Intrinsic Disorder in PTEN and its Interactome Confers Structural Plasticity and Functional Versatility

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Supplementary Material List

SUPPLEMENTARY FIGURES

Supplementary Figure Legends

Supplementary Figure S1: Mutational Analysis for the PTEN protein

PTEN mutations from two databases cBioPortal for Cancer Genomics and the Roche Cancer Genome Database were analyzed. The number of mutations occurring in each amino acid residue was plotted. The PTEN C-tail IDR region is indicated in red.

Supplementary Figure S2: Sequence alignments for PTEN catalytic dual phosphatase motif

Sequence alignments were performed for the PTEN protein from vertebrates and invertebrates. All of the species considered show a conserved catalytic motif HCKAGKGR. All FASTA sequences for the PTEN protein were retrieved from UniProt. The sequence alignments were performed using Clustal Omega.

Supplementary Figure S3: Sequence alignments for PTEN C-tail interacting proteins

A literature review helped identify the interaction domains/motifs in thirteen PTEN C-tail interacting proteins. The interaction domain details as well as the relevant references are part of the table. Sequence alignments were performed for these thirteen PTEN C-tail interacting proteins: neprilysin, NHERF1, NHERF2, MSP58, Prex2, sharpin, MAGI1, MAGI2, MAGI3, MAST1, MAST2, MAST3 and DLG1. The alignments are restricted to the PTEN interaction motifs in these proteins (as indicated in the table). The sequence alignments have been performed for vertebrate animals and invertebrate animals (wherever available).Conserved residues are indicated in red. Short motifs that are known to be critical for interaction with PTEN are highlighted in yellow. Most of these PTEN C-tail interaction motifs show good sequence conservation across species. This indicates that the PTEN tail has evolved in vertebrates so as to incorporate features that allow interaction with these conserved domains. All FASTA sequences for the proteins were retrieved from UniProt. The sequence alignments were performed using Clustal Omega.

Supplementary Figure S4: MoRF prediction for PTEN.

MoRFpred (Disfani et al, 2012), a computational tool, was used to identify MoRF regions within the PTEN protein. The output for PTEN is illustrated with the MoRF regions highlighted in red.

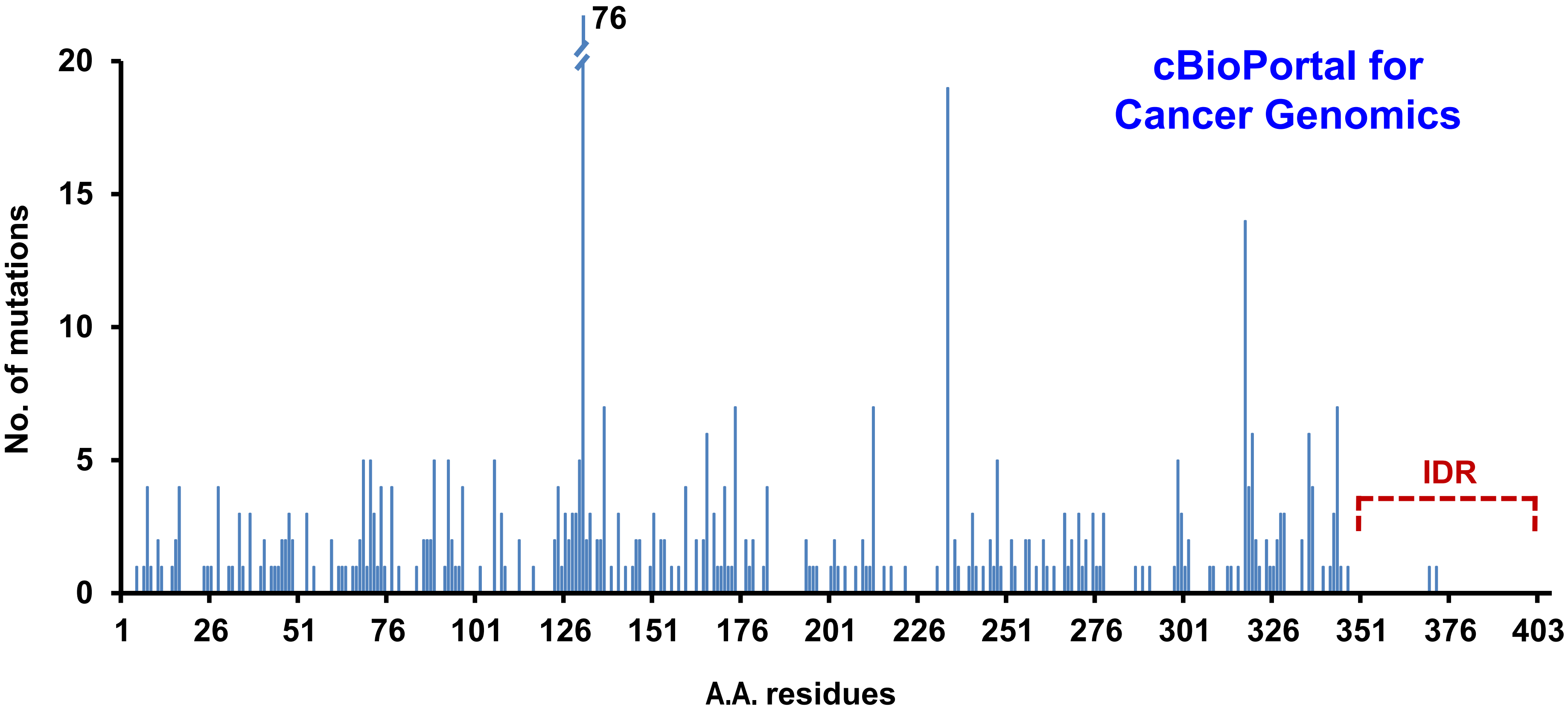
Supplementary Figure S5: ELMs output for PTEN

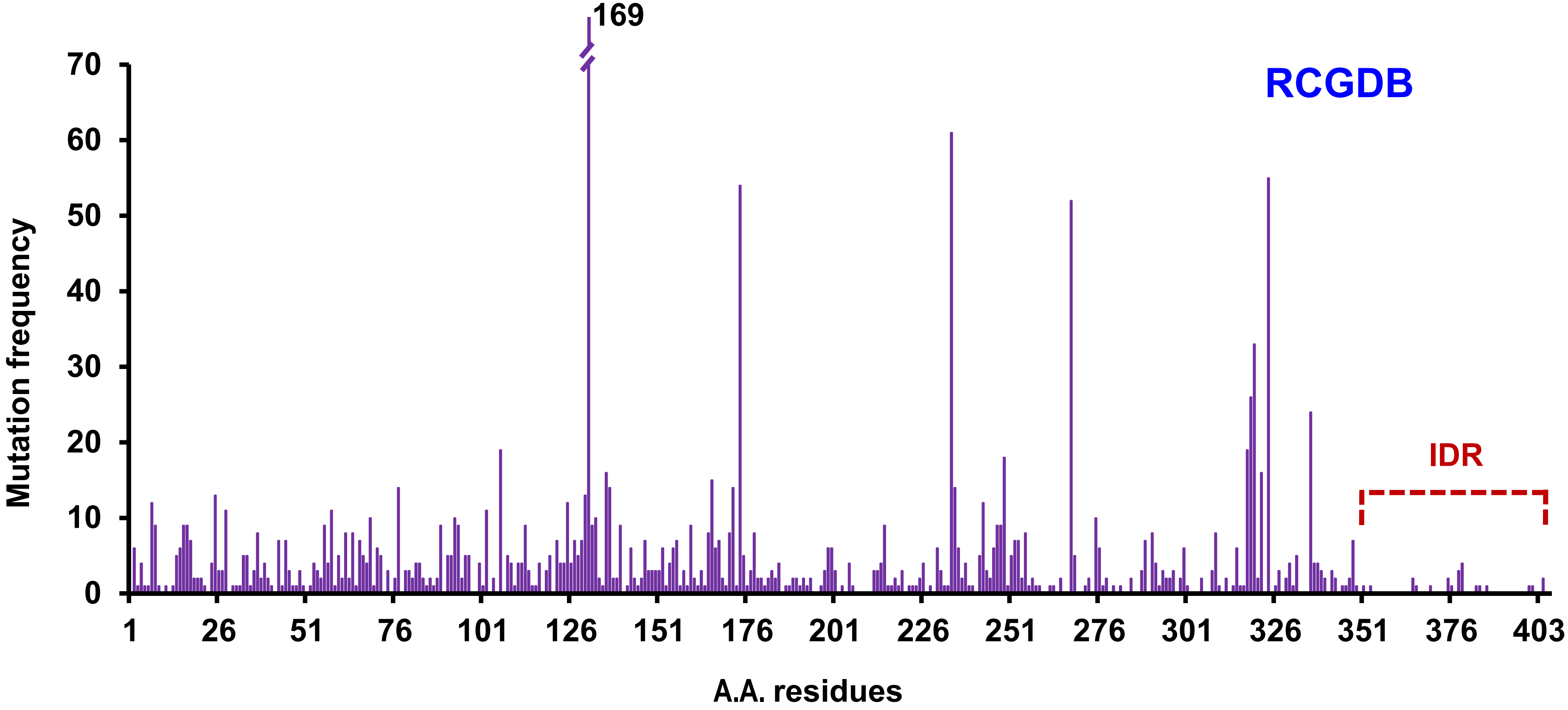
ELM output for PTEN (Redrawn from the output from ELM; http://elm.eu.org/). We ran the ELM software with PTEN as the query protein. The query protein is scanned for annotated ELMs. Several other tools are used in conjunction to reveal structural information about the query protein. SMART is used to detect protein domains. IUPred is used to predict any disorder within the protein structure. IUPred uses a cut-off of 0.5, regions having values above 0.5 are considered to be disordered and those below 0.5 are considered to be ordered. IUPred helps correlate the occurrence of ELMs with disorder in a protein structure. The output also shows a conservation score for each of the motifs. Generally, it is observed that the conserved motifs appear to be the ones which are functional. Conservation is calculated using a tree-based method with lighter shades of blue representing a lower conservation score while darker shades represent higher conservation scores. Details regarding the phosphorylation modifications occurring within the protein sequence are obtained from the Phospho.ELM database (Dinkel et al, 2012). The ELM output for PTEN shows that it possesses several linear motifs distributed throughout the length of the protein. It is interesting, however, to note that linear motifs with a high conservation score are restricted to the disordered C-tail region indicating its functional significance in PTEN function.

Supplementary Figure S6: DISPHOS prediction for PTEN.

DISPHOS (Iakoucheva, Radivojac et al, 2004), a structural disorder based phosphorylation prediction software was used to identify residues within the PTEN protein that are modified through phosphorylation events. The software predicts all of the serine and threonine sites modified by phosphorylation with the exception of T382 and T383. The software, however, fails to pick up any of the currently documented tyrosine phosphorylation sites.

Supplementary Figure S1
Mutational Analysis for the PTEN protein

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RCGDB
IDR
Mutation frequency
0
10
20
30
40
50
60
70
1
26
51
76
101
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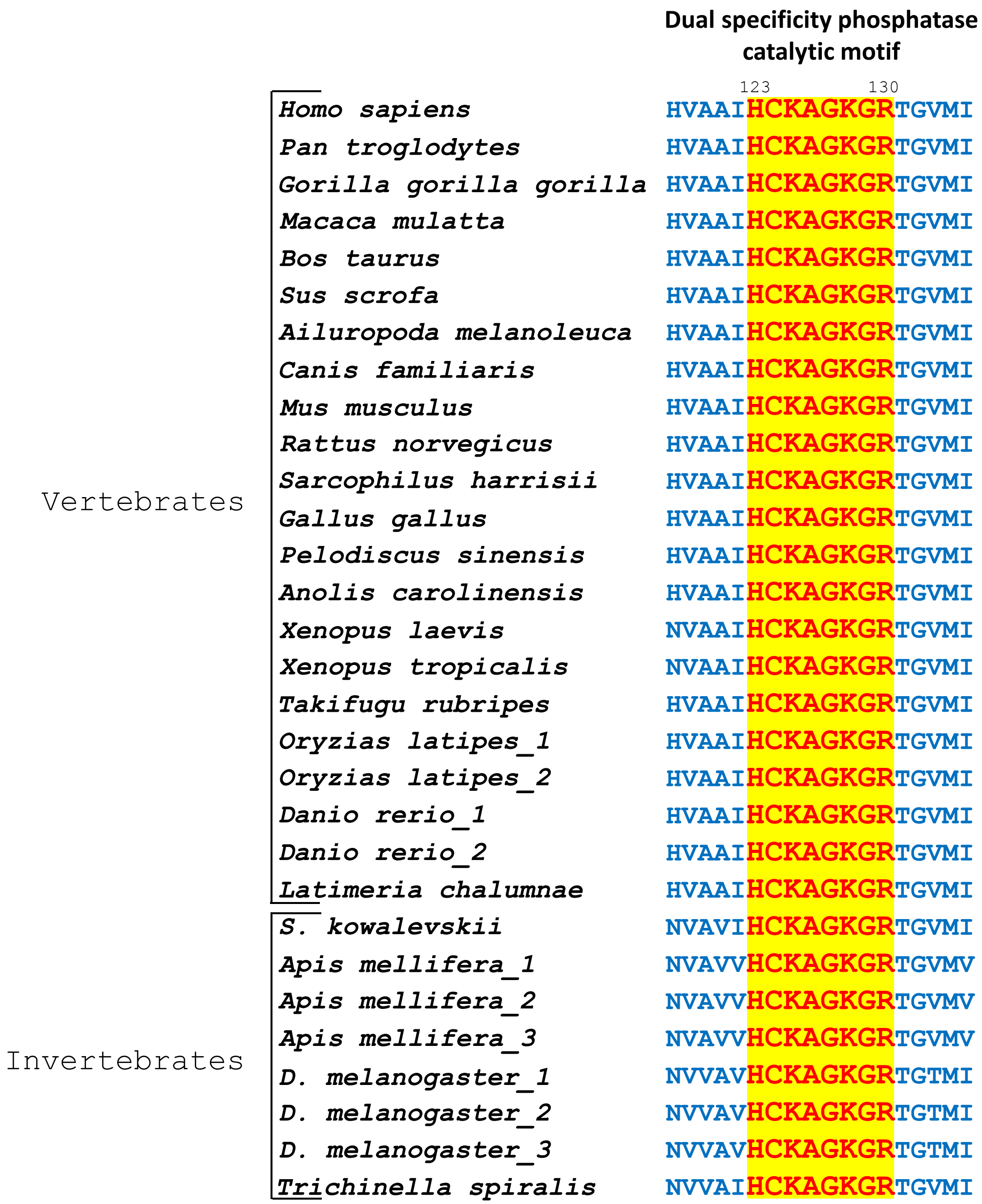
176
201
226
251
276
301
326
351
376
403
A.A. residues

Supplementary Figure S2
Sequence alignments for PTEN catalytic dual phosphatase motif



Dual specificity phosphatase catalytic motif

123 130

Vertebrates	*Homo sapiens*	HVAAI**HCKAGKGR**TGVMI
	Pan troglodytes	HVAAI**HCKAGKGR**TGVMI
	Gorilla gorilla gorilla	HVAAI**HCKAGKGR**TGVMI
	Macaca mulatta	HVAAI**HCKAGKGR**TGVMI
	Bos taurus	HVAAI**HCKAGKGR**TGVMI
	Sus scrofa	HVAAI**HCKAGKGR**TGVMI
	Ailuropoda melanoleuca	HVAAI**HCKAGKGR**TGVMI
	Canis familiaris	HVAAI**HCKAGKGR**TGVMI
	Mus musculus	HVAAI**HCKAGKGR**TGVMI
	Rattus norvegicus	HVAAI**HCKAGKGR**TGVMI
	Sarcophilus harrisii	HVAAI**HCKAGKGR**TGVMI
	Gallus gallus	HVAAI**HCKAGKGR**TGVMI
	Pelodiscus sinensis	HVAAI**HCKAGKGR**TGVMI
	Anolis carolinensis	HVAAI**HCKAGKGR**TGVMI
	Xenopus laevis	NVAAI**HCKAGKGR**TGVMI
	Xenopus tropicalis	NVAAI**HCKAGKGR**TGVMI
	Takifugu rubripes	HVAAI**HCKAGKGR**TGVMI
	Oryzias latipes_1	HVAAI**HCKAGKGR**TGVMI
	Oryzias latipes_2	HVAAI**HCKAGKGR**TGVMI
	Danio rerio_1	HVAAI**HCKAGKGR**TGVMI
	Danio rerio_2	HVAAI**HCKAGKGR**TGVMI
	Latimeria chalumnae	HVAAI**HCKAGKGR**TGVMI
Invertebrates	*S. kowalevskii*	NVAVI**HCKAGKGR**TGVMI
	Apis mellifera_1	NVAVV**HCKAGKGR**TGVMV
	Apis mellifera_2	NVAVV**HCKAGKGR**TGVMV
	Apis mellifera_3	NVAVV**HCKAGKGR**TGVMV
	D. melanogaster_1	NVVAV**HCKAGKGR**TGTMI
	D. melanogaster_2	NVVAV**HCKAGKGR**TGTMI
	D. melanogaster_3	NVVAV**HCKAGKGR**TGTMI
	Trichinella spiralis	NVVAI**HCKAGKGR**TGVMI

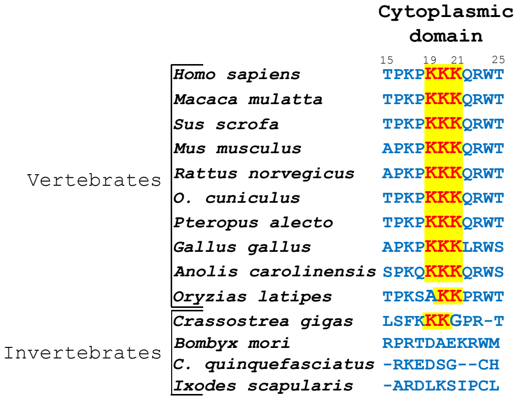
Supplementary Figure S3

Sequence alignments for PTEN C-tail interacting proteins

Binding partner	Interaction interface in PTEN C-tail	Interaction interface in the binding partner	Reference
Neprilysin	AA 379-385 of PTEN	A triple lysine residue in cytoplasmic domain	[1]
NHERF1	PDZ binding motif of PTEN	Q37 residue in the PDZ1 domain	[2]
NHERF2	PDZ binding motif of PTEN	PDZ1 domain	[2]
MSP58	C-terminal region of PTEN (interaction requires Thr366)	Forkhead Association (FHA) Domain	[3]
PREX2	C-terminal region of PTEN (not including the PDZ domain)	Pleckstrin Homology (PH) domain	[4]
Sharpin	Amino and C-terminus of PTEN	Ubiquitin Like (UBL) domain	[5]
MAGI-1b	PDZ binding motif	2nd PDZ domain	[6]
MAGI-2	PDZ binding motif	2nd PDZ domain	[7]
MAGI-3	PDZ binding motif	2nd PDZ domain	[8]
MAST1	PDZ binding motif	PDZ domain	[9]
MAST2	PDZ binding motif	PDZ domain	[9, 10]
MAST3	PDZ binding motif	PDZ domain	[9, 11]
DLG1	PDZ binding motif	2nd PDZ domain	[10]

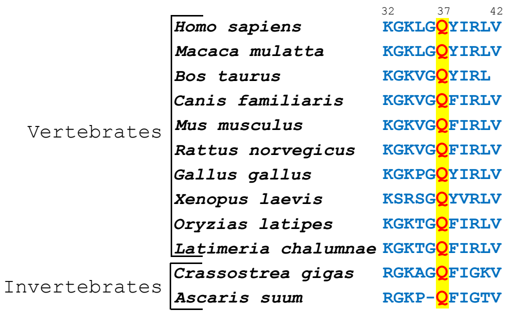
Sequence alignments for PTEN C-tail interacting proteins

Neprilysin



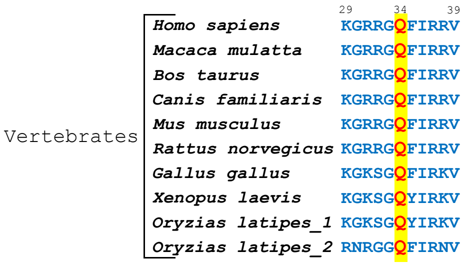
		Cytoplasmic domain 15 19 21 25
Vertebrates	*Homo sapiens*	TPKPKKKQRWT
	Macaca mulatta	TPKPKKKQRWT
	Sus scrofa	TPKPKKKQRWT
	Mus musculus	APKPKKKQRWT
	Rattus norvegicus	APKPKKKQRWT
	O. cuniculus	TPKPKKKQRWT
	Pteropus alecto	TPKPKKKQRWT
	Gallus gallus	APKPKKKLRWS
	Anolis carolinensis	SPKQKKKQRWS
	Oryzias latipes	TPKSAKKPRWT
Invertebrates	*Crassostrea gigas*	LSFKKKGPR-T
	Bombyx mori	RPRTDAEKRWM
	C. quinquefasciatus	-RKEDSG--CH
	Ixodes scapularis	-ARDLKSIPCL

NHERF1



		32 37 42
Vertebrates	*Homo sapiens*	KGKLGQYIRLV
	Macaca mulatta	KGKLGQYIRLV
	Bos taurus	KGKVGQYIRL
	Canis familiaris	KGKVGQFIRLV
	Mus musculus	KGKVGQFIRLV
	Rattus norvegicus	KGKVGQFIRLV
	Gallus gallus	KGKPGQYIRLV
	Xenopus laevis	KSRSGQYVRLV
	Oryzias latipes	KGKTGQFIRLV
	Latimeria chalumnae	KGKTGQFIRLV
Invertebrates	*Crassostrea gigas*	RGKAGQFIGKV
	Ascaris suum	RGKP-QFIGTV

NHERF2



		29 34 39
Vertebrates	*Homo sapiens*	KGRRGQFIRRV
	Macaca mulatta	KGRRGQFIRRV
	Bos taurus	KGRRGQFIRRV
	Canis familiaris	KGRRGQFIRRV
	Mus musculus	KGRRGQFIRRV
	Rattus norvegicus	KGRRGQFIRRV
	Gallus gallus	KGKSGQFIRKV
	Xenopus laevis	KGKSGQYIRKV
	Oryzias latipes_1	KGKSGQYIRKV
	Oryzias latipes_2	RNRGGQFIRNV

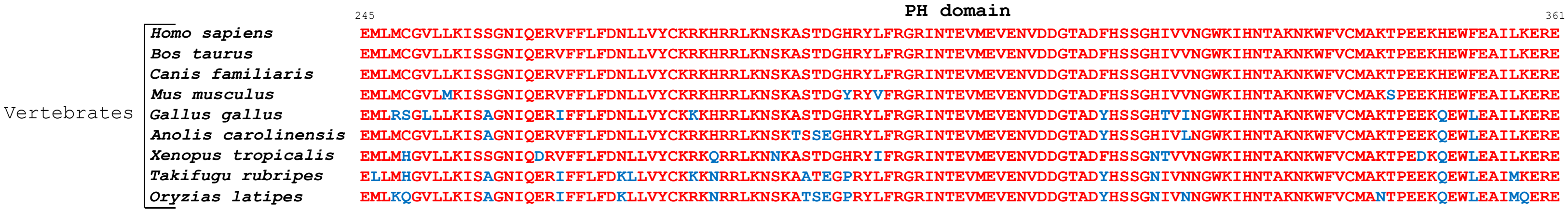
MSP58

		FHA domain 363 419
Vertebrates	*Homo sapiens*	EITLGRATKDNQIDVDLSLEGPAWKISRKQGVIKLKNNGDFFIANEGRRPIYIDGRP
	Macaca mulatta	EITLGRATKDNQIDVDLSLEGPAWKISRKQGVIKLKNNGDFFIANEGRRPIYIDGRP
	Bos taurus	EITLGRATKDNQIDVDLSLEGPAWKISRKQGVIKLKNNGDFFIANEGRRPIYIDGRP
	Canis familiaris	EITLGRATKDNQIDVDLSLEGPAWKISRKQGVIKLKNNGDFFIANEGRRPIYIDGRP
	Mus musculus	EITLGRATKDNQIDVDLSLEGPAWKISRKQGVIKLKNNGDFFIANEGRRPIYIDGRP
	Rattus norvegicus	EITLGRATKDNQIDVDLSLEGPAWKISRKQGVIKLKNNGDFFIANEGRRPIYIDGRP
	Gallus gallus	EITLGRATKDNQIDVDLALEGPAWKISRKQGVIKLKNNGDFFIANEGRRPIYIDGRP
	Xenopus laevis	EITLGRATKDNQIDVDLSLEGPAWKISRKQGVIKLKNNGDFFLANEGRRAIYIDGRP
	Oryzias latipes	EITLGRATKDKQVDVDLSLEGPAWKISRKQGIIKLKNNGDFFIANEGRRPIYIDGRP
	Latimeria chalumnae	EITLGRATKDNQIDVDLSLEGPAWKISRKQGIIKLKNNGDFFIANEGRRPVYIDGRP
Invertebrates	*Crassostrea gigas*	EITLGRATKDNQIDVDLSLEGPAWKISRRQGIIKLRSNGDFFLANEGKRPFYVDGKA
	Danaus plexippus	EIAVGRSTRDHTIDVDLSLEGPAAKVSRKQATIRLRNSGDFFMSSEGKRPIFVDGRP
	C. quinquefasciatus	EIVFGRSTKDATVDVDFSLEGPAYKVSRKQGTIKLRSNGDFFITNEGKRPLYIDGTA
	Ixodes scapularis	EITIGRATKDSAIDVDLSLEGPAWKVSRRQGVVKLRNTGEFIIANEGKRPIYIDGKP
	Trichinella spiralis	--TDKSPESVKTIINELTKGGSSVKCGQQIDKLTVRGGSE-----------------
	C. elegans	SVTMGRASLNEKIDIDLSKEGPATKVSRQQAVICHVADDKFTIQNVGQRIMYVDSKP

Sharpin

		UBL domain 240 300
Vertebrates	*Homo sapiens*	ALQVHPHCTVAALQEQVFSELGFPPAVQRWVIGRCLCVPERSLASYGVRQDGDPAFLYLLS
	Macaca mulatta	ALQVHPHCTVAALQEQVFSELGFPPAVQRWVIGRCLCVPERSLASYGVRQDGDPAFLYLLS
	Bos taurus	SLQVHPHCTIRALQEQVFSEFGFPPAVQRWVIGRCLCVPEHSLAFYGVQRDGDPAFLYLLS
	Sus scrofa	SLQVHPHCTIRALQEQVFSEFGFPPAVQRWVIGRCLCAPECSLASYGVRRDGDPAFLYLLS
	Mus musculus	SLQVHPHCTIATLQEQVFSEFGFPPAVQRWVIGQCLCVPERSLASYGVRRDGDPAFLYLLS
	Canis familiaris	SLKIHPHCSIAALQDQVFSEFGFPPAVQRWVIGRCLCMPERSLASYGVSQDGDPAFLYLLS
	Rattus norvegicus	SLQIHPHCSIAALQEQVFSEFGFPPAVQRWVIGRCLCMPERSLASYGVSQDGDPAFLYLLS
	Takifugu rubripes	TVKVFPHMTTAALKQQVFLEYGFHPRVQRWVIGQCLCADQRSLASYGVHQDGDTAFLYLLS

PREX2



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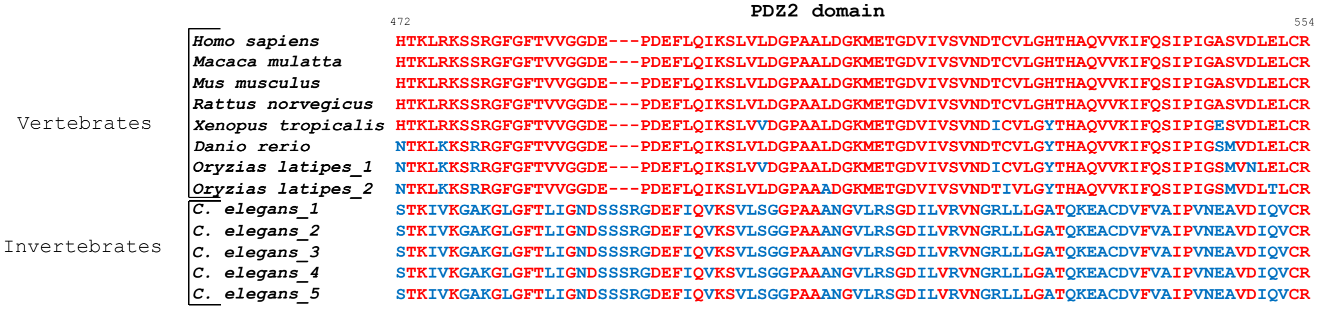
Bos taurus	EMLMCGVLLKISSGNIQERVFFLFDNLLVYCKRKHRRLKNSKASTDGHRYLFRGRINTEVMEVENVDDGTADFHSSGHIVVNGWKIHNTAKNKWFVCMAKTPEEKHEWFEAILKERE
Canis familiaris	EMLMCGVLLKISSGNIQERVFFLFDNLLVYCKRKHRRLKNSKASTDGHRYLFRGRINTEVMEVENVDDGTADFHSSGHIVVNGWKIHNTAKNKWFVCMAKTPEEKHEWFEAILKERE
Mus musculus	EMLMCGVLMKISSGNIQERVFFLFDNLLVYCKRKHRRLKNSKASTDGYRYVFRGRINTEVMEVENVDDGTADFHSSGHIVVNGWKIHNTAKNKWFVCMAKSPEEKHEWFEAILKERE
Gallus gallus	EMLRSGLLLKISAGNIQERIFFLFDNLLVYCKKKHRRLKNSKASTDGHRYLFRGRINTEVMEVENVDDGTADYHSSGHTVINGWKIHNTAKNKWFVCMAKTPEEKQEWLEAILKERE
Anolis carolinensis	EMLMCGVLLKISAGNIQERVFFLFDNLLVYCKRKHRRLKNSKTSSEGHRYLFRGRINTEVMEVENVDDGTADYHSSGHIVLNGWKIHNTAKNKWFVCMAKTPEEKQEWLEAILKERE
Xenopus tropicalis	EMLMHGVLLKISSGNIQDRVFFLFDNLLVYCKRKQRRLKNNKASTDGHRYIFRGRINTEVMEVENVDDGTADFHSSGNTVVNGWKIHNTAKNKWFVCMAKTPEDKQEWLEAILKERE
Takifugu rubripes	ELLMHGVLLKISAGNIQERIFFLFDKLLVYCKKKNRRLKNSKAATEGPRYLFRGRINTEVMEVENVDDGTADYHSSGNIVNNGWKIHNTAKNKWFVCMAKTPEEKQEWLEAIMKERE
Oryzias latipes	EMLKQGVLLKISAGNIQERIFFLFDKLLVYCKRKNRRLKNSKATSEGPRYLFRGRINTEVMEVENVDDGTADYHSSGNIVNNGWKIHNTAKNKWFVCMANTPEEKQEWLEAIMQERE

DLG1

Homo sapiens	EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCLEEVTHEEAVTALKNTSDFVYLKVAKP
Macaca mulatta	EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCLEEVTHEEAVTALKNTSDFVYLKVAKP
Canis familiaris	EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNSVCLEEVTHEEAVTALKNTSDFVYLKVAKP
Mus musculus	EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNSVCLEEVTHEEAVTALKNTSDFVYLKVAKP
Rattus norvegicus	EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNSVCLEEVTHEEAVTALKNTSDFVYLKVAKP
Xenopus tropicalis	DIKLVKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGRLQIGDKLLAVNTVCLEEVSHEDAVTALKNTSDFVNLKVAKP
Danio rerio	DVKLVKGPKGLGFSIAGGVGNQHIPGDNSIYITKIIEGGAAHKDGRLQIGDKLLAVNAVCLEEVTHEDAVAALKNTPDVVYLKVAKP
Oryzias latipes	EIKLVKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGSLQIGDKLLAVNSSCLEEVSHEHAVTALKNTPDVVYLKVAKP
Latimeria chalumnae	EIKLVKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGRLQIGDKLLAVNTVCLEEVTHEDAVTALKNTSDIVYLKVAKP

MAGI-1



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Macaca mulatta       HTKLRKSSRGFGFTVVGGDE---PDEFLQIKSLVLDGPAALDGKMETGDVIVSVNDTCVLGHTHAQVVKIFQSIPIGASVDLELCR
Mus musculus         HTKLRKSSRGFGFTVVGGDE---PDEFLQIKSLVLDGPAALDGKMETGDVIVSVNDTCVLGHTHAQVVKIFQSIPIGASVDLELCR
Rattus norvegicus    HTKLRKSSRGFGFTVVGGDE---PDEFLQIKSLVLDGPAALDGKMETGDVIVSVNDTCVLGHTHAQVVKIFQSIPIGASVDLELCR
Xenopus tropicalis   HTKLRKSSRGFGFTVVGGDE---PDEFLQIKSLVVDGPAALDGKMETGDVIVSVNDICVLGYTHAQVVKIFQSIPIGESVDLELCR
Danio rerio          NTKLKKSRRGFGFTVVGGDE---PDEFLQIKSLVLDGPAALDGKMETGDVIVSVNDTCVLGYTHAQVVKIFQSIPIGSMVDLELCR
Oryzias latipes_1    NTKLKKSRRGFGFTVVGGDE---PDEFLQIKSLVVDGPAALDGKMETGDVIVSVNDICVLGYTHAQVVKIFQSIPIGSMVNLELCR
Oryzias latipes_2    NTKLKKSRRGFGFTVVGGDE---PDEFLQIKSLVLDGPAAADGKMETGDVIVSVNDTIVLGYTHAQVVKIFQSIPIGSMVDLTLCR
C. elegans_1         STKIVKGAKGLGFTLIGNDSSSRGDEFIQVKSVLSGGPAANGVLRSGDILVRVNGRLLLGATQKEACDVFVAIPVNEAVDIQVCR
C. elegans_2         STKIVKGAKGLGFTLIGNDSSSRGDEFIQVKSVLSGGPAANGVLRSGDILVRVNGRLLLGATQKEACDVFVAIPVNEAVDIQVCR
C. elegans_3         STKIVKGAKGLGFTLIGNDSSSRGDEFIQVKSVLSGGPAANGVLRSGDILVRVNGRLLLGATQKEACDVFVAIPVNEAVDIQVCR
C. elegans_4         STKIVKGAKGLGFTLIGNDSSSRGDEFIQVKSVLSGGPAANGVLRSGDILVRVNGRLLLGATQKEACDVFVAIPVNEAVDIQVCR
C. elegans_5         STKIVKGAKGLGFTLIGNDSSSRGDEFIQVKSVLSGGPAANGVLRSGDILVRVNGRLLLGATQKEACDVFVAIPVNEAVDIQVCR
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MAGI-2

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                     426                                                                        510
Homo sapiens         STTLKKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMETGDVIVYINEVCVLGHTHADVVKLFQSVPIGQSVNLVLCRGY
Macaca mulatta       STTLKKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMETGDVIVYINEVCVLGHTHADVVKLFQSVPIGQSVNLVLCRGY
Mus musculus         STTLKKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMETGDVIVYINEVCVLGHTHADVVKLFQSVPIGQSVNLVLCRGY
Rattus norvegicus    STTLKKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMETGDVIVYINEVCVLGHTHADVVKLFQSVPIGQSVNLVLCRGY
Xenopus tropicalis   STILKKSNMGFGFTIIGGDEPDEFLQVKSVIPEGPAAQDGKMETGDVIVYINEACVLGYTHADVVKIFQSVPIGQSVNLVLCRGY
Danio rerio          STPLQKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMATGDVIVYINDVCVLGTTHADVVKLFQSVPIGQSVTLVLCRGY
Oryzias latipes_1    STSLQKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAADGKMATGDVIVYINDVCVLGTTHADVVKIFQSIPIGQSVTLVLCRGY
Oryzias latipes_2    STALQKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMDTGDVIVYINDICVLGTTHADVVKLFQSVPIGQSVTLVLCRGY
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MAGI-3

