as ATD2B. Scribble is not known to localize to the nucleus but it cannot be excluded that the proteins interact under specific circumstances. For example, ATD2B has been detected in the cytoplasm in some cancer cells (19). Under normal conditions, however, it is possible that the ATD2B C terminus is recognized by other class I PDZ proteins, such as NHERF2, that shuttle between the cytoplasm and the nucleus (20).

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^{4.} Quail MA, et al. (2008) A large genome center's improvements to the Illumina sequencing system. Nat Methods 5(12):1005-1010.

^{5.} Kim T, et al. (2012) MUSI: An integrated system for identifying multiple specificity from very large peptide or nucleic acid data sets. Nucleic Acids Res 40(6):e47.

^{6.} Monera OD, Sereda TJ, Zhou NE, Kay CM, Hodges RS (1995) Relationship of sidechain hydrophobicity and alpha-helical propensity on the stability of the single-stranded amphipathic alpha-helix. J Pept Sci 1(5):319-329.

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Fig. S1. Overview of the viral library design based on host organism.



Fig. S2. Comparison between logos derived from ProP-PD and conventional peptide-phage display. On the left logos as derived from the Tonikian et al. (1) study using a combinatorial peptide-phage library, on the right logos derived from ProP-PD experiments. "Accumulated hydrophobicity ratio ProP-PD/Tonikian" gives the ratio of the accumulated and normalized hydrophobicity (see *Methods*). Values smaller than one indicate a more hydrophobic PWM for the data obtained from the conventional phage library.



Fig. S3. Correlation between affinities and sequencing counts for Scribble PDZ3. Semilog scale plot of the sequencing counts versus affinities with a linear fit. The two red squares indicate outliers (the DNM1L peptide, to the left) and the GSPDSWV peptide (to the right).



Fig. S4. Colocalization of Scribble with CTNB1 and DNM1L, respectively. (A) Colocalization of GFP-tagged full-length Scribble with Flag-tagged CTNB1 and DNM1L 48 h after cotransfection in HEK293T cells (confocal micrographs). (Scale bars, 15 μm.)



Fig. S5. Comprehensive network of identified interactions. The bait proteins (Densin-180 PDZ; Erbin PDZ; Scribble PDZ1, PDZ2, and PDZ3; and DLG1 PDZ1, PDZ2, and PDZ3) are indicated by gray diamonds. Ligands identified by ProP-PD experiments are indicated by circles, in which colors indicate their biological processes. The width of the connecting lines reflect the frequency of a ligand in the sequencing data, with the ligands divided into three categories: high $[log_{10}(counts) > 3]$, medium $[3 > log_{10}(counts) > 2]$, and low $[log_{10}(counts) < 2]$. The color of the connecting branches indicates if the interactions are novel (gray), known (green), or here validated (yellow). The network was designed using the program Cytoscape (10).



Fig. S6. Frequency of mutated peptides versus designed parental peptides after the fifth round of selection. The comparison between the amount of sequences with point mutations (*x* axis) to the frequency of their parental sequences ("Frequency parental peptides," *y* axis, log-scale) illustrates that the more selected a wild-type peptide is, the more mutants of it will accumulate during the phage propagation.

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Table S1. Comprehensive list of selected targets for each domain with literature references when applicable