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                     435                                                                               517
Homo sapiens         RASLKKSTMGFGFTIIGGDRPDEFLQVKNVLKDGPAAQDGKIAPGDVIVDINGNCVLGHTHADVVQMFQLVPVNQYVNLTLCR
Macaca mulatta       RASLKKSTMGFGFTIIGGDRPDEFLQVKNVLKDGPAAQDGKIAPGDVIVDINGNCVLGHTHADVVQMFQLVPVNQYVNLTLCR
Mus musculus         RASLKKSTMGFGFTIIGGDRPDEFLQVKNVLKDGPAAQDGKIAPGDVIVDINGNCVLGHTHADVVQMFQLVPVNQYVNLTLCR
Rattus norvegicus    RASLKKSTMGFGFTIIGGDRPDEFLQVKNVLKDGPAAQDGKMAPGDVIVDINGNCVLGHTHADVVQMFQLVPVNQYVNLTLCR
Xenopus tropicalis   HTSLKKSAMGFGFTIIGGDRPDEFLQVKNVLKDGPAAQDGKIAPGDVIVDINGTCVLGHTHAEVVQMFQLIPINQYVNMTLCR
Danio rerio          RTTLKKSPQGFGFTIIGGDRPDEFLQVKNVLRDGPAAHDNKIASGDVIVDINGACVLGKTHADVVQMFQSIPVNQYVDMVLCR
Oryzias latipes_1    HTTLKKSLHGFGFTIIGGDRPDEFLQVKNVLPDGPAAHDKKIASGDVIVEINEACVLGKTHADVVQMFQSIPVNQYVDMVLCR
Oryzias latipes_2    HTSLKKSSQGFGFTIIGGDRTDEFLQVKNVLSDGPAAQDNKMASGDVIVEINRMCVLGRTHPEVVKMFQSVPINHYVDMVLCR
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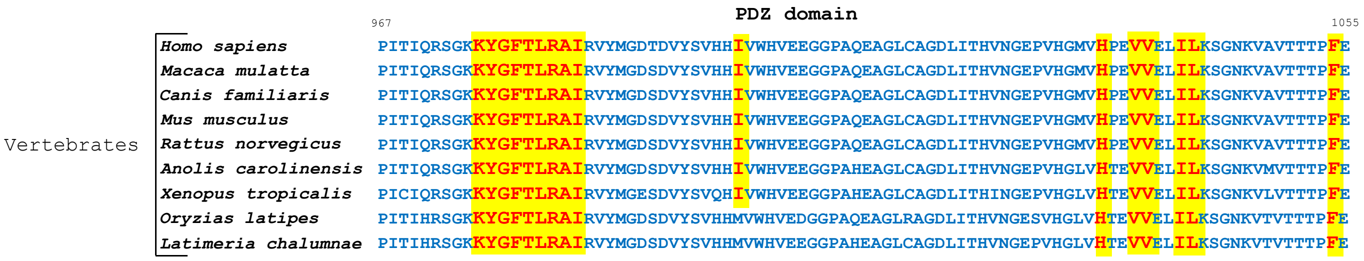
MAST1



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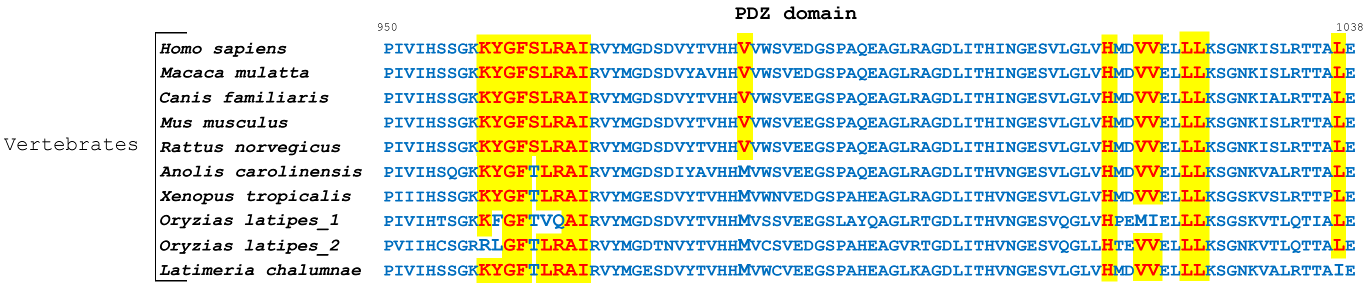
                                     PDZ domain
                         967                                                                                      1055
             Homo sapiens           PITIQRSGKKYGFTLRAIRVYMGDTDVYSVHHIVWHVEEGGPAQEAGLCAGDLITHVNGEPVHGMVHPEVVELILKSGNKVAVTTTPFE
             Macaca mulatta         PITIQRSGKKYGFTLRAIRVYMGDSDVYSVHHIVWHVEEGGPAQEAGLCAGDLITHVNGEPVHGMVHPEVVELILKSGNKVAVTTTPFE
             Canis familiaris       PITIQRSGKKYGFTLRAIRVYMGDSDVYSVHHIVWHVEEGGPAQEAGLCAGDLITHVNGEPVHGMVHPEVVELILKSGNKVAVTTTPFE
             Mus musculus           PITIQRSGKKYGFTLRAIRVYMGDSDVYSVHHIVWHVEEGGPAQEAGLCAGDLITHVNGEPVHGMVHPEVVELILKSGNKVAVTTTPFE
Vertebrates  Rattus norvegicus      PITIQRSGKKYGFTLRAIRVYMGDSDVYSVHHIVWHVEEGGPAQEAGLCAGDLITHVNGEPVHGMVHPEVVELILKSGNKVAVTTTPFE
             Anolis carolinensis    PITIQRSGKKYGFTLRAIRVYMGDSDVYSVHHIVWHVEEGGPAHEAGLCAGDLITHVNGEPVHGLVHTEVVELILKSGNKVMVTTTPFE
             Xenopus tropicalis     PICIQRSGKKYGFTLRAIRVYMGESDVYSVQHIVWHVEEGGPAHEAGLCAGDLITHINGEPVHGLVHTEVVELILKSGNKVLVTTTPFE
             Oryzias latipes        PITIHRSGKKYGFTLRAIRVYMGDSDVYSVHHMVWHVEDGGPAQEAGLRAGDLITHVNGESVHGLVHTEVVELILKSGNKVTVTTTPFE
             Latimeria chalumnae    PITIHRSGKKYGFTLRAIRVYMGDSDVYSVHHMVWHVEEGGPAHEAGLCAGDLITHVNGEPVHGLVHTEVVELILKSGNKVTVTTTPFE
```

MAST2

```
                                     PDZ domain
                         1104                                                                                     1192
             Homo sapiens           PPIIIHRAGKKYGFTLRAIRVYMGDSDVYTVHHMVWHVEDGGPASEAGLRQGDLITHVNGEPVHGLVHTEVVELILKSGNKVAISTTPL
             Macaca mulatta         PPIIIHRAGKKYGFTLRAIRVYMGDSDVYTVHHMVWHVEDGGPASEAGLRQGDLITHVNGEPVHGLVHTEVVELILKSGNKVAISTTPL
             Canis familiaris       PPIIIHRAGKKYGFTLRAIRVYMGDSDVYTVHHMVWHVEDGGPASEAGLRQGDLITHVNGEPVHGLVHTEVVELILKSGNKVSISTTPL
             Mus musculus           PPIIIHRAGKKYGFTLRAIRVYMGDTDVYTVHHMVWHVEDGGPASEAGLRQGDLITHVNGEPVHGLVHTEVVELVLKSGNKVSISTTPL
Vertebrates  Rattus norvegicus      PPIIIHRAGKKYGFTLRAIRVYMGDSDVYTVHHMVWHVEDGGPASEAGLRQGDLITHVNGEPVHGLVHTEVVELVLKSGNKVSISTTPL
             Anolis carolinensis    PPIIIHRAGKKYGFTLRAIRVYMGNSDIYTVHHMVWHVEEGGPASEAGLREGDLITHVNGEPVHGLVHTEVVELVLKSGNKVSISTTPF
             Xenopus tropicalis     PPIIIHRAGKKYGFTLRAIRVYMGESDVYTVHHMVWHVEEDGPAHDAGLREGDLITHVNGEPVHGLVHTEVVELILKSGNKVSISTTPF
             Oryzias latipes        PAITIHRAGKKYGFTLRAIRVYMGDTDIYTVHHMVWHVEEGGPAHEAGLREGDLITHVNGEPVHGLVHTEVVELILKSGAKVSISATPF
             Latimeria chalumnae    PPIIIHRAGKNYGFTLRAIRVYMGDTDVYTVHHMVWHVEDGGPAQEAGLREGDLITHVNGEPVHGLVHTEVVELILKSDNKVSISTTPF
```

MAST3



```
                                     PDZ domain
                         950                                                                                      1038
             Homo sapiens           PIVIHSSGKKYGFSLRAIRVYMGDSDVYTVHHVVWSVEDGSPAQEAGLRAGDLITHINGESVLGLVHMDVVELLLKSGNKISLRTTALE
             Macaca mulatta         PIVIHSSGKKYGFSLRAIRVYMGDSDVYAVHHVVWSVEDGSPAQEAGLRAGDLITHINGESVLGLVHMDVVELLLKSGNKISLRTTALE
             Canis familiaris       PIVIHSSGKKYGFSLRAIRVYMGDSDVYTVHHVVWSVEEGSPAQEAGLRAGDLITHINGESVLGLVHMDVVELLLKSGNKIALRTTALE
             Mus musculus           PIVIHSSGKKYGFSLRAIRVYMGDSDVYTVHHVVWSVEEGSPAQEAGLRAGDLITHINGESVLGLVHMDVVELLLKSGNKISLRTTALE
Vertebrates  Rattus norvegicus      PIVIHSSGKKYGFSLRAIRVYMGDSDVYTVHHVVWSVEEGSPAQEAGLRAGDLITHINGESVLGLVHMDVVELLLKSGNKISLRTTALE
             Anolis carolinensis    PIVIHSQGKKYGFTLRAIRVYMGDSDIYAVHHMVWSVEEGSPAQEAGLRAGDLITHVNGESVLGLVHMDVVELLLKSGNKVALRTTALE
             Xenopus tropicalis     PIIIHSSGKKYGFTLRAIRVYMGESDVYTVHHMVWNVEDGSPAHEAGLRAGDLITHVNGESVLGLVHMDVVELLLKSGSKVSLRTTPLE
             Oryzias latipes_1      PIVIHTSGKKFGFTVQAIRVYMGDSDVYTVHHMVSSVEEGSLAYQAGLRTGDLITHVNGESVQGLVHPEMIELLLKSGSKVTLQTIALE
             Oryzias latipes_2      PVIIHCSGRRLGFTLRAIRVYMGDTNVYTVHHMVCSVEDGSPAHEAGVRTGDLITHVNGESVQGLLHTEVVELLLKSGNKVTLQTTALE
             Latimeria chalumnae    PIVIHSSGKKYGFTLRAIRVYMGESDVYTVHHMVWCVEEGSPAHEAGLKAGDLITHVNGESVLGLVHMDVVELLLKSGNKVALRTTAIE
```

Supplementary Figure S4
MoRF prediction for PTEN

```
MTAIIKEIVSRNKRRYQEDGFDLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVR
nnnnnnnnnnMMnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
23262923272827393750545240393831232527273236343533394738443745413731272726232229333334262628323330414845343537

FLDSKHKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCEDLDQ
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnMnnnn
32272635333538322932343638394846383736373432333738384236454542463537343433354340403241353033374443485549444645

WLSEDDNHVAAIHCKAGKGRTGVMICAYLLHRGKFLKAQEALDFYGEVRTRDKKG
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VTIPSQRRYVYYYSYLLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQL
nnnnnnnnnnMMMnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
13172020212939374646585857454839403023212121182326272827332929343237413931242522211819242226241924273331374847

KVKIYSSNSGPTRREDKFMYFEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFWV
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45353329282420201515111215192627424647435453525432292822241726323635363735373532282322171615172326333541525859

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58595251453329273125222222262728313031282424262532343328242320171734353946434847535444515050403425171714161723

DKANRYFSPNFKVKLYFTKTVEEPSNPEASSSTSVTPDVSDNEPDHYRYSDTTDS
nnnnnnnnMMMMMMMMMnnnnnnnnnnnnnnnnnnnnnnnnnMMMnnnnnnnnnn
31272623272631455163686852566266554648474235211511100914172021232831303233353739484854525146454441363535312423

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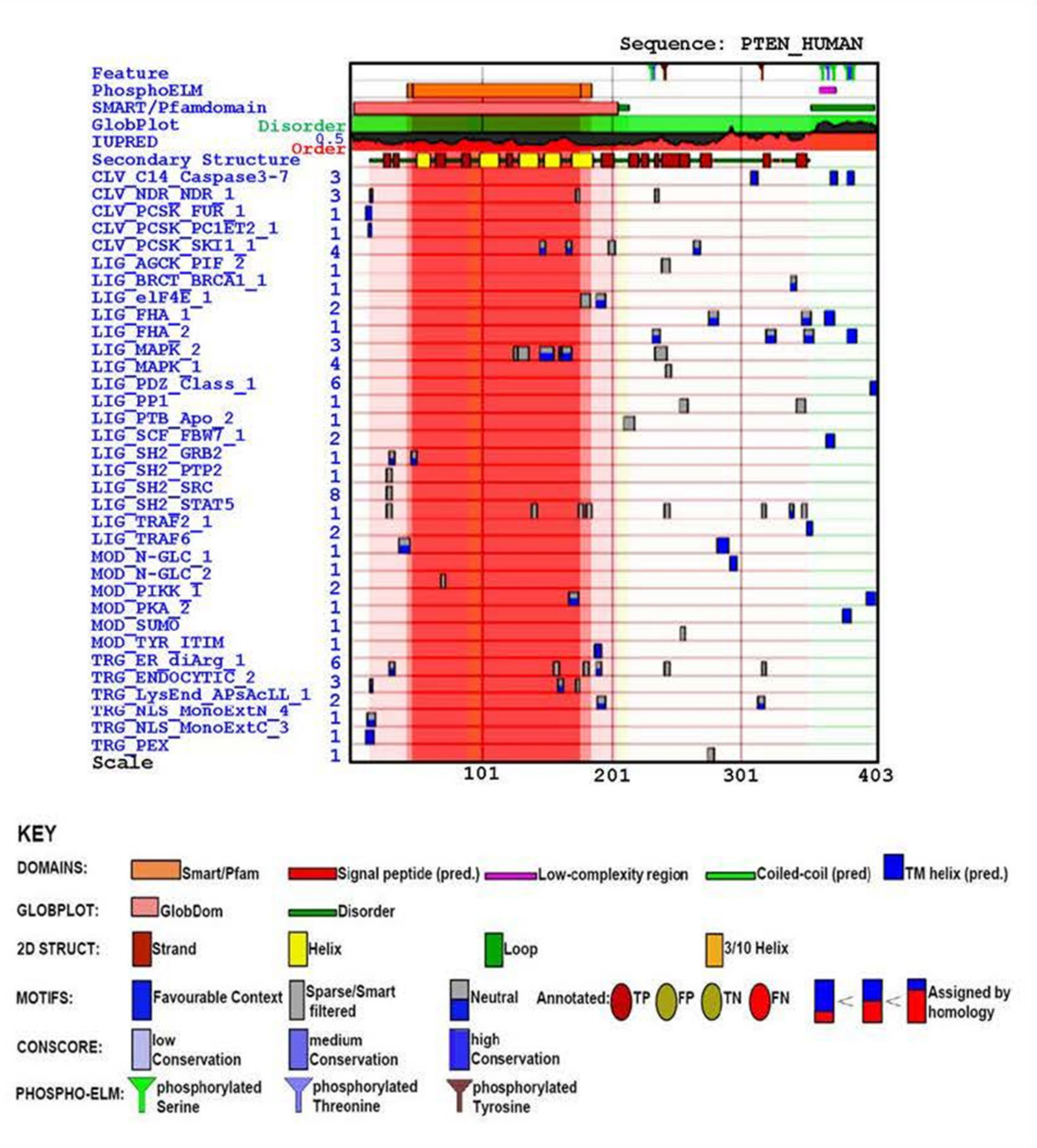
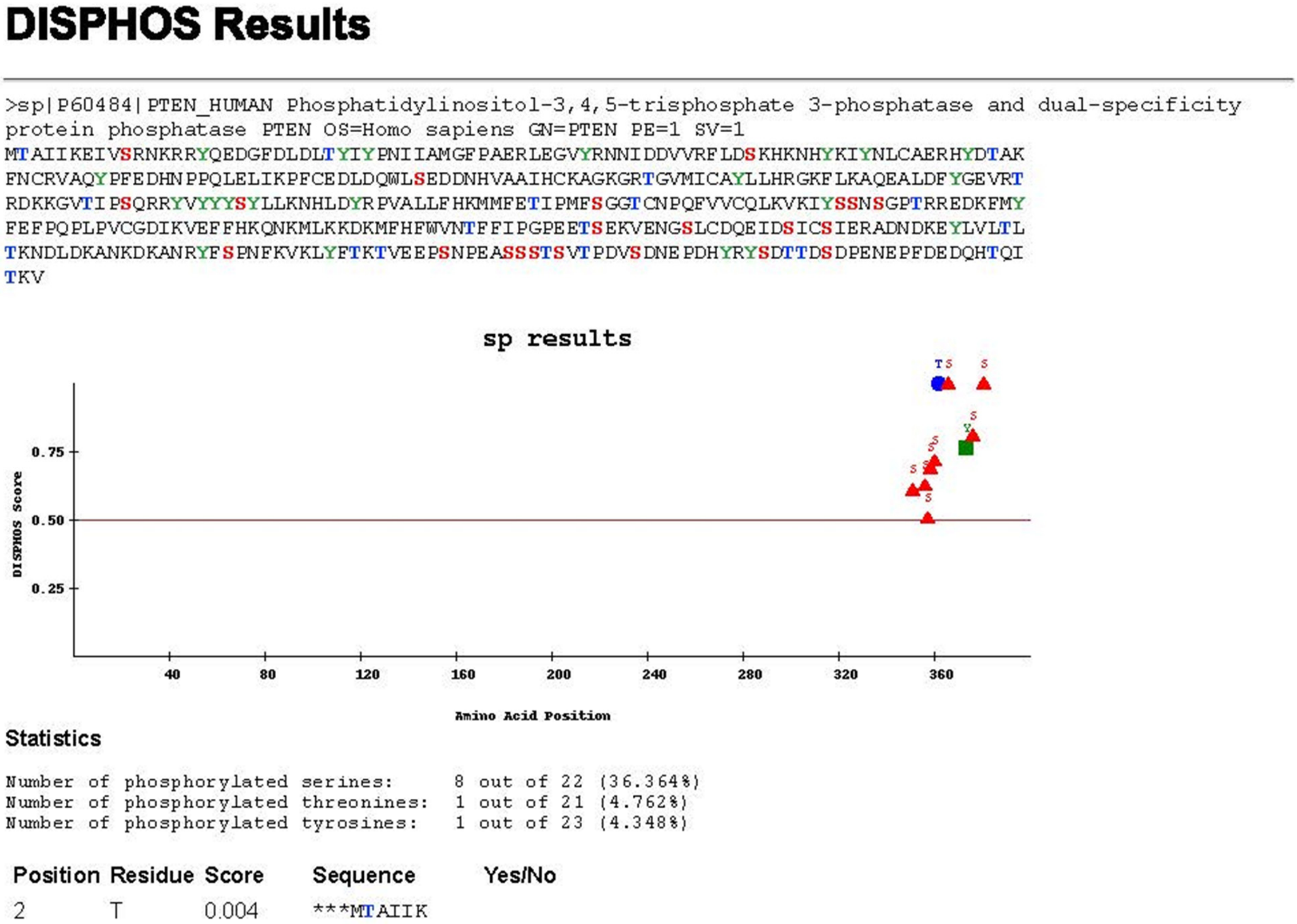
Supplementary Figure S5
ELM output for PTEN



Supplementary Figure S6
DISPHOS prediction for PTEN



DISPHOS Results

```
>sp|P60484|PTEN_HUMAN Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity
protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1
MTAIIKEIVSRNKRRYQEDGFDLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLCAERHYDTAK
FNCRVAQYPFEDHNPPQLELIKPFCEDLDQWLSEDDNHVAAIHCKAGKGRTGVMICAYLLHRGKFLKAQEALDFYGEVRT
RDKKGVTIPSQRRYVYYYSYLLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTRREDKFMY
FEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFWVNTFFIPGPEETSEKVENGSLCDQEIDSICSIERADNDKEYLVLTL
TKNDLDKANKDKANRYFSPNFKVKLYFTKTVEEPSNPEASSSTSVTPDVSDNEPDHYRYSDTTDSDPENEPFDEDQHTQI
TKV
```

Statistics

```
Number of phosphorylated serines:     8 out of 22 (36.364%)
Number of phosphorylated threonines:  1 out of 21 (4.762%)
Number of phosphorylated tyrosines:   1 out of 23 (4.348%)
```

Position	Residue	Score	Sequence	Yes/No
2	T	0.004	***MTAIIK	

10	S	0.151	KEIV**S**RNKR
16	Y	0.002	NKRR**Y**QEDG
26	T	0.051	DLDL**T**YIYP
27	Y	0.077	LDLT**Y**IYPN
29	Y	0.012	LTYI**Y**PNII
46	Y	0.038	LEGV**Y**RNNI
59	S	0.021	RFLD**S**KHKN
65	Y	0.011	HKNH**Y**KIYN
68	Y	0.014	HYKI**Y**NLCA
76	Y	0.024	AERH**Y**DTAK
78	T	0.055	RHYD**T**AKFN
88	Y	0.008	RVAQ**Y**PFED
113	S	0.039	DQWL**S**EDDN
131	T	0.004	GKGR**T**GVMI
138	Y	0.027	MICA**Y**LLHR
155	Y	0.215	ALDF**Y**GEVR
160	T	0.229	GEVR**T**RDKK
167	T	0.023	KKGV**T**IPSQ
170	S	0.227	VTIP**S**QRRY
174	Y	0.011	SQRR**Y**VYYY
176	Y	0.021	RRYV**Y**YYSY
177	Y	0.022	RYVY**Y**YSYL
178	Y	0.017	YVYY**Y**SYLL
179	S	0.072	VYYY**S**YLLK
180	Y	0.019	YYYS**Y**LLKN
188	Y	0.057	NHLD**Y**RPVA
202	T	0.010	MMFE**T**IPMF

207	S	0.022	IPMFSGGTC	
210	T	0.037	FSGGTCNPQ	
225	Y	0.031	KVKIYSSNS	
226	S	0.110	VKIYSSNSG	
227	S	0.159	KIYSSNSGP	
229	S	0.145	YSSNSGPTR	
232	T	0.093	NSGPTRRED	
240	Y	0.080	DKFMYFEFP	
277	T	0.012	FWVNTFFIP	
286	T	0.285	GPEETSEKV	
287	S	0.357	PEETSEKVE	
294	S	0.137	VENGSLCDQ	
302	S	0.211	QEIDSICSI	
305	S	0.392	DSICSIERA	
315	Y	0.037	NDKEYLVLT	
319	T	0.010	YLVLTLTKN	
321	T	0.025	VLTLTKNDL	
336	Y	0.024	KANRYFSPN	
338	S	0.243	NRYFSPNFK	
346	Y	0.016	KVKLYFTKT	
348	T	0.014	KLYFTKTVE	
350	T	0.075	YFTKTVEEP	
355	S	0.611	VEEPSNPEA	YES
360	S	0.628	NPEASSSTS	YES
361	S	0.508	PEASSSTSV	YES
362	S	0.692	EASSSTSVT	YES
363	T	0.064	ASSSTSVTP	

364	S	0.718	SSSTSVTPD	YES
366	T	1.000	STSVTPDVS	YES*
370	S	1.000	TPDVSDNEP	YES*
377	Y	0.765	EPDHYRYSD	YES
379	Y	0.298	DHYRYSDTT	
380	S	0.808	HYRYSDTTD	YES
382	T	0.236	RYSDTTDSD	
383	T	0.384	YSDTTDSDP	
385	S	1.000	DTTDSDPEN	YES*
398	T	0.080	EDQHTQITK	
401	T	0.083	HTQITKV**	

*An asterisk indicates prediction by similarity to the training sequences

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SUPPLEMENTARY TABLES

Supplementary Table Legends

Supplementary Table S1: PTEN Primary Interactome.

Mapped proteins: A list of 40 proteins, within the PTEN interactome, that have been mapped onto the PTEN structure. Approximate regions of PTEN involved in interaction with each of the 40 proteins are known. Unmapped proteins: A list of approx. 350 proteins that are known to interact with PTEN, determined either experimentally or through computational approaches. However, the exact region of PTEN involved in interaction with each of these proteins is yet to be determined. It is important to note that the 350 proteins may interact with PTEN directly or indirectly via another protein or scaffold.

Supplementary Table S2: GO of 40 interactome proteins.

Gene Ontology terms were mapped onto the list of 40 mapped proteins using a controlled vocabulary to describe gene and gene attributes as per the Gene Ontology project (GO) using UniProtKB database. The gene attributes were described under three disjointed categories: cellular component, molecular function and biological process.

Supplementary Table S3: Disorder score for mapped proteins.

A per residue disorder prediction was obtained for each of the 40 mapped proteins of the PTEN interactome using the PONDR-FIT software. A value of 0.5 is used as a cut-off to distinguish between ordered and disordered residues. The number of disordered residues throughout the entire length of the protein is calculated for each of the 40 proteins. Percent disorderliness is calculated as [(No. of disordered residues within a given protein/Total number of amino acid residues in the given protein)*100]. Protein is classified as disordered if it contains one or more long disordered regions (i.e disordered stretches greater than 30 amino acids). A plot of the percent disorderliness is part of Figure 2.

Supplementary Table S4: Identification of cancer as the most over represented disease in the primary interactome.

Functional Analysis using IPA (Ingenuity® Systems, www.ingenuity.com) identified the biological functions and/or diseases that were most significant in the primary PTEN interactome. 13 proteins were enriched as cancer-related from the analysis. Right-tailed Fisher's exact test was used to calculate a p-value determining the probability that each biological function and/or disease assigned to that data set is due to chance alone.

Supplementary Table S5: PTEN Secondary Interactome.

PTEN secondary interactome was derived using 37 of the 40 primary interacting proteins (individual interacting proteins for each of the primary interacting proteins are listed in separately). Disorder analysis was carried out for each of the secondary interacting proteins (using PONDR-FIT software) and disordered proteins were identified.

Supplementary Table S6: Disorder analysis of the PTEN-Cancer Interactome.

Secondary interactome was derived for the 13 cancer-related primary interacting proteins. Disorder analysis identified 193 disordered proteins from the secondary interactome. 31 disordered proteins occurred more than once in the individual interactomes of the 13 cancer related primary interacting proteins.

Supplementary Table S7: Derivation of PTEN associated cancer hubs using a human cancer signaling map

PTEN associated cancer network: Network associations for the PTEN related cancer associated genes were derived from the Cancer Signaling Map (Cui et al, 2007, Awan et al, 2007, Li et al, 2012 and Newman et al, 2013). The network was extended by adding PTEN protein-protein interactions from the primary interactome (Figure 2d, Supplementary Table S1) to the signaling map. The extended network associations were used for visualization and network topology analysis. Topological analysis of PTEN cancer network: Topological analysis identifies p53 as the most significant network hub. PTEN associated cancer network was analyzed using the Network Analysis tool, which calculates topological coefficients to identify topologically important proteins. Based on the statistically relevant scores p53 was identified as the top network hub in the PTEN associated cancer network.

Supplementary Table S8: Disorder prediction for kinases.

A per residue disorder prediction was obtained for all kinases that are known to phosphorylate PTEN using the PONDR-VLXT and PONDR-FIT softwares. A value of 0.5 is used as a cut-off to distinguish between ordered and disordered residues. The kinase is classified as disordered if it contains one or more long disordered regions (i.e disordered stretches greater than 30 amino acids). The exact location of the kinase domains is obtained from UniProt. It is observed that all the kinases have a relatively ordered catalytic domain supporting the concept of a D-O interaction between PTEN and a kinase.

SUPPLEMENTARY TABLE S1
PTEN PRIMARY INTERACTOME: MAPPED PROTEINS

Uniprot ID	Protein name	Region of PTEN that the protein interacts with
Q15796	Smad2	PD
P84022	Smad3	PD
O00308	WWP2	AA 100-187 of PTEN (PD)
P10275	AR	PD
P10599	Thioredoxin	Cys(212) of the C2 domain of PTEN
Q92831	PCAF	AA 186-202 of PTEN (C2)
P49407	ARRB1	C2 domain of PTEN
P32121	ARRB2	C2 domain of PTEN
P35226	BMI-1	AAs 186-286 of PTEN (C2)
Q06830	Prdx-1	AA 157-199 of PTEN (C2)
P42685	RAK	C2 domain of PTEN
P04637	p53	C2 domain of PTEN
Q03135	CAV	AA 271-278 (C2)
Q15831	STK11	N-terminal portion of C2 domain
Q14764	MVP	C2 domain of PTEN
Q9NZM5	PICT-1	AA 338-348 (C2)
P08473	NEP	AA 379-385 of PTEN (C-tail)
F1NK41	Myo5a	C-tail
G3X9Y9	Myo5b	C-tail
G7MXH2	Myo5c	C-tail
Q96EZ8	MSP58	C-tail

Q70Z35	PREX 2	C-tail
P30260	APC 3	C-tail
Q9UJX5	APC 4	C-tail
Q9UJX4	APC 5	C-tail
Q9UJX3	APC 7	C-tail
P49452	Cenpc 1	C-tail
P09619	PDGFRB	PDZ domain of PTEN
Q12959	DLG1	PDZ domain of PTEN
Q96QZ7	MAGI 1	PDZ domain of PTEN
O88382	MAGI2	PDZ domain of PTEN
Q9HBC4	MAGI3	PDZ domain of PTEN
Q9R1L5	Mast1	PDZ domain of PTEN
Q60592	Mast2	PDZ domain of PTEN
O60307	Mast3	PDZ domain of PTEN
O14745	NHERF 1	PDZ domain of PTEN
Q15599	NHERF2	PDZ domain of PTEN
O00254	Par3	PDZ domain of PTEN
P34968	5-HTR2C	PDZ domain of PTEN
Q9H0F6	Sharpin	N- and C- termninus of PTEN

PTEN PRIMARY INTERACTOME: UNMAPPED PROTEINS

Uniprot ID	Protein Name
P63279	SUMO-conjugating enzyme UBC9
P68036	Ubiquitin-conjugating enzyme E2 L3
P42574	Caspase-3
P46934	E3 ubiquitin-protein ligase NEDD4
P0CG48	Polyubiquitin-C
P03372	Estrogen receptor
Q81UK1	Alpha-acetolactate decarboxylase
P35222	Catenin beta-1
P49023	Paxillin
Q13464	ROCK1
Q9NZM5	Glioma tumor suppressor candidate region gene 2 protein/p60 (GLTSCR2)
Q01469	Fatty acid-binding protein, epidermal
Q4G0X9	Coiled-coil domain-containing protein 40
Q93084	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3
P43487	Ran-specific GTPase-activating protein
P11021	78 kDa glucose-regulated protein (GRP 78)
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit (PPP1CA)
P13693	Translationally-controlled tumor protein
P57721	Poly(rC)-binding protein 3
P37802	Transgelin-2
P19784	Casein kinase II subunit alpha
P31749	AKT1
P31751	AKT2
Q9Y243	AKT3
P02533	KRT14 keratin 14

Q99497	DJ1
Q68EM8	MAN2C1 protein
O60930	RNH1
O95136	Sphingosine 1-phosphate receptor 2
Q05586	Glutamate [NMDA] receptor subunit zeta-1
Q13224	Glutamate [NMDA] receptor subunit epsilon-2
Q92734	TRK-fused gene protein
Q9BT67	Ndfip 1
P17181	Interferon alpha/beta receptor 1
Q9Y5S9	RNA-binding protein 8A
P04117	FABP4
Q9QYJ3	HSP40
P97298	Serpinf1
Q9R118	Serine protease HTRA1
Q8IY57	YY1-associated factor 2
Q6PCB0	von Willebrand factor A domain-containing protein 1
P21796	Voltage-dependent anion-selective channel protein 1
P68104	Elongation factor 1-alpha 1
Q04323	UBX domain-containing protein 1
P70698	CTP synthase 1
Q3UEB3	Poly(U)-binding-splicing factor PUF60
Q8C338	Isocitrate dehydrogenase
Q8VEK3	Heterogeneous nuclear ribonucleoprotein U
Q61990	Poly(RC) binding protein 2
Q9Z2X1	Heterogeneous nuclear ribonucleoprotein F
P60335	Poly(rC)-binding protein 1
O88685	26S protease regulatory subunit 6A
O70251	Elongation factor 1-beta
Q3U4U6	Chaperonin containing Tcp1, subunit 3 (Gamma)
Q8CAY6	Acetyl-CoA acetyltransferase, cytosolic

P11983	T-complex protein 1 subunit alpha
B7STB7	Annexin
P09405	Nucleolin
Q01853	Transitional endoplasmic reticulum ATPase
P19324	47 kDa heat shock protein
Q5U415	Aldo-keto reductase family 1, member B3 (Aldose reductase)
F8WGL3	Cofilin 1
Q5M8R8	60S acidic ribosomal protein P0
Q68FD5	Clathrin heavy chain 1
P62082	40S ribosomal protein S7
Q571M2	Heat shock 70 kDa protein 4
P80313	T-complex protein 1 subunit eta
Q71LX8	Heat shock protein 90 alpha
P57776	Elongation factor 1-delta
Q3V117	ATP citrate lyase
Q03265	ATP synthase subunit alpha, mitochondrial
E9QPA6	Chaperonin containing Tcp1, subunit 6a (Zeta)
Q9R0P3	Esterase 10
Q9D0K2	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial
Q564E2	L-lactate dehydrogenase
P99024	Tubulin beta-5 chain
Q3TJ71	UDP-glucose 6-dehydrogenase
O08586	PTEN
Q658W2	Putative uncharacterized protein DKFZp666O0110
P80316	T-complex protein 1 subunit epsilon
B2RQQ5	Microtubule-associated protein 1B
Q9D8N0	Elongation factor 1-gamma
P68134	Actin, alpha skeletal muscle
Q3U7V7	Profilin
P63017	Heat shock cognate 71 kDa protein

P61164	Alpha-centractin
P58252	Elongation factor 2
Q9CQ65	S-methyl-5'-thioadenosine phosphorylase
Q3UMM1	Tubulin, beta 6
Q78PY7	Staphylococcal nuclease domain-containing protein 1
Q91ZH2	Proliferating cell nuclear antigen
Q564F4	T-complex protein 1 subunit delta
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1
P52480	Pyruvate kinase isozymes M1/M2
P62908	40S ribosomal protein S3
P28656	Nucleosome assembly protein 1-like 1
O35945	Aldehyde dehydrogenase, cytosolic 1
Q91V38	Endoplasmin
P19096	Fatty acid synthase
Q58E64	Elongation factor 1-alpha
Q61276	A-X actin
P60843	Eukaryotic initiation factor 4A-I
P05213	Tubulin alpha-1B chain
Q5FW97	Enolase 1, alpha non-neuron
P63038	60 kDa heat shock protein, mitochondrial
Q61937	Nucleophosmin
Q61598	Rab GDP dissociation inhibitor beta
Q80Y52	Heat shock protein 90, alpha (Cytosolic), class A member 1
P68372	Tubulin beta-4B chain
P46471	26S protease regulatory subunit 7
P62702	40S ribosomal protein S4, X isoform
Q5XJY5	Coatomer subunit delta
P62315	Small nuclear ribonucleoprotein Sm D1
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3
Q9CWF2	Tubulin beta-2B chain