Scribble PD21 RFLETKL 67.51 47.351 112.665 87.2271,HUMAN Audebert et al. (1) 15.227 2 3 Scribble PD21 MMETT 286 5 2.51 AHRG,HUMAN Audebert et al. (1) 15.22 4.61 15.52 4.61 15.52 4.61 15.52 4.61 15.52 4.61 15.52 4.61 15.52 4.61 15.52 4.61 15.52 4.61 14.469 15.52 4.61 14.469 12.100	Protein	Peptide	Library A	Library B	Total	Uniprot	Source	PMID	Rank ProP-PD	Rank Tonikian
Scribble PD21 MVDETNL 3,000 1,552 4,561 AHKG, HUMAN 1 155 Scribble PD21 TSRETDL 9 1 10 KCMAS, HUMAN 1 15 Scribble PD21 TSRETDL 9 1 10 KCMAS, HUMAN 1 12,927 Scribble PD21 REESTM 0 1 10 KCMAS, HUMAN 1 1,2297 Scribble PD22 ROSPSWV 0 6 168 618 618 614 NARES, HUMAN 2 1 2 168 Scribble PD22 VORTIVL 75 70 164 NARES, HUMAN 4 4 6 144,683 Scribble PD23 VORTIVL 75 70 144 NARES, HUMAN 4 146 146,833 Scribble PD23 VORTIVL 83 144,428 NYRES, HUMAN 4 146 Scribble PD23 REETH 2.21 12,738 2.04 CD2 1412 2.04 CD2 2.04 CD2 2.04 CD2 <	Scribble PDZ1	RFLETKL	67,514	45,351	112,865	B7Z2Y1_HUMAN			1	4
Scribble PD21 IMFETEL 286 5 291 AHKG, HUMAN Zhang et al. (2) 16737968 4 156 Scribble PD21 REESTM 0 8 8 VMCL, HUMAN 2 12,927 Scribble PD21 REFHUW 0 6 641,4691 2,100 Scribble PD22 SPDSWV 0 618 PKH_HUMAN 2 12,6 Scribble PD22 RETRIL 35 41 76 BYTMAN 4 4 Scribble PD22 RETRIL 35 31 3 5 5 3 3 3 Scribble PD23 RETRIL 30,601 27,064 SARAG/T, HUMAN Audebert et al. (1) 15182672 2 32 Scribble PD23 RETRIL 12,81 17,29 AUDE HUMAN 44 1,42 33 Scribble PD23 RETRIL 12 7,318 7,320 ATD2 HUMAN 49 1,22 Scribble PD23 RETRIL 12 7,320 ATD2 HUMAN <td>Scribble PDZ1</td> <td>AWDETNL</td> <td>3,009</td> <td>1,552</td> <td>4,561</td> <td>ARHG7_HUMAN</td> <td>Audebert et al. (1)</td> <td>15182672</td> <td>2</td> <td>25</td>	Scribble PDZ1	AWDETNL	3,009	1,552	4,561	ARHG7_HUMAN	Audebert et al. (1)	15182672	2	25
Scribble PD21 TSRETDL 9 1 10 KCMAS, HUMAN Zhang et al. (2) 16737968 4 186 Scribble PD21 REFHLW 7 0 7 DMML1, HUMAN 1 2,100 Scribble PD22 SGRSWV 0 618	Scribble PDZ1	HMFETFL	286	5	291	ARHG8_HUMAN			3	15
Scribble PD21 RGEESTM 0 8 8 VMCC_HUMAN 5 12,927 Scribble PD22 GSPDSWV 0 618 PKR4_HUMAN 1 2,100 Scribble PD22 GSPDSWV 0 618 PKR4_HUMAN 2 125 Scribble PD22 GSPDSWV 6 12 38 ARGE_THUMAN 4 46 Scribble PD22 KPLETKL 23 38 ARGE_THUMAN 4 46 Scribble PD22 KPUSTW 61 7.57 7.67 7.27 7.52 5.23 Scribble PD23 MVDTML 82.801 7.79 80 7.597 7.67 7.67 7.57 7.52 7.28 7.75	Scribble PDZ1	TSRETDL	9	1	10	KCNA5_HUMAN	Zhang et al. (2)	16737968	4	186
Scribble PD21 IRETHUW 7 0 7 DMML1_HUMAN 1 2,100 Scribble PD22 SPRSWU 6 16 RVPE_JHUMAN 2 126 Scribble PD22 AVMDETN 29 29 58 AHRG7_HUMAN 3 3 Scribble PD22 AVMDETN 29 29 58 AHRG7_HUMAN 4 46 Scribble PD22 AVMDETN 20 1 21 ZSWM1_HUMAN 4 46 Scribble PD22 AVMDETN 30,601 27,005 57,697 AHRG7_HUMAN 4 14 Scribble PD23 HWETTN 2 7,138 7,320 ADD23_HUMAN 4 14 Scribble PD23 HWETTN 7 1,271 30,000 P2271_HUMAN 5 166 Scribble PD23 HWETTN 7 1,272 ADADD HUMAN 4 14 Scribble PD23 FRETNL 7 10 5 10 12 2 7 Scribb	Scribble PDZ1	RGEESTM	0	8	8	VWCE_HUMAN			5	12,927
Scribble PD22 GSPDSWV 0 618 FRM, HUMAN 1 2,100 Scribble PD22 RFLETKL 35 1 16 NPE2, HUMAN 2 126 Scribble PD22 RFLETKL 35 4 1 6 NPE2, HUMAN 3 3 Scribble PD22 ARPDSWV 6 32 38 TIND2, HUMAN 4 46 Scribble PD23 VQHITWL 83,844 17,68 101,482 NPE2, HUMAN 4 1 55 Scribble PD23 RUETL 1,228 17,719 30,000 322,271, HUMAN 4 14 Scribble PD23 RUETL 7,318 73,20 ATD2, HUMAN 4 14 Scribble PD23 RUETL 7,318 73,20 ATD2, HUMAN 4 14 Scribble PD23 RUETL 7,738 73,20 ATD2, HUMAN 5 112 Scribble PD23 RUETL 1,823 GTA2, HUMAN 1 1 1,23 3 3 <t< td=""><td>Scribble PDZ1</td><td>IRETHLW</td><td>7</td><td>0</td><td>7</td><td>DNML1_HUMAN</td><td></td><td></td><td>6</td><td>41,469</td></t<>	Scribble PDZ1	IRETHLW	7	0	7	DNML1_HUMAN			6	41,469
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Scribble PD23 VQRHTWL 83,844 17,638 101,632 NXPEZ JUNAN 1 55 Scribble PD23 RFLETKL 12,281 17,719 30,000 872271,HUMAN 3 13 Scribble PD23 NIRETDI 784 494 1,729 ADATD_HUMAN 5 112 Scribble PD23 NIRETDI 784 494 1,739 ADATD_HUMAN 6 36,666 Scribble PD23 POKETOL 725 302 0 302 RBT_LHUMAN 9 99 Scribble PD23 DRKETSI 302 0 302 RBT_LHUMAN 9 99 Scribble PD23 DRKTSI 1 242 253 GCAVA_LHUMAN 10 1 1 Scribble PD23 DRKTSI 1 242 254 MARA_LHUMAN 12 342 Scribble PD23 DRKTSI 1 242 255 GCRESTI 12 215 236 Scribble PD23 DRKTSI 30 3	Scribble PDZ2	PYEQVQL	20	1	21	ZSWM1_HUMAN			6	14,689
Scribble PD23 AWDE INU 30,001 27,095 57,697 ARHG, JUMAN Audebert et al. (1) 1518,26/2 2 222 Scribble PD23 IMFETFL 2 7,318 7,320 ATD28 HUMAN 4 14 Scribble PD23 IRETHU 1 1,193 1,194 DMML, HUMAN 6 36,666 Scribble PD23 IRETTU 1 1,193 1,194 DMML, HUMAN 6 36,666 Scribble PD23 IRETTSL 1 222 Z53 GCYA2, HUMAN 10 1 Scribble PD23 IRETTSL 1 222 Z53 GCYA2, HUMAN 12 342 Scribble PD23 IRETAL 1 2215 MREA HUMAN 12 32 Scribble PD23 IRETAL 1 2215 MREA HUMAN 13 22 Scribble PD23 IRETAL 103 145 236 GCYA2, HUMAN 16 39,666 Scribble PD23 IRETAL 104 114 IRETAL 10	Scribble PDZ3	VQRHTWL	83,844	17,638	101,482	NXPE2 _HUMAN		45400670	1	55
Scribble PD23 NHETRL 12,231 17,719 30,000 87,227 114 Scribble PD23 NIRETD 784 494 1,728 ADATD_HUMAN 5 112 Scribble PD23 NIRETD 784 494 1,728 ADATD_HUMAN 5 112 Scribble PD23 SKETPL 782 302 707 501 101 1 Scribble PD23 DRKTSI 302 0 302 RBP_HUMAN 9 99 Scribble PD23 REKTSI 1 242 253 GCXA_2 HUMAN 10 1 Scribble PD23 REKTSI 1 242 215 MEPA_HUMAN 12 322 Scribble PD23 STEFTSI 1 242 215 MEPA_HUMAN 11 1.320 Scribble PD23 STEFTSI 10 11 111 IRK J_HUMAN Scribble PD23 SCRIbBP23 SCRIbBP23 SCRIbBP23 SCRIBBP23 SCRIBBP23 SCRIBBP23 SCRIBBP23 SCRIBBP23 SCRIBBP23	Scribble PDZ3	AWDEINL	30,601	27,096	57,697	ARHG/_HUMAN	Audebert et al. (1)	15182672	2	322
Scribble PD23 HMFETIL 2 7,318 7,320 A1228 AUARAN 4 14 Scribble PD23 IRETHU 1 1,193 1,194 DMML_HUMAN 6 36,666 Scribble PD23 IRETHU 1 1,193 1,141 MK12L,HUMAN 6 36,666 Scribble PD23 POKETG 775 0 775 SOICL_HUMAN 8 77 Scribble PD23 FIRETSL 1 222 223 GCYA2,HUMAN 10 1 Scribble PD23 FIRETSM 91 145 236 GCXA2,HUMAN 12 342 Scribble PD23 FIRETAN 91 145 236 GCXA2,HUMAN 12 342 Scribble PD23 STEFDL 174 0 174 GTM2 16737968 14 28 Scribble PD23 STEFTDL 7 86 37 14 30,860 Scribble PD23 STEFTDL 7 86 37 39 39 <td< td=""><td>Scribble PDZ3</td><td>RFLEIKL</td><td>12,281</td><td>1/,/19</td><td>30,000</td><td>B/Z2Y1_HUMAN</td><td></td><td></td><td>3</td><td>13</td></td<>	Scribble PDZ3	RFLEIKL	12,281	1/,/19	30,000	B/Z2Y1_HUMAN			3	13
Scribble PD23 NIRE IDI 784 494 1,22 ADAID_HUMAN 5 112 Scribble PD23 VSKTPL 782 359 1,141 MK12_HUMAN 7 179 Scribble PD23 PKRTSI 302 0 302 RBP1_HUMAN 9 99 Scribble PD23 RKTSI 302 0 302 RBP1_HUMAN 9 99 Scribble PD23 RKTSI 1 225 CSCA2_HUMAN 10 1 1,230 Scribble PD23 RWETSI 1 248 249 ADA22_HUMAN 13 2 323 Scribble PD23 RKETHL 203 12 215 MRP4_HUMAN Xhang et al. (2) 16737968 16 3.906 Scribble PD23 SKETHL 9 9 9 87 MET_HUMAN Xhang et al. (2) 16737968 17 5 Scribble PD23 SKETHL 9 8 MCAS_HUMAN Xhang et al. (2) 16737968 17 5 3.06	Scribble PDZ3	HMFEIFL	2	/,318	7,320	ATD2B_HUMAN			4	14
Scribble PD23 INETHUW 1 1,193 1,194 DNMIL_HUMAN 6 36,666 Scribble PD23 PKKETQL 775 0 775 501C1,HUMAN 7 779 Scribble PD23 FIRETSL 1 252 253 GCYA2,HUMAN 9 99 Scribble PD23 FIRETSL 1 248 249 ADA2 11 1,233 Scribble PD23 FIRETSL 1 248 249 ADA2 11 1,233 Scribble PD23 FIRETSL 93 12 ISMEHA 13 2 Scribble PD23 SKRTDL 174 0 174 CTNB1.HUMAN Xhang et al. (2) 16737968 14 228 Scribble PD23 SKRTDL 7 86 39 KCNA5,HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23 SKRTTAL 0 39 39 DKL2,HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23	Scribble PDZ3	NLRETDI	784	494	1,278	ADA1D_HUMAN			5	112