Q8BGQ7	Alanine--tRNA ligase, cytoplasmic
Q8BP47	Asparagine--tRNA ligase, cytoplasmic
P62830	60S ribosomal protein L23
Q5M9K9	Ribosomal protein L31
P16045	Galectin-1
Q8VEM8	Phosphate carrier protein, mitochondrial
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial
Q9D7S7	60S ribosomal protein L22-like 1
Q02053	Ubiquitin-like modifier-activating enzyme 1
P16110	Galectin-3
Q8VDD5	Myosin-9
Q3U0U5	Adenylyl cyclase-associated protein
Q62167	DEAD box protein 3, X-chromosomal
P48962	ADP/ATP translocase 1
P27659	60S ribosomal protein L3
P45591	Cofilin-2
Q64674	Spermidine synthase
P47955	60S acidic ribosomal protein P1
Q99JY9	Actin-related protein 3
P54775	26S protease regulatory subunit 6B
Q3TXH3	Lysyl oxidase
O08529	Calpain-2 catalytic subunit
Q4FK36	Destrin
Q9CXW4	60S ribosomal protein L11
Q61390	T-complex protein 1 subunit zeta-2
P56959	RNA-binding protein FUS
Q8BTM8	Filamin-A
Q498M9	Similar to glyceraldehyde-3-phosphate dehydrogenase
P00352	Retinal dehydrogenase 1
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1

P61978	Heterogeneous nuclear ribonucleoprotein K
P14866	Heterogeneous nuclear ribonucleoprotein L
P00558	Phosphoglycerate kinase 1
P62937	Peptidyl-prolyl cis-trans isomerase A
P60174	Triosephosphate isomerase
IPI00458204	similar to tubulin, β2
O00232	26S proteasome non-ATPase regulatory subunit 12
P63173	60S ribosomal protein L38
P08708	40S ribosomal protein S17
Q07020	60S ribosomal protein L18
B2RYU2	Similar to 60S ribosomal protein L12
B5T1L6	AHNAK nucleoprotein isoform 1
E4ZWE6	Similar to ubiquitin / ribosomal protein S27a
Q9Y4K1	Absent in melanoma 1 protein
P48681	Nestin
Q9HD26	Golgi-associated PDZ and coiled-coil motif-containing protein
P08670	Vimentin
Q15293	Reticulocalbin-1
Q93009	Ubiquitin carboxyl-terminal hydrolase 7
P00338	L-lactate dehydrogenase A chain
P04792	Heat shock protein beta-1
Q5TBT2	Dystonin
P07384	Calpain-1 catalytic subunit
Q15582	TGFB1
P50402	Emerin
O14979	Heterogeneous nuclear ribonucleoprotein D-like
O15027	Protein transport protein Sec16A
Q92841	Probable ATP-dependent RNA helicase DDX17
P02545	Prelamin-A/C
P46940	Ras GTPase-activating-like protein IQGAP1

Q53HU2	Guanine nucleotide-binding protein subunit beta-2-like 1
Q01813	6-phosphofructokinase type C
P31946	14-3-3 protein beta/alpha
Q16555	Dihydropyrimidinase-related protein 2
P27348	14-3-3 protein theta
P50454	Serpin H1
P62244	40S ribosomal protein S15a
Q9Y678	Coatomer subunit gamma-1
Q9NX63	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial
A7BI36	p180/ribosome receptor
Q16891	Mitochondrial inner membrane protein
P18085	ADP-ribosylation factor 4
P52272	Heterogeneous nuclear ribonucleoprotein M
B4DW28	40S ribosomal protein S20
A7E2F8	182 kDa tankyrase-1-binding protein
P84098	60S ribosomal protein L19
P68366	Tubulin alpha-4A chain
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
P62913	60S ribosomal protein L11
P33947	ER lumen protein retaining receptor 2
Q9Y3F4	Serine-threonine kinase receptor-associated protein
P63010	AP-2 complex subunit beta
P04632	Calpain small subunit 1
P55072	Transitional endoplasmic reticulum ATPase
P52597	Heterogeneous nuclear ribonucleoprotein F
P49411	Elongation factor Tu, mitochondrial
P46781	40S ribosomal protein S9
Q5HY50	Ribosomal protein L10
P62280	40S ribosomal protein S11
P42766	60S ribosomal protein L35

P61247	40S ribosomal protein S3a
P11940	Polyadenylate-binding protein 1
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
Q5QPK0	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
P46782	40S ribosomal protein S5
P31689	DnaJ homolog subfamily A member 1
Q01082	Spectrin beta chain, brain 1
P53621	Coatomer subunit alpha
P17844	Probable ATP-dependent RNA helicase DDX5
P40429	60S ribosomal protein L13a
Q9UNF1	Melanoma-associated antigen D2
P60660	Myosin light polypeptide 6
P18621	60S ribosomal protein L17
Q13200	26S proteasome non-ATPase regulatory subunit 2
P62241	40S ribosomal protein S8
P36542	ATP synthase subunit gamma, mitochondrial
P61353	60S ribosomal protein L27
Q9BQA1	Methylosome protein 50
P62195	26S protease regulatory subunit 8
Q9NRX2	39S ribosomal protein L17, mitochondrial
P12268	Inosine-5'-monophosphate dehydrogenase 2
Q9NVI7	ATPase family AAA domain-containing protein 3A
O94832	Unconventional myosin-Id
Q12789	General transcription factor 3C polypeptide 1
Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial
Q9BRJ7	Protein syndesmos
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial
Q9UNA1	Rho GTPase-activating protein 26
P58166	Inhibin beta E chain
Q16671	Anti-Muellerian hormone type-2 receptor

O14654	Insulin receptor substrate 4
P52564	Dual specificity mitogen-activated protein kinase kinase 6
Q16513	Serine/threonine-protein kinase N2
P16234	Platelet-derived growth factor receptor alpha
Q9BXM7	Serine/threonine-protein kinase PINK1, mitochondrial
Q92791	Synaptonemal complex protein SC65
A8K6H6	cDNA FLJ76875, highly similar to Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mR
Q15678	Tyrosine-protein phosphatase non-receptor type 14
Q8TEX0	Protein DBF4 homolog B
O60606	Ras GTPase-activating protein-binding protein 2
Q96TC6	Cerebral protein-13
P46109	Crk-like protein
Q14795	Caspase-8
Q6PID4	Protein-tyrosine kinase 2-beta
P56705	Protein Wnt-4
B3DIF4	Zgc:55701 protein
Q8TDT3	Probable G-protein coupled receptor 113
O15316	GDNF family receptor alpha-2
Q8WWW1	Smoothelin
Q3MI93	RNA polymerase II transcription factor SIII subunit A3-like-1
Q05397	Focal Adhesion Kinase (FAK)
A2A5Z6	E3 ubiquitin-protein ligase SMURF2
P35568	Insulin receptor substrate 1
Q9Y4H2	Insulin receptor substrate 2
Q6PIZ9	T-cell receptor-associated transmembrane adapter 1 (TRAT 1)
P61247	40S ribosomal protein S3a
O43460	PTENP1
Q8TDY2	RB1-inducible coiled-coil protein 1
Q92835	SHIP-1
O43426	Synaptojanin-1

O15056	Synaptojanin-2
Q96D37	VAV1 protein
P01116	KRAS
P01111	NRAS
P01112	GTPase HRas
Q07889	Son of sevenless homolog 1
P21860	Receptor tyrosine-protein kinase erbB-3
P18146	Early growth response protein 1
Q99418	Cytohesin-2
P29353	SHC-transforming protein 1
Q13480	GRB2-associated-binding protein 1
P11274	Breakpoint cluster region protein
P11912	CD79A
P40259	CD79B
P62993	Growth factor receptor-bound protein 2
Q8WZA2	RAPGEF4
Q96PE3	Type I inositol-3,4-bisphosphate 4-phosphatase
O15327	Type II inositol-3,4-bisphosphate 4-phosphatase
P32019	Type II inositol-1,4,5-trisphosphate 5-phosphatase
Q8WUK0	Protein-tyrosine phosphatase mitochondrial 1
P05556	Integrin beta-1
Q59F77	Phospholipase C, beta 2 variant
O14735	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
Q8TCU6	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein
Q4LE43	PLCG1 variant protein
P42336	PIK3CA
O00443	PIK3C2A
Q68DL0	PIK3CB
O00750	PIK3C2B
O00329	PIK3CD

P48736	PIK3CG
O75747	PIK3C2G
Q8NEB9	PIK3C3
O00334	Phosphatidylinositol 3-kinase delta catalytic subunit
P27986	PIK3R1
O00459	PIK3R2
Q92569	PIK3R3
Q8WYR1	PIK3R5
Q9NRR6	72 kDa inositol polyphosphate 5-phosphatase
Q9NQ66	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-1
Q01970	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3
Q15147	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-4
Q8N3E9	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-3
Q9BRC7	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-4
Q9P212	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase epsilon-1
P16885	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-2
Q86YW0	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase zeta-1
Q68CY7	Putative uncharacterized protein DKFZp686P05226
Q6A1A2	Putative 3-phosphoinositide-dependent protein kinase 2
B3KR14	Phospholipase C, delta 1
P42356	Phosphatidylinositol 4-kinase alpha
Q9UBF8	Phosphatidylinositol 4-kinase beta
Q99755	Phosphatidylinositol-4-phosphate 5-kinase type-1 alpha
P48426	Phosphatidylinositol-5-phosphate 4-kinase type-2 alpha
O14986	Phosphatidylinositol-4-phosphate 5-kinase type-1 beta
P78356	Phosphatidylinositol-5-phosphate 4-kinase type-2 beta
O60331	Phosphatidylinositol-4-phosphate 5-kinase type-1 gamma
Q8TBX8	Phosphatidylinositol-5-phosphate 4-kinase type-2 gamma
Q01968	Inositol polyphosphate 5-phosphatase OCRL-1
Q9Y2I7	1-phosphatidylinositol-3-phosphate 5-kinase

O15530	3-phosphoinositide-dependent protein kinase 1
P08069	Insulin-like growth factor 1 receptor
P42345	MTOR
Q9UPR6	Zinc finger RNA-binding protein 2
Q14240	Eukaryotic initiation factor 4A-II
refseq:NP_0578	Tat [Human immunodeficiency virus 1]
Q9BVJ6	U3 small nucleolar RNA-associated protein 14 homolog A
P05060	Secretogranin-1
P03950	Angiogenin
P69905	Hemoglobin subunit alpha/ Alpha 2 globin variant (HBA1)
Q7L5N1	COP9 signalosome complex subunit 6
P42229	Signal transducer and activator of transcription 5A (STAT5A)
Q53XB4	Full-length cDNA clone CS0DF032YM23 of Fetal brain of Homo sapiens
P46527	p27Kip1
Q9P0U4	Methyl-CpG-binding domain protein 1
O00423	Echinoderm microtubule-associated protein-like 1
Q9Y6B2	EP300-interacting inhibitor of differentiation 1
Q6WCQ1	Myosin phosphatase Rho-interacting protein
Q9NRD5	PRKCA-binding protein
P29350	Tyrosine-protein phosphatase non-receptor type 6
P23443	Ribosomal protein S6 kinase beta-1
Q9UBS0	Ribosomal protein S6 kinase beta-2
Q8N488	RING1 and YY1-binding protein
P98170	E3 ubiquitin-protein ligase XIAP
Q640N1	Adipocyte enhancer-binding protein 1

SUPPLEMENTARY TABLE S2
GO CLASSIFICATION FOR MAPPED PROTEINS

Entry	Entry name	Gene names	Length	Gene ontology (GO)
P34968	5HT2C_MOUSE	Htr2c 5ht1c Htr1c	459	1-(4-iodo-2,5-dimethoxyphenyl)propan-2-amine binding; ERK1 and ERK2 cascade; cGMP biosynthetic process; cytoplasm; drug binding; integral to membrane; nucleus; phosphatidylinositol biosynthetic process; phosphatidylinositol phospholipase C activity; plasma membrane; release of sequestered calcium ion into cytosol; response to drug; serotonin binding; serotonin receptor activity
P10275	ANDR_HUMAN	AR DHTR NR3C4	919	activation of prostate induction by androgen receptor signaling pathway; androgen binding; androgen receptor activity; axon; cell death; cell growth; cell proliferation; cell-cell signaling; chromatin binding; cytoplasm; dendrite; epithelial cell differentiation involved in prostate gland development; in utero embryonic development; lateral sprouting involved in mammary gland duct morphogenesis; male genitalia morphogenesis; male gonad development; male somatic sex determination; mammary gland alveolus development; morphogenesis of an epithelial fold; negative regulation of apoptotic process; negative regulation of epithelial cell proliferation; negative regulation of integrin biosynthetic process; nuclear chromatin; nucleoplasm; organ formation; positive regulation of MAPK cascade; positive regulation of NF-kappaB transcription factor activity; positive regulation of cell proliferation; positive regulation of insulin-like growth factor receptor signaling pathway; positive regulation of integrin biosynthetic process; positive regulation of intracellular estrogen receptor signaling pathway; positive regulation of phosphorylation; positive regulation of transcription from RNA polymerase II promoter; positive regulation of transcription from RNA polymerase III promoter; prostate gland development; prostate gland epithelium morphogenesis; prostate gland growth; regulation of catalytic activity; regulation of developmental growth; regulation of establishment of protein localization in plasma membrane; regulation of prostatic bud formation; response to insulin stimulus; sequence-specific DNA binding; sex differentiation; tertiary branching involved in mammary gland duct morphogenesis; transcription initiation from RNA polymerase II promoter; transcription regulatory region DNA binding; transport; zinc ion binding
Q9UJX5	APC4_HUMAN	ANAPC4 APC4	808	G2/M transition of mitotic cell cycle; anaphase-promoting complex; anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process; cell division; cytosol; mitotic anaphase; mitotic cell cycle spindle assembly checkpoint; negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; nucleoplasm; positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; protein K11-linked ubiquitination; ubiquitin-protein ligase activity
Q9UJX4	APC5_HUMAN	ANAPC5 APC5	755	G2/M transition of mitotic cell cycle; anaphase-promoting complex; anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process; cell division; cytosol; mitotic anaphase; mitotic cell cycle spindle assembly checkpoint; negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; nucleoplasm; positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; protein K11-linked ubiquitination; ubiquitin-protein ligase activity
P49407	ARRB1_HUMAN	ARRB1 ARR1	418	G-protein coupled receptor internalization; GTPase activator activity; Golgi membrane; Notch signaling pathway; cellular membrane organization; chromatin; coated pit; cytoplasmic vesicle membrane; cytosol; enzyme inhibitor activity; histone H4 acetylation; lysosomal membrane; membrane fraction; negative regulation of NF-kappaB transcription factor activity; negative regulation of interleukin-6 production; negative regulation of interleukin-8 production; negative regulation of protein ubiquitination; nucleus; plasma membrane; platelet activation; positive regulation of ERK1 and ERK2 cascade; positive regulation of Rho protein signal transduction; positive regulation of histone acetylation; positive regulation of transcription from RNA polymerase II promoter; post-Golgi vesicle-mediated transport; proteasomal ubiquitin-dependent protein catabolic process; protein transport; protein ubiquitination; pseudopodium; soluble fraction; stress fiber assembly; transcription from RNA polymerase II promoter; transcription regulatory region DNA binding
P35226	BMI1_HUMAN	BMI1 PCGF4 RNF51	326	PRC1 complex; brain development; chromatin binding; cytoplasm; embryonic skeletal system morphogenesis; hemopoiesis; histone acetylation; histone ubiquitination; humoral immune response; in utero embryonic development; negative regulation of apoptotic process; negative regulation of transcription from RNA polymerase II promoter; nuclear body; nucleolus; positive regulation of B cell proliferation; positive regulation of fibroblast proliferation; positive regulation of immature T cell proliferation in thymus; positive regulation of ubiquitin-protein ligase activity; rostrocaudal neural tube patterning; segment specification; sequence-specific DNA binding; somatic stem cell division; transcription, DNA-dependent; ubiquitin ligase complex; ubiquitin-protein ligase activity; zinc ion binding
Q03135	CAV1_HUMAN	CAV1 CAV	178	Golgi membrane; MAPK cascade; T cell costimulation; acrosomal membrane; apical plasma membrane; basal plasma membrane; basolateral plasma membrane; blood coagulation; calcium ion transport; caveola; caveola assembly; caveolin-mediated endocytosis; cell cortex; cell surface; cellular response to hyperoxia; cellular response to starvation; cholesterol binding; cholesterol efflux; cholesterol homeostasis; cholesterol transport; cytosol; cytosolic calcium ion homeostasis; endocytic vesicle membrane; endoplasmic reticulum; endosome; flagellum; focal adhesion; inactivation of MAPK activity; induction of apoptosis by extracellular signals; integral to membrane of membrane fraction; integral to plasma membrane; interspecies interaction between organisms; lactation; leukocyte migration; lipid particle; lipid storage; maintenance of protein location in cell; mammary gland involution; membrane depolarization; microtubule polymerization; mitochondrion; negative regulation of BMP signaling pathway; negative regulation of JAK-STAT cascade; negative regulation of canonical Wnt receptor signaling pathway; negative regulation of cytokine-mediated signaling pathway; negative regulation of endothelial cell proliferation; negative regulation of epithelial cell differentiation; negative regulation of nitric oxide biosynthetic process; negative regulation of peptidyl-serine phosphorylati negative regulation of protein binding; negative regulation of transcription from RNA polymerase II promoter; negative regulation of tyrosine phosphorylation of Stat5 protein; nitric oxide homeostasis; nitric oxide metabolic process; peptidase activator activity; perinuclear region of cytoplasm; positive regulation of anti-apoptosis; positive regulation of calcium ion transport into cytosol; positive regulation of canonical Wnt receptor signaling pathway; positive regulation of endocytosis; positive regulation of extrinsic apoptotic signaling pathway; positive regulation of intrinsic apoptotic signaling pathway; positive regulation of metalloenzyme activity; positive regulation of microtubule polymerization; positive regulation of peptidyl-serine phosphorylation; positive regulation of vasoconstriction; protein complex; protein homooligomerization; receptor internalization involved in canonical Wnt receptor signaling pathway; regulation of blood coagulation; regulation of fatty acid metabolic process; regulation of nitric-oxide synthase activity; regulation of smooth muscle contraction; response to calcium ion; response to drug; response to estrogen stimulus; response to gamma radiation; response to glucocorticoid stimulus; response to hypoxia; response to mechanical stimulus; response to nutrient; response to progesterone stimulus; skeletal muscle tissue development; soluble fraction; structural molecule activity; triglyceride metabolic process; vasculogenesis; vasoconstriction; vesicle organization
P49452	CENPC_MOUSE	Cenpc1 Cenpc	906	DNA binding; cell division; centromeric heterochromatin; chromosome segregation; condensed chromosome kinetochore; condensed nuclear chromosome, centromeric region; kinetochore; kinetochore assembly; mitosis; mitotic cell cycle
Q12959	DLG1_HUMAN	DLG1	904	MPP7-DLG1-LIN7 complex; actin filament organization; axon guidance; basolateral plasma membrane; cell-cell adhesion; cortical actin cytoskeleton organization; cytosol; endoplasmic reticulum membrane; endothelial cell proliferation; establishment or maintenance of cell polarity; guanylate kinase activity; immunological synapse; interspecies interaction between organisms; mitotic cell cycle G1/S transition checkpoint; negative regulation of mitotic cell cycle; nucleus; phosphoprotein phosphatase activity; postsynaptic density; postsynaptic membrane; potassium channel regulator activity; protein localization in plasma membrane; sarcolemma; synaptic transmission; tight junction; tight junction assembly
P42685	FRK_HUMAN	FRK PTK5 RAK	505	ATP binding; cell differentiation; cytoplasm; negative regulation of cell proliferation; non-membrane spanning protein tyrosine kinase activity; nucleus; plasma membrane

Q92831	KAT2B_HUMAN	KAT2B PCAF	832	A band; Ada2/Gcn5/Ada3 transcription activator complex; I band; N-terminal peptidyl-lysine acetylation; Notch signaling pathway; PCAF complex; actomyosin; cell cycle arrest; cellular response to insulin stimulus; chromatin remodeling; chromatin remodeling complex; cyclin-dependent protein kinase inhibitor activity; histone H3 acetylation; histone acetyltransferase activity; interspecies interaction between organisms; kinetochore; lysine N-acetyltransferase activity; negative regulation of cell proliferation; negative regulation of cyclin-dependent protein kinase activity; positive regulation of transcription from RNA polymerase II promoter; transcription coactivator activity; transcription initiation from RNA polymerase I promoter; transcription initiation from RNA polymerase II promoter
Q96QZ7	MAGI1_HUMAN	MAGI1 AIP3 BAIAP1 BAP1 TNRC19	1491	ATP binding; cell adhesion; cell projection; cell surface receptor signaling pathway; cell-cell junction; cytoplasm; plasma membrane; protein complex assembly; tight junction
O88382	MAGI2_RAT	Magi2 Acvrinp1 Aip1 Sscam	1277	SMAD protein signal transduction; glomerular filtration; glomerular visceral epithelial cell development; mitotic cell cycle arrest; negative regulation of activin receptor signaling pathway; negative regulation of cell migration; negative regulation of cell proliferation; negative regulation of protein kinase B signaling cascade; nucleus; perinuclear region of cytoplasm; positive regulation of phosphoprotein phosphatase activity; positive regulation of receptor internalization; postsynaptic density; protein complex; protein heterooligomerization; receptor clustering; signal transducer activity; slit diaphragm; synaptosome; tight junction
Q5TCQ9	MAGI3_HUMAN	MAGI3 KIAA1634	1506	ATP binding; apoptotic process; guanylate kinase activity; interspecies interaction between organisms; intracellular; intracellular signal transduction; membrane; nucleus; tight junction
Q9R1L5	MAST1_MOUSE	Mast1 Kiaa0973 Sast	1570	ATP binding; cytoplasm; cytoskeleton; cytoskeleton organization; intracellular protein kinase cascade; magnesium ion binding; membrane; plasma membrane; protein serine/threonine kinase activity
Q60592	MAST2_MOUSE	Mast2 Mast205	1734	ATP binding; cell junction; cytoplasm; magnesium ion binding; membrane; microtubule cytoskeleton; protein serine/threonine kinase activity; regulation of interleukin-12 biosynthetic process; spermatid differentiation
O60307	MAST3_HUMAN	MAST3 KIAA0561	1309	ATP binding; magnesium ion binding; protein serine/threonine kinase activity
P08473	NEP_HUMAN	MME EPN	750	axon; beta-amyloid metabolic process; brush border; cellular response to UV-A; cellular response to UV-B; cellular response to cytokine stimulus; creatinine metabolic process; dendrite; integral to plasma membrane; kidney development; membrane fraction; metalloendopeptidase activity; neuron projection terminus; peptide binding; peptide metabolic process; proteolysis; replicative senescence; sensory perception of pain; synaptic vesicle; zinc ion binding
O14745	NHRF1_HUMAN	SLC9A3R1 NHERF NHERF1	358	Wnt receptor signaling pathway; actin cytoskeleton; actin cytoskeleton organization; adenylate cyclase-activating dopamine receptor signaling pathway; apical plasma membrane; apoptotic process; bile acid secretion; brush border membrane; cellular phosphate ion homeostasis; cellular protein localization; centrosome; chloride channel regulator activity; endomembrane system; filopodium; glutathione transport; intracellular membrane-bounded organelle; microvillus assembly; microvillus membrane; negative regulation of ERK1 and ERK2 cascade; negative regulation of cell migration; negative regulation of cell proliferation; negative regulation of phosphatidylinositol 3-kinase cascade; negative regulation of platelet-derived growth factor receptor signaling pathway; negative regulation of protein kinase B signaling cascade; negative regulation of sodium ion transport; negative regulation of sodium:hydrogen antiporter activity; phospholipase C-activating dopamine receptor signaling pathway; protein complex assembly; regulation of excretion; regulation of protein kinase activity; regulation of sodium:hydrogen antiporter activity; renal phosphate ion absorption; renal sodium ion transport; ruffle
Q15599	NHRF2_HUMAN	SLC9A3R2 NHERF2	337	apical plasma membrane; channel regulator activity; cytoplasm; endomembrane system; inner ear development; negative regulation of phosphatidylinositol 3-kinase cascade; nucleus; plasma membrane; positive regulation of membrane potential; protein complex assembly
P04637	P53_HUMAN	TP53 P53	393	ATP binding; B cell lineage commitment; DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest; DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis; DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator; DNA strand annealing activity; ER overload response; PML body; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription; Ras protein signal transduction; T cell differentiation in thymus; T cell lineage commitment; T cell proliferation involved in immune response; apoptotic process; base-excision repair; blood coagulation; cell cycle arrest; cell differentiation; cell proliferation; cellular protein localization; cellular response to UV; cellular response to glucose starvation; cellular response to hypoxia; cellular response to ionizing radiation; central nervous system development; chromatin assembly complex; chromatin binding; chromosome organization; copper ion binding; cytoplasm; cytosol; damaged DNA binding; determination of adult lifespan; double-strand break repair; endoplasmic reticulum; gastrulation; histone deacetylase regulator activity; in utero embryonic development; insoluble fraction; interspecies interaction between organisms; mitochondrion; mitotic cell cycle arrest; multicellular organism growth; negative regulation of DNA replication; negative regulation of apoptotic process; negative regulation of cell growth; negative regulation of fibroblast proliferation; negative regulation of helicase activity; negative regulation of neuroblast proliferation; negative regulation of transcription from RNA polymerase II promoter; negative regulation of transforming growth factor beta receptor signaling pathway; nuclear chromatin; nuclear matrix; nucleolus; nucleotide-excision repair; nucleus; oxidative stress-induced premature senescence; positive regulation of cell aging; positive regulation of histone deacetylation; positive regulation of intrinsic apoptotic signaling pathway; positive regulation of neuron apoptotic process; positive regulation of peptidyl-tyrosine phosphorylation; positive regulation of protein oligomerization; positive regulation of reactive oxygen species metabolic process; positive regulation of release of cytochrome c from mitochondria; positive regulation of thymocyte apoptotic process; positive regulation of transcription from RNA polymerase II promoter; protein import into nucleus, translocation; protein localization; protein tetramerization; rRNA transcription; regulation of mitochondrial membrane permeability; release of cytochrome c from mitochondria; replication fork; replicative senescence; response to X-ray; response to antibiotic; response to gamma radiation; sequence-specific DNA binding transcription factor activity; somitogenesis; transcription regulatory region DNA binding; transcription repressor activity; zinc ion binding
O00254	PAR3_HUMAN	F2RL2 PAR3	374	apical plasma membrane; extracellular region; integral to plasma membrane; phosphatidylinositol phospholipase C activity; platelet activation; thrombin receptor activity
P09619	PGFRB_HUMAN	PDGFRB PDGFR PDGFR1	1106	ATP binding; adrenal gland development; aorta morphogenesis; apical plasma membrane; cardiac myofibril assembly; cell migration involved in coronary angiogenesis; cell migration involved in vasculogenesis; cytoplasm; cytoplasmic membrane-bounded vesicle; in utero embryonic development; integral to plasma membrane; intrinsic to plasma membrane; lysosomal lumen; metanephric glomerular capillary formation; metanephric glomerular mesangial cell proliferation involved in metanephros development; nitrogen compound metabolic process; nucleus; peptidyl-tyrosine phosphorylation; phosphatidylinositol metabolic process; phosphatidylinositol-mediated signaling; platelet activating factor receptor activity; platelet-derived growth factor beta-receptor activity; positive regulation of DNA biosynthetic process; positive regulation of ERK1 and ERK2 cascade; positive regulation of MAP kinase activity; positive regulation of calcium ion import; positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor signaling pathway; positive regulation of chemotaxis; positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway; positive regulation of mitosis; positive regulation of phosphatidylinositol 3-kinase activity; positive regulation of phosphatidylinositol 3-kinase cascade; positive regulation of phospholipase C activity; positive regulation of phosphoprotein phosphatase activity; positive regulation of reactive oxygen species metabolic process; positive regulation of smooth muscle cell migration; positive regulation of smooth muscle cell proliferation; protein autophosphorylation; regulation of actin cytoskeleton organization; regulation of peptidyl-tyrosine phosphorylation; retina vasculature development in camera-type eye; skeletal system morphogenesis; smooth muscle cell chemotaxis; smooth muscle tissue development; tissue homeostasis; vascular endothelial growth factor receptor signaling pathway; vascular endothelial growth factor-activated receptor activity
Q06830	PRDX1_HUMAN	PRDX1 PAGA PAGB TDPX2	199	cell proliferation; hydrogen peroxide catabolic process; melanosome; mitochondrion; nucleus; skeletal system development; thioredoxin peroxidase activity

Q70Z35	PREX2_HUMAN	PREX2 DEPDC2	1606	G-protein coupled receptor signaling pathway; Rac GTPase activator activity; Rac guanyl-nucleotide exchange factor activity; intracellular; intracellular signal transduction; phospholipid binding
Q9H0F6	SHRPN_HUMAN	SHARPIN SIPL1 PSEC0216	387	LUBAC complex; apoptotic nuclear change; brain development; cytosol; keratinization; mitochondrion organization; negative regulation of inflammatory response; positive regulation of I-kappaB kinase/NF-kappaB cascade; postsynaptic density; protein homooligomerization; protein linear polyubiquitination; regulation of CD40 signaling pathway; regulation of tumor necrosis factor-mediated signaling pathway; zinc ion binding
Q15796	SMAD2_HUMAN	SMAD2 MADH2 MADR2	467	SMAD protein complex; SMAD protein complex assembly; activin responsive factor complex; anterior/posterior pattern specification; cell fate commitment; chromatin binding; common-partner SMAD protein phosphorylation; cytosol; developmental growth; double-stranded DNA binding; embryonic cranial skeleton morphogenesis; embryonic foregut morphogenesis; endoderm development; in utero embryonic development; insulin secretion; intracellular signal transduction; lung development; mesoderm formation; negative regulation of cell proliferation; negative regulation of transcription, DNA-dependent; nodal signaling pathway; organ growth; palate development; pancreas development; paraxial mesoderm morphogenesis; pericardium development; positive regulation of BMP signaling pathway; positive regulation of epithelial to mesenchymal transition; positive regulation of nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry; positive regulation of transcription from RNA polymerase II promoter; post-embryonic development; primary miRNA processing; regulation of binding; regulation of transforming growth factor beta receptor signaling pathway; response to cholesterol; response to glucose stimulus; sequence-specific DNA binding transcription factor activity; transcription, DNA-dependent; transforming growth factor beta receptor signaling pathway; transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity; ureteric bud development; zygotic specification of dorsal/ventral axis
P84022	SMAD3_HUMAN	SMAD3 MADH3	425	SMAD protein complex; SMAD protein complex assembly; T cell activation; activation of cysteine-type endopeptidase activity involved in apoptotic process; activation of pro-apoptotic gene products; cell cycle arrest; cell-cell junction organization; chromatin DNA binding; core promoter proximal region sequence-specific DNA binding; cytosol; developmental growth; double-stranded DNA binding; embryonic cranial skeleton morphogenesis; embryonic foregut morphogenesis; embryonic pattern specification; endoderm development; evasion of host defenses by virus; heart looping; immune response; immune system development; in utero embryonic development; induction of apoptosis; lens fiber cell differentiation; liver development; mesoderm formation; negative regulation of apoptotic process; negative regulation of cell growth; negative regulation of inflammatory response; negative regulation of mitotic cell cycle; negative regulation of osteoblast differentiation; negative regulation of osteoblast proliferation; negative regulation of protein catabolic process; negative regulation of protein phosphorylation; negative regulation of transcription from RNA polymerase II promoter; negative regulation of wound healing; nodal signaling pathway; nuclear inner membrane; nucleoplasm; osteoblast development; paraxial mesoderm morphogenesis; pericardium development; plasma membrane; positive regulation of alkaline phosphatase activity; positive regulation of bone mineralization; positive regulation of canonical Wnt receptor signaling pathway; positive regulation of catenin import into nucleus; positive regulation of cell migration; positive regulation of chondrocyte differentiation; positive regulation of epithelial to mesenchymal transition; positive regulation of focal adhesion assembly; positive regulation of interleukin-1 beta production; positive regulation of positive chemotaxis; positive regulation of stress fiber assembly; positive regulation of transcription factor import into nucleus; positive regulation of transcription from RNA polymerase II promoter; positive regulation of transforming growth factor beta3 production; primary miRNA processing; protein stabilization; receptor complex; regulation of binding; regulation of epithelial cell proliferation; regulation of immune response; regulation of striated muscle tissue development; regulation of transforming growth factor beta receptor signaling pathway; regulation of transforming growth factor beta2 production; release of cytochrome c from mitochondria; response to hypoxia; sequence-specific DNA binding transcription factor activity; somitogenesis; thyroid gland development; transcription factor complex; transcription, DNA-dependent; transdifferentiation; transforming growth factor beta receptor signaling pathway; transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity; transport; ureteric bud development; wound healing; zinc ion binding
Q15831	STK11_HUMAN	STK11 LKB1 PJS	433	ATP binding; Golgi localization; anoikis; autophagy; axonogenesis; canonical Wnt receptor signaling pathway; cell cycle arrest; cytoplasm; cytosol; energy reserve metabolic process; establishment of cell polarity glucose homeostasis; insulin receptor signaling pathway; magnesium ion binding; membrane; mitochondrion; negative regulation of cell growth; negative regulation of cell proliferation; negative regulation of epithelial cell proliferation involved in prostate gland development; nucleus; positive regulation of axonogenesis; positive regulation of gluconeogenesis; positive regulation of transforming growth factor beta receptor signaling pathway; protein autophosphorylation; protein complex; protein heterooligomerization; protein kinase activator activity; protein serine/threonine kinase activity; regulation of Wnt receptor signaling pathway; regulation of fatty acid biosynthetic process; regulation of fatty acid oxidation; regulation of protein kinase B signaling cascac response to DNA damage stimulus; response to glucagon stimulus; response to ionizing radiation; response to lipid; signal transduction by p53 class mediator resulting in induction of apoptosis; small molecule metabolic process; spermatid development; tissue homeostasis; vasculature development
P10599	THIO_HUMAN	TXN TRDX TRX TRX1	105	cell proliferation; cell redox homeostasis; cell-cell signaling; cellular component movement; cytosol; electron carrier activity; electron transport chain; extracellular region; glycerol ether metabolic process; innate immune response; mitochondrion; negative regulation of protein export from nucleus; nucleobase-containing small molecule interconversion; nucleoplasm; nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway; oxidation-reduction process; peptide disulfide oxidoreductase activity; positive regulation of DNA binding; protein disulfide oxidoreductase activity; regulation of protein import into nucleus, translocation; regulation of transcription, DNA-dependent; response to radiation; transcription, DNA-dependent; transport
O00308	WWP2_HUMAN	WWP2	870	cytoplasm; negative regulation of protein transport; negative regulation of sequence-specific DNA binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter; negative regulation of transporter activity; nucleus; proteasomal ubiquitin-dependent protein catabolic process; protein K63-linked ubiquitination; protein ubiquitination involved in ubiquitin-dependent protein catabolic process; ubiquitin ligase complex; ubiquitin-protein ligase activity; viral entry into host cell
G7MXH2	G7MXH2_MACMU	EGK_17502	1792	ATP binding; motor activity; myosin complex; zinc ion binding
G3X9Y9	G3X9Y9_MOUSE	Myo5b mCG_123286	1844	ATP binding; motor activity; myosin complex
F1NK41	F1NK41_CHICK	MYO5A	1857	ATP binding; Golgi apparatus; actin filament-based movement; actomyosin; anagen; calcium ion binding; endoplasmic reticulum localization; exocytosis; insulin secretion; intermediate filament; locomotion involved in locomotory behavior; long-chain fatty acid biosynthetic process; melanin biosynthetic process; melanocyte differentiation; melanosome; melanosome transport; microfilament motor activity myelination; myosin complex; neuronal cell body; odontogenesis; photoreceptor outer segment; regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity; ruffle; secretory granule; secretory granule localization; synapse organization; synaptic transmission; visual perception
Q9UJX3	APC7_HUMAN	ANAPC7 APC7	599	anaphase-promoting complex; anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process; cell division; cytosol; mitosis; mitotic cell cycle spindle assembly checkpoint; negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; nucleoplasm; positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; protein K11-linked ubiquitina
P32121	ARRB2_HUMAN	ARRB2 ARB2 ARR2	409	G-protein coupled receptor internalization; Notch signaling pathway; adult walking behavior; cell chemotaxis; coated pit; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle; cytosol; desensitization of G-protein coupled receptor protein signaling pathway by arrestin; negative regulation of NF-kappaB transcription factor activity; negative regulation of interleukin-1 beta production; negative regulation of interleukin-12 production; negative regulation of interleukin-6 production; negative regulation of natural killer cell mediated cytotoxicity; negative regulation of protein ubiquitination; negative regulation of toll-like receptor signaling pathway; negative regulation of tumor necrosis factor production; nucleus; plasma membrane; platelet activation; positive regulation of ERK1 and ERK2 cascade; positive regulation of protein kinase B signaling cascade; positive regulation of protein ubiquitination; positive regulation of synaptic transmission, dopaminergic; proteasomal ubiquitin-dependent protein catabolic process; protein transport; protein ubiquitination; regulation of androgen receptor signaling pathway; regulation of protein phosphorylation; transcription from RNA polymerase II promoter; transforming growth factor beta receptor signaling pathway

P30260	CDC27_HUMAN	CDC27 ANAPC3 D0S1430E D17S978E	824	anaphase-promoting complex; anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process; cell proliferation; centrosome; cytosol; mitotic cell cycle spindle assembly checkpoint; mitotic metaphase/anaphase transition; negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; nucleoplasm; positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; protein K11-linked ubiquitination; spindle microtubule
Q9NZM5	GSCR2_HUMAN	GLTSCR2	478	nucleolus
Q96EZ8	MCRS1_HUMAN	MCRS1 INO80Q MSP58	462	DNA recombination; DNA repair; Ino80 complex; MLL1 complex; cytoplasm; histone H4-K16 acetylation; histone H4-K5 acetylation; histone H4-K8 acetylation; histone acetyltransferase complex; nucleolus; regulation of transcription, DNA-dependent; transcription, DNA-dependent
Q14764	MVP_HUMAN	MVP LRP	893	cytoplasm; mRNA transport; nuclear pore; nucleus; protein transport; response to drug; ribonucleoprotein complex

SUPPLEMENTARY TABLE S3
DISORDER SCORE FOR MAPPED PROTEINS

Uniprot ID	Protein name	No. of AA	No. of residues disordered	No. of disordered stretches (>30)	D/O	% of protein disordered
Q15796	SMAD-2	467	86	1	D	18.41541756
P84022	SMAD-3	425	88	1	D	20.70588235
O00308	WWP-2	870	252	1	D	28.96551724
P10275	AR	919	392	3	D	42.65505985
P10599	TRDX	105	22	0	O	20.95238095
Q92831	PCAF	832	223	2	D	26.80288462
P49407	ARRB1	418	91	1	D	21.77033493
P32121	ARRB2	409	45	0	O	11.00244499
P35226	BMI-1	326	148	1	D	45.39877301
Q06830	Prdx-1	199	27	0	O	13.5678392
P42685	RAK	505	30	0	O	5.940594059
P04637	p53	393	216	3	D	54.96183206
Q03135	CAV1	178	18	0	O	10.11235955
Q15831	STK-11	433	109	1	D	25.17321016
Q14764	MVP	893	162	2	D	18.14109742
Q9NZM5	PICT-1	478	396	4	D	82.84518828
P08473	NEP	750	53	0	O	7.066666667
F1NK41	Myo5a	1857	520	5	D	28.00215401
G3X9Y9	Myo5b	1844	408	4	D	22.12581345
G7MXH2	Myo5c	1792	266	3	D	14.84375
Q96EZ8	MSP-58	462	161	1	D	34.84848485
Q70Z35	PREX-2	1606	212	2	D	13.20049813
P30260	APC-3	824	274	2	D	33.25242718
Q9UJX5	APC-4	808	72	1	D	8.910891089
Q9UJX4	APC-5	755	100	1	D	13.24503311
Q9UJX3	APC-7	599	118	1	D	19.69949917
P49452	Cenpc-1	906	702	3	D	77.48344371
Q9H0F6	Sharpin	387	188	2	D	48.57881137
P09619	PDGFRB	1106	149	1	D	13.47197107
Q12959	DLG-1	904	259	3	D	28.65044248
Q96QZ7	MAGI-1	1491	686	7	D	46.00938967
O88382	MAGI-2	1277	500	5	D	39.15426782
Q5TCQ9	MAGI-3	1506	589	5	D	39.11022576
Q9R1L5	MAST-1	1570	987	5	D	62.86624204
Q60592	MAST-2	1734	1138	8	D	65.62860438
O60307	MAST-3	1309	765	3	D	58.44155844
O14745	NHERF-1	358	187	3	D	52.23463687
Q15599	NHERF-2	337	209	3	D	62.01780415

O00254	Par-3	374	13	0	O	3.475935829
P34968	HTR2C	459	66	1	D	14.37908497

SUPPLEMENTARY TABLE S4

IDENTIFICATION OF CANCER AS THE MOST OVERREPRESENTED DISEASE IN THE PRIMARY INTERACTOME

Category	p-value	Molecules
Cancer	2.32E-05-6.24E-03	TP53 (includes EG:22059),SMAD2,SLC9A3R1,STK11,BMI1,SMAD3,KAT2B,HTR2C,GLTSCR2,AR,ARRB1,SLC9A3R2,MCRS1,PDGFRB
Cardiovascular Disease	1.77E-03-6.24E-03	TP53 (includes EG:22059),SMAD2,AR,SMAD3,PDGFRB
Connective Tissue Disorders	2.59E-04-6.24E-03	TP53 (includes EG:22059),SMAD2,AR,SMAD3,STK11,BMI1
Dermatological Diseases and Conditions	2.09E-03-4.17E-03	TP53 (includes EG:22059),STK11,SMAD3
Developmental Disorder	3.24E-04-6.24E-03	MYO5A,TP53 (includes EG:22059),DLG1,SMAD2,ARRB1,AR,SLC9A3R1,STK11,SMAD3,MYO5B
Endocrine System Disorders	9.1E-04-4.17E-03	TP53 (includes EG:22059),SMAD2,AR,PDGFRB
Gastrointestinal Disease	4.21E-06-6.24E-03	TP53 (includes EG:22059),SMAD2,BMI1,SMAD3,STK11,MYO5B,PDGFRB
Hematological Disease	7.04E-04-5.83E-03	TP53 (includes EG:22059),AR,STK11,PDGFRB
Hepatic System Disease	3.28E-03-5.63E-03	TP53 (includes EG:22059),SMAD2,SMAD3,STK11
Hereditary Disorder	2.09E-03-4.17E-03	MYO5A,TP53 (includes EG:22059),AR,SLC9A3R1,STK11
Hypersensitivity Response	2.09E-03-2.09E-03	SMAD3
Immunological Disease	7.04E-04-5.83E-03	MYO5A,TP53 (includes EG:22059),PDGFRB
Infectious Disease	9.47E-04-4.17E-03	TP53 (includes EG:22059),MYO5B
Inflammatory Disease	4.21E-06-3.35E-03	TP53 (includes EG:22059),SMAD2,AR,SMAD3
Inflammatory Response	2.09E-03-6.24E-03	SMAD3
Metabolic Disease	2.13E-03-4.17E-03	MYO5A,TP53 (includes EG:22059),SLC9A3R1
Neurological Disease	5.07E-04-4.78E-03	TP53 (includes EG:22059),SMAD2,GLTSCR2,AR,ARRB1,SLC9A3R1,STK11,SMAD3,BMI1,PDGFRB
Ophthalmic Disease	2.09E-03-2.09E-03	TP53 (includes EG:22059)
Organismal Injury and Abnormalities	1.5E-04-6.24E-03	TP53 (includes EG:22059),HTR2C,SMAD2,AR,STK11,SMAD3,PDGFRB
Renal and Urological Disease	3.24E-04-2.09E-03	DLG1,SMAD2,SMAD3,PDGFRB
Reproductive System Disease	1.82E-03-6.24E-03	TP53 (includes EG:22059),KAT2B,GLTSCR2,AR,STK11,BMI1,PDGFRB
Respiratory Disease	2.09E-03-6.24E-03	TP53 (includes EG:22059),DLG1,ARRB1,AR,PDGFRB
Skeletal and Muscular Disorders	2.59E-04-4.17E-03	TP53 (includes EG:22059),SMAD2,AR,BMI1,SMAD3,STK11

SUPPLEMENTARY TABLE 5
DISORDER PREDICTION FOR PTEN SECONDARY INTERACTOME

Name	N	R%_meta	CH_dist2	dCDFs
Q9UIS9	605	0.534	0.03	-0.332
Q9BS18	74	0.703	0.192	-0.183
Q8NHZ8	85	1	0.103	-0.534
Q99459	802	0.522	0.034	-0.304
Q13573	536	0.513	0.122	-0.256
Q9BS18	74	0.703	0.192	-0.183
Q8NHZ8	85	1	0.103	-0.534
Q9BS18	74	0.703	0.192	-0.183
Q8NHZ8	85	1	0.103	-0.534
A0JLT2	244	0.693	0.117	-0.398
Q9BS18	74	0.703	0.192	-0.183
Q8NHZ8	85	1	0.103	-0.534
Q99459	802	0.522	0.034	-0.304
Q99933	345	0.53	0.016	-0.26
P38398	1863	0.583	0.014	-0.325
Q00987	491	0.601	0.057	-0.261
Q9Y252	685	0.758	0.087	-0.377
P82094	1093	0.801	0.046	-0.491
P35269	517	0.723	0.138	-0.357
P63165	101	0.307	0.066	-0.199
O95251	611	0.489	0.047	-0.133
Q9UER7	740	0.704	0.061	-0.31
Q9JLQ4	704	0.518	0.015	-0.261
P31946	246	0.354	0.017	-0.092
P61981	247	0.328	0.006	-0.042
Q99933	345	0.53	0.016	-0.26
Q9NYF8	920	0.907	0.305	-0.508
Q05682	793	0.909	0.273	-0.531
P62158	149	0.43	0.098	-0.152
P09496	248	0.661	0.054	-0.348
O54946	365	0.762	0.042	-0.471
Q13283	466	0.575	0.026	-0.198
P16403	213	0.808	0.204	-0.493
Q92522	213	0.77	0.224	-0.338
P23527	126	0.437	0.105	-0.151
P84243	136	0.551	0.073	-0.038
P62805	103	0.505	0.071	-0.033
O35387	280	0.843	0.124	-0.501
Q7Z4V5	671	0.768	0.162	-0.393

Q00839	825	0.541	0.051	-0.185
P23588	611	0.81	0.242	-0.486
Q9Y496	699	0.381	0.007	-0.149
Q86UP2	1357	0.553	0.039	-0.471
Q9UHB6	759	0.773	0.073	-0.454
P46821	2468	0.718	0.061	-0.332
Q00987	491	0.601	0.057	-0.261
Q6WCQ1	1025	0.597	0.05	-0.32
P35579	1960	0.544	0.022	-0.205
Q60795	597	0.625	0.035	-0.36
Q14978	699	0.903	0.144	-0.481
Q9NPE3	64	0.375	0.106	-0.212
P06748	294	0.588	0.115	-0.189
P19338	710	0.687	0.165	-0.398
Q13523	1007	0.601	0.235	-0.221
P98175	930	0.661	0.073	-0.363
P61313	204	0.539	0.212	-0.079
P09651	372	0.573	0.028	-0.264
P51991	378	0.606	0.06	-0.264
Q13464	1354	0.525	0.037	-0.186
O15446	510	0.869	0.041	-0.465
P62241	208	0.471	0.212	-0.081
Q92541	710	0.703	0.108	-0.38
Q13435	895	0.715	0.063	-0.391
P62314	119	0.37	0.049	-0.002
Q13813	2472	0.114	0.024	-0.054
Q14247	550	0.351	0.109	-0.383
Q9UQ35	2752	0.996	0.299	-0.534
Q13428	1488	0.952	0.029	-0.499
Q86V81	257	0.615	0.061	-0.271
P67936	248	0.907	0.149	-0.515
Q9Y2W1	955	0.913	0.316	-0.51
P25490	414	0.551	0.019	-0.307
P08670	466	0.515	0.029	-0.321
P20152	466	0.53	0.032	-0.331
P67809	324	0.799	0.236	-0.394
O95218	330	0.782	0.357	-0.458
Q3MIH3	128	0.219	0.061	-0.012
Q5RKT7	156	0.359	0.09	-0.132
Q8TBK5	288	0.438	0.142	-0.179
Q13428	1488	0.952	0.029	-0.499
Q14978	699	0.903	0.144	-0.481
Q92522	213	0.77	0.224	-0.338
Q02539	215	0.8	0.216	-0.48

O43719	755	0.675	0.31	-0.305
P30414	1462	0.83	0.249	-0.423
Q14247	550	0.351	0.109	-0.383
P55209	391	0.368	0.166	-0.138
Q8TBK5	288	0.438	0.142	-0.179
Q9NPE3	64	0.375	0.106	-0.212
Q9BUA3	381	0.856	0.022	-0.495
Q9NQ92	184	0.837	0.208	-0.364
Q5RKT7	156	0.359	0.09	-0.132
Q3MIH3	128	0.219	0.061	-0.012
P09497	229	0.703	0.089	-0.438
Q16643	649	0.732	0.098	-0.364
P23527	126	0.437	0.105	-0.151
P46821	2468	0.718	0.061	-0.332
Q7Z4V5	671	0.768	0.162	-0.393
Q8WVC0	666	0.878	0.39	-0.444
P35580	1976	0.562	0.029	-0.196
P16403	213	0.808	0.204	-0.493
P98175	930	0.661	0.073	-0.363
Q13813	2472	0.114	0.024	-0.054
P67809	324	0.799	0.236	-0.394
P19338	710	0.687	0.165	-0.398
P54105	237	0.684	0.123	-0.277
P23588	611	0.81	0.242	-0.486
P09651	372	0.573	0.028	-0.264
P46778	160	0.531	0.164	-0.122
Q01082	2364	0.204	0.009	-0.004
P08670	466	0.515	0.029	-0.321
Q9NYF8	920	0.907	0.305	-0.508
Q86V81	257	0.615	0.061	-0.271
P31946	246	0.354	0.017	-0.092
P07910	306	0.634	0.074	-0.322
P46779	137	0.664	0.183	-0.189
O43390	633	0.43	0.027	-0.132
Q9Y2W1	955	0.913	0.316	-0.51
Q15233	471	0.569	0.052	-0.305
P61313	204	0.539	0.212	-0.079
P61981	247	0.328	0.006	-0.042
P16989	372	0.823	0.109	-0.423
P23246	707	0.748	0.099	-0.353
P50914	215	0.591	0.075	-0.169
Q07020	188	0.452	0.155	-0.094
Q14103	355	0.561	0.022	-0.353
P35579	1960	0.544	0.022	-0.205

P62316	118	0.61	0.046	-0.147
P09496	248	0.661	0.054	-0.348
P39019	145	0.331	0.02	-0.083
Q9UHB6	759	0.773	0.073	-0.454
Q8NC51	408	0.841	0.138	-0.485
Q00839	825	0.541	0.051	-0.185
P62241	208	0.471	0.212	-0.081
P41227	235	0.306	0.01	-0.057
O95218	330	0.782	0.357	-0.458
P62314	119	0.37	0.049	-0.002
Q9UQ35	2752	0.996	0.299	-0.534
P62753	249	0.594	0.194	-0.179
Q9UN86	482	0.61	0.07	-0.217
O14974	1030	0.739	0.086	-0.346
Q14004	1512	0.689	0.031	-0.318
Q13435	895	0.715	0.063	-0.391
P84098	196	0.653	0.301	-0.26
P36578	427	0.45	0.09	-0.079
P49454	3210	0.653	0.06	-0.476
P78362	688	0.465	0.034	-0.1
P61254	145	0.628	0.247	-0.265
P42766	123	0.707	0.3	-0.361
P55196	1824	0.524	0.013	-0.172
P06748	294	0.588	0.115	-0.189
P62158	149	0.43	0.098	-0.152
Q13523	1007	0.601	0.235	-0.221
Q9Y3U8	105	0.79	0.229	-0.346
S100A9	113	0.54	0.014	-0.352
Q00987	491	0.601	0.057	-0.261
Q8VDS3	158	0.677	0.035	-0.26
P30658	519	0.744	0.015	-0.376
Q9HC52	389	0.614	0.099	-0.259
O00257	560	0.839	0.041	-0.41
Q8IY57	180	0.939	0.19	-0.531
Q8N488	228	0.886	0.152	-0.498
P62805	103	0.505	0.071	-0.033
Q8NFW9	859	0.522	0.015	-0.302
O95810	425	0.795	0.066	-0.436
Q60865	707	0.791	0.053	-0.435
Q9CR02	221	0.538	0.102	-0.259
P24788	784	0.588	0.177	-0.188
Q6PDQ2	1915	0.409	0.02	-0.101
Q9DA19	450	0.716	0.319	-0.434
O35492	638	0.469	0.079	-0.108

Q61545	655	0.899	0.103	-0.473
Q61584	677	0.465	0.007	-0.106
P70696	127	0.425	0.052	-0.142
P84228	136	0.544	0.069	-0.042
Q5SVQ0	613	0.491	0.03	-0.134
P14733	588	0.541	0.025	-0.386
Q8K310	846	0.635	0.042	-0.27
P97434	1024	0.6	0.035	-0.311
Q91W39	579	0.748	0.097	-0.366
P30415	1453	0.866	0.239	-0.44
A2AR02	752	0.783	0.436	-0.389
Q61136	1007	0.599	0.231	-0.217
Q9DBU5	667	0.763	0.023	-0.36
Q9D083	201	0.547	0.007	-0.178
Q569Z6	951	0.925	0.317	-0.512
Q8K4P0	1330	0.706	0.079	-0.304
A2A9P5	784	0.588	0.177	-0.188
B9EI85	136	0.544	0.069	-0.042
Q5BL18	846	0.635	0.042	-0.27
A2AJI4	951	0.925	0.317	-0.512
Q8R5E6	350	0.623	0.224	-0.283
Q8BR71	708	0.579	0.096	-0.251
E9PYL1	1952	0.373	0.009	-0.084
Q3UFG2	569	0.608	0.021	-0.427
Q3V0L1	475	0.811	0.044	-0.476
A2AWQ8	450	0.716	0.319	-0.434
Q3TLX0	948	0.575	0.06	-0.246
Q3TFD9	466	0.541	0.034	-0.336
P70281	254	0.52	0.032	-0.424
Q8CJI4	398	0.847	0.265	-0.448
Q9CV89	235	0.936	0.14	-0.505
Q3TWV0	466	0.515	0.025	-0.295
P15331	475	0.674	0.01	-0.437
A0PJG9	587	1	0.216	-0.534
Q05BN4	194	0.851	0.137	-0.503
Q8BU35	315	0.695	0.117	-0.277
Q8CIA8	1201	0.523	0.005	-0.334
O94850	711	0.902	0.051	-0.46
P97837	1059	0.557	0.016	-0.383
P01106	439	0.608	0.002	-0.351
Q13573	536	0.513	0.122	-0.256
Q99459	802	0.522	0.034	-0.304
Q86WP2	473	0.825	0.119	-0.471
Q96CN9	775	0.613	0.019	-0.391

Q9Y2W2	641	0.888	0.044	-0.492
P51116	673	0.483	0.003	-0.119
P0C1Z6	253	0.85	0.063	-0.426
Q9BZI7	483	0.799	0.302	-0.425
Q9C086	356	0.978	0.044	-0.53
Q9UER7	740	0.704	0.061	-0.31
P02545	664	0.738	0.005	-0.421
P46783	165	0.491	0.076	-0.19
Q9H1E3	243	1	0.376	-0.534
Q9BRK5	362	0.138	0.033	-0.067
Q86UE4	582	0.845	0.09	-0.442
Q14978	699	0.903	0.144	-0.481
Q05519	484	0.731	0.214	-0.383
P35579	1960	0.544	0.022	-0.205
Q16630-1	551	0.719	0.037	-0.345
P05305	212	0.443	0.065	-0.287
P26043	583	0.515	0.058	-0.125
P26038	577	0.51	0.045	-0.095
Q5VIY5	522	0.157	0.063	-0.138
Q9R0W0	84	0.56	0.066	-0.178
P15311	586	0.519	0.049	-0.108
Q9NWQ8	432	0.852	0.051	-0.458
P26043	583	0.515	0.058	-0.125
Q9R0W0	84	0.56	0.066	-0.178
Q05066	204	0.456	0.091	-0.356
P61981	247	0.328	0.006	-0.042
Q86WX3	136	0.882	0.195	-0.505
P38398	1863	0.583	0.014	-0.325
Q9NPI1	651	0.473	0.04	-0.195
Q5VTR2	975	0.547	0.073	-0.319
O75150	1001	0.616	0.018	-0.381
Q9BWC9	280	0.568	0.035	-0.272
Q8N726	132	0.689	0.035	-0.247
Q64364	169	0.716	0.051	-0.214
P38936	164	0.622	0.013	-0.308
Q9UER7	740	0.704	0.061	-0.31
P09429	215	0.744	0.252	-0.46
P20042	333	0.526	0.069	-0.135
Q9UNL4	249	0.333	0.004	-0.158
P46821	2468	0.718	0.061	-0.332
P56273	473	0.571	0.072	-0.276
Q8IZD2	1858	0.729	0.013	-0.403
Q99547	160	0.362	0.072	-0.329
P01106	439	0.608	0.002	-0.351

O60936	219	0.689	0.136	-0.37
P06748	294	0.588	0.115	-0.189
P19338	710	0.687	0.165	-0.398
Q9BTK6	254	1	0.204	-0.534
Q13526	163	0.571	0.023	-0.417
Q8N488	228	0.886	0.152	-0.498
P04271	92	0.337	0.039	-0.157
Q15424	915	0.937	0.188	-0.491
Q14151	953	0.887	0.154	-0.472
Q92922	1105	0.461	0.017	-0.187
Q9Y675	71	0.901	0.124	-0.534
P63165	101	0.307	0.066	-0.199
Q9NS56	1045	0.7	0.121	-0.326
Q12888	1972	0.785	0.026	-0.38
P62328	44	1	0.277	-0.534
Q9H9J4	1324	0.721	0.035	-0.31
Q9C0J8	1336	0.704	0.082	-0.304
Q8TBK6	192	0.677	0.091	-0.295
Q8TAQ5	688	0.128	0.101	-0.305
P17028	368	0.356	0.012	-0.212
Q13746	386	0.764	0.064	-0.37
Q14DJ8	832	0.716	0.011	-0.353
Q9PST7	573	0.281	0.106	-0.026
Q9C0J8	1336	0.704	0.082	-0.304
P62979	156	0.365	0.097	-0.122
P62987	128	0.219	0.061	-0.012
O75528	432	0.637	0.042	-0.394
P84040	103	0.515	0.071	-0.033
P02299	136	0.544	0.069	-0.042
O12161	101	0.822	0.206	-0.391
P03129	98	0.582	0.004	-0.124
Q05209	780	0.494	0.005	-0.212
Q15599	337	0.62	0.014	-0.415
Q9NQ29	371	0.558	0.205	-0.316
P01106	439	0.608	0.002	-0.351
P54257	671	0.557	0.023	-0.317
Q96RL1	719	0.673	0.043	-0.391
Q00987	491	0.601	0.057	-0.261
P01106	439	0.608	0.002	-0.351
P18101	128	0.234	0.055	-0.019
P55196	1824	0.524	0.013	-0.172
Q9ULX6	646	0.706	0.094	-0.394
P84996	626	0.899	0.043	-0.517
P55789	205	0.522	0.034	-0.211

P30533	357	0.392	0.027	-0.284
Q92688	251	0.506	0.359	-0.181
Q9BTT0	268	0.552	0.395	-0.189
Q9NRL2	1556	0.455	0.003	-0.137
Q9NWK9	470	0.264	0.003	-0.151
Q00994	111	0.919	0.148	-0.521
P62158	149	0.43	0.098	-0.152
Q86WR0	208	0.385	0.023	-0.067
P09496	248	0.661	0.054	-0.348
Q9BVG4	233	0.369	0.068	-0.026
Q9H501	851	0.67	0.161	-0.36
P50502	369	0.612	0.037	-0.287
Q96MY7	647	0.813	0.061	-0.492
P14136	432	0.488	0.003	-0.342
Q15651	99	1	0.365	-0.534
O60841	1220	0.531	0.087	-0.137
Q14919	205	0.688	0.081	-0.319
Q96SB3	815	0.698	0.042	-0.416
P07197	916	0.585	0.157	-0.424
P55209	391	0.368	0.166	-0.138
Q13438	667	0.49	0.069	-0.231
P40855	299	0.793	0.044	-0.49
Q8WXF1	523	0.65	0.01	-0.3
P20962	102	1	0.632	-0.534
Q9H6Z4	567	0.716	0.026	-0.352
Q8IUD2	1116	0.8	0.064	-0.465
Q86UR5	1692	0.668	0.056	-0.292
P62987	128	0.219	0.061	-0.012
P51991	378	0.606	0.06	-0.264
Q13464	1354	0.525	0.037	-0.186
Q96T23	1441	0.745	0.156	-0.404
P08621	437	0.78	0.342	-0.408
P05060	677	0.799	0.29	-0.428
Q9HC62	589	0.401	0.001	-0.106
Q13435	895	0.715	0.063	-0.391
Q92922	1105	0.461	0.017	-0.187
Q13573	536	0.513	0.122	-0.256
Q7KZ85	1726	0.321	0.063	-0.005
Q05519	484	0.731	0.214	-0.383
Q13243	272	0.632	0.283	-0.249
Q9NQ55	473	0.459	0.034	-0.109
O75683	361	0.925	0.281	-0.528
Q5VWG9	929	0.73	0.059	-0.391
Q6IPX3	200	1	0.328	-0.534

Q9UPQ9	1833	0.871	0.036	-0.469
P11387	765	0.442	0.175	-0.154
P12270	2363	0.815	0.086	-0.503
Q9H2G4	693	0.645	0.195	-0.255
P25490	414	0.551	0.019	-0.307
O60315	1214	0.53	0.042	-0.311
Q9H2Y7	1883	0.691	0.001	-0.331
Q15326	562	0.384	0.047	-0.074
P51814	821	0.173	0.06	-0.076
Q5RKT7	156	0.359	0.09	-0.132
Q8N6E6	398	0.857	0.15	-0.474
P11171	864	0.538	0.006	-0.216
Q9NY61	560	0.471	0.085	-0.197
Q9UEE9	299	0.806	0.188	-0.496
Q7Z3E2	898	0.682	0.075	-0.419
Q9HDC5	661	0.504	0.01	-0.238
P02545	664	0.738	0.005	-0.421
Q13526	163	0.571	0.023	-0.417
Q8NG27	643	0.782	0.083	-0.358
Q9BZL4	782	0.738	0.023	-0.353
Q8WXF1	523	0.65	0.01	-0.3
Q9H6Z4	567	0.716	0.026	-0.352
P36578	427	0.45	0.09	-0.079
Q86UC2	560	0.561	0.003	-0.277
P08621	437	0.78	0.342	-0.408
Q9BYW2	2564	0.649	0.045	-0.392
Q13573	536	0.513	0.122	-0.256
Q05066	204	0.456	0.091	-0.356
P06753	284	0.831	0.156	-0.501
P25490	414	0.551	0.019	-0.307
P08670	466	0.515	0.029	-0.321
O60315	1214	0.53	0.042	-0.311
Q15326	562	0.384	0.047	-0.074
Q86UD4	541	0.124	0.072	-0.208
Q8NFZ5	429	0.513	0.022	-0.408
Q16543	378	0.452	0.08	-0.215
Q02241	960	0.392	0.001	-0.134
Q92922	1105	0.461	0.017	-0.187
Q8TEW0	1356	0.607	0.024	-0.294
P09429	215	0.744	0.252	-0.46
Q96BK5	328	0.793	0.192	-0.435
O95990	144	0.799	0.169	-0.471
P40337	213	0.418	0.059	-0.116
P11171	864	0.538	0.006	-0.216

P01106	439	0.608	0.002	-0.351
P38936	164	0.622	0.013	-0.308
P54259	1190	0.886	0.007	-0.5
Q01844	656	0.907	0.102	-0.477
Q16630	551	0.719	0.037	-0.345
Q15637	639	0.786	0.003	-0.439
Q9BTC0	2240	0.814	0.034	-0.407
Q9BWA2	656	0.907	0.102	-0.477

INTERACTOME FOR 5HT-2C

P41595	5-hydroxytryptamine receptor 2B
P28223	5-hydroxytryptamine receptor 2A
P50148	Guanine nucleotide-binding protein G(q) subunit alpha
Q9UIS9	Methyl-CpG-binding domain protein 1
Q99JA2	Agouti-signaling protein
P17752	Tryptophan 5-hydroxylase 1
P30679	Guanine nucleotide-binding protein subunit alpha-15
P29992	Guanine nucleotide-binding protein subunit alpha-11
B1ALW3	Guanine nucleotide binding protein (G protein), alpha 14
Q00169	Phosphatidylinositol transfer protein alpha isoform

INTERACTOME FOR APC3

Q13042	Cell division cycle protein 16 homolog
Q9UJX2	Cell division cycle protein 23 homolog
P27986	Phosphatidylinositol 3-kinase regulatory subunit alpha
P06241	Tyrosine-protein kinase Fyn
P62993	Growth factor receptor-bound protein 2
A2A6Q5	Cell division cycle protein 27 homolog
Q9BS18	Anaphase-promoting complex subunit 13
Q96DE5	Anaphase-promoting complex subunit 16
Q9UJX5	Anaphase-promoting complex subunit 4
Q9UJX6	Anaphase-promoting complex subunit 2
P00519	Tyrosine-protein kinase ABL1
P16333	Cytoplasmic protein NCK1
Q9UJX4	Anaphase-promoting complex subunit 5
Q9H1A4	Anaphase-promoting complex subunit 1
Q12834	Cell division cycle protein 20 homolog
P12830	Cadherin-1
Q8NHZ8	Anaphase-promoting complex subunit CDC26
Q5NI33	Ribonuclease II family protein
Q9CPV2	Anaphase-promoting complex subunit 16
Q9UKT4	F-box only protein 5
Q9JJ66	Cell division cycle protein 20 homolog
P51784	Ubiquitin carboxyl-terminal hydrolase 11
P11440	Cyclin-dependent kinase 1
Q9Z1B5	Mitotic spindle assembly checkpoint protein MAD2A
Q9Z1S0	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta
Q96C86	Scavenger mRNA-decapping enzyme DcpS
Q9H2P0	Activity-dependent neuroprotector homeobox protein
Q8VDQ8	NAD-dependent deacetylase sirtuin-2
Q9UI95	Mitotic spindle assembly checkpoint protein MAD2B
Q9NS71	Gastrokine-1
Q6NZQ4	PAX-interacting protein 1
Q9UJX3	Anaphase-promoting complex subunit 7
Q9UM11	Fizzy-related protein homolog
P60484	PTEN
P31016	Disks large homolog 4
P51955	Serine/threonine-protein kinase Nek2
Q99459	Cell division cycle 5-like protein
Q13573	SNW domain-containing protein 1

INTERACTOME FOR APC4

Q9BS18	Anaphase-promoting complex subunit 13
Q9UJX2	Cell division cycle protein 23 homolog
Q13042	Cell division cycle protein 16 homolog
Q96DE5	Anaphase-promoting complex subunit 16
Q9UJX4	Anaphase-promoting complex subunit 5
Q9H1A4	Anaphase-promoting complex subunit 1
Q12834	Cell division cycle protein 20 homolog
Q8NHZ8	Anaphase-promoting complex subunit CDC26
P30260	Cell division cycle protein 27 homolog
P11440	Cyclin-dependent kinase 1
Q9Z1B5	Mitotic spindle assembly checkpoint protein MAD2A
Q9Z1S0	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta
Q6NZQ4	PAX-interacting protein 1
Q8VDQ8	NAD-dependent deacetylase sirtuin-2
P60484	PTEN

INTERACTOME FOR APC5

Q96DE5	Anaphase-promoting complex subunit 16
Q9UJX2	Cell division cycle protein 23 homolog
Q13042	Cell division cycle protein 16 homolog
Q9UJX5	Anaphase-promoting complex subunit 4
Q9BS18	Anaphase-promoting complex subunit 13
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta
Q8NHZ8	Anaphase-promoting complex subunit CDC26
Q9UJX6	Anaphase-promoting complex subunit 2
O43684	Mitotic checkpoint protein BUB3
Q9H1A4	Anaphase-promoting complex subunit 1
P30260	Cell division cycle protein 27 homolog
Q9UJX3	Anaphase-promoting complex subunit 7
Q12834	Cell division cycle protein 20 homolog
A0JLT2	Mediator of RNA polymerase II transcription subunit 19
Q9Z1B5	Mitotic spindle assembly checkpoint protein MAD2A
O14867	Transcription regulator protein BACH1
Q92731	Estrogen receptor beta
Q6NZQ4	PAX-interacting protein 1
P60484	PTEN
Q05516	Zinc finger and BTB domain-containing protein 16

INTERACTOME FOR APC7

Q9BS18	Anaphase-promoting complex subunit 13
Q96DE5	Anaphase-promoting complex subunit 16
Q9UJX2	Cell division cycle protein 23 homolog
Q13042	Cell division cycle protein 16 homolog
Q9UJX4	Anaphase-promoting complex subunit 5
P11440	Cyclin-dependent kinase 1
Q9H1A4	Anaphase-promoting complex subunit 1
Q12834	Cell division cycle protein 20 homolog
Q8NHZ8	Anaphase-promoting complex subunit CDC26
Q92560	Ubiquitin carboxyl-terminal hydrolase BAP1
Q9JJ66	Cell division cycle protein 20 homolog
Q9Z1B5	Mitotic spindle assembly checkpoint protein MAD2A
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta
P60484	PTEN
P30260	Cell division cycle protein 27 homolog
Q99459	Cell division cycle 5-like protein

INTERACTOME FOR AR

Q9UBS8	E3 ubiquitin-protein ligase RNF14
O43294	Transforming growth factor beta-1-induced transcript 1 protein
Q99933	BAG family molecular chaperone regulator 1
O95238	SAM pointed domain-containing Ets transcription factor
Q92993	Histone acetyltransferase KAT5
P49116	Nuclear receptor subfamily 2 group C member 2
P63279	SUMO-conjugating enzyme UBC9
P38398	BRCA1
Q05086	Ubiquitin-protein ligase E3A
P46406	Glyceraldehyde-3-phosphate dehydrogenase
Q00987	E3 ubiquitin-protein ligase Mdm2
P06396	Gelsolin
P11308	Transcriptional regulator ERG
Q9Y252	E3 ubiquitin-protein ligase RNF6
O88850	Homeodomain-interacting protein kinase 3
P62826	GTP-binding nuclear protein Ran
Q13772	Nuclear receptor coactivator 4
P82094	TATA element modulatory factor
P05412	Transcription factor AP-1
Q03135	Caveolin-1
P35269	General transcription factor IIF subunit 1
P24385	G1/S-specific cyclin-D1
P51946	Cyclin-H
P50613	Cyclin-dependent kinase 7
P25491	Mitochondrial protein import protein MAS5
Q15596	Nuclear receptor coactivator 2
Q9Y265	RuvB-like 1
P21333	Filamin-A
P07288	Prostate-specific antigen
P56524	Histone deacetylase 4