Scribble PD23 SKRETPL 7/8 353 1,141 MR12_HUMAN 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7	Scribble PDZ3	IRETHLW	1	1,193	1,194	DNM1L_HUMAN			6	36,666
Scribble PD23 PKRETSL 1 252 253 GCYA2, HUMAN 9 9 Scribble PD23 FRETSL 1 252 253 GCYA2, HUMAN 10 1 Scribble PD23 FRETSL 1 254 249 ADA22, HUMAN 12 342 Scribble PD23 TIFETAL 203 12 215 MRP4, HUMAN 12 342 Scribble PD23 TIFETAL 203 14 CTNB1, HUMAN Mang et al. (2) 16737968 14 228 Scribble PD23 GEKETHL 94 76 170 S6A12, HUMAN Geller et al. (3) 2152870 15 23 Scribble PD23 GEKETHL 9 9 87 KETML 18 30.660 Scribble PD23 SGRETAL 0 39 43 RKR4, HUMAN 12 16737968 19 87 Scribble PD23 SGRETAL 0 39 13 ALREA, HUMAN 21 26 26 21 26 26	Scribble PDZ3	VSKETPL	/82	359	1,141	MK12_HUMAN			/	179
Scribble PD23 EIRETSL 1 252 253 CYA2_HUMAN 1 1 1 Scribble PD23 RLWETSI 1 248 249 ADA22_HUMAN 11 1,1,230 Scribble PD23 TIFETAL 203 12 215 MRPA_HUMAN 13 2 Scribble PD23 SWETSL 10 174 00 174 CTBL_HUMAN 16 3,906 Scribble PD23 SWETSL 10 111 111 IK12_HUMAN 56 3,906 Scribble PD23 SKETEHL 94 76 170 S6A12_HUMAN Xhang et al. (2) 16737968 17 5 Scribble PD23 SKETENL 7 86 93 KCMAS_HUMAN Xhang et al. (2) 16737968 18 3,080 Scribble PD23 SVESDE 55 0 55 ACTN1,2,3,4_HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23 SVESDE 3 26 25 S1540 17 <t< td=""><td>Scribble PDZ3</td><td>PGKETQL</td><td>//5</td><td>0</td><td>//5</td><td>SO1C1_HUMAN</td><td></td><td></td><td>8</td><td>//</td></t<>	Scribble PDZ3	PGKETQL	//5	0	//5	SO1C1_HUMAN			8	//
Scribble PD23 FIKEISL 1 2.52 CCYA2_HUMAN 10 1 Scribble PD23 FIKETSM 91 145 2.25 GCYA2_HUMAN 12 342 Scribble PD23 TIFETAL 203 12 215 MRP4_HUMAN 12 342 Scribble PD23 SEKETHL 94 76 170 SGA12_HUMAN 16737968 14 228 Scribble PD23 SRESTDL 7 86 93 KCNA5_HUMAN Khang et al. (2) 16737968 17 5 Scribble PD23 SRESTDL 7 86 93 KCNA5_HUMAN Xhang et al. (2) 16737968 19 377 Scribble PD23 VRESDL 5 0 85 ACTN12_3.4_HUMAN Xhang et al. (2) 16737968 19 377 Scribble PD23 VRESDL 2 3 21 268 29 14 14K4_HUMAN 22 104 Scribble PD23 VRESTAL 0 13 ANR50_HUMAN 23	Scribble PDZ3	DRKETSI	302	0	302	RBP1_HUMAN			9	99
Schlabe PD23 RVER13 I 248 249 AUA22_FUMAN I I I, 230 Scribble PD23 TRETAL 203 12 215 MRP4_HUMAN Xhang et al. (2) 16737968 14 228 Scribble PD23 GKERTHL 94 76 170 S6A12_HUMAN Chang et al. (2) 16737968 15 23 Scribble PD23 SRESEL 100 11 111 IRK12_HUMAN Geller et al. (3) 21525870 15 23 Scribble PD23 SRESEL 7 86 93 KCNA5_HUMAN Xhang et al. (2) 16737968 17 5 Scribble PD23 SRESEAL 2 39 41 IRK12_HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23 VEGEDL 5 0 54 ACTN12_JA_HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23 VEGEDL 0 1 11 RARE_HUMAN 21 268 Scribble PD23	Scribble PDZ3	FLREISL	1	252	253	GCYA2_HUMAN			10	1
Scribble PD23 FirkLish 91 145 236 KLNB2_HUMAN 12 12 245 Scribble PD23 AWFDTDL 174 0 174 CTNB1 16737968 14 228 Scribble PD23 SGRETH 94 76 170 Scribble PD23 15228870 15 238 Scribble PD23 SFRESEI 100 11 111 IRK1_HUMAN Khang et al. (2) 16737968 17 5 Scribble PD23 SFWETS 87 0 87 MET_HUMAN Xhang et al. (2) 16737968 19 30,860 Scribble PD23 SFWETS 87 0 87 MET_HUMAN 20 42 Scribble PD23 VRKTAL 0 39 39 DLK2_HUMAN 21 268 22 104 Scribble PD23 SKETGL 3 26 29 S15A5_HUMAN 23 21 26 Scribble PD23 SKETGL 0 1 1 17 18	Scribble PDZ3	RLVVEISI	1	248	249	ADA22_HUMAN			11	1,230
Scribble PD23 SKRETPL 12 215 MKP4_HUMAN Xhang et al. (2) 16737968 14 228 Scribble PD23 GKERTHL 94 76 170 SCAL SCAL SCAL SCAL	Scribble PDZ3	PIREISM	91	145	236	KCNB2_HUMAN			12	342
Schnbie PD23 Schnbie PD23 Serk PD4 Schnbie PD3	Scribble PDZ3	TIFETAL	203	12	215	MRP4_HUMAN) (I) (D)	46727060	13	2
Schnbie PD23 GREATER PLAS GREATER PLAS Construction Construction<	Scribble PDZ3	AWFDIDL	1/4	0	174	CINB1_HUMAN	Xhang et al. (2)	16/3/968	14	228
Scribble PD23 TRKESH 100 11 111 IKR12_HUMAN Xhang et al. (2) 16737968 17 5 Scribble PD23 STRKETS 87 0 87 MET_HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23 VKRESAL 2 39 41 IRK1_HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23 YKRETSAL 2 39 41 IRK4_HUMAN 20 422 Scribble PD23 YKKETPL 30 1 31 ANR50_HUMAN 223 21 Scribble PD23 GKRTGL 3 26 29 ISA5_HUMAN 223 21 Scribble PD23 GKRETGL 0 26 F189B_HUMAN 26 472 Scribble PD23 GKRETGL 0 14 14 ZN563_HUMAN 27 2,136 Scribble PD23 SKPETAL 0 15 STARS_HUMAN 27 2,136 Scribble PD23 MKYES1	Scribble PDZ3	GEKETHL	94	/6	170	S6A12_HUMAN	Gfeller et al. (3)	21525870	15	23
Scribble PD23 SKRIDL 7 86 93 RKNAS_HUMAN Khang et al. (2) 16737968 17 5 Scribble PD23 LYGESDL 55 0 55 ACTN1,2,3,4_HUMAN Xhang et al. (2) 16737968 19 877 Scribble PD23 YRRESAI 2 39 41 IRK4_HUMAN Xhang et al. (2) 16737968 19 42 Scribble PD23 YRKETPL 30 1 31 ANRS0_HUMAN 22 104 Scribble PD23 DKKETPL 30 1 31 ANRS0_HUMAN 23 21 Scribble PD23 GSKETGL 0 26 29 515AS_HUMAN 23 21 Scribble PD23 GDLSTD 0 21 21 RFRTB_HUMAN 26 472 Scribble PD23 SGRETGL 0 15 15 STA8_HUMAN 28 48,049 Scribble PD23 SKPGTFL 0 14 14 20563_HUMAN 29 352 Scribble PD23 SKPGTFL 0 16 54,450 10 1172 11	Scribble PDZ3	YRRESEI	100	11	111	IRK12_HUMAN) (I) (D)	46727060	16	3,906
Scribble PD23 Stribble PD23 Viet Stribble PD2	Scribble PDZ3	ISREIDL	/	86	93	KCNA5_HUMAN	Xhang et al. (2)	16/3/968	17	5
Scribble PD23 YRESAI 2 39 41 IRX4_HUMAN 20 42 Scribble PD23 YRKETAL 0 39 39 DLV2_HUMAN 21 268 Scribble PD23 YKKETPL 30 1 31 ANRS0_HUMAN 23 21 Scribble PD23 DLWETAL 3 26 25 S15A5_HUMAN 23 21 Scribble PD23 GRUETGL 0 26 26 189B_HUMAN 26 27 9794 Scribble PD23 GRUETGL 0 21 21 RPR1B_HUMAN 26 472 Scribble PD23 GRUETSTL 0 15 15 STAR8_HUMAN 29 352 Scribble PD23 SGRUETTL 0 10 10 S4A4_HUMAN 29 352 Scribble PD23 SGRUETTL 0 10 10 S4A4_HUMAN 30 577 Scribble PD23 SVGRUETL 0 7 ILVX1_HUMAN 112049 2 35 Scribble PD23 SVGVETL 0 71,560 PKP4_HUMAN Lau	Scribble PDZ3	ASEVVETS	8/	0	8/)/h a mar at a [(2)	10727000	18	30,860
Scribble PD23 PKKTEDAL 2 39 41 INKA_HOMAN 20 42 Scribble PD23 PKKETPL 30 1 31 ANR50_HUMAN 22 104 Scribble PD23 DLWETAL 3 26 29 S15A5_HUMAN 23 21 Scribble PD23 GSRETGL 0 26 F1898_HUMAN 23 21 Scribble PD23 GSRETGL 0 21 21 RPR1B_HUMAN 26 472 Scribble PD23 GAGETKL 0 15 STAR_HUMAN 26 472 Scribble PD23 THWRETI 0 14 14 ZN563_HUMAN 29 352 Scribble PD23 SKPGTFL 0 7 7 LNX1_HUMAN 30 377 Scribble PD23 SVPGTFL 0 7 7 LNX1_HUMAN 10 30 577 Scribble PD23 SVPGTFL 0 7 7 LNX1_HUMAN Laura et al. (4) 1172919 2 35 Densin-180 ASPDSWV Failed 5,450 PKP4_HUMAN	Scribble PDZ3		55	0	55	ACINI,2,3,4_HUMAN	Xhang et al. (2)	16/3/968	19	877
Scribble PD23 YKKETPL 30 1 31 ANRSD, HUMAN 22 104 Scribble PD23 UKETAL 3 26 29 S15A5, HUMAN 23 21 Scribble PD23 GSRETGL 0 26 26 F189B, HUMAN 24 58 Scribble PD23 GDLFSTD 0 21 17 18 TMG1, HUMAN 26 472 Scribble PD23 AGPETKL 0 15 15 STAR8, HUMAN 26 472 Scribble PD23 THSTTL 0 14 42 14 2NS63, HUMAN 29 352 Scribble PD23 GKTETTL 0 10 10 54A4, HUMAN 31 356 Scribble PD23 SWPGTFL 0 7 1 NT1, HUMAN 31 356 Densin-180 GSPDSWV Failed 5,450 PK44, HUMAN 11 170 Densin-180 GSPDSWV 64,274 71,946 136,220 CTND2, HUMAN Laura et al. (4) 11729199 2 35 Erbin GPDSWV 0 17,	Scribble PDZ3	TRRESAL	2	39	41				20	42
Scribble PD23 DWETAL 30 1 31 ANRSO_HOMAN 22 104 Scribble PD23 GSRETGL 0 26 29 515AS_HUMAN 23 21 Scribble PD23 GSRETGL 0 21 21 RPR18_HUMAN 23 9794 Scribble PD23 AGPETKL 0 15 15 STAR8_HUMAN 26 472 Scribble PD23 AGPETKL 0 15 15 STAR8_HUMAN 27 2,136 Scribble PD23 KGTETTL 0 10 14 2056_HUMAN 29 352 Scribble PD23 MYKSSDI 0 8 8 NR2E1_HUMAN 30 577 Scribble PD23 MYKSSDI 0 8 8 NR2E1_HUMAN 30 577 Scribble PD23 SVPGTFL 0 7 LNX1_HUMAN 11 170 Densin-180 GSPDSWV Failed 5,459 PKP4_HUMAN Lzawa et al. (4) 11221434 1 2 Erbin GSPDSWV 17,680 PKP4_HUMAN Lawa et al. (5) <	Scribble PDZ3		20	39	39				21	208