P07900	Heat shock protein HSP 90-alpha
Q92793	CREB-binding protein
P63165	Small ubiquitin-related modifier 1
P10592	Heat shock protein SSA2
Q15788	Nuclear receptor coactivator 1
Q15652	Probable JmjC domain-containing histone demethylation protein 2C
O95251	Histone acetyltransferase KAT7
P22202	Heat shock protein SSA4
Q99497	Protein DJ-1
Q14686	Nuclear receptor coactivator 6
Q16665	Hypoxia-inducible factor 1-alpha
P60709	Actin, cytoplasmic 1
Q9R1E0	Forkhead box protein O1
P00925	Enolase 2
P60010	Actin
O14672	Disintegrin and metalloproteinase domain-containing protein 10
Q06830	Peroxiredoxin-1
P20711	Aromatic-L-amino-acid decarboxylase
O14976	Cyclin-G-associated kinase
Q9UER7	Death domain-associated protein 6
Q9UQ80	Proliferation-associated protein 2G4
P35222	Catenin beta-1
P10275	Androgen Receptor
P15108	ATP-dependent molecular chaperone HSC82
P00359	Glyceraldehyde-3-phosphate dehydrogenase 3
P10591	Heat shock protein SSA1
P02994	Elongation factor 1-alpha
Q14192	Four and a half LIM domains protein 2
Q16666	Gamma-interferon-inducible protein 16
O96028	Probable histone-lysine N-methyltransferase NSD2
O14595	Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 2
P14921	Protein C-ets-1
O89110	Caspase-8

Q04917	14-3-3 protein eta
P04637	p53
P19447	TFIIH basal transcription factor complex helicase XPB subunit
Q15797	SMAD1
Q9JLQ4	Pleiomorphic adenoma gene-like 1

INTERACTOME FOR ARRB1

P31946	14-3-3 protein beta/alpha
P62258	14-3-3 protein epsilon
Q04917	14-3-3 protein eta
P61981	14-3-3 protein gamma
P27348	14-3-3 protein theta
P63104	14-3-3 protein zeta/delta
P97288	5-hydroxytryptamine receptor 4
Q13085	Acetyl-CoA carboxylase 1
Q562R1	Beta-actin-like protein 2
Q9BYX7	Putative beta-actin-like protein 3
P60709	Actin, cytoplasmic 1 (Beta-actin)
P68133	Actin, alpha skeletal muscle
P28332	Alcohol dehydrogenase 6
P08588	Beta-1 adrenergic receptor
P30556	Type-1 angiotensin II receptor
Q16352	Alpha-internexin
P31750	RAC-alpha serine/threonine-protein kinase
O14744	Protein arginine N-methyltransferase 5
P07355	Annexin A2
O00203	AP-3 complex subunit beta-1
O14617	AP-3 complex subunit delta-1
P51693	Amyloid-like protein 1
O15511	Actin-related protein 2/3 complex subunit 5
P32121	Beta-arrestin-2
P36575	Arrestin-C
P10523	S-arrestin
P25705	ATP synthase subunit alpha, mitochondrial
P06576	ATP synthase subunit beta, mitochondrial
Q13535	Serine/threonine-protein kinase ATR
O15169	Axin-1
Q9BYV9	Transcription regulator protein BACH2
Q99933	BAG family molecular chaperone regulator 1
Q9NYF8	Bcl-2-associated transcription factor 1
O35607	Bone morphogenetic protein receptor type-2
Q14137	Ribosome biogenesis protein BOP1
Q06187	Tyrosine-protein kinase BTK
Q05682	Caldesmon
P62158	Calmodulin
P05814	Beta-casein
P15085	Carboxypeptidase A1
Q16627	C-C motif chemokine 14
P60953	Cell division control protein 42 homolog

Q07065	Cytoskeleton-associated protein 4
P09496	Clathrin light chain A
Q00610	Clathrin heavy chain 1
Q96DG6	Carboxymethylenebutenolidase homolog
Q16281	Cyclic nucleotide-gated cation channel alpha-3
P23528	Cofilin-1
Q86YQ8	Copine-8
P68400	Casein kinase II subunit alpha
Q96GQ7	Probable ATP-dependent RNA helicase DDX27
P52429	Diacylglycerol kinase epsilon
P49619	Diacylglycerol kinase gamma
Q86XP1	Diacylglycerol kinase eta
Q13574	Diacylglycerol kinase zeta
Q13268	Dehydrogenase/reductase SDR family member 2
O60832	H/ACA ribonucleoprotein complex subunit 4
P11532	Dystrophin
O54946	DnaJ homolog subfamily B member 6
Q9C005	Protein dpy-30 homolog
Q8TD57	Dynein heavy chain 3, axonemal
Q05193	Dynamin-1
P25101	Endothelin-1 receptor
Q05639	Elongation factor 1-alpha 2
Q13347	Eukaryotic translation initiation factor 3 subunit I
Q16875	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3
P49327	Fatty acid synthase
P21333	Filamin-A
Q13283	Ras GTPase-activating protein-binding protein 1
P06396	Gelsolin
P43220	Glucagon-like peptide 1 receptor
Q14749	Glycine N-methyltransferase
P98192	Dihydroxyacetone phosphate acyltransferase
P34947	G protein-coupled receptor kinase 5
P38646	Stress-70 protein, mitochondrial
P11021	78 kDa glucose-regulated protein
P16403	Histone H1.2
Q92522	Histone H1x
P0C0S8	Histone H2A type 1
Q8IUE6	Histone H2A type 2-B
P16104	Histone H2A.x
P23527	Histone H2B type 1-O
P84243	Histone H3.3
P62805	Histone H4
O35387	HCLS1-associated protein X-1
Q7Z4V5	Hepatoma-derived growth factor-related protein 2
P31943	Heterogeneous nuclear ribonucleoprotein H

P61978	Heterogeneous nuclear ribonucleoprotein K
P52272	Heterogeneous nuclear ribonucleoprotein M
Q00839	Heterogeneous nuclear ribonucleoprotein U
P07900	Heat shock protein HSP 90-alpha
P08107	Heat shock 70 kDa protein 1A/1B
P48741	Putative heat shock 70 kDa protein 7
P11142	Heat shock cognate 71 kDa protein
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2
P23588	Eukaryotic translation initiation factor 4B
P25963	NF-kappa-B inhibitor alpha
O00505	Importin subunit alpha-3
P05412	Transcription factor AP-1
Q9Y597	BTB/POZ domain-containing protein KCTD3
P50053	Ketohexokinase
Q9ULI4	Kinesin-like protein KIF26A
Q99661	Kinesin-like protein KIF2C
Q9Y496	Kinesin-like protein KIF3A
P14618	Pyruvate kinase isozymes M1/M2
Q86UP2	Kinectin
P42166	Lamina-associated polypeptide 2, isoform alpha
Q81LR7	Elongation factor 4
Q9UHB6	LIM domain and actin-binding protein 1
Q9NZR2	Low-density lipoprotein receptor-related protein 1B
O75096	Low-density lipoprotein receptor-related protein 4
Q13233	Mitogen-activated protein kinase kinase kinase 1
Q99683	Mitogen-activated protein kinase kinase kinase 5
P46821	Microtubule-associated protein 1B
Q00987	E3 ubiquitin-protein ligase Mdm2
Q9BQA1	Methylosome protein 50
P45984	Mitogen-activated protein kinase 9
P53779	Mitogen-activated protein kinase 10
O14950	Myosin regulatory light chain 12B
P45985	Dual specificity mitogen-activated protein kinase kinase 4
Q6WCQ1	Myosin phosphatase Rho-interacting protein
P04731	Metallothionein-1A
Q9R0L9	Sialomucin core protein 24
P12882	Myosin-1
P35579	Myosin-9
P60660	Myosin light polypeptide 6
O00159	Unconventional myosin-Ic
Q9QY36	N-alpha-acetyltransferase 10
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial
Q9HC98	Serine/threonine-protein kinase Nek6
Q60795	Nuclear factor erythroid 2-related factor 2
Q14978	Nucleolar and coiled-body phosphoprotein 1

Q9NPE3	H/ACA ribonucleoprotein complex subunit 3
P06748	Nucleophosmin
P19338	Nucleolin
O00443	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha
O00459	Phosphatidylinositol 3-kinase regulatory subunit beta
P07237	Protein disulfide-isomerase (PDI)
O00541	Pescadillo homolog
Q53H76	Phospholipase A1 member A
P62937	Peptidyl-prolyl cis-trans isomerase A
P35813	Protein phosphatase 1A
O75688	Protein phosphatase 1B
Q13523	Serine/threonine-protein kinase PRP4 homolog
Q9Y6C5	Protein patched homolog 2
P62820	Ras-related protein Rab-1A
Q96S59	Ran-binding protein 9
P98175	RNA-binding protein 10
Q9BXF6	Rab11 family-interacting protein 5
P49796	Regulator of G-protein signaling 3
A7KAX9	Rho GTPase-activating protein 32
P61313	60S ribosomal protein L15
P35268	60S ribosomal protein L22
P39023	60S ribosomal protein L3
P62424	60S ribosomal protein L7a
Q6DKI1	60S ribosomal protein L7-like 1
P09651	Heterogeneous nuclear ribonucleoprotein A1
P51991	Heterogeneous nuclear ribonucleoprotein A3
Q13464	Rho-associated protein kinase 1
O95602	DNA-directed RNA polymerase I subunit RPA1
O15446	DNA-directed RNA polymerase I subunit RPA34
Q9GZS1	DNA-directed RNA polymerase I subunit RPA49
P19388	DNA-directed RNA polymerases I, II, and III subunit RPABC1
O15160	DNA-directed RNA polymerases I and III subunit RPAC1
P08708	40S ribosomal protein S17
P15880	40S ribosomal protein S2
P61247	40S ribosomal protein S3a
P62241	40S ribosomal protein S8
Q92541	RNA polymerase-associated protein RTF1 homolog
Q9ES97	Reticulon-3
Q6P3W7	SCY1-like protein 2
O75056	Syndecan-3
Q13435	Splicing factor 3B subunit 2
P62314	Small nuclear ribonucleoprotein Sm D1
Q9QX47	Protein SON
Q9Y657	Spindlin-1
Q13813	Spectrin alpha chain, brain

Q12772	Sterol regulatory element-binding protein 2
Q14247	Src substrate cortactin
P12931	Proto-oncogene tyrosine-protein kinase Src
Q9UQ35	Serine/arginine repetitive matrix protein 2
Q9Y2H1	Serine/threonine-protein kinase 38-like
Q15208	Serine/threonine-protein kinase 38
Q5T5C0	Syntaxin-binding protein 5
Q9BQE3	Tubulin alpha-1C chain
Q13748	Tubulin alpha-3C/D chain
P68366	Tubulin alpha-4A chain
Q13885	Tubulin beta-2A chain
P07437	Tubulin beta chain
Q13428	Treacle protein
Q86V81	THO complex subunit 4
Q8WZ42	Titin
Q9NYL9	Tropomodulin-3
Q01320	DNA topoisomerase 2-alpha
P67936	Tropomyosin alpha-4 chain
Q9Y2W1	Thyroid hormone receptor-associated protein 3
Q9Y4K3	TNF receptor-associated factor 6
P25490	Transcriptional repressor protein YY1
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24
Q00341	Vigilin
P08670	Vimentin
P20152	Vimentin
P13010	X-ray repair cross-complementing protein 5
P67809	Nuclease-sensitive element-binding protein 1
P07947	Tyrosine-protein kinase Yes
O43298	Zinc finger and BTB domain-containing protein 43
O95218	Zinc finger Ran-binding domain-containing protein 2
Q15942	Zyxin (Zyxin-2)
Q3MIH3	Ubiquitin A-52 residue ribosomal protein fusion product 1
Q5U5U6	Ubiquitin B
Q5JU97	Zinc finger and BTB domain containing 43
Q5RKT7	Ribosomal protein S27a
Q5UGI3	Ubiquitin C splice variant
Q8TBK5	60S ribosomal protein L6
Q7Z3R3	Putative uncharacterized protein DKFZp686J1593
Q5NET8	ATp-dependent helicase
Q5NGW2	Chitinase family 18 protein
Q8R542	Matrilin-2

INTERACTOME FOR ARRB2

P25101	Endothelin-1 receptor
P12931	Proto-oncogene tyrosine-protein kinase Src
Q08499	cAMP-specific 3',5'-cyclic phosphodiesterase 4D
Q9Y4K3	TNF receptor-associated factor 6
P49407	Beta-arrestin-1
Q96GQ7	Probable ATP-dependent RNA helicase DDX27
Q13428	Treacle protein
O00541	Pescadillo homolog
Q6DKI1	60S ribosomal protein L7-like 1
P51148	Ras-related protein Rab-5C
Q8N983	39S ribosomal protein L43, mitochondrial
O00203	AP-3 complex subunit beta-1
Q14137	Ribosome biogenesis protein BOP1
P53779	Mitogen-activated protein kinase 10
P08588	Beta-1 adrenergic receptor
O00505	Importin subunit alpha-3
Q14978	Nucleolar and coiled-body phosphoprotein 1
P22087	rRNA 2'-O-methyltransferase fibrillarin
O00629	Importin subunit alpha-4
Q99683	Mitogen-activated protein kinase kinase kinase 5
Q9H9J2	39S ribosomal protein L44, mitochondrial
P32121	Beta-arrestin-2
P45985	Dual specificity mitogen-activated protein kinase kinase 4
Q92522	Histone H1x
Q02539	Histone H1.1
Q9NYL9	Tropomodulin-3
O43719	HIV Tat-specific factor 1
P30414	NK-tumor recognition protein
Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein

Q14247	Src substrate cortactin
P34931	Heat shock 70 kDa protein 1-like
P84090	Enhancer of rudimentary homolog
P55209	Nucleosome assembly protein 1-like 1
Q562R1	Beta-actin-like protein 2
Q9BYX7	Putative beta-actin-like protein 3
P81605	Dermcidin
Q8TBK5	60S ribosomal protein L6
Q9NPE3	H/ACA ribonucleoprotein complex subunit 3
Q9BUA3	Uncharacterized protein C11orf84
Q9H3K6	BolA-like protein 2
Q9NQ92	Cooperator of PRMT5
Q9UL80	Myosin-reactive immunoglobulin light chain variable region
Q5RKT7	Ribosomal protein S27a
Q3MIH3	Ubiquitin A-52 residue ribosomal protein fusion product 1
Q3B726	Q3B726
P09497	Clathrin light chain B
IGKV1-5	Ig kappa chain V-I region HK102
Q8IUE6	Histone H2A type 2-B
Q16643	Drebrin
Q5UGI3	Ubiquitin C splice variant
P23527	Histone H2B type 1-O
P46821	Microtubule-associated protein 1B
P27348	14-3-3 protein theta
Q7Z4V5	Hepatoma-derived growth factor-related protein 2
Q5JUX0	Spindlin-3
O75056	Syndecan-3
Q8N752	Casein kinase I isoform alpha-like
Q9Y657	Spindlin-1
Q86VZ4	Low-density lipoprotein receptor-related protein 11
P17066	Heat shock 70 kDa protein 6
O00567	Nucleolar protein 56
Q5U5U6	Ubiquitin B

Q8WVC0	RNA polymerase-associated protein LEO1
O76061	Stanniocalcin-2
P35813	Protein phosphatase 1A
P35580	Myosin-10
Q9H9Y6	DNA-directed RNA polymerase I subunit RPA2
P16403	Histone H1.2
P05814	Beta-casein
Q5NHX5	Phosphatidate cytidylyltransferase
Q96G25	Mediator of RNA polymerase II transcription subunit 8
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial
P98175	RNA-binding protein 10
P11021	78 kDa glucose-regulated protein
Q13813	Spectrin alpha chain, brain
P67809	Nuclease-sensitive element-binding protein 1
P19338	Nucleolin
O95071	E3 ubiquitin-protein ligase UBR5
Q6P3W7	SCY1-like protein 2
Q5T5U3	Rho GTPase-activating protein 21
P54105	Methylosome subunit pICln
P30050	60S ribosomal protein L12
P60660	Myosin light polypeptide 6
P23588	Eukaryotic translation initiation factor 4B
O75688	Protein phosphatase 1B
P09651	Heterogeneous nuclear ribonucleoprotein A1
Q05639	Elongation factor 1-alpha 2
P35268	60S ribosomal protein L22
Q9H361	Polyadenylate-binding protein 3
Q15750	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1
Q99829	Copine-1
P61978	Heterogeneous nuclear ribonucleoprotein K
Q12906	Interleukin enhancer-binding factor 3
P46778	60S ribosomal protein L21
Q9BXF6	Rab11 family-interacting protein 5

O75533	Splicing factor 3B subunit 1
Q9BQE3	Tubulin alpha-1C chain
Q15208	Serine/threonine-protein kinase 38
P63267	Actin, gamma-enteric smooth muscle
Q15393	Splicing factor 3B subunit 3
Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1
O95602	DNA-directed RNA polymerase I subunit RPA1
Q01082	Spectrin beta chain, brain 1
Q13310	Polyadenylate-binding protein 4
P05388	60S acidic ribosomal protein P0
Q04917	14-3-3 protein eta
Q9H7D7	WD repeat-containing protein 26
P08670	Vimentin
Q99873	Protein arginine N-methyltransferase 1
P07355	Annexin A2
P39023	60S ribosomal protein L3
Q9NYF8	Bcl-2-associated transcription factor 1
P13639	Elongation factor 2
O00299	Chloride intracellular channel protein 1
P04406	Glyceraldehyde-3-phosphate dehydrogenase
Q13574	Diacylglycerol kinase zeta
Q86V81	THO complex subunit 4
O60832	H/ACA ribonucleoprotein complex subunit 4
P14618	Pyruvate kinase isozymes M1/M2
P23396	40S ribosomal protein S3
P31946	14-3-3 protein beta/alpha
Q14722	Voltage-gated potassium channel subunit beta-1
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2
Q96QK1	Vacuolar protein sorting-associated protein 35
P46060	Ran GTPase-activating protein 1
P52429	Diacylglycerol kinase epsilon
P25205	DNA replication licensing factor MCM3
Q9P2K8	Eukaryotic translation initiation factor 2-alpha kinase 4

P46779	60S ribosomal protein L28
P68366	Tubulin alpha-4A chain
O14617	AP-3 complex subunit delta-1
O43390	Heterogeneous nuclear ribonucleoprotein R
P35221	Catenin alpha-1
P07384	Calpain-1 catalytic subunit
P52907	F-actin-capping protein subunit alpha-1
Q9Y2W1	Thyroid hormone receptor-associated protein 3
P62258	14-3-3 protein epsilon
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
Q15233	Non-POU domain-containing octamer-binding protein
P61313	60S ribosomal protein L15
O00159	Unconventional myosin-Ic
P04350	Tubulin beta-4A chain
P36575	Arrestin-C
Q15029	116 kDa U5 small nuclear ribonucleoprotein component
P61981	14-3-3 protein gamma
P08708	40S ribosomal protein S17
P31943	Heterogeneous nuclear ribonucleoprotein H
Q92499	ATP-dependent RNA helicase DDX1
P40227	T-complex protein 1 subunit zeta
Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta
Q9NY65	Tubulin alpha-8 chain
P16989	DNA-binding protein A
P11940	Polyadenylate-binding protein 1
P62277	40S ribosomal protein S13
P23246	Splicing factor, proline- and glutamine-rich
P52272	Heterogeneous nuclear ribonucleoprotein M
O60716	Catenin delta-1
P55795	Heterogeneous nuclear ribonucleoprotein H2
P50914	60S ribosomal protein L14
P62424	60S ribosomal protein L7a
P11142	Heat shock cognate 71 kDa protein

P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
Q00526	Cyclin-dependent kinase 3
P18124	60S ribosomal protein L7
P61247	40S ribosomal protein S3a
Q07020	60S ribosomal protein L18
Q14103	Heterogeneous nuclear ribonucleoprotein D0
P08238	Heat shock protein HSP 90-beta
Q13885	Tubulin beta-2A chain
P47755	F-actin-capping protein subunit alpha-2
P35579	Myosin-9
P52597	Heterogeneous nuclear ribonucleoprotein F
O14744	Protein arginine N-methyltransferase 5
P62316	Small nuclear ribonucleoprotein Sm D2
Q13509	Tubulin beta-3 chain
P17812	CTP synthase 1
Q71U36	Tubulin alpha-1A chain
Q13748	Tubulin alpha-3C/D chain
P09496	Clathrin light chain A
P60709	Actin, cytoplasmic 1
P39019	40S ribosomal protein S19
P05387	60S acidic ribosomal protein P2
P07237	Protein disulfide-isomerase
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
Q9UHB6	LIM domain and actin-binding protein 1
P05386	60S acidic ribosomal protein P1
C2orf6	MOB kinase activator 1A
Q15052	Rho guanine nucleotide exchange factor 6
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
Q13151	Heterogeneous nuclear ribonucleoprotein A0
Q00839	Heterogeneous nuclear ribonucleoprotein U
Q14739	Lamin-B receptor
Q13263	Transcription intermediary factor 1-beta
Q16875	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3

P06396	Gelsolin
P62241	40S ribosomal protein S8
P62081	40S ribosomal protein S7
P26599	Polypyrimidine tract-binding protein 1
P62899	60S ribosomal protein L31
P10523	S-arrestin
O00571	ATP-dependent RNA helicase DDX3X
P41227	N-alpha-acetyltransferase 10
O95218	Zinc finger Ran-binding domain-containing protein 2
P62314	Small nuclear ribonucleoprotein Sm D1
Q9UQ35	Serine/arginine repetitive matrix protein 2
P68371	Tubulin beta-4B chain
P62753	40S ribosomal protein S6
P23528	Cofilin-1
P08107	Heat shock 70 kDa protein 1A/1B
Q9UN86	Ras GTPase-activating protein-binding protein 2
O14974	Protein phosphatase 1 regulatory subunit 12A
Q14204	Cytoplasmic dynein 1 heavy chain 1
Q9BQA1	Methylosome protein 50
Q14004	Cyclin-dependent kinase 13
Q13435	Splicing factor 3B subunit 2
P84098	60S ribosomal protein L19
Q93034	Cullin-5
P30291	Wee1-like protein kinase
P62888	60S ribosomal protein L30
Q13367	AP-3 complex subunit beta-2
P62701	40S ribosomal protein S4, X isoform
Q9P286	Serine/threonine-protein kinase PAK 7
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase
P36578	60S ribosomal protein L4
P18077	60S ribosomal protein L35a
P46019	Phosphorylase b kinase regulatory subunit alpha, liver isoform
Q9NZN5	Rho guanine nucleotide exchange factor 12

P49454	Centromere protein F
P68104	Elongation factor 1-alpha 1
P16104	Histone H2A.x
P27694	Replication protein A 70 kDa DNA-binding subunit
Q9Y2J2	Band 4.1-like protein 3
O00443	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha
P78362	SRSF protein kinase 2
P61254	60S ribosomal protein L26
P55072	Transitional endoplasmic reticulum ATPase
P42766	60S ribosomal protein L35
P19388	DNA-directed RNA polymerases I, II, and III subunit RPABC1
P55196	Afadin
O15160	DNA-directed RNA polymerases I and III subunit RPAC1
P11802	Cyclin-dependent kinase 4
Q14974	Importin subunit beta-1
P68032	Actin, alpha cardiac muscle 1
Q99558	Mitogen-activated protein kinase kinase kinase 14
Q68EM7	Rho GTPase-activating protein 17
P42166	Lamina-associated polypeptide 2, isoform alpha
P17844	Probable ATP-dependent RNA helicase DDX5
P21333	Filamin-A
O15111	Inhibitor of nuclear factor kappa-B kinase subunit alpha
P49327	Fatty acid synthase
Q9HBA0	Transient receptor potential cation channel subfamily V member 4
P12956	X-ray repair cross-complementing protein 6
P68400	Casein kinase II subunit alpha
P06748	Nucleophosmin
P62158	Calmodulin
P13010	X-ray repair cross-complementing protein 5
O95782	AP-2 complex subunit alpha-1
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
Q92769	Histone deacetylase 2
P62937	Peptidyl-prolyl cis-trans isomerase A

O94973	AP-2 complex subunit alpha-2
O43318	Mitogen-activated protein kinase kinase kinase 7
P42224	Signal transducer and activator of transcription 1-alpha/beta
P62913	60S ribosomal protein L11
Q8IZQ8	Myocardin
Q13523	Serine/threonine-protein kinase PRP4 homolog
O15085	Rho guanine nucleotide exchange factor 11
Q13233	Mitogen-activated protein kinase kinase kinase 1
Q9UPA5	Protein bassoon
Q9Y3U8	60S ribosomal protein L36
S100A9	Protein S100-A9
Q5NGD0	Isoleucine--tRNA ligase
Q8TAQ2	SWI/SNF complex subunit SMARCC2
Q6ZWR4	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform
P45984	Mitogen-activated protein kinase 9
P28482	Mitogen-activated protein kinase 1
P63010	AP-2 complex subunit beta
O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial
P50613	Cyclin-dependent kinase 7
P31750	RAC-alpha serine/threonine-protein kinase
Q9WV60	Glycogen synthase kinase-3 beta
P60953	Cell division control protein 42 homolog
Q00987	E3 ubiquitin-protein ligase Mdm2
P97288	5-hydroxytryptamine receptor 4
P40417	Mitogen-activated protein kinase ERK-A
Q08499-2	cAMP-specific 3',5'-cyclic phosphodiesterase 4D
Q9H422	Homeodomain-interacting protein kinase 3
P26769	Adenylate cyclase type 2
Q9HBX9	Relaxin receptor 1

INTERACTOME FOR BMI1

P63279	SUMO-conjugating enzyme UBC9
Q8VDS3	Chromobox protein homolog 7
O14508	Suppressor of cytokine signaling 2
P30658	Chromobox protein homolog 2
Q9HC52	Chromobox protein homolog 8
O95503	Chromobox protein homolog 6
P67870	Casein kinase II subunit beta
Q06587	E3 ubiquitin-protein ligase RING1
Q99496	E3 ubiquitin-protein ligase RING2
Q8IXK0	Polyhomeotic-like protein 2
P78364	Polyhomeotic-like protein 1
Q8NDX5	Polyhomeotic-like protein 3
P68400	Casein kinase II subunit alpha
O00257	E3 SUMO-protein ligase CBX4
Q8IY57	YY1-associated factor 2
O75461	Transcription factor E2F6
P51784	Ubiquitin carboxyl-terminal hydrolase 11
P0CG48	Polyubiquitin-C
Q93009	Ubiquitin carboxyl-terminal hydrolase 7
P60484	PTEN
Q9ULT8	E3 ubiquitin-protein ligase HECTD1
Q8N488	RING1 and YY1-binding protein
P62805	Histone H4
O76075	DNA fragmentation factor subunit beta
P62258	14-3-3 protein epsilon

INTERACTOME FOR CAVEOLIN

P10275	Androgen receptor
P35354	Prostaglandin G/H synthase 2
Q13586	Stromal interaction molecule 1
P01876	Ig alpha-1 chain C region
Q9H1Q7	Protein FAM113A
P20264	POU domain, class 3, transcription factor 3
P01834	Ig kappa chain C region
Q9UGM3	Deleted in malignant brain tumors 1 protein
Q96JH8	Ras-associating and dilute domain-containing protein
O00194	Ras-related protein Rab-27B
Q8NFW9	Rab effector MyRIP
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit
P48995	Short transient receptor potential channel 1
Q15843	NEDD8
P61081	NEDD8-conjugating enzyme Ubc12
P11021	78 kDa glucose-regulated protein
P22307	Non-specific lipid-transfer protein
O75955	Flotillin-1
Q8ZAQ2	Phosphomethylpyrimidine synthase
P41134	DNA-binding protein inhibitor ID-1
P25116	Proteinase-activated receptor 1
Q7CL81	PTS system enzyme IIBC
P25445	Tumor necrosis factor receptor superfamily member 6
Q9UNN8	Endothelial protein C receptor
P13987	CD59 glycoprotein
P55957	BH3-interacting domain death agonist
P49755	Transmembrane emp24 domain-containing protein 10
Q15363	Transmembrane emp24 domain-containing protein 2
Q14254	Flotillin-2
P51636	Caveolin-2
P10586	Receptor-type tyrosine-protein phosphatase F
P18031	Tyrosine-protein phosphatase non-receptor type 1
P00533	Epidermal growth factor receptor
P03301	Genome polyprotein
P20936	Ras GTPase-activating protein 1
P41240	Tyrosine-protein kinase CSK
O95810	Serum deprivation-response protein
P12931	Proto-oncogene tyrosine-protein kinase Src
P60484	PTEN
P08183	Multidrug resistance protein 1
Q03160	Growth factor receptor-bound protein 7
Q12933	TNF receptor-associated factor 2

P01112	GTPase HRas
P29350	Tyrosine-protein phosphatase non-receptor type 6
Q16881	Thioredoxin reductase 1, cytoplasmic
Q969G5	Protein kinase C delta-binding protein
Q06124	Tyrosine-protein phosphatase non-receptor type 11
Q14108	Lysosome membrane protein 2

INTERACTOME FOR CENPC1

Q5SUE7	Adenosine deaminase domain-containing protein 1
Q9ES28	Rho guanine nucleotide exchange factor 7
Q8CDM1	ATPase family AAA domain-containing protein 2
Q925I1	ATPase family AAA domain-containing protein 3
Q03265	ATP synthase subunit alpha, mitochondrial
P46737	Lys-63-specific deubiquitinase BRCC36
Q9WVA3	Mitotic checkpoint protein BUB3
Q60865	Caprin-1
Q66JQ7	Protein CASC5
Q9CWN7	UPF0760 protein C2orf29 homolog
Q9CR02	UPF0534 protein C4orf43 homolog
P24788	Cyclin-dependent kinase 11B
O35216	Histone H3-like centromeric protein A
Q8K1K4	Centromere protein I
Q9ESN5	Centromere protein K
Q9CQA0	Centromere protein M
Q9CZW2	Centromere protein N
Q8K015	Centromere protein O
Q9CZ92	Centromere protein P
Q9CPQ5	Centromere protein Q
Q6PDQ2	Chromodomain-helicase-DNA-binding protein 4
Q9DA19	Corepressor interacting with RBPJ 1
Q68FD5	Clathrin heavy chain 1
O35492	Dual specificity protein kinase CLK3
Q9CQF3	Cleavage and polyadenylation specificity factor subunit 5
Q60737	Casein kinase II subunit alpha
O54833	Casein kinase II subunit alpha'
P67871	Casein kinase II subunit beta
Q64368	Deleted in azoospermia-like
Q91VR5	ATP-dependent RNA helicase DDX1

Q9QY15	ATP-dependent RNA helicase DDX25
O35286	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
O70133	ATP-dependent RNA helicase A
Q9DA79	Dipeptidase 3
P51807	Dynein light chain Tctex-type 1
Q61545	RNA-binding protein EWS
Q69ZR9	Protein FAM208A
Q5DTT3	Protein FAM208B
P35550	rRNA 2'-O-methyltransferase fibrillarin
P35922	Fragile X mental retardation protein 1 homolog
Q61584	Fragile X mental retardation syndrome-related protein 1
Q9WVR4	Fragile X mental retardation syndrome-related protein 2
Q68FF6	ARF GTPase-activating protein GIT1
Q9JLQ2	ARF GTPase-activating protein GIT2
Q8CGP6	Histone H2A type 1-H
P70696	Histone H2B type 1-A
P84228	Histone H3.2
Q9Z0R0	Serine/threonine-protein kinase haspin
O09106	Histone deacetylase 1
P70288	Histone deacetylase 2
Q6PAV2	Probable E3 ubiquitin-protein ligase HERC4
P16627	Heat shock 70 kDa protein 1-like
Q60960	Importin subunit alpha-1
P70168	Importin subunit beta-1
Q5SVQ0	Histone acetyltransferase KAT7
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta
P06151	L-lactate dehydrogenase A chain
P00342	L-lactate dehydrogenase C chain
P14733	Lamin-B1
Q8K310	Matrin-3
Q9CY25	Protein MIS12 homolog
P97434	Myosin phosphatase Rho-interacting protein
P54276	DNA mismatch repair protein Msh6

Q8K4B0	Metastasis-associated protein MTA1
Q9R190	Metastasis-associated protein MTA2
Q6DID5	PWWP domain-containing protein MUM1
Q8C854	Myelin expression factor 2 (MEF-2) (MyEF-2)
Q91W39	Nuclear receptor coactivator 5 (NCoA-5)
P30415	NK-tumor recognition protein
Q8R0G9	Nuclear pore complex protein Nup133
Q9JIH2	Nuclear pore complex protein Nup50
Q9DAK2	Parkin coregulated gene protein homolog
Q9JMB7	Piwi-like protein 1
Q8CDG1	Piwi-like protein 2
Q9CPV5	Polyamine-modulated factor 1
A2AR02	Peptidyl-prolyl cis-trans isomerase G
Q61136	Serine/threonine-protein kinase PRP4 homolog
P60484	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN
Q60973	Histone-binding protein RBBP7
Q8C2Q3	RNA-binding protein 14
Q8VH51	RNA-binding protein 39
A2AU37	Double-strand-break repair protein rad21-like protein 1
Q99J62	Replication factor C subunit 4
Q99MV7	RING finger protein 17
Q9DBU5	E3 ubiquitin-protein ligase RNF6
P08775	DNA-directed RNA polymerase II subunit RPB1
P60122	RuvB-like 1
Q9WTM5	RuvB-like 2
Q9QX47	Protein SON
Q9D083	Kinetochore protein Spc24
Q9CUU3	Synaptonemal complex protein 2 (SCP-2)
Q9ERA6	Tuftelin-interacting protein 11
Q01320	DNA topoisomerase 2-alpha
Q569Z6	Thyroid hormone receptor-associated protein 3
O08810	116 kDa U5 small nuclear ribonucleoprotein component
Q8K4P0	pre-mRNA 3' end processing protein WDR33

Q5U4F6	WD repeat-containing protein 34
Q0GGX2	Zinc finger protein 541
Q3TTV6	Tuftelin-interacting protein 11
Q543F1	Elongation factor Tu GTP binding domain containing 2
A3QK68	MIS12 homolog
A3KPD0	Histone H2A
B8JK54	Centromere protein O
Q0VB91	PARK2 co-regulated
A2A9P5	Cell division cycle 2-like 1
B1AV89	Centromere protein I
Q3TXT7	RuvB-like protein 2
B9EI85	Histone H3
Q8BTS0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5
Q6ZQG1	MCG21756, isoform CRA_a
Q80U43	MKIAA0310 protein (SEC16 homolog A (S. cerevisiae)) (Fragment)
Q7TSF9	Protein 2610020H08Rik
A1L347	Heat shock protein 1-like
Q8BIZ8	Protein Scaper
D3Z3J7	Protein 2610020H08Rik (RIKEN cDNA 2610020H08, isoform CRA_h)
Q58E49	Histone deacetylase
Q91VA7	Isocitrate dehydrogenase 3 (NAD+) beta
Q3U1C2	MCG130614
Q548Z6	L-lactate dehydrogenase
Q3UKJ6	DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_a
Q5BL18	Matrin 3
Q564E2	L-lactate dehydrogenase
B2RVI6	Centromere protein P
A2AJI4	Thyroid hormone receptor associated protein 3
Q8R5E6	Ythdc1 protein (Fragment)
Q545V8	Putative uncharacterized protein
Q8BR71	Putative uncharacterized protein (Fragment)
Q8C5H3	Putative uncharacterized protein
E9PYL1	Protein Chd5

Q3UE68	Putative uncharacterized protein
Q3UHW8	Putative uncharacterized protein
Q8CDH5	Putative uncharacterized protein (Fragment)
Q3UFG2	Putative uncharacterized protein (Fragment)
Q8BJ53	Putative uncharacterized protein
Q3U057	Putative uncharacterized protein
A0AUV1	Histone H2A (Fragment)
Q3V0L1	Putative uncharacterized protein
Q3UXK4	Putative uncharacterized protein
A2AWQ8	Novel protein, possible orthologue of human CBF1 interacting corepressor
Q3TLX0	Putative uncharacterized protein (Fragment)
Q3TFD9	Putative uncharacterized protein
Q9ERA8	ATP synthase gamma chain
Q69ZZ3	MKIAA0788 protein (Fragment)
Q61464	Zinc finger protein 638
Q8C854	Myelin expression factor 2
Q5SS40	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
I49707	germ cell specific gene 3 protein
Q9D2X5	MAU2 chromatid cohesion factor homolog
Q8K305	kinetochore-associated protein NSL1 homolog
P70281	synaptonemal complex protein 3
P62259	14-3-3 protein epsilon
NP_940810	tudor domain-containing protein 6 isoform 2
Q9CQL1	Protein mago nashi homolog 1-related
Q8BJ01	ubiquitin associated protein 2-like
Q8CJI4	H1 histone family, member N, testis-specific
Q8R081	Heterogeneous nuclear ribonucleoprotein L
Q9CV89	pinin
Q3TWV0	vimentin
Q3TLK3	expressed sequence AU014645; nuclear cap binding protein subunit 1
P15331	Peripherin
A0PJG9	retinoblastoma binding protein 6
Q3UJZ7	predicted gene 5243; NOP56 ribonucleoprotein homolog (yeast)

P68040	Guanine nucleotide-binding protein subunit beta-2-like 1
B2DD01	Retinoic acid induced 14
Q05BN4	serine/arginine repetitive matrix 2; similar to Serine/arginine repetitive matrix protein 2; similar to retinitis pigmen GTPase regulator
Q58E64	predicted gene 5869; predicted gene 7161; predicted gene 7105; predicted gene 5822; similar to eukaryotic translation elongation factor 1 alpha 1; predicted gene 6192; predicted gene 6392; predicted gene 6767; predicted gene 6170; predicted gene 6548; predicted gene 6789; eukaryotic translation elongation factor 1 alpha 1
Q45VK5	interleukin enhancer binding factor 3
D3ZIF7	mediator complex subunit 1
Q6P5B5	fragile X mental retardation, autosomal homolog 2
Q8BU35	RNA binding motif protein 25
Q8CIA8	uveal autoantigen with coiled-coil domains and ankyrin repeats
A2AU37	Double-strand-break repair protein rad21-like protein 1
Q8C211	ankyrin repeat domain 32
Q9Z2U6	spermatogenesis associated 5
Q05C68	mitochondrial carrier homolog 2 (C. elegans)
Q8BRY5	topoisomerase (DNA) II beta
Q3UXI9	interleukin enhancer binding factor 2
Q3U7T8	heat shock protein 5
Q99MV7	RING finger protein 17

INTERACTOME FOR DLG1

P78536	Disintegrin and metalloproteinase domain-containing protein 17
Q4VCS5	Angiomotin
A1A5B4	Anoctamin-9
Q9ULH1	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1
P23634	Plasma membrane calcium-transporting ATPase 4
Q9NS75	Cysteinyl leukotriene receptor 2
P89079	E4-ORF1
O70421	Frizzled-1
Q61088	Frizzled-4
Q61090	Frizzled-7
P22001	Potassium voltage-gated channel subfamily A member 3
P15385	Potassium voltage-gated channel subfamily A member 4
Q9NQT8	Kinesin-like protein KIF13B
P06239	Tyrosine-protein kinase Lck
Q99759	Mitogen-activated protein kinase kinase kinase 3
P36507	Dual specificity mitogen-activated protein kinase kinase 2
Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase
P06428	Protein E6
Q4ZGA4	Tax (Fragment)

INTERACTOME FOR MAGI2

O43424	Glutamate receptor delta-2 subunit
O35116	Catenin delta-2
O94850	Dendrin
P35439	Glutamate [NMDA] receptor subunit zeta-1
P62630	Elongation factor 1-alpha 1
Q00959	Glutamate [NMDA] receptor subunit epsilon-1
Q00961	Glutamate [NMDA] receptor subunit epsilon-3
Q02563	Synaptic vesicle glycoprotein 2A
Q62640	Glutamate receptor delta-1 subunit
Q62765	Neuroligin-1
Q62824	Exocyst complex component 4
Q9WU82	Catenin beta-1
P31424	Metabotropic glutamate receptor 5
P97838	Disks large-associated protein 3
P97837	Disks large-associated protein 2
Q6GMN2	Brain-specific angiogenesis inhibitor 1-associated protein 2
P97839	Disks large-associated protein 4
P38444	Activin receptor type-2A
O54857	PTEN
Q8R4T5	General receptor for phosphoinositides 1-associated scaffold protein
Q63374	Neurexin-2-alpha
P97836	Disks large-associated protein 1
Q9R012	Serine/threonine-protein kinase PLK2
Q96B97	SH3 domain-containing kinase-binding protein 1
P23471	Receptor-type tyrosine-protein phosphatase zeta

INTERACTOME FOR MAGI3

Q70EL4	Ubiquitin carboxyl-terminal hydrolase 43
Q8TD84	Down syndrome cell adhesion molecule-like protein 1
Q9ULL4	Plexin-B3
P08588	Beta-1 adrenergic receptor
Q92823	Neuronal cell adhesion molecule

INTERACTOME FOR MAGI1

Q12959	Disks large homolog 1
P01106	Myc proto-oncogene protein
Q5NHE7	DNA gyrase subunit B
Q5NEC0	Phosphoribosylformylglycinamidine synthase
P08588	Beta-1 adrenergic receptor
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1
A5XAW2	Kinesin heavy chain
P63000	Ras-related C3 botulinum toxin substrate 1
Q7CGN3	rtn5
O94868	FCH and double SH3 domains protein 2
Q81XA4	Preprotein translocase, SecG subunit
F1PTW8	FCHSD2
Q9NSI5	Immunoglobulin superfamily member 5
O43707	Alpha-actinin-4
Q8N3V7	Synaptopodin
P98164	Low-density lipoprotein receptor-related protein 2
Q9Y624	Junctional adhesion molecule A
Q96AP7	Endothelial cell-selective adhesion molecule
Q96J66	ATP-binding cassette sub-family C member 11
Q16774	Guanylate kinase
O00548	Delta-like protein 1
P12814	Alpha-actinin-1

INTERACTOME FOR MVP

Q14764	Major vault protein
Q81N92	Putative uncharacterized protein
Q7CL30	Putative uncharacterized protein
Q07065	Cytoskeleton-associated protein 4
Q81TT4	Chaperone protein ClpB
Q81ZA2	Methyl-accepting chemotaxis protein
Q81ME0	Phosphopentomutase
P00738	Haptoglobin
P34913	Epoxide hydrolase 2
P52292	Importin subunit alpha-2
O15162	Phospholipid scramblase 1
Q14161	ARF GTPase-activating protein GIT2
Q13423	NAD(P) transhydrogenase, mitochondrial
Q9NUX5	Protection of telomeres protein 1
P00156	Cytochrome b
P63104	14-3-3 protein zeta/delta
Q9WMX2	Genome polyprotein
Q13573	SNW domain-containing protein 1
Q99459	Cell division cycle 5-like protein

INTERACTOME FOR MAST2

Q12933	TNF receptor-associated factor 2
Q9Y4K3	TNF receptor-associated factor 6
P60484	PTEN
P0CG47	Polyubiquitin-B
Q61235	Beta-2-syntrophin
Q61983	Sodium-dependent phosphate transport protein 1
Q60825	Sodium-dependent phosphate transport protein 2A

INTERACTOME FOR MAST3

Q9C0A0	Contactin-associated protein-like 4
Q04917	14-3-3 protein eta
O43741	5'-AMP-activated protein kinase subunit beta-2
P54646	5'-AMP-activated protein kinase catalytic subunit alpha-2
P60484	PTEN

INTERACTOME FOR MAST1

Q61235	Beta-2-syntrophin
P29476	Nitric oxide synthase, brain
P60484	PTEN

INTERACTOME FOR MSP58

O95071	E3 ubiquitin-protein ligase UBR5
Q63HN8	E3 ubiquitin-protein ligase RNF213
P56537	Eukaryotic translation initiation factor 6
Q8WZ42	Titin
Q9NZM3	Intersectin-2
O14986	Phosphatidylinositol 4-phosphate 5-kinase type-1 beta
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit
P68400	Casein kinase II subunit alpha
Q5T4S7	E3 ubiquitin-protein ligase UBR4
P67870	Casein kinase II subunit beta
Q9Y3C0	WASH complex subunit CCDC53
Q86WP2	Vasculin
Q96CN9	GRIP and coiled-coil domain-containing protein 1
Q81LM9	Phenylalanine-4-hydroxylase, putative
P62312	U6 snRNA-associated Sm-like protein LSm6
P40425	Pre-B-cell leukemia transcription factor 2
Q9BQD3	KxDL motif-containing protein 1
Q8NBZ0	INO80 complex subunit E
P43364	Melanoma-associated antigen 11
Q9C0F1	Centrosomal protein of 44 kDa
Q15834	Coiled-coil domain-containing protein 85B
Q86SE5	RNA-binding Raly-like protein
Q9Y2W2	WW domain-binding protein 11
P51116	Fragile X mental retardation syndrome-related protein 2
P0C1Z6	TCF3 fusion partner
Q6PI98	INO80 complex subunit C
Q9D1P2	Histone acetyltransferase KAT8
Q53TQ3	INO80 complex subunit D
Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5
Q9BZI7	Regulator of nonsense transcripts 3B
O94972	E3 ubiquitin-protein ligase TRIM37
Q8IXK0	Polyhomeotic-like protein 2
P61964	WD repeat-containing protein 5
Q9NPJ6	Mediator of RNA polymerase II transcription subunit 4
Q6P4R8	Nuclear factor related to kappa-B-binding protein
Q9H9F9	Actin-related protein 5
Q9C086	INO80 complex subunit B
Q9H981	Actin-related protein 8
O96019	Actin-like protein 6A
Q9ULG1	DNA helicase INO80
Q9UER7	Death domain-associated protein 6
O14641	Segment polarity protein dishevelled homolog DVL-2

Q9Y265	RuvB-like 1
Q9Y230	RuvB-like 2
B7ZL83	DGKB protein

INTERACTOME FOR NEPRILYSIN

P51648	Fatty aldehyde dehydrogenase
Q14554	Protein disulfide-isomerase A5
Q92973	Transportin-1
P02545	Prelamin-A/C
P04792	Heat shock protein beta-1
P46783	40S ribosomal protein S10
Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial
P62266	40S ribosomal protein S23
O43187	Interleukin-1 receptor-associated kinase-like 2
P36776	Lon protease homolog, mitochondrial
P68104	Elongation factor 1-alpha 1
P62888	60S ribosomal protein L30
O15321	Transmembrane 9 superfamily member 1
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinases substrate
P13645	Keratin, type I cytoskeletal 10
Q9BRK5	45 kDa calcium-binding protein
Q86UE4	Protein LYRIC
Q9H9J2	39S ribosomal protein L44, mitochondrial
P40616	ADP-ribosylation factor-like protein 1
Q92835	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1
O00519	Fatty-acid amide hydrolase 1
P53985	Monocarboxylate transporter 1
Q04609	Glutamate carboxypeptidase 2
Q3ZCM7	Tubulin beta-8 chain
P54707	Potassium-transporting ATPase alpha chain 2
P12268	Inosine-5'-monophosphate dehydrogenase 2
O75844	CAAX prenyl protease 1 homolog
P46939	Utrophin
P60709	Actin, cytoplasmic 1
Q14978	Nucleolar and coiled-body phosphoprotein 1

Q9Y265	RuvB-like 1
Q9Y6F6	Protein MRVI1
Q8NBM4	Ubiquitin-associated domain-containing protein 2
P12004	Proliferating cell nuclear antigen
O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4
Q9Y230	RuvB-like 2
Q13423	NAD(P) transhydrogenase, mitochondrial
Q96JB5-1	CDK5 regulatory subunit-associated protein 3
Q14254	Flotillin-2
P11586	C-1-tetrahydrofolate synthase, cytoplasmic
P22830	Ferrochelatase, mitochondrial
Q8NEG4	Protein FAM83F
P13010	X-ray repair cross-complementing protein 5
Q05519	Serine/arginine-rich splicing factor 11
Q9NXW2	DnaJ homolog subfamily B member 12
P61225	Ras-related protein Rap-2b
P08107	Heat shock 70 kDa protein 1A/1B
Q8N2F6	Armadillo repeat-containing protein 10
P45880	Voltage-dependent anion-selective channel protein 2
Q92597	Protein NDRG1
P51571	Translocon-associated protein subunit delta
P0C0S8	Histone H2A type 1
O60313-2	Dynamin-like 120 kDa protein, mitochondrial
P35579	Myosin-9
P56134	ATP synthase subunit f, mitochondrial
Q8NAB2	Kelch repeat and BTB domain-containing protein 3
Q6P587	Acylpyruvase FAHD1, mitochondrial
Q9H8H3	Methyltransferase-like protein 7A
P11142	Heat shock cognate 71 kDa protein
Q16630-1	Cleavage and polyadenylation specificity factor subunit 6
Q9H2X3	C-type lectin domain family 4 member M
Q6IAA8	Ragulator complex protein LAMTOR1
Q14498	RNA-binding protein 39

P82663	28S ribosomal protein S25, mitochondrial
O95299	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial
Q9H0X4	Protein ITFG3
Q6S545	POTE ankyrin domain family member H
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
P01160	Natriuretic peptides A
P20366	Protachykinin-1
P08246	Neutrophil elastase
P05067	Amyloid beta A4 protein
P15144	Aminopeptidase N
P05305	Endothelin-1
Q5T208	Nicastrin
P14735	Insulin-degrading enzyme
P23582	C-type natriuretic peptide
P20800	Endothelin-2

INTERACTOME FOR NHERF1

O14745	NHERF1
P26043	Radixin
P13569	Cystic fibrosis transmembrane conductance regulator
Q9ULV1	Frizzled-4
p35240-1	Mediator of RNA polymerase II transcription subunit 28
P08473	Neprilysin
Q6ZVD8	PH domain leucine-rich repeat-containing protein phosphatase 2
P26038	Moesin
P51790	H(+)/Cl(-) exchange transporter 3
Q5VIY5	Zinc finger protein 468
O95999	B-cell lymphoma/leukemia 10
P41145	Kappa-type opioid receptor
P47900	P2Y purinoceptor 1
Q9R0W0	Metabotropic glutamate receptor type 1
O08586	Pten
P23508	Colorectal mutant cancer protein
P07550	Beta-2 adrenergic receptor
P05622	Platelet-derived growth factor receptor beta
P07947	Tyrosine-protein kinase Yes
P46937	Yorkie homolog
P15311	Ezrin
Q9BXI6	TBC1 domain family member 10A
Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3
P41231	P2Y purinoceptor 2
Q9Y6Q1	Calpain-6
Q68EM7	Rho GTPase-activating protein 17
Q9NWQ8	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1

INTERACTOME FOR NHERF2

P26043	Radixin
Q8CZH6	Putative fimbrial chaperone
Q9HBW0	Lysophosphatidic acid receptor 2
Q6GQQ9	OTU domain-containing protein 7B
Q6ZVD8	PH domain leucine-rich repeat-containing protein phosphatase 2
O60346	PH domain leucine-rich repeat-containing protein phosphatase 1
P58700	Trp operon repressor
P13569	Cystic fibrosis transmembrane conductance regulator
Q9R0W0	Metabotropic glutamate receptor type 1
P23508	Colorectal mutant cancer protein
P40879	Chloride anion exchanger
P51432	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3
P60484	PTEN
Q05066	Sex-determining region Y protein
P09619	Platelet-derived growth factor receptor beta
Q8IUQ4	E3 ubiquitin-protein ligase SIAH1
P46937	Yorkie homolog
Q9BXI6	TBC1 domain family member 10A
Q01814	Plasma membrane calcium-transporting ATPase 2

INTERACTOME FOR P53

P62258	14-3-3 protein epsilon
P61981	14-3-3 protein gamma
P31947	14-3-3 protein sigma
P63103	14-3-3 protein zeta/delta
Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
Q8ZHG0	Putative agmatine deiminase
Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2
P10275	Androgen receptor
Q01484	Ankyrin-2
P12429	Annexin A3
P20073	Annexin A7
P02749	Beta-2-glycoprotein 1
Q7Z2E3	Aprataxin
O95376	E3 ubiquitin-protein ligase ARIH2
P36405	ADP-ribosylation factor-like protein 3
Q86WX3	Active regulator of SIRT1)
Q96KQ4	Apoptosis-stimulating of p53 protein 1
Q13625	Apoptosis-stimulating of p53 protein 2
P18847	Cyclic AMP-dependent transcription factor ATF-3
Q13315	Serine-protein kinase ATM
Q13535	Serine/threonine-protein kinase ATR
O15169	Axin-1
Q07817	Bcl-2-like protein 1
Q8N9N5	Protein BANP
Q99728	BRCA1-associated RING domain protein 1
O70445	BRCA1-associated RING domain protein 1
P10415	Apoptosis regulator Bcl-2
O14503	Class E basic helix-loop-helix protein 40

P13497	Bone morphogenetic protein 1
P51813	Cytoplasmic tyrosine-protein kinase BMX
P38398	Breast cancer type 1 susceptibility protein
P51587	Breast cancer type 2 susceptibility protein
Q9NPI1	Bromodomain-containing protein 7
Q5VTR2	E3 ubiquitin-protein ligase BRE1A
O75150	E3 ubiquitin-protein ligase BRE1B
Q9BX70	BTB/POZ domain-containing protein 2
Q8TDN4	CDK5 and ABL1 enzyme substrate 1
Q9ESJ1	CDK5 and ABL1 enzyme substrate 1
Q92793	CREB-binding protein
P45481	CREB-binding protein
Q9BWC9	Coiled-coil domain-containing protein 106
P55774	C-C motif chemokine 18
Q8N726	Cyclin-dependent kinase inhibitor 2A, isoform 4
Q64364	Cyclin-dependent kinase inhibitor 2A, isoform 3
P60953	Cell division control protein 42 homolog
P06493	Cyclin-dependent kinase 1 (CDK1)
P38936	Cyclin-dependent kinase inhibitor 1
P42773	Cyclin-dependent kinase 4 inhibitor C
P17676	CCAAT/enhancer-binding protein beta (C/EBP beta)
Q03701	CCAAT/enhancer-binding protein zeta
O14757	Serine/threonine-protein kinase Chk1
O96017	Serine/threonine-protein kinase Chk2
Q99966	Cbp/p300-interacting transactivator 1
Q14061	Cytochrome c oxidase copper chaperone
Q14999	Cullin-7
Q8IWT3	Cullin-9
Q9UER7	Death domain-associated protein 6
O14576	Cytoplasmic dynein 1 intermediate chain 1
Q92841	Probable ATP-dependent RNA helicase DDX17
P17844	Probable ATP-dependent RNA helicase DDX5
P0A6Y8	Chaperone protein DnaK (HSP70)

Q9BV47	Dual specificity protein phosphatase 26
O14641	Segment polarity protein dishevelled homolog DVL-2
P03244	E1B protein, large T-antigen
P04489	Probable early E4 11 kDa protein
P18146	Early growth response protein 1
Q09472	Histone acetyltransferase p300
P84090	Enhancer of rudimentary homolog
Q15910	Histone-lysine N-methyltransferase EZH2
Q9BQD7	Protein FAM173A
Q05397	Focal adhesion kinase 1
Q86XK2	F-box only protein 11
Q8WWV6	High affinity immunoglobulin alpha and immunoglobulin mu Fc receptor
Q8ZJL7	Cation-efflux pump FieF
O43524	Forkhead box protein O3
Q9H0Q3	FXYD domain-containing ion transport regulator 6
P24522	Growth arrest and DNA damage-inducible protein GADD45 alpha
Q5NIP5	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein
Q9BVP2	Guanine nucleotide-binding protein-like 3
P18283	Glutathione peroxidase 2
P38646	Stress-70 protein, mitochondrial
P11021	78 kDa glucose-regulated protein
P49841	Glycogen synthase kinase-3 beta
Q03013	Glutathione S-transferase Mu 4
Q15486	Putative beta-glucuronidase-like protein SMA3
Q13547	Histone deacetylase 1
O15379	Histone deacetylase 3
Q9BY41	Histone deacetylase 8
P42858	Huntingtin
Q86Z02	Homeodomain-interacting protein kinase 1
Q9H2X6	Homeodomain-interacting protein kinase 2
P09429	High mobility group protein B1
P61978	Heterogeneous nuclear ribonucleoprotein K

P34931	Heat shock 70 kDa protein 1-like
P04792	Heat shock protein beta-1
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1
Q8WUF5	RelA-associated inhibitor
P20042	Eukaryotic translation initiation factor 2 subunit 2
Q08619	Interferon-activable protein 205-B
O14920	Inhibitor of nuclear factor kappa-B kinase subunit beta
Q9UNL4	Inhibitor of growth protein 4
Q15181	Inorganic pyrophosphatase
Q8N9B5	Junction-mediating and -regulatory protein
Q14695	Uncharacterized protein KIAA0087
Q92831	Histone acetyltransferase KAT2B
Q92993	Histone acetyltransferase KAT5
Q9H7Z6	Histone acetyltransferase KAT8
Q06486	Casein kinase I isoform delta
P04183	Thymidine kinase, cytosolic
Q16363	Laminin subunit alpha-4
O43261	Leukemia-associated protein 1
P03070	Large T antigen
P43356	Melanoma-associated antigen 2
Q96M61	Melanoma-associated antigen B18
Q9UBF1	Melanoma-associated antigen C2
P46821	Microtubule-associated protein 1B
Q8IW41	MAP kinase-activated protein kinase 5
Q15013	MAD2L1-binding protein (Caught by MAD2 protein)
P56273	E3 ubiquitin-protein ligase Mdm2
O15151	Protein Mdm4
Q15648	Mediator of RNA polymerase II transcription subunit 1
O00255	Menin
P45983	Mitogen-activated protein kinase 8 (MAP kinase 8)
Q15759	Mitogen-activated protein kinase 11
P47811	Mitogen-activated protein kinase 14
Q9UHC7	E3 ubiquitin-protein ligase makorin-1

Q03164	Histone-lysine N-methyltransferase MLL
Q8IZD2	Histone-lysine N-methyltransferase MLL5
Q99547	M-phase phosphoprotein 6
P04731	Metallothionein-1A
P42345	Serine/threonine-protein kinase mTOR
P01106	Myc proto-oncogene protein
Q15596	Nuclear receptor coactivator 2
P23511	Nuclear transcription factor Y subunit alpha
P25208	Nuclear transcription factor Y subunit beta
P30419	Glycylpeptide N-tetradecanoyltransferase 1
O60551	Glycylpeptide N-tetradecanoyltransferase 2
Q9Y3T9	Nucleolar complex protein 2 homolog
O60936	Nucleolar protein 3
Q9WYW0	NAD-dependent deacetylase
P06748	Nucleophosmin (NPM)
P15559	NAD(P)H dehydrogenase [quinone] 1
P22736	Nuclear receptor subfamily 4 group A member 1
O60285	NUAK family SNF1-like kinase 1
P19338	Nucleolin
Q96G74	OTU domain-containing protein 5
P02340	Cellular tumor antigen p53
Q9H3D4	Tumor protein 63
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
Q9BTK6	PAXIP1-associated protein 1
P09874	Poly [ADP-ribose] polymerase 1
Q9UN74	Protocadherin alpha-4
P35232	Prohibitin
O75925	E3 SUMO-protein ligase PIAS1
O75928	E3 SUMO-protein ligase PIAS2
Q8N2W9	E3 SUMO-protein ligase PIAS4
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
P53350	Serine/threonine-protein kinase PLK1
P29590	Protein PML

P00491	Purine nucleoside phosphorylase
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
O00231	26S proteasome non-ATPase regulatory subunit 11
P61289	Proteasome activator complex subunit 3
P20338	Ras-related protein Rab-4A
Q06609	DNA repair protein RAD51 homolog 1
P61224	Ras-related protein Rap-1b
Q15291	Retinoblastoma-binding protein 5
P06400	Retinoblastoma-associated protein
P18754	Regulator of chromosome condensation
P27694	Replication protein A 70 kDa DNA-binding subunit
Q8NHY2	E3 ubiquitin-protein ligase RFWD2
Q13972	Ras-specific guanine nucleotide-releasing factor 1
Q7LG56	Ribonucleoside-diphosphate reductase subunit M2 B
P31350	Ribonucleoside-diphosphate reductase subunit M2
P62081	40S ribosomal protein S7
P63162	Small nuclear ribonucleoprotein-associated protein N
Q8N488	RING1 and YY1-binding protein
P04271	Protein S100-B
P26447	Protein S100-A4
Q9UBE0	SUMO-activating enzyme subunit 1
Q15424	Scaffold attachment factor B1
Q14151	Scaffold attachment factor B2
P21673	Diamine acetyltransferase 1
O15126	Secretory carrier-associated membrane protein 1
Q8WTS6	Histone-lysine N-methyltransferase SETD7
Q96ST3	Paired amphipathic helix protein Sin3a
Q96EB6	NAD-dependent deacetylase sirtuin-1
Q15796	Mothers against decapentaplegic homolog 2 (MAD homolog 2)
Q8BUN5	Mothers against decapentaplegic homolog 3 (MAD homolog 3)
P51532	Transcription activator BRG1
Q16637	Survival motor neuron protein
Q92922	SWI/SNF complex subunit SMARCC1

O95863	Zinc finger protein SNAI1
Q9Y675	SNRPN upstream reading frame protein
Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2
P08047	Transcription factor Sp1
P50453	Serpin B9
Q12772	Sterol regulatory element-binding protein 2
Q96SB4	SRSF protein kinase 1
P49888	Estrogen sulfotransferase
Q15831	Serine/threonine-protein kinase STK11
Q13190	Syntaxin-5
P63165	Small ubiquitin-related modifier 1 (SUMO-1)
Q86TM6	E3 ubiquitin-protein ligase synoviolin
P49847	Transcription initiation factor TFIID subunit 6
Q16594	Transcription initiation factor TFIID subunit 9
P20226	TATA-box-binding protein
P48643	T-complex protein 1 subunit epsilon
P13693	Translationally-controlled tumor protein
P32780	General transcription factor IIH subunit 1
Q8NA92	THAP domain-containing protein 8
Q13263	Transcription intermediary factor 1-beta
Q96GM8	Target of EGR1 protein 1
Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase
Q9NS56	E3 ubiquitin-protein ligase Topors
Q12888	Tumor suppressor p53-binding protein 1
Q15672	Twist-related protein 1
P62328	Thymosin beta-4
P0CG47	Polyubiquitin-B
P63279	SUMO-conjugating enzyme UBC9
P0CG48	Polyubiquitin-C
P49459	Ubiquitin-conjugating enzyme E2 A
Q05086	Ubiquitin-protein ligase E3A
P51784	Ubiquitin carboxyl-terminal hydrolase 11
Q9HBJ7	Ubiquitin carboxyl-terminal hydrolase 29

Q9H9J4	Ubiquitin carboxyl-terminal hydrolase 42
Q93009	Ubiquitin carboxyl-terminal hydrolase 7
Q92890	Ubiquitin fusion degradation protein 1 homolog
P11473	Vitamin D3 receptor
P03120	Regulatory protein E2
P04019	Protein E6
Q99986	Serine/threonine-protein kinase VRK1
Q9C0J8	pre-mRNA 3' end processing protein WDR33
Q8TAF3	WD repeat-containing protein 48
P61964	WD repeat-containing protein 5
Q14191	Werner syndrome ATP-dependent helicase
Q9NZC7	WW domain-containing oxidoreductase
O14980	Exportin-1
P55060	Exportin-2
P18887	DNA repair protein XRCC11)
P12956	X-ray repair cross-complementing protein 6
Q96PM9	Zinc finger protein 385A
Q8TBK6	Zinc finger CCHC domain-containing protein 10
Q96PM5	RING finger and CHY zinc finger domain-containing protein 1
Q8TAQ5	Zinc finger protein 420
P17028	Zinc finger protein 24
Q6LET9	LAMA4 protein
Q5JYX0	Cell division control protein 42 homolog
Q2KN33	RING finger and CHY zinc finger domain-containing protein 1
Q7Z566	Activating transcription factor 3
Q13746	Bcr-abl mRNA of acute lymphocytic leukaemia (ALL) patients
Q7L7W2	PP2A B56 gamma 3
E1BAP5	Uncharacterized protein
Q81RG7	Putative uncharacterized protein
Q9X365	PXO1-95
Q14DJ8	Axin-1
Q9DH70	Large T antigen
Q9PST7	Zinc finger protein XFDL 156

Q9C0J8	pre-mRNA 3' end processing protein WDR33
P62979	Ubiquitin-40S ribosomal protein S27a
P62987	Ubiquitin-60S ribosomal protein L40

INTERACTOME FOR PAR3

P12931	Proto-oncogene tyrosine-protein kinase Src
P06241	Tyrosine-protein kinase Fyn
P62993	Growth factor receptor-bound protein 2
Q9Z101	Partitioning defective 6 homolog alpha
P16333	Cytoplasmic protein NCK1
P19174	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1
P00519	Tyrosine-protein kinase ABL1
P46108	Adapter molecule crk
Q8NI35	InaD-like protein

INTERACTOME FOR PCAF

P22415	Upstream stimulatory factor 1
P23511	Nuclear transcription factor Y subunit alpha
Q9EPK5	WW domain-containing transcription regulator protein 1
O75529	TAF5-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 5L
q16514-1	Transcription initiation factor TFIID subunit 12
Q9Y6J9	TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L
Q86YP4	Transcriptional repressor p66-alpha
O75478	Transcriptional adapter 2-alpha
Q8WXI9	Transcriptional repressor p66-beta
O75486	Transcription initiation protein SPT3 homolog
Q12962	Transcription initiation factor TFIID subunit 10
Q92830	Histone acetyltransferase KAT2A
O75528	Transcriptional adapter 3
Q09472	Histone acetyltransferase p300
Q16594	Transcription initiation factor TFIID subunit 9
P26358	DNA (cytosine-5)-methyltransferase 1
Q15672	Twist-related protein 1
P15172	Myoblast determination protein 1
Q92793	CREB-binding protein
Q01094	Transcription factor E2F1
P84040	Histone H4
P02299	Histone H3
P06400	Retinoblastoma-associated protein
P31749	AKT1
P04637	p53
P03255	Early E1A 32 kDa protein
Q16665	Hypoxia-inducible factor 1-alpha
Q96EB6	NAD-dependent deacetylase sirtuin-1
P06790	Regulatory protein E2
O12161	Protein Tat

P03129	Protein E7
Q04206	Transcription factor p65
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta
P16104	Histone H2A.x

INTERACTOME FOR PDGFR

P09619	Platelet-derived growth factor receptor beta
P42229	Signal transducer and activator of transcription 5A
P27986	Phosphatidylinositol 3-kinase regulatory subunit alpha
P20936	Ras GTPase-activating protein 1
P62993	Growth factor receptor-bound protein 2
Q9Y2R2	Tyrosine-protein phosphatase non-receptor type 22
P23469	Receptor-type tyrosine-protein phosphatase epsilon
Q15256	Receptor-type tyrosine-protein phosphatase R
Q16827	Receptor-type tyrosine-protein phosphatase O
P23467	Receptor-type tyrosine-protein phosphatase beta
P08575	Receptor-type tyrosine-protein phosphatase C
P29350	Tyrosine-protein phosphatase non-receptor type 6
P19174	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1
P01127	Platelet-derived growth factor subunit B
P23470	Receptor-type tyrosine-protein phosphatase gamma
P18031	Tyrosine-protein phosphatase non-receptor type 1
Q12913	Receptor-type tyrosine-protein phosphatase eta
Q05209	Tyrosine-protein phosphatase non-receptor type 12
Q15262	Receptor-type tyrosine-protein phosphatase kappa
Q00944	Focal adhesion kinase 1
P00519	Tyrosine-protein kinase ABL1
O00750	PIK3C2B
Q9BQ66	Keratin-associated protein 4-12
P25020	Tyrosine-protein kinase transforming protein Src
P0CK45	Protein E5
O00459	PIK3R2
P19174	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1
P07947	Tyrosine-protein kinase Yes
O43639	Cytoplasmic protein NCK2
P46108	Adapter molecule crk

P41499	Tyrosine-protein phosphatase non-receptor type 11
Q13239	Src-like-adapter
O14492	SH2B adapter protein 2
P06241	Tyrosine-protein kinase Fyn
P16333	Cytoplasmic protein NCK1
P22681	E3 ubiquitin-protein ligase CBL
P23956	V-type proton ATPase 16 kDa proteolipid subunit
Q13322	Growth factor receptor-bound protein 10
Q14451	Growth factor receptor-bound protein 7
Q15599	Na(+)/H(+) exchange regulatory cofactor NHE-RF2
Q28619	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
P60484	PTEN

INTERACTOME FOR PEROXIREDOXIN

Q3KTM2	Glycerophosphodiester phosphodiesterase domain-containing protein 5
Q00005	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform
Q9HCK5	Protein argonaute-4
Q6UXB4	C-type lectin domain family 4 member G
P68587	Yop proteins translocation protein P
Q6FG91	GABA(A) receptor-associated protein-like 2, isoform CRA_b
P43351	DNA repair protein RAD52 homolog
Q9NQ29	Putative RNA-binding protein Luc7-like 1
Q96GL3	IRF3 protein
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
Q9H492	Microtubule-associated proteins 1A/1B light chain 3A
Q9GZQ8	Microtubule-associated proteins 1A/1B light chain 3B
O95166	Gamma-aminobutyric acid receptor-associated protein
Q9H0R8	Gamma-aminobutyric acid receptor-associated protein-like 1
P11766	Alcohol dehydrogenase class-3
Q9Y572	Receptor-interacting serine/threonine-protein kinase 3
Q96GM5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1
O14796	SH2 domain-containing protein 1B
Q15051	IQ calmodulin-binding motif-containing protein 1
Q13162	Peroxiredoxin-4
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
P04406	Glyceraldehyde-3-phosphate dehydrogenase
Q99836	Myeloid differentiation primary response protein MyD88
P01106	Myc proto-oncogene protein
P10275	Androgen receptor
Q9Y297	F-box/WD repeat-containing protein 1A
P00533	Epidermal growth factor receptor
P62993	Growth factor receptor-bound protein 2
P10599	Thioredoxin
P60484	PTEN

Q7Z5G6	IRF3 protein
P00519	Tyrosine-protein kinase ABL1
Q16186	Proteasomal ubiquitin receptor ADRM1

INTERACTOME FOR PICT1

Q8IY92	Structure-specific endonuclease subunit SLX4
Q5NEP4	Hypothetical membrane protein
Q81T55	D-isomer specific 2-hydroxyacid dehydrogenase family protein
Q9X365	PXO1-95
Q81WS3	Arylsulfatase
Q7CGW9	Putative uncharacterized protein
Q8ZFX5	Histidinol dehydrogenase
P54257	Huntingtin-associated protein 1
Q70EL2	Ubiquitin carboxyl-terminal hydrolase 45
Q96RL1	BRCA1-A complex subunit RAP80
Q81Z87	Chitinase B
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
Q00987	E3 ubiquitin-protein ligase Mdm2

INTERACTOME FOR PREX2

P63000	RAC1
P60953	CDC42
P31749	AKT1
P42345	mTOR
Q9NR83	SLC2A4 regulator
Q9JHK5	Pleckstrin
Q7KZI7	Serine/threonine-protein kinase MARK2
P21730	C5a anaphylatoxin chemotactic receptor
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
P01106	Myc proto-oncogene protein
Q15796	SMAD2

INTERACTOME FOR RAK

P60484	PTEN
P06400	Retinoblastoma-associated protein
P63000	RAC1
Q8IZP0	Abl interactor 1

INTERACTOME FOR SHARPIN

P01583	Interleukin-1 alpha
P17301	Integrin alpha-2
P08648	Integrin alpha-5
Q99757	Thioredoxin, mitochondrial
P05556	Integrin beta-1
P18101	Ubiquitin-60S ribosomal protein L40
Q9BYM8	RanBP-type and C3HC4-type zinc finger-containing protein 1
Q96EP0	RING finger protein 31