Scribble PD23 GNUVETAL 3 20 29 STAS_FUNMAN 23 21 Scribble PD23 GDLFSTD 0 21 21 RPR1B_HUMAN 26 472 Scribble PD23 AGPETKL 1 17 18 TMIG1_HUMAN 26 472 Scribble PD23 AGPETKL 0 15 STARB_HUMAN 27 2,136 Scribble PD23 THWRETI 0 14 14 ZN563_HUMAN 28 48,049 Scribble PD23 MYKSSDI 0 8 8 NR2E1_HUMAN 29 352 Scribble PD23 SWPGTL 0 7 T LNX1_HUMAN 30 577 Scribble PD23 SVPGTFL 0 7 T LNX1_HUMAN 112awa et al. (4) 11729199 2 35 Densin-180 ASPDSWV Failed 5,450 PKP4_HUMAN Lawa et al. (5) 11821434 1 2 Erbin QPVDSWV 17,680 PKP4_HUMAN Lawa et al. (6) 12047349 2 3 Erbin QVDYDW 114 2 116	Scribble PDZ3	YKKEIPL	30	1	31	ANK50_HUMAN			22	104
Scribble PD23 GDL FD23 GDL FD24 GDR FGL 0 20 F189E_PUMAN 24 38 Scribble PD23 GDL FSTD 0 21 21 RFR1E_HUMAN 26 472 Scribble PD23 FMSETAL 1 17 18 TMIG1_HUMAN 26 472 Scribble PD23 KGPETKL 0 15 15 STAR8_HUMAN 27 2,136 Scribble PD23 KGTETTL 0 10 10 S44_HUMAN 29 352 Scribble PD23 KYKSDI 0 8 8 NR2E1_HUMAN 30 577 Scribble PD23 SVPSTFL 0 7 TLN1_HUMAN 30 356 Densin-180 GSPDSWV Failed 5,450 PKP4_HUMAN Laura et al. (4) 1172919 2 35 Erbin GSPDSWV Failed 17,680 PKP4_HUMAN Laura et al. (5) 11821434 1 2 Erbin GSPDSWV 1,748 18,35 ARVC_HUMAN Laura et al. (5) 11821434 3 4 Erbin	Scribble PDZ3		3	20	29	SISAS_HUIVIAN			23	21
Actinatione PD23 PISETAL 1 17 18 NRME_HOMAN 25 9,794 Scribble PD23 AGPETKL 0 15 15 STAR8_HUMAN 27 2,136 Scribble PD23 KGTETTL 0 14 14 ZN563_HUMAN 28 48,049 Scribble PD23 KGTETTL 0 10 10 StaR8_HUMAN 29 352 Scribble PD23 SKGTETTL 0 7 7 LNX1_HUMAN 30 577 Scribble PD23 SVPGTFL 0 7 7 LNX1_HUMAN 31 356 Densin-180 GSPDSWV Failed 2,794 27,94 CTND2_HUMAN Laura et al. (4) 11729199 2 35 Erbin ASPDSWV 64,274 71,946 136,220 CTND2_HUMAN Laura et al. (5) 11821434 1 2 Erbin GSPDSWV 0 17,680 PKP4_HUMAN Laura et al. (5) 11821434 1 2 Erbin YDVTDV 114 2 116 GR87_HUMAN Laura et al. (5) 11821434 <td>Scribble PDZ3</td> <td>GSREIGL</td> <td>0</td> <td>20</td> <td>20</td> <td></td> <td></td> <td></td> <td>24</td> <td>56 0 704</td>	Scribble PDZ3	GSREIGL	0	20	20				24	56 0 704
Scribble PD23 FINETAL 1 17 18 TMINE_HUMAN 20 4/2 Scribble PD23 THWRETI 0 14 14 ZN563_HUMAN 28 48,049 Scribble PD23 KGTETTL 0 10 10 SA4A_HUMAN 29 352 Scribble PD23 SKGTETL 0 10 SA4A_HUMAN 30 577 Scribble PD23 SWGTFL 0 7 7 INX1_HUMAN 31 356 Densin-180 GSPDSWV Failed 5,450 5,450 PKP4_HUMAN Izawa et al. (4) 11729199 2 35 Erbin GSPDSWV 64,274 71,946 136,220 CTND2_HUMAN Izawa et al. (6) 12047349 2 3 Erbin GSPDSWV 1,747 88 1,835 ARVC_HUMAN Izawa et al. (5) 11821434 4 1,357 Erbin VPDYDTDV 114 2 116 GRR2_HUMAN Laura et al. (5) 11821434 3 4 Erbin VPDYDTDV 114 12 NS2_HUMAN Laura et al. (5	Scribble PDZ3		1	17	21				25	5,754 470
Scribble PD23 HVRETI 0 10 10 SGRIDMEND 28 48,049 Scribble PD23 KKRETI 0 10 10 S4A4_HUMAN 29 352 Scribble PD23 SWPGTFL 0 7 7 LINX1_HUMAN 30 5777 Scribble PD23 SWPGTFL 0 7 7 LINX1_HUMAN 31 356 Densin-180 GSPDSWV Failed 5,450 FKP4_HUMAN Lawa et al. (4) 11729199 2 35 Erbin GSPDSWV Failed 2,794 2,794 CTND2_HUMAN Lawa et al. (5) 11821434 1 2 Erbin GSPDSWV 64,274 71,680 PKP4_HUMAN Lawa et al. (5) 11821434 3 4 Erbin QPVDSWV 1,747 88 1,835 ARVC_HUMAN Lawa et al. (5) 11821434 3 4 Erbin VQRHTWL 21 1 22 NPE2_HUMAN Lawa et al. (5) 11821434 4 1,357 Erbin VQRHTWL 11 71,40 BG422_HUMAN	Scribble PDZ3		0	17	10				20	472
Actingue PD23 NTMKLTI 0 14 14 24 20 46,049 Scribble PD23 MYKSSDI 0 8 8 NR2E1_HUMAN 30 577 Scribble PD23 SWPGTFL 0 7 7 LNX1_HUMAN 31 356 Densin-180 GSPDSWV Failed 2,794 2,794 CTND2_HUMAN 1 170 Densin-180 ASPDSWV Failed 2,794 2,794 CTND2_HUMAN Laura et al. (4) 11729199 2 35 Erbin ASPDSWV 64,274 71,946 136,220 CTND2_HUMAN Laura et al. (5) 11821434 1 2 Erbin GSPDSWV 0 17,680 17,680 PKP4_HUMAN Laura et al. (5) 11821434 3 4 Erbin VQPNDSWV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin VQPNTVL 21 1 22 NXPE2_HUMAN Laura et al. (5) 11821434 3 4 DLG1 PD21 RKETKL 569	Scribble PDZ3		0	1/	1/				27	18 0/0
Actioner PD23 NKRLTTL 0 10 577 Scribble PD23 SWPGTFL 0 7 7 LNX1_HUMAN 11 10 11 170 Densin-180 GSPDSWV Failed 2,794 CTND2_HUMAN Laura et al. (4) 11729199 2 35 Erbin ASPDSWV 64,274 71,946 136,220 CTND2_HUMAN Laura et al. (5) 11821434 1 2 3 Erbin QPVDSWV 1,747 88 1,835 ARVC_HUMAN Laura et al. (5) 11821434 3 4 1,357 Erbin YDYDV 114 2 116 GPR3_HUMAN Laura et al. (5) 11821434 3 4 Erbin YDYDV 114 2 116 GPR3_HUMAN Laura et al. (5) 11821434 3 4 DL	Scribble PDZ3	KGTETTI	0	14	14				20	40,049
Densine FD23 SWPGTFL 0 7 7 LIX1_HUMAN 31 356 Densin-180 GSPDSWV Failed 5,450 5,450 PKP4_HUMAN 1 170 Densin-180 ASPDSWV Failed 2,794 2,794 CTND2_HUMAN Lava et al. (4) 11729199 2 35 Erbin ASPDSWV 64,274 71,946 136,220 CTND2_HUMAN Laura et al. (5) 11821434 1 2 Erbin QSPDSWV 1,747 88 1,835 ARVC_HUMAN Laura et al. (5) 11821434 3 4 Erbin YPYDTDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YPYDTDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin VPYDTVV 114 2 173 GA212_HUMAN Laura et al. (5) 11821434 3 4 DLG1 PD21 RMSVHWV 11 0 131 TBX15_HUMAN 1 721 1 721 </td <td>Scribble PDZ3</td> <td></td> <td>0</td> <td>8</td> <td>8</td> <td>NR2E1 HUMAN</td> <td></td> <td></td> <td>30</td> <td>577</td>	Scribble PDZ3		0	8	8	NR2E1 HUMAN			30	577
Densin-180 GSPDSWV Failed 5,450 PKP4_HUMAN 1 170 Densin-180 ASPDSWV Failed 2,794 2,794 CTND2_HUMAN Laura et al. (4) 11729199 2 35 Erbin ASPDSWV 64,274 71,946 136,220 CTND2_HUMAN Laura et al. (5) 11821434 1 2 Erbin GSPDSWV 0 17,680 PKP4_HUMAN Laura et al. (5) 11821434 3 4 Erbin GVDSWVV 1,747 88 1,835 ARVC_HUMAN Laura et al. (5) 11821434 3 4 Erbin YPDYDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YQPTDV 114 5 19 GA2L2_HUMAN Laura et al. (5) 11821434 3 4 Erbin VQRHTWL 21 1 22 RXPE2_HUMAN Laura et al. (5) 11821434 3 4 DLG1 PDZ1 RFLETKL 569 77 646 B722Y1_HUMAN Laura et al. (3) 21525870	Scribble PD73	SWPGTEI	0	7	7				31	356
Densin-180 ASPDSWV Failed 2,794 CTND2_HUMAN Izawa et al. (4) 11729199 2 35 Erbin ASPDSWV 64,274 71,946 136,220 CTND2_HUMAN Laura et al. (5) 11821434 1 2 Erbin GSPDSWV 0 17,680 17,680 PKP4_HUMAN Laura et al. (5) 11821434 3 4 Erbin QPVDSWV 1,747 88 1,835 ARVC_HUMAN Laura et al. (5) 11821434 3 4 Erbin YPDYDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YPDYDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YQRHTWL 21 1 22 NXF2_HUMAN Laura et al. (5) 11821434 3 4 DLG1 PDZ1 RFLETKL 569 77 646 B722Y1_HUMAN Laura et al. (3) 21525870 1 24 DLG1 PDZ2 RKETLV 58,320 29,164 87,484 CTR2_	Densin-180	GSPDSWV	Failed	, 5 450	, 5 450	PKP4 HUMAN			1	170
Brish no. ASPDSWV 64,274 71,946 136,220 CTND2_HUMAN Laura et al. (5) 11821434 1 2 Erbin GSPDSWV 0 17,680 PKP4_HUMAN Laura et al. (5) 11821434 3 4 Erbin QPVDSWV 1,747 88 1,835 ARVC_HUMAN Laura et al. (5) 11821434 3 4 Erbin YYDYTDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YQDYTDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YQDYTDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YQPTDV 114 5 19 GA2L2_HUMAN Laura et al. (5) 11821434 1 2 1,230 DLG1 PDZ1 RKETKL 569 77 646 B722Y1_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RKETRV 58,320 29,164 87,484	Densin-180	ASPDSWV	Failed	2 794	2 794	CTND2 HUMAN	Izawa et al. (4)	11729199	2	35
Erbin GSPDSWV 0 17,680 PKP4_HUMAN Izawa et al. (6) 12047349 2 3 Erbin QPVDSWV 1,747 88 1,835 ARVC_HUMAN Laura et al. (5) 11821434 3 4 Erbin YYDYDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YQDYTDV 114 2 116 GPR87_HUMAN Laura et al. (5) 11821434 3 4 Erbin YQRHTWL 21 1 22 NXPE2_HUMAN 4 1,357 Erbin VQRHTWL 21 1 22 NXPE2_HUMAN 6 44 Erbin PEEESWV 14 5 19 GA2L2_HUMAN 6 46 DLG1 PDZ1 RKETKL 569 77 646 B7221_HUMAN 1 721 DLG1 PDZ2 LRKETRV 58,320 29,164 87,484 CLTR2_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RSISTDV 14,224 24,273 38,497	Frbin	ASPDSWV	64.274	71,946	136,220	CTND2_HUMAN	Laura et al. (5)	11821434	1	2
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Erbin YYDYTDV 114 2 116 GPR87_HUMAN 4 1,357 Erbin VQRHTWL 21 1 22 NXPE2_HUMAN 5 44 Erbin PEEESWV 14 5 19 GA2L2_HUMAN 6 46 DLG1 PDZ1 RFLETKL 569 77 646 B7Z2Y1_HUMAN 1 721 DLG1 PDZ1 QMSVHMV 131 0 131 TBX15_HUMAN Geller et al. (3) 21525870 1 24 DLG1 PDZ2 LRKETRV 58,320 29,164 87,484 CLTR2_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RKETLV 21,909 11,998 33,907 ARHG8_HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gare et al. (3) 21525870 4 1 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gare et al. (3) 21525870 4 1 DLG1 PDZ2 SKETVV 421 <td>Erbin</td> <td>OPVDSWV</td> <td>1.747</td> <td>88</td> <td>1.835</td> <td>ARVC HUMAN</td> <td>Laura et al. (5)</td> <td>11821434</td> <td>3</td> <td>4</td>	Erbin	OPVDSWV	1.747	88	1.835	ARVC HUMAN	Laura et al. (5)	11821434	3	4
Erbin VQRHTWL 21 1 22 NXPE2_HUMAN 5 44 Erbin PEEESWV 14 5 19 GA2L2_HUMAN 6 46 DLG1 PDZ1 RFLETKL 569 77 646 B722Y1_HUMAN 1 721 DLG1 PDZ1 QMSVHMV 131 0 131 TBX15_HUMAN 2 1,230 DLG1 PDZ2 LRKETRV 58,320 29,164 87,484 CLTR2_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RSISTDV 14,224 24,273 38,497 F163B_HUMAN 2 2 2 2 DLG1 PDZ2 KRKETLV 21,909 11,998 33,907 ARHG8_HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 NSKETVV 421 <td>Erbin</td> <td>YYDYTDV</td> <td>, 114</td> <td>2</td> <td>116</td> <td>GPR87 HUMAN</td> <td></td> <td></td> <td>4</td> <td>1.357</td>	Erbin	YYDYTDV	, 114	2	116	GPR87 HUMAN			4	1.357
Erbin PEEESWV 14 5 19 GA2L2_HUMAN 6 46 DLG1 PDZ1 RFLETKL 569 77 646 B7Z2Y1_HUMAN 1 721 DLG1 PDZ1 QMSVHMV 131 0 131 TBX15_HUMAN 2 1,230 DLG1 PDZ2 LRKETRV 58,320 29,164 87,484 CLTR2_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RSISTDV 14,224 24,273 38,497 F163B_HUMAN 2	Erbin	VORHTWL	21	1	22	NXPE2 HUMAN			5	44
DLG1 PDZ1 RFLETKL 569 77 646 B7Z2Y1_HUMAN 1 721 DLG1 PDZ1 QMSVHMV 131 0 131 TBX15_HUMAN 2 1,230 DLG1 PDZ2 LRKETRV 58,320 29,164 87,484 CLTR2_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RSISTDV 14,224 24,273 38,497 F163B_HUMAN 2 2 2 DLG1 PDZ2 RSISTDV 14,224 24,273 38,497 F163B_HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN Yamamoto et al. (9) 15021905 </td <td>Erbin</td> <td>PEEESWV</td> <td>14</td> <td>5</td> <td>19</td> <td>GA2L2 HUMAN</td> <td></td> <td></td> <td>6</td> <td>46</td>	Erbin	PEEESWV	14	5	19	GA2L2 HUMAN			6	46
DLG1 PDZ1 QMSVHMV 131 0 131 TBX15_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 LRKETRV 58,320 29,164 87,484 CLTR2_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RSISTDV 14,224 24,273 38,497 F163B_HUMAN 2 2 2 DLG1 PDZ2 KRKETLV 21,909 11,998 33,907 ARHG8_HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 AGRETTV 719 10,401 11,120 KIF1B_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 15	DLG1 PDZ1	RFLETKL	569	77	646	B7Z2Y1 HUMAN			1	721
DLG1 PDZ2 LRKETRV 58,320 29,164 87,484 CLTR2_HUMAN Gfeller et al. (3) 21525870 1 24 DLG1 PDZ2 RSISTDV 14,224 24,273 38,497 F1638_HUMAN 2 2 DLG1 PDZ2 KRKETLV 21,909 11,998 33,907 ARHG8_HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 AGRETTV 719 10,401 11,120 KIF1B_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 WKHETTV 483 90 573 GP125_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 155 <t< td=""><td>DLG1 PDZ1</td><td>QMSVHMV</td><td>131</td><td>0</td><td>131</td><td>TBX15 HUMAN</td><td></td><td></td><td>2</td><td>1,230</td></t<>	DLG1 PDZ1	QMSVHMV	131	0	131	TBX15 HUMAN			2	1,230
DLG1 PDZ2 RSISTDV 14,224 24,273 38,497 F163B_HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 KRKETLV 21,909 11,998 33,907 ARHG8_HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 AGRETTV 719 10,401 11,120 KIF1B_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 WKHETTV 483 90 573 GP125_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 155 340 F163A_HUMAN Yamamoto et	DLG1 PDZ2	LRKETRV	58,320	29,164	87,484	CLTR2_HUMAN	Gfeller et al. (3)	21525870	1	24
DLG1 PDZ2 KRKETLV 21,909 11,998 33,907 ARHG2 HUMAN Carr et al. (7) 19586902 3 3 DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 AGRETTV 719 10,401 11,120 KIF1B_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 WKHETTV 483 90 573 GP125_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 155 340 F163A_HUMAN 8 18 DLG1 PDZ2 WKNETTV 255 35 290 GP123_HUMAN 9 218 DLG1 PDZ2 <t< td=""><td>DLG1 PDZ2</td><td>RSISTDV</td><td>14,224</td><td>24,273</td><td>38,497</td><td>F163B_HUMAN</td><td></td><td></td><td>2</td><td>2</td></t<>	DLG1 PDZ2	RSISTDV	14,224	24,273	38,497	F163B_HUMAN			2	2
DLG1 PDZ2 SARSTDV 4,643 16,686 21,329 ANO9_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 AGRETTV 719 10,401 11,120 KIF1B_HUMAN Gfeller et al. (3) 21525870 4 1 DLG1 PDZ2 AGRETTV 719 10,401 11,120 KIF1B_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN 6 5 DLG1 PDZ2 WKHETTV 483 90 573 GP125_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 155 340 F163A_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 WKNETTV 255 35 290 GP123_HUMAN 9 218 DLG1 PDZ2 GTKSTTV 0 269 269 DCNL1_HUMAN 10 43	DLG1 PDZ2	KRKETLV	21,909	11,998	33,907	ARHG8_HUMAN	Carr et al. (7)	19586902	3	3
DLG1 PDZ2 AGRETTV 719 10,401 11,120 KIF1B_HUMAN Mok et al. (8) 12097473 5 13 DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN 6 5 DLG1 PDZ2 WSKETVV 421 279 700 MARH3_HUMAN 6 5 DLG1 PDZ2 WKHETTV 483 90 573 GP125_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 155 340 F163A_HUMAN 8 18 DLG1 PDZ2 WKNETTV 255 35 290 GP123_HUMAN 9 218 DLG1 PDZ2 GTKSTTV 0 269 269 DCNL1_HUMAN 10 43	DLG1 PDZ2	SARSTDV	4,643	16,686	21.329	ANO9 HUMAN	Gfeller et al. (3)	21525870	4	- 1
DLG1 PDZ2 NSKETVV 421 279 700 MARH3_HUMAN 6 5 DLG1 PDZ2 WKHETTV 483 90 573 GP125_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 155 340 F163A_HUMAN 8 18 DLG1 PDZ2 WKNETTV 255 35 290 GP123_HUMAN 9 218 DLG1 PDZ2 GTKSTTV 0 269 269 DCNL1_HUMAN 10 43	DLG1 PDZ2	AGRETTV	719	10,401	11,120	KIF1B HUMAN	Mok et al. (8)	12097473	5	13
DLG1 PDZ2 WKHETTV 483 90 573 GP125_HUMAN Yamamoto et al. (9) 15021905 7 41 DLG1 PDZ2 RAISTDV 185 155 340 F163A_HUMAN 8 18 DLG1 PDZ2 WKNETTV 255 35 290 GP123_HUMAN 9 218 DLG1 PDZ2 GTKSTTV 0 269 269 DCNL1_HUMAN 10 43	DLG1 PDZ2	NSKETVV	421	279	700	MARH3_HUMAN	.,		6	5
DLG1 PDZ2 RAISTDV 185 155 340 F163A_HUMAN 8 18 DLG1 PDZ2 WKNETTV 255 35 290 GP123_HUMAN 9 218 DLG1 PDZ2 GTKSTTV 0 269 269 DCNL1_HUMAN 10 43	DLG1 PDZ2	WKHETTV	483	90	573	GP125_HUMAN	Yamamoto et al. (9)	15021905	7	41
DLG1 PDZ2 WKNETTV 255 35 290 GP123_HUMAN 9 218 DLG1 PDZ2 GTKSTTV 0 269 269 DCNL1_HUMAN 10 43	DLG1 PDZ2	RAISTDV	185	155	340	F163A_HUMAN			8	18
DLG1 PDZ2 GTKSTTV 0 269 269 DCNL1_HUMAN 10 43	DLG1 PDZ2	WKNETTV	255	35	290	GP123_HUMAN			9	218
	DLG1 PDZ2	GTKSTTV	0	269	269	DCNL1_HUMAN			10	43