INTERACTOME FOR SMAD2

P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
Q969K4	Ankyrin repeat and BTB/POZ domain-containing protein 1
P05141	ADP/ATP translocase 2
P12236	ADP/ATP translocase 3
P55196	Afadin
Q9ULX6	A-kinase anchor protein 8-like
P84996	Protein ALEX
P55789	FAD-linked sulfhydryl oxidase ALR
P30533	Alpha-2-macroglobulin receptor-associated protein
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E
Q9UJX6	Anaphase-promoting complex subunit 2
Q12955	Ankyrin-3
P58335	Anthrax toxin receptor 2
P05023	Sodium/potassium-transporting ATPase subunit alpha-1
P05026	Sodium/potassium-transporting ATPase subunit beta-1
P56385	ATP synthase subunit e, mitochondrial
Q9NRL2	Bromodomain adjacent to zinc finger domain protein 1A
Q9NWK9	Box C/D snoRNA protein 1
Q00994	Protein BEX3
Q9BX70	BTB/POZ domain-containing protein 2
P62158	Calmodulin
Q92793	CREB-binding protein
Q86WR0	Coiled-coil domain-containing protein 25
P10809	60 kDa heat shock protein, mitochondrial
Q9NSE2	Cytokine-inducible SH2-containing protein
P09496	Clathrin light chain A
P05108	Cholesterol side-chain cleavage enzyme, mitochondrial
P01243	Chorionic somatomammotropin hormone
Q92905	COP9 signalosome complex subunit 5

Q93034	Cullin-5
Q9BVG4	UPF0368 protein Cxorf26
O14576	Cytoplasmic dynein 1 intermediate chain 1
P61962	DDB1- and CUL4-associated factor 7
Q96GG9	DCN1-like protein 1
Q92499	ATP-dependent RNA helicase DDX1
Q14562	ATP-dependent RNA helicase DHX8
Q92988	Homeobox protein DLX-4
O60884	DnaJ homolog subfamily A member 2
Q99615	DnaJ homolog subfamily C member 7
Q8NF50	Dedicator of cytokinesis protein 8
Q9BZ29	Dedicator of cytokinesis protein 9
Q8N608	Inactive dipeptidyl peptidase 10
P68104	Elongation factor 1-alpha 1
O15371	Eukaryotic translation initiation factor 3 subunit D
Q9Y262	Eukaryotic translation initiation factor 3 subunit L
Q09472	Histone acetyltransferase p300
O15197	Ephrin type-B receptor 6 (HEP)
P19447	TFIIH basal transcription factor complex helicase XPB subunit
Q9H501	ESF1 homolog
P50502	Hsc70-interacting protein
Q96MY7	Protein FAM161B
A6ND36	Protein FAM83G
P01100	Proto-oncogene c-Fos
P14136	Glial fibrillary acidic protein
Q92769	Histone deacetylase 2
Q5T447	E3 ubiquitin-protein ligase HECTD3
Q15651	High mobility group nucleosome-binding domain-containing protein 3
P08107	Heat shock 70 kDa protein 1A/1B
O60841	Eukaryotic translation initiation factor 5B)
Q14240	Eukaryotic initiation factor 4A-II
Q9NWB7	Intraflagellar transport protein 57 homolog
O15111	Inhibitor of nuclear factor kappa-B kinase subunit alpha

Q9NPH3	Interleukin-1 receptor accessory protein)
Q14974	Importin subunit beta-1
P05412	Transcription factor AP-1
Q2LD37	Uncharacterized protein KIAA1109
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
P33176	Kinesin-1 heavy chain
Q13887	Krueppel-like factor 5
O15230	Laminin subunit alpha-5
Q9WUH2	LIM/homeobox protein Lhx9
Q9Y2U8	Inner nuclear membrane protein Man1
O15068	Guanine nucleotide exchange factor DBS
Q96RN5	Mediator of RNA polymerase II transcription subunit 15
O75448	Mediator of RNA polymerase II transcription subunit 24
O75586	Mediator of RNA polymerase II transcription subunit 6
Q9NXB0	Meckel syndrome type 1 protein
Q9NZJ7	Mitochondrial carrier homolog 1
Q9NYA4	Myotubularin-related protein 4
Q92614	Unconventional myosin-XVIIIa
Q9Y4I1	Unconventional myosin-Va
Q9UJ70	N-acetyl-D-glucosamine kinase
Q14919	Dr1-associated corepressor
Q14686	Nuclear receptor coactivator 6
Q96SB3	Neurabin-2
Q96PU5	E3 ubiquitin-protein ligase NEDD4-like
P07197	Neurofilament medium polypeptide
P55209	Nucleosome assembly protein 1-like 1
Q8TAK6	Oligodendrocyte transcription factor 1
Q13438	Protein OS-9
P04637	Cellular tumor antigen p53
Q9H3D4	Tumor protein 63 (p63)
Q8WXI9	Transcriptional repressor p66-beta
P51003	Poly(A) polymerase alpha

Q6ZW49	PAX-interacting protein 1
P40855	Peroxisomal biogenesis factor 19
O60664	Perilipin-3
Q70Z35	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein (P-Rex2)
O00231	26S proteasome non-ATPase regulatory subunit 11
P48556	26S proteasome non-ATPase regulatory subunit 8
Q8WXF1	Paraspeckle component 1
P20962	Parathymosin
P27708	CAD protein
Q9H6Z4	Ran-binding protein 3
Q96S59	Ran-binding protein 9
P62826	GTP-binding nuclear protein Ran
P10826	Retinoic acid receptor beta
Q8IUD2	ELKS/Rab6-interacting/CAST family member 1
Q96LT9	RNA-binding protein 40
Q9D8T3	GTPase RhebL1
P61586	Transforming protein RhoA
P97348	Rho-related GTP-binding protein RhoD
Q86UR5	Regulating synaptic membrane exocytosis protein 1
Q13671	Ras and Rab interactor 1
P62888	60S ribosomal protein L30
P62987	Ubiquitin-60S ribosomal protein L40
P32969	60S ribosomal protein L9
Q5XPI4	E3 ubiquitin-protein ligase RNF123
O60518	Ran-binding protein 6 (RanBP6)
P51991	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)
Q13464	Rho-associated protein kinase 1
P05423	DNA-directed RNA polymerase III subunit RPC4
Q969S9	Ribosome-releasing factor 2, mitochondrial
P62263	40S ribosomal protein S14
P61247	40S ribosomal protein S3a
Q96T23	Remodeling and spacing factor 1
P08621	U1 small nuclear ribonucleoprotein 70 kDa

P19793	Retinoic acid receptor RXR-alpha
P07602	Proactivator polypeptide
Q9BW04	Specifically androgen-regulated gene protein
P05060	Secretogranin-1
Q9H2E6	Semaphorin-6A
Q9HC62	Sentrin-specific protease 2
Q13435	Splicing factor 3B subunit 2
P12757	Ski-like protein
P12755	Ski oncogene
P84022	Mothers against decapentaplegic homolog 3 (MAD homolog 3)
Q13485	Mothers against decapentaplegic homolog 4 (MAD homolog 4)
O15198	Mothers against decapentaplegic homolog 9 (MAD homolog 9)
Q92922	SWI/SNF complex subunit SMARCC1
Q9HCE7	E3 ubiquitin-protein ligase SMURF1
Q9HAU4	E3 ubiquitin-protein ligase SMURF2
O95295	SNARE-associated protein Snapin
Q13573	SNW domain-containing protein 1
P00441	Superoxide dismutase
P30626	Sorcin
Q8N0X7	Spartin
Q7KZ85	Transcription elongation factor SPT6
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial
Q9BX66	Sorbin and SH3 domain-containing protein 1
Q05519	Serine/arginine-rich splicing factor 11
Q13243	Serine/arginine-rich splicing factor 5
Q9NQ55	Suppressor of SWI4 1 homolog
P78524	Suppression of tumorigenicity 5 protein
O75683	Surfeit locus protein 6
P21579	Synaptotagmin-1
Q5VWG9	Transcription initiation factor TFIID subunit 3
P68363	Tubulin alpha-1B chain
P68366	Tubulin alpha-4A chain
Q86TI0	TBC1 domain family member 1

Q6IPX3	Transcription elongation factor A protein-like 6
P40227	T-complex protein 1 subunit zeta
P13693	Translationally-controlled tumor protein
P54274	Telomeric repeat-binding factor 1
Q12800	Alpha-globin transcription factor CP2
P36897	TGF-beta receptor type-1
P21980	Protein-glutamine gamma-glutamyltransferase 2
Q9UPQ9	Trinucleotide repeat-containing gene 6B protein
P11387	DNA topoisomerase 1
P12270	Nucleoprotein TPR
Q9UPN9	E3 ubiquitin-protein ligase TRIM33
Q9BVG3	Tripartite motif-containing protein 62
Q9H2G4	Testis-specific Y-encoded-like protein 2
P25490	Transcriptional repressor protein YY1
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase
O95071	E3 ubiquitin-protein ligase UBR5
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X
Q9Y5K8	V-type proton ATPase subunit D
Q2M389	WASH complex subunit 7
O00308	NEDD4-like E3 ubiquitin-protein ligase WWP2
O60315	Zinc finger E-box-binding homeobox 2
Q9H2Y7	Zinc finger protein 106 homolog
Q96KR1	Zinc finger RNA-binding protein
O95405	Zinc finger FYVE domain-containing protein 9
Q15326	Zinc finger MYND domain-containing protein 11
P51814	Zinc finger protein 41
Q15227	Pregnancy specific beta-1-glycoprotein 9
Q9H5C5	CDNA: FLJ23584 fis, clone LNG14307
Q5RKT7	Ribosomal protein S27a
Q13484	Ankyrin G119
Q8N6E6	C21orf66 protein
Q9NRC3	Cytoplasmic dynein heavy chain (Fragment)
Q96T67	TOB3

Q9CQB1	ADP-ribosylation factor 4-like (ADP-ribosylation factor-like 4D) (ADP-ribosylation factor-like protein 4D)

INTERACTOME FOR SMAD3

P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
P11171	Protein 4.1
Q9NY61	Protein AATF
P60709	Actin, cytoplasmic 1
Q9HDC9	Adipocyte plasma membrane-associated protein
P04114	Apolipoprotein B-100
O60563	Cyclin-T1
P17676	CCAAT/enhancer-binding protein beta (C/EBP beta)
P08603	Complement factor H
Q9UEE9	Craniofacial development protein 1
O15519	CASP8 and FADD-like apoptosis regulator
Q9H2X0	Chordin
Q7Z3E2	Uncharacterized protein C10orf118
O75746	Calcium-binding mitochondrial carrier protein Aralar1
P31146	Coronin-1A
P05108	Cholesterol side-chain cleavage enzyme, mitochondrial
P46108	Adapter molecule crk
Q7LFL8	CXXC-type zinc finger protein 5
Q9UI36	Dachshund homolog 1
P61962	DDB1- and CUL4-associated factor 7
P11926	Ornithine decarboxylase
O75618	Death effector domain-containing protein
Q14562	ATP-dependent RNA helicase DHX8
O60884	DnaJ homolog subfamily A member 2
Q9UDY4	DnaJ homolog subfamily B member 4
Q9BZ29	Dedicator of cytokinesis protein 9
P51141	Segment polarity protein dishevelled homolog DVL-1
Q99814	Endothelial PAS domain-containing protein 1
A6ND36	Protein FAM83G
P23142	Fibulin-1

P21333	Filamin-A
O43524	Forkhead box protein O3
P35573	Glycogen debranching enzyme
Q9H7M9	Platelet receptor Gi24
Q14161	ARF GTPase-activating protein GIT2
Q5TA50	Glycolipid transfer protein domain-containing protein 1
Q9Y692	Glucocorticoid modulatory element-binding protein 1
P62993	Growth factor receptor-bound protein 2
Q9UHL9	General transcription factor II-I repeat domain-containing protein 1
Q9Y5J3	Hairy/enhancer-of-split related with YRPW motif protein 1
Q9NQ87	Hairy/enhancer-of-split related with YRPW motif-like protein
P61978	Heterogeneous nuclear ribonucleoprotein K
P00738	Haptoglobin
P08107	Heat shock 70 kDa protein 1A/1B
Q9UBH0	Interleukin-36 receptor antagonist protein
O15111	Inhibitor of nuclear factor kappa-B kinase subunit alpha
Q14213	Interleukin-27 subunit beta
Q9NZH6	Interleukin-37
P35568	Insulin receptor substrate 1
P61371	Insulin gene enhancer protein ISL-1
Q9HDC5	Junctophilin-1
Q8WXH2	Junctophilin-3
P13645	Keratin, type I cytoskeletal 10
P35908	Keratin, type II cytoskeletal 2 epidermal
Q7Z3B3	KAT8 regulatory NSL complex subunit 1
Q9Y2K7	Lysine-specific demethylase 2A
Q9P2J3	Kelch-like protein 9
Q80TH2	Protein LAP2
P18428	Lipopolysaccharide-binding protein
P02545	Prelamin-A/C [Cleaved into: Lamin-A/C
Q9Y2U8	Inner nuclear membrane protein Man1
O60318	80 kDa MCM3-associated protein
Q96RN5	Mediator of RNA polymerase II transcription subunit 15

P28482	Mitogen-activated protein kinase 1
Q9UMN6	Histone-lysine N-methyltransferase MLL4
P30304	M-phase inducer phosphatase 1
Q9Y483	Metal-response element-binding transcription factor 2
Q9NYA4	Myotubularin-related protein 4
Q99836	Myeloid differentiation primary response protein MyD88
Q9ULV0	Unconventional myosin-Vb
Q14686	Nuclear receptor coactivator 6
Q01705	Neurogenic locus notch homolog protein 1 (Notch 1)
P22736	Nuclear receptor subfamily 4 group A member 1
O88898	Tumor protein 63
P09466	Glycodelin
O08675	Proteinase-activated receptor 3 (PAR-3)
Q9UKK3	Poly [ADP-ribose] polymerase 4
Q08174	Protocadherin-1
Q16822	Phosphoenolpyruvate carboxykinase
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
Q8NG27	E3 ubiquitin-protein ligase Praja-1
Q6DJT9	Zinc finger protein PLAG1 (Pleiomorphic adenoma gene 1 protein)
Q9UM63	Zinc finger protein PLAGL1 (Lost on transformation 1) (LOT-1) (Pleiomorphic adenoma-like protein 1) (Tumor supressor ZAC)
P00747	Plasminogen
Q9BZL4	Protein phosphatase 1 regulatory subunit 12C
Q9UKN5	PR domain zinc finger protein 4
Q92786	Prospero homeobox protein 1
P24158	Myeloblastin
O00231	26S proteasome non-ATPase regulatory subunit 11
Q8WXF1	Paraspeckle component 1
P06737	Glycogen phosphorylase, liver form
Q9H6Z4	Ran-binding protein 3
Q96S59	Ran-binding protein 9
P35243	Recoverin
P27694	Replication protein A 70 kDa DNA-binding subunit

Q9BXF6	Rab11 family-interacting protein 5
Q9BVS4	Serine/threonine-protein kinase RIO2
P39023	60S ribosomal protein L3
P36578	60S ribosomal protein L4
P05388	60S acidic ribosomal protein P0
Q96EP0	RING finger protein 31
Q86UC2	Radial spoke head protein 3 homolog
P08621	U1 small nuclear ribonucleoprotein 70 kDa
Q9BW04	Specifically androgen-regulated gene protein
Q9BYW2	Histone-lysine N-methyltransferase SETD2
Q15459	Splicing factor 3A subunit 1
Q9UJ37	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
P12757	Ski-like protein
P12755	Ski oncogene
Q15796	SMAD2
Q8BUN5	SMAD3
Q13485	SMAD$
Q9HCE7	E3 ubiquitin-protein ligase SMURF1
Q9HAU4	E3 ubiquitin-protein ligase SMURF2
Q13573	SNW domain-containing protein 1
Q9H0E3	Histone deacetylase complex subunit SAP130
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial
Q13501	Sequestosome-1
Q12772	Sterol regulatory element-binding protein 2
Q9UHV2	SERTA domain-containing protein 1
Q05066	Sex-determining region Y protein
Q9Y3Q8	TSC22 domain family protein 4
Q92844	TRAF family member-associated NF-kappa-B activator
P17987	T-complex protein 1 subunit alpha
Q04206	Transcription factor p65
P21980	Protein-glutamine gamma-glutamyltransferase 2
O00206	Toll-like receptor 4
Q13445	Transmembrane emp24 domain-containing protein 1

P06753	Tropomyosin alpha-3 chain
P02787	Serotransferrin
Q9UPN9	E3 ubiquitin-protein ligase TRIM33
O95551	Tyrosyl-DNA phosphodiesterase 2
P25490	Transcriptional repressor protein YY1
Q93009	Ubiquitin carboxyl-terminal hydrolase 7
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X
P52735	Guanine nucleotide exchange factor VAV2 (VAV-2)
P08670	Vimentin
P47810	Wee1-like protein kinase
O00308	NEDD4-like E3 ubiquitin-protein ligase WWP2
P12956	X-ray repair cross-complementing protein 6
Q05516	Zinc finger and BTB domain-containing protein 16
Q5D1E8	Ribonuclease ZC3H12A
Q8WYQ9	Zinc finger CCHC domain-containing protein 14
Q9NPG8	Probable palmitoyltransferase ZDHHC4
O60315	Zinc finger E-box-binding homeobox 2
P15822	Zinc finger protein 40
O95405	Zinc finger FYVE domain-containing protein 9
Q15326	Zinc finger MYND domain-containing protein 11
Q86UD4	Zinc finger protein 329
P51522	Zinc finger protein 83
P78451	Somatomammotropin
Q13484	Ankyrin G119
Q96RS2	Laminin receptor-like protein LAMRL5
Q86YA9	ADP-ribosylation factor-binding protein GGA1
Q8NBT9	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1

INTERACTOME FOR STK11

Q7RTN6	STE20-related kinase adapter protein alpha
Q99LC8	Translation initiation factor eIF-2B subunit alpha
Q96CW1	AP-2 complex subunit mu
Q9Y376	Calcium-binding protein 39
Q9H6T3	RNA polymerase II-associated protein 3
Q15831	STK11
Q9NNW5	WD repeat-containing protein 6
Q8NFZ5	TNFAIP3-interacting protein 2
Q9C0K7	STE20-related kinase adapter protein beta
Q96L34	MAP/microtubule affinity-regulating kinase 4
Q8TAF3	WD repeat-containing protein 48
Q81LC5	Glutamyl-tRNA reductase
Q16543	Hsp90 co-chaperone Cdc37
Q7CG03	Metalloprotease
Q9H9S4	Calcium-binding protein 39-like
Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5
P48059	LIM and senescent cell antigen-like-containing domain protein 1
Q02241	Kinesin-like protein KIF23
Q92922	SWI/SNF complex subunit SMARCC1
P51784	Ubiquitin carboxyl-terminal hydrolase 11
O60285	NUAK family SNF1-like kinase 1
P08107	Heat shock 70 kDa protein 1A/1B
Q9Y3A3	MOB-like protein phocein
P51532	Transcription activator BRG1
Q8TEW0	Partitioning defective 3 homolog
P07900	Heat shock protein HSP 90-alpha
Q923E4	NAD-dependent deacetylase sirtuin-1
P04637	p53
Q9NRH2	SNF-related serine/threonine-protein kinase

INTERACTOME FOR THIOREDOXIN

P09429	High mobility group protein B1
P27695	DNA-(apurinic or apyrimidinic site) lyase
Q99683	Mitogen-activated protein kinase kinase kinase 5
O60739	Eukaryotic translation initiation factor 1b
Q9HC24	Protein lifeguard 4
Q6FG91	GABA(A) receptor-associated protein-like 2, isoform CRA_b
Q96D09	G-protein coupled receptor-associated sorting protein 2
P78330	Phosphoserine phosphatase
Q96BK5	PIN2/TERF1-interacting telomerase inhibitor 1
Q86XK2	F-box only protein 11
Q53HC9	Protein TSSC1
O95990	Protein FAM107A
P40337	Von Hippel-Lindau disease tumor suppressor
P11171	Protein 4.1
P30480	HLA class I histocompatibility antigen, B-42 alpha chain
Q9H3M7	Thioredoxin-interacting protein
P04406	Glyceraldehyde-3-phosphate dehydrogenase
Q9H492	Microtubule-associated proteins 1A/1B light chain 3A
Q81NX1	Conserved domain protein
Q9H0R8	Gamma-aminobutyric acid receptor-associated protein-like 1
Q9GZQ8	Microtubule-associated proteins 1A/1B light chain 3B
O14879	Interferon-induced protein with tetratricopeptide repeats 3
O95166	Gamma-aminobutyric acid receptor-associated protein
Q99836	Myeloid differentiation primary response protein MyD88
P40692	DNA mismatch repair protein Mlh1
Q8IUQ4	E3 ubiquitin-protein ligase SIAH1
Q16621	Transcription factor NF-E2 45 kDa subunit
O43707	Alpha-actinin-4
P63172	Dynein light chain Tctex-type 1
Q9Y4K3	TNF receptor-associated factor 6
P01106	Myc proto-oncogene protein
Q92905	COP9 signalosome complex subunit 5
P25942	Tumor necrosis factor receptor superfamily member 5
P63104	14-3-3 protein zeta/delta
P32119	Peroxiredoxin-2
P38936	Cyclin-dependent kinase inhibitor 1
P00533	Epidermal growth factor receptor
Q06830	Peroxiredoxin-1

INTERACTOME FOR WWP2

P54259	Atrophin-1
Q93009	Ubiquitin carboxyl-terminal hydrolase 7
O00308	NEDD4-like E3 ubiquitin-protein ligase WWP2
Q15796	SMAD2
P84022	SMAD3
O15105	SMAD7
Q01844	RNA-binding protein EWS
P50552	Vasodilator-stimulated phosphoprotein
Q9NR12	PDZ and LIM domain protein 7
Q16630	Cleavage and polyadenylation specificity factor subunit 6
Q15637	Splicing factor 1
Q9BTC0	Death-inducer obliterator 1
P0CG47	Polyubiquitin-B
Q14820	Splicing factor 1, isoform CRA_b
Q9BWA2	EWSR1 protein
P0CG48	Polyubiquitin-C
Q9Y3C5	RING finger protein 11

SUPPLEMENTARY TABLE S6
DISORDERED PROTEINS IN THE PTEN CANCER INTERACTOME

Entry	Entry name	Protein names	Gene names	Length
P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAB	246
P61981	1433G_HUMAN	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	YWHAG	247
P11171	41_HUMAN	Protein 4.1 (P4.1) (4.1R) (Band 4.1) (EPB4.1)	EPB41 E41P	864
Q9NY61	AATF_HUMAN	Protein AATF (Apoptosis-antagonizing transcription factor) (Rb-binding protein Che-1)	AATF CHE1 DED HSPC277	560
P55196	AFAD_HUMAN	Afadin (ALL1-fused gene from chromosome 6 protein) (Protein AF-6)	MLLT4 AF6	1824
Q9ULX6	AKP8L_HUMAN	A-kinase anchor protein 8-like (AKAP8-like protein) (Helicase A-binding protein 95) (HAP95) (Homologous to AKAP95 protein) (HA95) (Neighbor of A-kinase-anchoring protein 95) (Neighbor of AKAP95)	AKAP8L NAKAP NAKAP95 HRIHFB2018	646
P84996	ALEX_HUMAN	Protein ALEX (Alternative gene product encoded by XL-exon)	GNAS GNAS1	626
P55789	ALR_HUMAN	FAD-linked sulfhydryl oxidase ALR (EC 1.8.3.2) (Augmenter of liver regeneration) (hERV1) (Hepatopoietin)	GFER ALR HERV1 HPO	205
P30533	AMRP_HUMAN	Alpha-2-macroglobulin receptor-associated protein (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-associated protein 1) (RAP)	LRPAP1 A2MRAP	357
Q92688	AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B (Acidic protein rich in leucines) (Putative HLA-DR-associated protein I-2) (PHAPI2) (Silver-stainable protein SSP29)	ANP32B APRIL PHAPI2	251
Q9BTT0	AN32E_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member E (LANP-like protein) (LANP-L)	ANP32E	268
Q86WX3	AROS_HUMAN	Active regulator of SIRT1 (40S ribosomal protein S19-binding protein 1) (RPS19-binding protein 1) (S19BP)	RPS19BP1 AROS	136
Q99933	BAG1_HUMAN	BAG family molecular chaperone regulator 1 (BAG-1) (Bcl-2-associated athanogene 1)	BAG1 HAP	345
Q9NRL2	BAZ1A_HUMAN	Bromodomain adjacent to zinc finger domain protein 1A (ATP-dependent chromatin-remodeling protein) (ATP-utilizing chromatin assembly and remodeling factor 1) (hACF1) (CHRAC subunit ACF1) (Williams syndrome transcription factor-related chromatin-remodeling factor 180) (WCRF180) (hWALp1)	BAZ1A ACF1 WCRF180 HSPC317	1556
Q9NWK9	BCD1_HUMAN	Box C/D snoRNA protein 1 (Serologically defined breast cancer antigen NY-BR-75) (Zinc finger HIT domain-containing protein 6)	ZNHIT6 BCD1 C1orf181	470
Q9NYF8	BCLF1_HUMAN	Bcl-2-associated transcription factor 1 (Btf)	BCLAF1 BTF KIAA0164	920
Q00994	BEX3_HUMAN	Protein BEX3 (Brain-expressed X-linked protein 3) (Nerve growth factor receptor-associated protein 1) (Ovarian granulosa cell 13.0 kDa protein HGR74) (p75NTR-associated cell death executor)	NGFRAP1 BEX3 DXS6984E NADE	111
P38398	BRCA1_HUMAN	Breast cancer type 1 susceptibility protein (EC 6.3.2.-) (RING finger protein 53)	BRCA1 RNF53	1863
Q9NPI1	BRD7_HUMAN	Bromodomain-containing protein 7 (75 kDa bromodomain protein) (Protein CELTIX-1)	BRD7 BP75 CELTIX1	651
Q5VTR2	BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A (BRE1-A) (hBRE1) (EC 6.3.2.-) (RING finger protein 20)	RNF20 BRE1A	975
O75150	BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B (BRE1-B) (EC 6.3.2.-) (95 kDa retinoblastoma-associated protein) (RBP95) (RING finger protein 40)	RNF40 BRE1B KIAA0661	1001
Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1 CAD CDM	793
P62158	CALM_HUMAN	Calmodulin (CaM)	CALM1 CALM CAM CAM1; CALM2 CAM2 CAMB; CALM3 CALML2 CAM3 CAMC CAMIII	149
P30658	CBX2_MOUSE	Chromobox protein homolog 2 (M33) (Modifier 3 protein)	Cbx2 M33	519
O00257	CBX4_HUMAN	E3 SUMO-protein ligase CBX4 (EC 6.3.2.-) (Chromobox protein homolog 4) (Polycomb 2 homolog) (Pc2) (hPc2)	CBX4	560
Q8VDS3	CBX7_MOUSE	Chromobox protein homolog 7	Cbx7 D15Ertd417e	158
Q9HC52	CBX8_HUMAN	Chromobox protein homolog 8 (Polycomb 3 homolog) (Pc3) (hPc3) (Rectachrome 1)	CBX8 PC3 RC1	389
Q9BWC9	CC106_HUMAN	Coiled-coil domain-containing protein 106	CCDC106	280
Q86WR0	CCD25_HUMAN	Coiled-coil domain-containing protein 25	CCDC25	208
Q8N726	CD2A2_HUMAN	Cyclin-dependent kinase inhibitor 2A, isoform 4 (p14ARF) (p19ARF)	CDKN2A CDKN2 MLM	132

Q64364	CD2A2_MOUSE	Cyclin-dependent kinase inhibitor 2A, isoform 3 (p19ARF)	Cdkn2a	169
Q16543	CDC37_HUMAN	Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (p50Cdc37)	CDC37 CDC37A	378
P38936	CDN1A_HUMAN	Cyclin-dependent kinase inhibitor 1 (CDK-interacting protein 1) (Melanoma differentiation-associated protein 6) (MDA-6) (p21)	CDKN1A CAP20 CDKN1 CIP1 MDA6 PIC1 SDI1 WAF1	164
Q9UEE9	CFDP1_HUMAN	Craniofacial development protein 1 (Bucentaur)	CFDP1 BCNT	299
Q7Z3E2	CJ118_HUMAN	Uncharacterized protein C10orf118 (CTCL tumor antigen HD-CL-01/L14-2)	C10orf118	898
P09496	CLCA_HUMAN	Clathrin light chain A (Lca)	CLTA	248
Q9BVG4	CX026_HUMAN	UPF0368 protein Cxorf26	CXorf26	233
Q9UER7	DAXX_HUMAN	Death domain-associated protein 6 (Daxx) (hDaxx) (ETS1-associated protein 1) (EAP1) (Fas death domain-associated protein)	DAXX BING2 DAP6	740
O54946	DNJB6_MOUSE	DnaJ homolog subfamily B member 6 (Heat shock protein J2) (HSJ-2) (MRJ) (mDj4)	Dnajb6 Hsj2 Mrj	365
Q9H501	ESF1_HUMAN	ESF1 homolog (ABT1-associated protein)	ESF1 ABTAP C20orf6 HDCMC28P	851
P15311	EZRI_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR VIL2	586
P50502	F10A1_HUMAN	Hsc70-interacting protein (Hip) (Progesterone receptor-associated p48 protein) (Protein FAM10A1) (Putative tumor suppressor ST13) (Renal carcinoma antigen NY-REN-33) (Suppression of tumorigenicity 13 protein)	ST13 FAM10A1 HIP SNC6	369
Q96MY7	F161B_HUMAN	Protein FAM161B	FAM161B C14orf44	647
P51116	FXR2_HUMAN	Fragile X mental retardation syndrome-related protein 2	FXR2 FMR1L2	673
Q13283	G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 (G3BP-1) (EC 3.6.4.12) (EC 3.6.4.13) (ATP-dependent DNA helicase VIII) (hDH VIII) (GAP SH3 domain-binding protein 1)	G3BP1 G3BP	466
Q96CN9	GCC1_HUMAN	GRIP and coiled-coil domain-containing protein 1 (Golgi coiled-coil protein 1)	GCC1	775
P14136	GFAP_HUMAN	Glial fibrillary acidic protein (GFAP)	GFAP	432
Q86WP2	GPBP1_HUMAN	Vasculin (GC-rich promoter-binding protein 1) (Vascular wall-linked protein)	GPBP1 GPBP SSH6	473
P16403	H12_HUMAN	Histone H1.2 (Histone H1d)	HIST1H1C H1F2	213
Q92522	H1X_HUMAN	Histone H1x	H1FX	213
P23527	H2B1O_HUMAN	Histone H2B type 1-O (Histone H2B.2) (Histone H2B.n) (H2B/n)	HIST1H2BO H2BFH H2BFN	126
P84243	H33_HUMAN	Histone H3.3	H3F3A H3.3A H3F3 PP781; H3F3B H3.3B	136
P62805	H4_HUMAN	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	103
P54257	HAP1_HUMAN	Huntingtin-associated protein 1 (HAP-1) (Neuroan 1)	HAP1 HAP2 HLP1	671
O35387	HAX1_MOUSE	HCLS1-associated protein X-1 (HS1-associating protein X-1) (HAX-1) (HS1-binding protein 1) (HSP1BP-1)	Hax1 Hs1bp1	280
Q7Z4V5	HDGR2_HUMAN	Hepatoma-derived growth factor-related protein 2 (HRP-2) (Hepatoma-derived growth factor 2) (HDGF-2)	HDGFRP2 HDGF2 UNQ785/PRO1604	671
P09429	HMGB1_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1 HMG1	215
Q15651	HMGN3_HUMAN	High mobility group nucleosome-binding domain-containing protein 3 (Thyroid receptor-interacting protein 7) (TR-interacting protein 7) (TRIP-7)	HMGN3 TRIP7 PNAS-24	99
Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU HNRPU SAFA U21.1	825
P20042	IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2 (Eukaryotic translation initiation factor 2 subunit beta) (eIF-2-beta)	EIF2S2 EIF2B	333
O60841	IF2P_HUMAN	Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2)	EIF5B IF2 KIAA0741	1220

P23588	IF4B_HUMAN	Eukaryotic translation initiation factor 4B (eIF-4B)	EIF4B	611
Q9C086	IN80B_HUMAN	INO80 complex subunit B (High mobility group AT-hook 1-like 4) (IES2 homolog) (hIes2) (PAP-1-associated protein 1) (PAPA-1) (Zinc finger HIT domain-containing protein 4)	INO80B HMGA1L4 PAPA1 ZNHIT4	356
Q9UNL4	ING4_HUMAN	Inhibitor of growth protein 4 (p29ING4)	ING4 My036	249
Q9HDC5	JPH1_HUMAN	Junctophilin-1 (JP-1) (Junctophilin type 1)	JPH1 JP1	661
O95251	KAT7_HUMAN	Histone acetyltransferase KAT7 (EC 2.3.1.48) (Histone acetyltransferase binding to ORC1) (Lysine acetyltransferase 7) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 2) (MYST-2)	KAT7 HBO1 HBOa MYST2	611
Q02241	KIF23_HUMAN	Kinesin-like protein KIF23 (Kinesin-like protein 5) (Mitotic kinesin-like protein 1)	KIF23 KNSL5 MKLP1	960
Q9Y496	KIF3A_HUMAN	Kinesin-like protein KIF3A (Microtubule plus end-directed kinesin motor 3A)	KIF3A KIF3	699
Q86UP2	KTN1_HUMAN	Kinectin (CG-1 antigen) (Kinesin receptor)	KTN1 CG1 KIAA0004	1357
Q9UHB6	LIMA1_HUMAN	LIM domain and actin-binding protein 1 (Epithelial protein lost in neoplasm)	LIMA1 EPLIN SREBP3 PP624	759
P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA LMN1	664
P46821	MAP1B_HUMAN	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B	2468
Q9UIS9	MBD1_HUMAN	Methyl-CpG-binding domain protein 1 (CXXC-type zinc finger protein 3) (Methyl-CpG-binding protein MBD1) (Protein containing methyl-CpG-binding domain 1)	MBD1 CXXC3 PCM1	605
Q00987	MDM2_HUMAN	E3 ubiquitin-protein ligase Mdm2 (EC 6.3.2.-) (Double minute 2 protein) (Hdm2) (Oncoprotein Mdm2) (p53-binding protein Mdm2)	MDM2	491
P56273	MDM2_XENLA	E3 ubiquitin-protein ligase Mdm2 (EC 6.3.2.-) (Double minute 2 protein) (Xdm2) (p53-binding protein Mdm2)	mdm2	473
Q8IZD2	MLL5_HUMAN	Histone-lysine N-methyltransferase MLL5 (EC 2.1.1.43) (Lysine N-methyltransferase 2E) (KMT2E) (Myeloid/lymphoid or mixed-lineage leukemia protein 5)	MLL5 KMT2E	1858
P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN	577
Q99547	MPH6_HUMAN	M-phase phosphoprotein 6	MPHOSPH6 MPP6	160
Q6WCQ1	MPRIP_HUMAN	Myosin phosphatase Rho-interacting protein (M-RIP) (Rho-interacting protein 3) (RIP3) (p116Rip)	MPRIP KIAA0864 MRIP RHOIP3	1025
P01106	MYC_HUMAN	Myc proto-oncogene protein (Class E basic helix-loop-helix protein 39) (bHLHe39) (Proto-oncogene c-Myc) (Transcription factor p64)	MYC BHLHE39	439
P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9	1960
Q14919	NC2A_HUMAN	Dr1-associated corepressor (Dr1-associated protein 1) (Negative co-factor 2-alpha) (NC2-alpha)	DRAP1	205
Q96SB3	NEB2_HUMAN	Neurabin-2 (Neurabin-II) (Protein phosphatase 1 regulatory subunit 9B) (Spinophilin)	PPP1R9B PPP1R6	815
Q60795	NF2L2_MOUSE	Nuclear factor erythroid 2-related factor 2 (NF-E2-related factor 2) (NFE2-related factor 2) (Nuclear factor, erythroid derived 2, like 2)	Nfe2l2 Nrf-2 Nrf2	597
P07197	NFM_HUMAN	Neurofilament medium polypeptide (NF-M) (160 kDa neurofilament protein) (Neurofilament 3) (Neurofilament triplet M protein)	NEFM NEF3 NFM	916
Q15599	NHRF2_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 (NHERF-2) (NHE3 kinase A regulatory protein E3KARP) (SRY-interacting protein 1) (SIP-1) (Sodium-hydrogen exchanger regulatory factor 2) (Solute carrier family 9 isoform A3 regulatory factor 2) (Tyrosine kinase activator protein 1) (TKA-1)	SLC9A3R2 NHERF2	337
O60936	NOL3_HUMAN	Nucleolar protein 3 (Apoptosis repressor with CARD) (Muscle-enriched cytoplasmic protein) (Myp) (Nucleolar protein of 30 kDa) (Nop30)	NOL3 ARC NOP	219
Q14978	NOLC1_HUMAN	Nucleolar and coiled-body phosphoprotein 1 (140 kDa nucleolar phosphoprotein) (Nopp140) (Hepatitis C virus NS5A-transactivated protein 13) (HCV NS5A-transactivated protein 13) (Nucleolar 130 kDa protein) (Nucleolar phosphoprotein p130)	NOLC1 KIAA0035 NS5ATP13	699
Q9NPE3	NOP10_HUMAN	H/ACA ribonucleoprotein complex subunit 3 (Nucleolar protein 10) (Nucleolar protein family A member 3) (snoRNP protein NOP10)	NOP10 NOLA3	64
P55209	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP)	NAP1L1 NRP	391
P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1 NPM	294
P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL	710
Q13438	OS9_HUMAN	Protein OS-9 (Amplified in osteosarcoma 9)	OS9	667
Q9BTK6	PA1_HUMAN	PAXIP1-associated protein 1 (PTIP-associated protein 1)	PA1 C16orf53	254
Q8TEW0	PARD3_HUMAN	Partitioning defective 3 homolog (PAR-3) (PARD-3) (Atypical PKC isotype-specific-interacting protein) (ASIP) (CTCL tumor antigen se2-5) (PAR3-alpha)	PARD3 PAR3 PAR3A	1356