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Table S1. Cont.

Protein	Peptide	Library A	Library B	Total	Uniprot	Source	PMID	Rank ProP-PD	Rank Tonikian
DLG1 PDZ2	RHRNTVV	42	147	189	ERBB4_HUMAN	Huang et al. (10)	12175853	11	12
DLG1 PDZ2	MTKDTLV	60	18	78	PL8L1_HUMAN			12	42
DLG1 PDZ2	QRTHTRV	73	5	78	ZSC30_HUMAN			13	372
DLG1 PDZ2	SGISTIV	27	33	60	IQEC1_HUMAN			14	29
DLG1 PDZ2	GSPDSWV	0	54	54	PKP4_HUMAN	Izawa et al. (4)	12047349	15	314
DLG1 PDZ2	WKSETTV	42	5	47	GP124_HUMAN	Yamamoto et al. (9)	15021905	16	148
DLG1 PDZ2	GNRESVV	0	45	45	RNF12_HUMAN			17	17
DLG1 PDZ2	GGRQSVV	0	38	38	PRR5_HUMAN			18	16
DLG1 PDZ2	SSIESDV	18	18	36	NMDE2_HUMAN	Inanobe et al. (11)	11997254	19	28
DLG1 PDZ2	RDRESIV	19	16	35	SCN5A_HUMAN	Petitprez et al. (12)	21164104	20	19
DLG1 PDZ2	PGKETQL	2	29	31	SO1C1_HUMAN			21	108
DLG1 PDZ2	KIKETTV	15	12	27	FRPD4_HUMAN	Lee et al. (13)	19118189	22	38
DLG1 PDZ2	IKTETTV	12	12	24	RASF6_HUMAN			23	270
DLG1 PDZ2	DKKITTV	13	9	22	EXOC4_HUMAN	Bolis et al. (14)	19587293	24	451
DLG1 PDZ2	VQRHTWL	15	3	18	NXPE2_HUMAN			25	33
DLG1 PDZ2	DRKETSI	8	9	17	RBP1_HUMAN			26	70
DLG1 PDZ2	TSRETDL	13	0	13	KCNA5_HUMAN	Mathur et al. (15)	16466689	27	4
DLG1 PDZ2	KAVETDV	5	5	10	KCNA4_HUMAN	Kim et al. (16)	7477295	28	9
DLG1 PDZ2	YRRESEI	7	0	7	IRK12_HUMAN	Leonoudakis et al. (17)	14960569	29	267
DLG1 PDZ2	ASPDSWV	1	6	7	CTND2_HUMAN			30	429
DLG1 PDZ3	LRKETRV	146285	89,316	235,601	CLTR2_HUMAN	Gfeller et al. (3)	21525870	1	2
DLG1 PDZ3	NYKQTSV	287	622	909	CRIPT_HUMAN	Cai et al. (18)	12070168	2	1
DLG1 PDZ3	KRKETLV	18	4	22	ARHG8_HUMAN	Carr (6)	19586902	3	5

Library A and Library B, the sequencing counts for a given peptide from the replicate selection; Peptide, the selected C-terminal peptides; Protein, the identity of the bait PDZ domain; Rank ProP-PD, the rank of a peptide based on the selection (1: sequence with the highest total sequencing counts); Rank Tonikian PWM, predicted rank of a selected peptide using position specific scoring matrices based on the data of Tonikian et al. (18) among all sequences in the designed human ProP-PD library Reference, reference to a supporting publication with Pubmed id in PMID; Total, total sequencing counts of a given peptide; Uniprot, the Uniprot entry corresponding to a selected peptide.

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Table S2. Comprehensive list of identified viral targets stating interacting PDZ domains, peptide sequences, sequencing counts, and literature reference, when applicable

							Source (for the protein,	
Protein	Pentide	Count A	Count B	Total	Uniprot	Name	not always the exact variant)	PMID
		count A	21 596	21 506			Nakagawa	11027202
SCHOOLE PDZ1	RREIAL	x	21,500	21,300	VE0_HPV35	type 33 protein E6	and Huibregtse (1)	11027295
Scribble PDZ1	TRRETQL	х	175	175	VE6_HPV16	Human papillomavirus	Nakagawa	11027293
Scribble PDZ1	PDTDWLV	x	62	62	LRP2 HHV1F	type 16 protein E6 Human herpesvirus 1	and Hulbregtse (1)	
					_	latency-related protein 2		
Scribble PDZ2	HFREIEV	3,827	49,903	53,/30	IAX_HIL1F	virus 1 protein Tax-1	Arpin-Andre and Mesnard (2)	1/8553/2
Scribble PDZ2	HFHETEV	26	474	500	TAX_HTL1L	Human T-cell leukemia	Arpin-André and Mesnard (2)	17855372
Scribble PDZ3	RRRETAL	118,682	69,771	188,453	VE6 HPV33	Human papillomavirus	Nakagawa	11027293
	TRAFTO	20 722	20.067	50.000		type 33 protein E6	and Huibregtse (1)	44007000
Scribble PDZ3	TRRETQL	28,733	29,867	58,600	VE6_HPV16	type 16 protein E6	and Huibregtse (1)	11027293
Scribble PDZ3	HFRETEV	110	589	699	TAX_HTL1F	Human T-cell leukemia	Arpin-André (2)	17855372
Scribble PDZ3	TRRETEV	81	130	211	VE6 HPV35	virus 1 protein Tax-1 Human papillomavirus	Nakagawa	11027293
						type 35 protein E6	and Huibregtse (1)	
Scribble PDZ3	TRRETQV	39	145	184	VE6_HPV39	Human papillomavirus	Nakagawa and Huibregtse (1)	11027293
Scribble PDZ3	AIFSTDI	1	81	82	YVDA_VACCW	Vaccinia virus uncharacterized		
Scribble DD72	SCOTTRI	2	75	77		9.2 kDa protein		
Scribble PDZ3	TGRSTTL	2	64	72	VGLG_KABVV	Sheeppox virus putative		
						fusion protein		
Scribble PDZ3	IRRETQV	24	41	65	VE6_HPV70	Human papillomavirus	Nakagawa and Huibreatse (1)	11027293
Scribble PDZ3	RRRETQV	2	61	63	VE6_HPV45	Human papillomavirus	Nakagawa	11027293
Scribble PD73		6	20	45		type 45, protein E6 Human T. coll Joukomia	and Huibregtse (1)	18661220
SCIDDLE FDZS	HEHEV	0	29	45	TAA_HILIL	virus 1 protein Tax-1	Okajima et al. (5)	10001220
Scribble PDZ3	PFSSSDL	4	15	19	GAG_MLVAB	Abelson murine leukemia		
Scribble PDZ3	LNYETNL	1	13	14	ENV_HTL3P	Human T-cell leukemia		
						virus 3 envelope		
Frhin		7	3 235	3 242	VEMP ВСНКА	glycoprotein gp63 Bat coronavirus Envelope		
		,	5,255	5,242	VEINI _DCI IIC4	small membrane protein		
Erbin	YPPEDWV	5	699	704	VEMP_BCHK5	Bat coronavirus Envelope		
Erbin	RRRETAL	4	407	411	VE6_HPV33	Human papillomavirus		
Frhin		2	210	221		type 33 protein E6		
Erdin	DKLDINVVV	2	319	321	VPU_HVIYB	protein Vpu		
Erbin	IDQDNWV	4	220	224	VPU_SIVEK	Simina immunodeficiency		
Erbin	TRRETQL	0	168	168	VE6 HPV16	virus protein Vpu Human papillomavirus		
					_	type 16 protein E6		
Erbin	ATCTFTL	2	106	108	VP23_ELHVK	Elephantid herpesvirus 1, triplex capsid protein U56		
Erbin	IRRETQV	6	92	98	VE6_HPV70	Human papillomavirus		
Frhin	ΔΤΗΙ ΙΝΙΔ	5	83	88	11021 ASEW/A	type 70, protein E6 African swine fever virus		
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	5	05	00	11022_/01107	protein MGF 110–2L		
Erbin	APSVLTV	2	80	82	NS3D_BCHK5	Bat coronavirus KHU5		
Erbin	AVNFSTL	1	74	75	OBP_HHV2H	Human herpesvirus 2 replication		
Frhin	HEBETE//	0	7/	7/	TAX HTI 15	origin-binding protein	Song et al. (1)	10/77101
		U	/4	/4		protein Tax-1	Jong et al. (4)	1,5412131
DLG1 PDZ1	IRRETQV	283	539	822	VE6_HPV70	Human papillomavirus type 70,	Gardiol et al. (5)	10523825
DLG1 PDZ1	TRRETQV	406	132	538	VE6_HPV39	Human papillomavirus type 39 protein E6	Gardiol et al. (5)	10523825

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Protein	Peptide	Count A	Count B	Total	Uniprot	Name	Source (for the protein, not always the exact variant)	PMID
DLG1 PDZ2	IRRETQV	102,877	71,200	174,077	VE6_HPV70	Human papillomavirus type 70. protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	TRRETQV	17,861	24,016	41,877	VE6_HPV39	Human papillomavirus type 39 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	TRRETEV	4,089	4,716	8,805	VE6_HPV35	Human papillomavirus type 35 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	TGRSTEV	1,223	6,115	7,338	VU47_HHV6U	Human herpesvirus 6A glycoprotein U47	Blot et al. (6)	15286176
DLG1 PDZ2	RRRETQV	2,679	4,196	6,875	VE6_HPV18/45	Human papillomavirus type 18/45 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	RGIESEV	329	1,321	1,650	NS1_I63A1	Influenza A virus (Avian) nonstructural protein 1	Liu et al. (7)	20702615
DLG1 PDZ2	RRRETAL	382	706	1,088	VE6_HPV33	Human papillomavirus type 33 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	HFRETEV	100	534	634	TAX_HTL1F	Human T-cell leukemia virus 1 protein Tax-1	Lee et al. (8)	9192623
DLG1 PDZ2	TRRETQL	175	359	534	VE6_HPV16	Human papillomavirus type 16 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	TRQETQV	22	323	345	VE6_HPVME	Human papillomavirus type ME180 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	IRQETQV	46	293	339	VE6_HPV68	Human papillomavirus type 68 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	RHRETYV	25	133	158	US32_HCMVA	Human cytomegalovirus, uncharacterized protein HHRF7		
DLG1 PDZ2	PRTETQV	9	139	148	VE6_HPV31	Human papillomavirus type 31 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	RQTETQV	8	101	109	VE6_HPV26	Human papillomavirus type 26 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	QRNETQV	24	72	96	VE6_HPV51	Human papillomavirus type 51 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	RRIESEV	3	22	25	NS1_I49A1	Influenza A virus (Avian) nonstructural protein 1	Liu et al. (7)	20702615
DLG1 PDZ2	RRVESEV	3	18	21	NS1_I82A8	Influenza A virus (Avian) nonstructural protein 1	Liu et al. (7)	20702615
DLG1 PDZ2	RRRQTQV	0	11	11	VE6_HPV58	Human papillomavirus type 58 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ2	TGRSTTL	1	9	10	VFUS_SHEVK	Sheeppox virus putative fusion protein		
DLG1 PDZ3	IRRETQV	61,437	31,152	92,589	VE6_HPV70,	Human papillomavirus type 70, protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ3	TRRETQV	19,459	10,283	29,742	VE6_HPV39,	Human papillomavirus type 39 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ3	RRRETQV	2,336	8,525	10,861	VE6_HPV45,	Human papillomavirus type 18/45 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ3	RRRETAL	1,213	1,297	2,510	VE6_HPV33,	Human papillomavirus type 33 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ3	TRRETEV	90	227	317	VE6_HPV35,	Human papillomavirus type 35 protein E6	Gardiol et al. (5)	10523825
DLG1 PDZ3	RHRETYV	26	49	75	US32_HCMVA	Human cytomegalovirus, uncharacterized protein HHRF7		

Column labels are as in Table S1, plus a "Name" describing the protein and virus.

1. Nakagawa S, Huibregtse JM (2000) Human scribble (Vartul) is targeted for ubiquitin-mediated degradation by the high-risk papillomavirus E6 proteins and the E6AP ubiquitin-protein ligase. Mol Cell Biol 20(21):8244–8253.

2. Arpin-André C, Mesnard JM (2007) The PDZ domain-binding motif of the human T cell leukemia virus type 1 tax protein induces mislocalization of the tumor suppressor hScrib in T cells. J Biol Chem 282(45):33132–33141.

3. Okajima M, et al. (2008) Human T-cell leukemia virus type 1 Tax induces an aberrant clustering of the tumor suppressor Scribble through the PDZ domain-binding motif dependent and independent interaction. Virus Genes 37(2):231–240.

4. Song C, et al. (2009) Tax1 enhances cancer cell proliferation via Ras-Raf-MEK-ERK signaling pathway. IUBMB Life 61(6):685–692.

 Gardiol D, et al. (1999) Oncogenic human papillomavirus E6 proteins target the discs large tumour suppressor for proteasome-mediated degradation. Oncogene 18(40):5487–5496.
Blot V, et al. (2004) Human Dlg protein binds to the envelope glycoproteins of human T-cell leukemia virus type 1 and regulates envelope mediated cell-cell fusion in T lymphocytes. J Cell Sci 117(Pt 17):3983–3993.

7. Liu H, et al. (2010) The ESEV PDZ-binding motif of the avian influenza A virus NS1 protein protects infected cells from apoptosis by directly targeting Scribble. J Virol 84(21):11164–11174.

8. Lee SS, Weiss RS, Javier RT (1997) Binding of human virus oncoproteins to hDlg/SAP97, a mammalian homolog of the Drosophila discs large tumor suppressor protein. Proc Natl Acad Sci USA 94(13):6670–6675.

Table S3. Selected peptides of low interest to this study

PDZ domain	Peptide	Protein	# Library A	# Library B	Total count
Additional target pe	ptides from the prote	olytic TopFind set			
Scribble PDZ1	DRDYMGW	CCKN_HUMAN, CLEAVAGE-8141	343	0	343
Scribble PDZ2	GFYESDV	A2MG_HUMAN CLEAVAGE-593	1	328	329
Scribble PDZ3	GFYESDV	A2MG_HUMAN CLEAVAGE-593	0	242	242
Scribble PDZ3	WTTSTDL	AMPH_HUMAN INFERRED FROM	1,823	62	1,885
		CLEAVAGE-4706			
Additional target pe	ptides from the ENSEN	/IBL-only set			
Scribble PDZ1	KTYETDL	ENSP00000447314	1,326	56	1,382
Scribble PDZ3	KTYETDL	ENSP00000447314	2,224	12,398	14,622
Scribble PDZ3	LLRETSL	ENSP00000420911	97	0	97
Scribble PDZ3	VSRETKL	ENSP00000415771	0	85	85
Scribble PDZ3	GIRESKL	ENSP00000399301	0	79	79
Scribble PDZ3	GVRKETA	ENSP00000451805	0	20	20
Scribble PDZ3	FSEGTDL	ENSP00000440057	0	10	10
Scribble PDZ3	AGKTTIL	ENSP00000450315	0	8	8
Erbin	QENDWWV	ENSP00000398110	28,359	1,117	29,476
Erbin	QHHWESW	ENSP00000270281	0	40	40
DLG1 PDZ2	FPKETQV	ENSP00000442101	0	2,275	2,275
DLG1 PDZ2	SGTAYLL	ENSP00000449745	8	7	1

The peptides correspond to protein C termini either only supported by an experiment in TopFind (resulting from proteolytic cleavage or COFRADIC-based complementary positional proteomics experiments) or only found in ENSEMBL. PDZ domain, the identity of the bait PDZ domain; Peptide, the selected C-terminal peptides; Protein, the identifier corresponding to a selected peptide and the cleavage site when applicable; # Library A and # Library B, the sequencing counts for a given peptide from the replicate selection.

Other Supporting Information Files

Dataset S1 (XLSX) Dataset S2 (XLSX)

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