P40855	PEX19_HUMAN	Peroxisomal biogenesis factor 19 (33 kDa housekeeping protein) (Peroxin-19) (Peroxisomal farnesylated protein)	PEX19 HK33 PXF OK/SW-cl.22	299
Q9NWQ8	PHAG1_HUMAN	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1 (Csk-binding protein) (Transmembrane adapter protein PAG) (Transmembrane phosphoprotein Cbp)	PAG1 CBP PAG	432
Q13526	PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase Pin1) (PPIase Pin1) (Rotamase Pin1)	PIN1	163
Q8NG27	PJA1_HUMAN	E3 ubiquitin-protein ligase Praja-1 (Praja1) (EC 6.3.2.-) (RING finger protein 70)	PJA1 RNF70	643
Q9BZL4	PP12C_HUMAN	Protein phosphatase 1 regulatory subunit 12C (Protein phosphatase 1 myosin-binding subunit of 85 kDa) (Protein phosphatase 1 myosin-binding subunit p85)	PPP1R12C LENG3 MBS85	782
Q13523	PRP4B_HUMAN	Serine/threonine-protein kinase PRP4 homolog (EC 2.7.11.1) (PRP4 kinase) (PRP4 pre-mRNA-processing factor 4 homolog)	PRPF4B KIAA0536 PRP4 PRP4H PRP4K	1007
Q8WXF1	PSPC1_HUMAN	Paraspeckle component 1 (Paraspeckle protein 1)	PSPC1 PSP1	523
P20962	PTMS_HUMAN	Parathymosin	PTMS	102
Q05209	PTN12_HUMAN	Tyrosine-protein phosphatase non-receptor type 12 (EC 3.1.3.48) (PTP-PEST) (Protein-tyrosine phosphatase G1) (PTPG1)	PTPN12	780
P26043	RADI_MOUSE	Radixin (ESP10)	Rdx	583
Q9H6Z4	RANB3_HUMAN	Ran-binding protein 3 (RanBP3)	RANBP3	567
Q8IUD2	RB6I2_HUMAN	ELKS/Rab6-interacting/CAST family member 1 (ERC-1) (Rab6-interacting protein 2)	ERC1 ELKS KIAA1081 RAB6IP2	1116
P98175	RBM10_HUMAN	RNA-binding protein 10 (G patch domain-containing protein 9) (RNA-binding motif protein 10) (RNA-binding protein S1-1) (S1-1)	RBM10 DXS8237E GPATC9 GPATCH9 KIAA0122	930
Q9BZI7	REN3B_HUMAN	Regulator of nonsense transcripts 3B (Nonsense mRNA reducing factor 3B) (Up-frameshift suppressor 3 homolog B) (hUpf3B) (Up-frameshift suppressor 3 homolog on chromosome X) (hUpf3p-X)	UPF3B RENT3B UPF3X	483
Q86UR5	RIMS1_HUMAN	Regulating synaptic membrane exocytosis protein 1 (Rab-3-interacting molecule 1) (RIM 1) (Rab-3-interacting protein 2)	RIMS1 KIAA0340 RAB3IP2 RIM1 Nbla00761	1692
P61313	RL15_HUMAN	60S ribosomal protein L15	RPL15 EC45 TCBAP0781	204
P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40]	UBA52 UBCEP2	128
P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1)	RPL4 RPL1	427
Q9Y252	RNF6_HUMAN	E3 ubiquitin-protein ligase RNF6 (EC 6.3.2.-)	RNF6 SPG2	685
P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1)	HNRNPA1 HNRPA1	372
P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3 HNRPA3	378
Q13464	ROCK1_HUMAN	Rho-associated protein kinase 1 (EC 2.7.11.1) (Renal carcinoma antigen NY-REN-35) (Rho-associated, coiled-coil-containing protein kinase 1) (Rho-associated, coiled-coil-containing protein kinase I) (ROCK-I) (p160 ROCK-1) (p160ROCK)	ROCK1	1354
O15446	RPA34_HUMAN	DNA-directed RNA polymerase I subunit RPA34 (A34.5) (Antisense to ERCC-1 protein) (ASE-1) (CD3-epsilon-associated protein) (CAST) (CD3E-associated protein) (RNA polymerase I-associated factor PAF49)	CD3EAP ASE1 CAST PAF49	510
P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a]	RPS27A UBA80 UBCEP1	156
P62241	RS8_HUMAN	40S ribosomal protein S8	RPS8 OK/SW-cl.83	208
Q96T23	RSF1_HUMAN	Remodeling and spacing factor 1 (Rsf-1) (HBV pX-associated protein 8) (Hepatitis B virus X-associated protein) (p325 subunit of RSF chromatin-remodeling complex)	RSF1 HBXAP XAP8	1441
Q86UC2	RSPH3_HUMAN	Radial spoke head protein 3 homolog (Radial spoke head-like protein 2)	RSPH3 RSHL2 RSP3	560
Q92541	RTF1_HUMAN	RNA polymerase-associated protein RTF1 homolog	RTF1 KIAA0252	710
P08621	RU17_HUMAN	U1 small nuclear ribonucleoprotein 70 kDa (U1 snRNP 70 kDa) (U1-70K) (snRNP70)	SNRNP70 RNPU1Z RPU1 SNRP70 U1AP1	437
Q8N488	RYBP_HUMAN	RING1 and YY1-binding protein (Apoptin-associating protein 1) (APAP-1) (Death effector domain-associated factor) (DED-associated factor) (YY1 and E4TF1-associated factor 1)	RYBP DEDAF YEAF1	228
P04271	S100B_HUMAN	Protein S100-B (S-100 protein beta chain) (S-100 protein subunit beta) (S100 calcium-binding protein B)	S100B	92
Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB HAP HET SAFB1	915
Q14151	SAFB2_HUMAN	Scaffold attachment factor B2 (SAF-B2)	SAFB2 KIAA0138	953

P05060	SCG1_HUMAN	Secretogranin-1 (Chromogranin-B) (CgB) (Secretogranin I) (SgI) [Cleaved into: GAWK peptide; CCB peptide]	CHGB SCG1	677
Q9HC62	SENP2_HUMAN	Sentrin-specific protease 2 (EC 3.4.22.68) (Axam2) (SMT3-specific isopeptidase 2) (Smt3ip2) (Sentrin/SUMO-specific protease SENP2)	SENP2 KIAA1331	589
Q9BYW2	SETD2_HUMAN	Histone-lysine N-methyltransferase SETD2 (EC 2.1.1.43) (HIF-1) (Huntingtin yeast partner B) (Huntingtin-interacting protein 1) (HIP-1) (Huntingtin-interacting protein B) (Lysine N-methyltransferase 3A) (SET domain-containing protein 2) (hSET2) (p231HBP)	SETD2 HIF1 HYPB KIAA1732 KMT3A SET2 HSPC069	2564
Q13435	SF3B2_HUMAN	Splicing factor 3B subunit 2 (Pre-mRNA-splicing factor SF3b 145 kDa subunit) (SF3b145) (SF3b150) (Spliceosome-associated protein 145) (SAP 145)	SF3B2 SAP145	895
P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	SNRPD1	119
Q92922	SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1 (BRG1-associated factor 155) (BAF155) (SWI/SNF complex 155 kDa subunit) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 1)	SMARCC1 BAF155	1105
Q9Y675	SNURF_HUMAN	SNRPN upstream reading frame protein	SNURF	71
Q13573	SNW1_HUMAN	SNW domain-containing protein 1 (Nuclear protein SkiP) (Nuclear receptor coactivator NCoA-62) (Ski-interacting protein)	SNW1 SKIIP SKIP	536
Q7KZ85	SPT6H_HUMAN	Transcription elongation factor SPT6 (hSPT6) (Tat-cotransactivator 2 protein) (Tat-CT2 protein)	SUPT6H KIAA0162 SPT6H	1726
Q13813	SPTN1_HUMAN	Spectrin alpha chain, non-erythrocytic 1 (Alpha-II spectrin) (Fodrin alpha chain) (Spectrin, non-erythroid alpha subunit)	SPTAN1 NEAS SPTA2	2472
Q14247	SRC8_HUMAN	Src substrate cortactin (Amplaxin) (Oncogene EMS1)	CTTN EMS1	550
Q9UQ35	SRRM2_HUMAN	Serine/arginine repetitive matrix protein 2 (300 kDa nuclear matrix antigen) (Serine/arginine-rich splicing factor-related nuclear matrix protein of 300 kDa) (SR-related nuclear matrix protein of 300 kDa) (Ser/Arg-related nuclear matrix protein of 300 kDa) (Splicing coactivator subunit SRm300) (Tax-responsive enhancer element-binding protein 803) (TaxREB803)	SRRM2 KIAA0324 SRL300 SRM300 HSPC075	2752
Q05519	SRS11_HUMAN	Serine/arginine-rich splicing factor 11 (Arginine-rich 54 kDa nuclear protein) (p54) (Splicing factor, arginine/serine-rich 11)	SRSF11 SFRS11	484
Q13243	SRSF5_HUMAN	Serine/arginine-rich splicing factor 5 (Delayed-early protein HRS) (Pre-mRNA-splicing factor SRP40) (Splicing factor, arginine/serine-rich 5)	SRSF5 HRS SFRS5 SRP40	272
Q05066	SRY_HUMAN	Sex-determining region Y protein (Testis-determining factor)	SRY TDF	204
Q9NQ55	SSF1_HUMAN	Suppressor of SWI4 1 homolog (Ssf-1) (Brix domain-containing protein 3) (Peter Pan homolog)	PPAN BXDC3 SSF1	473
P63165	SUMO1_HUMAN	Small ubiquitin-related modifier 1 (SUMO-1) (GAP-modifying protein 1) (GMP1) (SMT3 homolog 3) (Sentrin) (Ubiquitin-homology domain protein PIC1) (Ubiquitin-like protein SMT3C) (Smt3C) (Ubiquitin-like protein UBL1)	SUMO1 SMT3C SMT3H3 UBL1 OK/SW-cl.43	101
O75683	SURF6_HUMAN	Surfeit locus protein 6	SURF6 SURF-6	361
P35269	T2FA_HUMAN	General transcription factor IIF subunit 1 (General transcription factor IIF 74 kDa subunit) (Transcription initiation factor IIF subunit alpha) (TFIIF-alpha) (Transcription initiation factor RAP74)	GTF2F1 RAP74	517
Q5VWG9	TAF3_HUMAN	Transcription initiation factor TFIID subunit 3 (140 kDa TATA box-binding protein-associated factor) (TBP-associated factor 3) (Transcription initiation factor TFIID 140 kDa subunit) (	TAF3	929
Q6IPX3	TCAL6_HUMAN	Transcription elongation factor A protein-like 6 (TCEA-like protein 6) (Transcription elongation factor S-II protein-like 6)	TCEAL6	200
Q13428	TCOF_HUMAN	Treacle protein (Treacher Collins syndrome protein)	TCOF1	1488
P0C1Z6	TFPT_HUMAN	TCF3 fusion partner (INO80 complex subunit F) (Protein FB1)	TFPT INO80F	253
Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF ALY BEF THOC4	257
P82094	TMF1_HUMAN	TATA element modulatory factor (TMF) (Androgen receptor coactivator 160 kDa protein) (Androgen receptor-associated protein of 160 kDa)	TMF1 ARA160	1093
Q8NFZ5	TNIP2_HUMAN	TNFAIP3-interacting protein 2 (A20-binding inhibitor of NF-kappa-B activation 2) (ABIN-2) (Fetal liver LKB1-interacting protein)	TNIP2 ABIN2 FLIP1	429
Q9UPQ9	TNR6B_HUMAN	Trinucleotide repeat-containing gene 6B protein	TNRC6B KIAA1093	1833
P11387	TOP1_HUMAN	DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	TOP1	765
Q9NS56	TOPRS_HUMAN	E3 ubiquitin-protein ligase Topors (EC 6.3.2.-) (SUMO1-protein E3 ligase Topors) (Topoisomerase I-binding RING finger protein) (Topoisomerase I-binding arginine/serine-rich protein) (Tumor suppressor p53-binding protein 3) (p53-binding protein 3) (p53BP3)	TOPORS LUN TP53BPL	1045
Q12888	TP53B_HUMAN	Tumor suppressor p53-binding protein 1 (53BP1) (p53-binding protein 1) (p53BP1)	TP53BP1	1972
P06753	TPM3_HUMAN	Tropomyosin alpha-3 chain (Gamma-tropomyosin) (Tropomyosin-3) (Tropomyosin-5) (hTM5)	TPM3	284
P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4	248
P12270	TPR_HUMAN	Nucleoprotein TPR	TPR	2363

Q9Y2W1	TR150_HUMAN	Thyroid hormone receptor-associated protein 3 (Thyroid hormone receptor-associated protein complex 150 kDa component) (Trap150)	THRAP3 TRAP150	955
Q9H2G4	TSYL2_HUMAN	Testis-specific Y-encoded-like protein 2 (TSPY-like protein 2) (Cell division autoantigen 1) (Cutaneous T-cell lymphoma-associated antigen se20-4) (CTCL-associated antigen se20-4) (Differentially-expressed nucleolar TGF-beta1 target protein) (Nuclear protein of 79 kDa) (NP79)	TSPYL2 CDA1 DENTT TSPX HRIHFB2216	693
P62328	TYB4_HUMAN	Thymosin beta-4 (T beta-4) (Fx) [Cleaved into: Hematopoietic system regulatory peptide (Seraspenide)]	TMSB4X TB4X THYB4 TMSB4	44
P25490	TYY1_HUMAN	Transcriptional repressor protein YY1 (Delta transcription factor) (INO80 complex subunit S) (NF-E1) (Yin and yang 1) (YY-1)	YY1 INO80S	414
Q9H9J4	UBP42_HUMAN	Ubiquitin carboxyl-terminal hydrolase 42 (EC 3.4.19.12) (Deubiquitinating enzyme 42) (Ubiquitin thioesterase 42) (Ubiquitin-specific-processing protease 42)	USP42	1324
Q96RL1	UIMC1_HUMAN	BRCA1-A complex subunit RAP80 (Receptor-associated protein 80) (Retinoid X receptor-interacting protein 110) (Ubiquitin interaction motif-containing protein 1)	UIMC1 RAP80 RXRIP110	719
P08670	VIME_HUMAN	Vimentin	VIM	466
P20152	VIME_MOUSE	Vimentin	Vim	466
Q9Y2W2	WBP11_HUMAN	WW domain-binding protein 11 (WBP-11) (Npw38-binding protein) (NpwBP) (SH3 domain-binding protein SNP70) (Splicing factor that interacts with PQBP-1 and PP1)	WBP11 NPWBP SIPP1 SNP70	641
Q9C0J8	WDR33_HUMAN	pre-mRNA 3' end processing protein WDR33 (WD repeat-containing protein 33) (WD repeat-containing protein WDC146)	WDR33 WDC146	1336
Q8IY57	YAF2_HUMAN	YY1-associated factor 2	YAF2	180
P67809	YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 (CCAAT-binding transcription factor I subunit A) (CBF-A) (DNA-binding protein B) (DBPB) (Enhancer factor I subunit A) (EFI-A) (Y-box transcription factor) (Y-box-binding protein 1) (YB-1)	YBX1 NSEP1 YB1	324
Q8TBK6	ZCH10_HUMAN	Zinc finger CCHC domain-containing protein 10	ZCCHC10	192
O60315	ZEB2_HUMAN	Zinc finger E-box-binding homeobox 2 (Smad-interacting protein 1) (SMADIP1) (Zinc finger homeobox protein 1b)	ZEB2 KIAA0569 SIP1 ZFHX1B ZFX1B HRIHFB2411	1214
Q9H2Y7	ZF106_HUMAN	Zinc finger protein 106 homolog (Zfp-106) (Zinc finger protein 474)	ZFP106 SH3BP3 ZNF474	1883
Q15326	ZMY11_HUMAN	Zinc finger MYND domain-containing protein 11 (Adenovirus 5 E1A-binding protein) (Protein BS69)	ZMYND11 BS69	562
Q86UD4	ZN329_HUMAN	Zinc finger protein 329	ZNF329	541
Q8TAQ5	ZN420_HUMAN	Zinc finger protein 420	ZNF420	688
Q5VIY5	ZN468_HUMAN	Zinc finger protein 468	ZNF468	522
P17028	ZNF24_HUMAN	Zinc finger protein 24 (Retinoic acid suppression protein A) (RSG-A) (Zinc finger and SCAN domain-containing protein 3) (Zinc finger protein 191) (Zinc finger protein KOX17)	ZNF24 KOX17 ZNF191 ZSCAN3	368
P51814	ZNF41_HUMAN	Zinc finger protein 41	ZNF41	821
O95218	ZRAB2_HUMAN	Zinc finger Ran-binding domain-containing protein 2 (Zinc finger protein 265) (Zinc finger, splicing)	ZRANB2 ZIS ZNF265	330
Q3MIH3	Q3MIH3_HUMAN	Ubiquitin A-52 residue ribosomal protein fusion product 1 (Ubiquitin A-52 residue ribosomal protein fusion product 1, isoform CRA_a) (cDNA, FLJ95576, Homo sapiens ubiquitin A-52 residue ribosomal protein fusionproduct 1 (UBA52), mRNA)	UBA52 hCG_37048	128
Q8N6E6	Q8N6E6_HUMAN	C21orf66 protein	C21orf66	398
Q8TBK5	Q8TBK5_HUMAN	60S ribosomal protein L6	RPL6	288
Q5RKT7	Q5RKT7_HUMAN	Ribosomal protein S27a	RPS27A	156
Q13746	Q13746_HUMAN	Bcr-abl mRNA of acute lymphocytic leukaemia (ALL) patients (Fragment)		386
Q14DJ8	Q14DJ8_MOUSE	Axin-1 (Axin1 protein)	Axin1	832
Q9JLQ4	Q9JLQ4_MOUSE	Pleiomorphic adenoma gene-like 1 (Pleiomorphic adenoma gene-like 1, isoform CRA_d) (Protein Plagl1) (Zinc finger protein ZAC1)	Plagl1 Zac1 AL713985.1-001 mCG_12864	704
Q9R0W0	Q9R0W0_RAT	Metabotropic glutamate receptor type 1 (Fragment)	Grm1 mGluR1a	84
Q9PST7	Q9PST7_XENLA	Zinc finger protein XFDL 156	znf585b	573

DISORDERED PROTEINS WITH MULTIPLE OCCURENCES IN THE PTEN CANCER INTERACTOME

Entry	Entry name	Protein names	Gene names	Organism	Length	Gene ontology (GO)
P61981	1433G_HUMAN	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	YWHAG	Homo sapiens (Human)	247	G2/M transition of mitotic cell cycle; cytosol; protein kinase C inhibitor activity; protein targeting; regulation of neuron differentiation; regulation of signal transduction; regulation of synaptic plasticity
Q99933	BAG1_HUMAN	BAG family molecular chaperone regulator 1 (BAG-1) (Bcl-2-associated athanogene 1)	BAG1 HAP	Homo sapiens (Human)	345	anti-apoptosis; apoptotic process; cell surface receptor signaling pathway; chaperone cofactor-dependent protein refolding; cytoplasm; cytosol; intermediate filament cytoskeleton; mitochondrion; neuron differentiation; nucleus; perinuclear region of cytoplasm; positive regulation of neuron apoptotic process; positive regulation of transcription from RNA polymerase II promoter; receptor signaling protein activity; response to drug; response to lithium ion; response to nicotine; response to stress
P38398	BRCA1_HUMAN	Breast cancer type 1 susceptibility protein (EC 6.3.2.-) (RING finger protein 53)	BRCA1 RNF53	Homo sapiens (Human)	1863	BRCA1-A complex; BRCA1-BARD1 complex; DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator; DNA damage response, signal transduction resulting in induction of apoptosis; DNA replication; G2/M transition DNA damage checkpoint; RNA binding; androgen receptor signaling pathway; apoptotic process; brain development; cellular response to indole-3-methanol; centrosome cycle; chordate embryonic development; chromosome segregation; condensed nuclear chromosome; damaged DNA binding; dosage compensation by inactivation of X chromosome; double-strand break repair via homologous recombination; fatty acid biosynthetic process; gamma-tubulin ring complex; mitochondrial matrix; negative regulation of centriole replication; negative regulation of fatty acid biosynthetic process; negative regulation of histone H3-K9 methylation; negative regulation of transcription, DNA-dependent; nucleoplasm; plasma membrane; positive regulation of DNA repair; positive regulation of cell cycle arrest; positive regulation of histone H3-K4 methylation; positive regulation of histone H3-K9 acetylation; positive regulation of histone H4-K16 acetylation; positive regulation of histone H4-K20 methylation; positive regulation of protein ubiquitination; positive regulation of transcription from RNA polymerase II promoter; postreplication repair; protein K6-linked ubiquitination; protein autoubiquitination; regulation of cell motility; regulation of cell proliferation; regulation of transcription from RNA polymerase III promoter; response to estradiol stimulus; response to estrogen stimulus; response to ionizing radiation; response to lipid; response to nutrient; ribonucleoprotein complex; ruffle; substrate adhesion-dependent cell spreading; transcription coactivator activity; transcription regulatory region DNA binding; ubiquitin-protein ligase activity; zinc ion binding
P62158	CALM_HUMAN	Calmodulin (CaM)	CALM1 CALM CAM CAM1; CALM2 CAM2 CAMB; CALM3 CALML2 CAM3 CAMC CAMIII	Homo sapiens (Human)	149	G-protein coupled receptor signaling pathway; activation of phospholipase C activity; calcium ion binding; centrosome; cytosol; epidermal growth factor receptor signaling pathway; extracellular region; fibroblast growth factor receptor signaling pathway; glucose metabolic process; glycogen catabolic process; muscle contraction; negative regulation of ryanodine-sensitive calcium-release channel activity; nerve growth factor receptor signaling pathway; nitric oxide metabolic process; nucleoplasm; plasma membrane; platelet activation; platelet degranulation; positive regulation of ryanodine-sensitive calcium-release channel activity; regulation of cytokinesis; regulation of nitric-oxide synthase activity; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum; response to calcium ion; small molecule metabolic process; spindle microtubule; spindle pole; synaptic transmission
P09496	CLCA_HUMAN	Clathrin light chain A (Lca)	CLTA	Homo sapiens (Human)	248	axon guidance; cellular membrane organization; clathrin coat; clathrin coat of coated pit; clathrin coat of trans-Golgi network vesicle; clathrin-coated endocytic vesicle membrane; cytoplasmic membrane-bounded vesicle; cytosol; endocytosis; epidermal growth factor receptor signaling pathway; intracellular protein transport; negative regulation of epidermal growth factor receptor signaling pathway; nerve growth factor receptor signaling pathway; peptide binding; plasma membrane; post-Golgi vesicle-mediated transport; structural molecule activity
Q9UER7	DAXX_HUMAN	Death domain-associated protein 6 (Daxx) (hDaxx) (ETS1-associated protein 1) (EAP1) (Fas death domain-associated protein)	DAXX BING2 DAP6	Homo sapiens (Human)	740	PML body; activation of JUN kinase activity; androgen receptor signaling pathway; apoptotic process; cell body; cell cortex; chromosome, centromeric region; cytokinesis after mitosis; cytosol; heterochromatin; induction of apoptosis via death domain receptors; interspecies interaction between organisms; negative regulation of transcription, DNA-dependent; neuron projection; nucleolus; receptor signaling protein activity; regulation of protein ubiquitination; transcription, DNA-dependent
P62805	H4_HUMAN	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	Homo sapiens (Human)	103	CenH3-containing nucleosome assembly at centromere; DNA binding; extracellular region; negative regulation of megakaryocyte differentiation; nucleoplasm; nucleosome; phosphatidylinositol-mediated signaling; telomere maintenance
P46821	MAP1B_HUMAN	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B	Homo sapiens (Human)	2468	axon; axon extension involved in development; cell junction; cellular process; central nervous system development; cytosol; dendrite development; developmental maturation; embryo development; establishment of monopolar cell polarity; growth cone; induction of synaptic plasticity by chemical substance; microtubule; microtubule associated complex; microtubule bundle formation; mitochondrion transport along microtubule; negative regulation of intracellular transport; negative regulation of microtubule depolymerization; perikaryon; perinuclear region of cytoplasm; peripheral nervous system axon regeneration; plasma membrane; positive regulation of axon extension; positive regulation of microtubule polymerization; positive regulation of neuron differentiation; postsynaptic density; response to carbohydrate stimulus; response to drug; response to estradiol stimulus; response to inorganic substance; response to insecticide; response to mechanical stimulus; response to peptide hormone stimulus; response to vitamin A; soluble fraction; structural molecule activity; synapse assembly
Q00987	MDM2_HUMAN	E3 ubiquitin-protein ligase	MDM2	Homo sapiens (Human)	491	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest; cellular response to hypoxia; cytosol; endocytic vesicle membrane;

		Mdm2 (EC 6.3.2.-) (Double minute 2 protein) (Hdm2) (Oncoprotein Mdm2) (p53-binding protein Mdm2)				epidermal growth factor receptor signaling pathway; establishment of protein localization; fibroblast growth factor receptor signaling pathway; interspecies interaction between organisms; negative regulation of DNA damage response, signal transduction by p53 class mediator; negative regulation of apoptotic process; negative regulation of cell cycle arrest; negative regulation of transcription from RNA polymerase II promoter; nerve growth factor receptor signaling pathway; nucleolus; nucleoplasm; peptidyl-lysine modification; phosphatidylinositol-mediated signaling; plasma membrane; positive regulation of cell proliferation; positive regulation of mitotic cell cycle; positive regulation of proteasomal ubiquitin-dependent protein catabolic process; protein complex; protein complex assembly; protein destabilization; protein localization to nucleus; protein ubiquitination involved in ubiquitin-dependent protein catabolic process; response to antibiotic; synaptic transmission; traversing start control point of mitotic cell cyc ubiquitin-protein ligase activity; zinc ion binding
P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1 NPM	Homo sapiens (Human)	294	CenH3-containing nucleosome assembly at centromere; DNA repair; RNA binding; anti-apoptosis; cell aging; centrosome cycle; interspecies interaction between organisms; intracellular protein transport; negative regulation of cell proliferation; negative regulation of centrosome duplication; nucleocytoplasmic transport; nucleolus; nucleoplasm; positive regulation of NF-kappaB transcription factor activity; protein oligomerization; regulation of centriole replication; regulation of endodeoxyribonuclease activity; regulation of endoribonuclease activity; ribonucleoprotein complex; ribosomal large subunit binding; ribosomal small subunit binding; ribosome assembly; signal transduction; spindle pole centrosome; transcription coactivator activity
P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL	Homo sapiens (Human)	710	RNA binding; angiogenesis; cell cortex; nucleolus; nucleoplasm; nucleotide binding; ribonucleoprotein complex; telomeric DNA binding
Q13526	PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase Pin1) (PPIase Pin1) (Rotamase Pin1)	PIN1	Homo sapiens (Human)	163	cell cycle; cytokine-mediated signaling pathway; cytoplasm; innate immune response; midbody; negative regulation of ERK1 and ERK2 cascade; negative regulation of cell motility; negative regulation of transforming growth factor beta receptor signaling pathway; negative regulation of type I interferon production; nuclear speck; nucleoplasm; peptidyl-prolyl cis-trans isomerase activity; positive regulation of Rho GTPase activity; positive regulation of protein phosphorylation; positive regulation of ubiquitin-protein ligase activity; protein folding; regulation of cell proliferation; regulation of cytokinesis; regulation of mitosis; regulation of pathway-restricted SMAD protein phosphorylation
Q8WXF1	PSPC1_HUMAN	Paraspeckle component 1 (Paraspeckle protein 1)	PSPC1 PSP1	Homo sapiens (Human)	523	RNA binding; cytoplasm; nuclear matrix; nuclear speck; nucleolus; nucleotide binding; paraspeckles; regulation of transcription, DNA-dependent; transcription, DNA-dependent
P26043	RADI_MOUSE	Radixin (ESP10)	Rdx	Mus musculus (Mouse)	583	actin filament capping; apical part of cell; apical protein localization; cleavage furrow; cytoplasm; cytoskeleton; extrinsic to membrane; filopodium; lamellipodium; microvillus assembly; plasma membrane; ruffle; stereocilium
Q9H6Z4	RANB3_HUMAN	Ran-binding protein 3 (RanBP3)	RANBP3	Homo sapiens (Human)	567	cytoplasm; intracellular transport; nucleus; protein transport
P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40]	UBA52 UBCEP2	Homo sapiens (Human)	128	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest; DNA repair; G1 phase of mitotic cell cycle; G1/S transition of mitotic cell cycle; I-kappaB kinase/NF-kappaB cascade; JNK cascade; M/G1 transition of mitotic cell cycle; MyD88-dependent toll-like receptor signaling pathway; Notch receptor processing; Notch signaling pathway; S phase of mitotic cell cycle; SRP-dependent cotranslational protein targeting to membrane; T cell receptor signaling pathway; TRIF-dependent toll-like receptor signaling pathway; Toll signaling pathwa activation of MAPK activity; anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process; anti-apoptosis; antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent; apoptotic process; cellular membrane organization; cytokine-mediated signaling pathway; cytosol; cytosolic large ribosomal subunit; egress of virus within host cell; endocytic vesicle membrane; endosomal transport; endosome membrane; epidermal growth factor receptor signaling pathway; fibroblast growth factor receptor signaling pathway; induction of apoptosis by extracellular signal innate immune response; negative regulation of epidermal growth factor receptor signaling pathway; negative regulation of type I interferon production; negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; nerve growth factor receptor signaling pathway; nuclear-transcribed mRNA catabolic process, nonsense-mediated decay; nucleoplasm; nucleotide-binding oligomerization domain containing signaling pathway; plasma membrane; positive regulation of I-kappaB kinase/NF-kappaB cascade; positive regulation of NF-kappaB transcription factor activity; positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; protein polyubiquitination; ribosome; structural constituent of ribosome; toll-like receptor 1 signaling pathway; toll-like receptor 2 signaling pathway; toll-like receptor 3 signaling pathway; toll-like receptor 4 signaling pathway; translation; translational elongation; translational initiation; translational termination; viral transcription
P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3 HNRPA3	Homo sapiens (Human)	378	RNA binding; catalytic step 2 spliceosome; nuclear mRNA splicing, via spliceosome; nucleolus; nucleoplasm; nucleotide binding
Q13464	ROCK1_HUMAN	Rho-associated protein kinase 1 (EC 2.7.11.1) (Renal carcinoma antigen NY-REN-35) (Rho-associated, coiled-coil-containing protein kinase 1) (Rho-associated, coiled-coil-containing protein kinase I) (ROCK-I) (p160 ROCK-1) (p160ROCK)	ROCK1	Homo sapiens (Human)	1354	ATP binding; Golgi membrane; Rho protein signal transduction; actin cytoskeleton organization; axon guidance; bleb; bleb assembly; cellular component disassembly involved in apoptotic process; centriole; cytokinesis; cytosol; leukocyte tethering or rolling; membrane to membrane docking; metal ion binding;negative regulation of angiogenesis; negative regulation of neuron apoptotic process; phospholipid binding; protein serine/threonine kinase activity; regulation of cell motility; regulation of establishment of cell polarity; regulation of focal adhesion assembly; regulation of keratinocyte differentiation; regulation of stress fiber assembly; smooth muscle contraction
P08621	RU17_HUMAN	U1 small nuclear ribonucleoprotein 70 kDa (U1 snRNP 70 kDa) (U1-70K) (snRNP70)	SNRNP70 RNPU1Z RPU1 SNRP70 U1AP1	Homo sapiens (Human)	437	RNA binding; nuclear mRNA splicing, via spliceosome; nucleoplasm; nucleotide binding; regulation of RNA splicing; spliceosomal complex
Q8N488	RYBP_HUMAN	RING1 and YY1-binding proteir (Apoptin-associating protein 1) (APAP-1) (Death effector domain-associated factor) (DED-associated factor)	RYBP DEDAF YEAF1	Homo sapiens (Human)	228	DNA binding; apoptotic process; cytoplasm; histone H2A monoubiquitination; multicellular organismal development; negative regulation of transcription from RNA polymerase II promoter; nucleoplasm; transcription corepressor activity; transcription, DNA-dependent; zinc ion binding

		(YY1 and E4TF1-associated factor 1)				
Q13435	SF3B2_HUMAN	Splicing factor 3B subunit 2 (Pre-mRNA-splicing factor SF3b 145 kDa subunit) (SF3b145) (SF3b150) (Spliceosome-associated protein 145) (SAP 145)	SF3B2 SAP145	Homo sapiens (Human)	895	U12-type spliceosomal complex; catalytic step 2 spliceosome; interspecies interaction between organisms; nuclear mRNA splicing, via spliceosome; nucleic acid binding; nucleoplasm
Q92922	SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1 (BRG1-associated factor 155) (BAF155) (SWI/SNF complex 155 kDa subunit) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 1)	SMARCC1 BAF155	Homo sapiens (Human)	1105	DNA binding; SWI/SNF complex; WINAC complex; XY body; chromatin binding; chromatin remodeling; insulin receptor signaling pathway; nBAF complex; nervous system development; npBAF complex; nucleosome disassembly; organ morphogenesis; positive regulation of transcription from RNA polymerase II promoter; positive regulation of transcription, DNA-dependent; regulation of transcription from RNA polymerase II promoter; soluble fraction; transcription coactivator activity; transcription, DNA-dependent
Q13573	SNW1_HUMAN	SNW domain-containing protein 1 (Nuclear protein SkiP) (Nuclear receptor coactivator NCoA-62) (Ski-interacting protein)	SNW1 SKIIP SKIP	Homo sapiens (Human)	536	Notch signaling pathway; catalytic step 2 spliceosome; cellular response to retinoic acid; chromatin; negative regulation of transcription, DNA-dependent; nuclear mRNA splicing, via spliceosome; nucleoplasm; positive regulation of neurogenesis; positive regulation of transcription from RNA polymerase II promoter; retinoic acid receptor signaling pathway; transcription initiation from RNA polymerase II promoter
Q05066	SRY_HUMAN	Sex-determining region Y protein (Testis-determining factor)	SRY TDF	Homo sapiens (Human)	204	DNA binding; RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity; cell differentiation; cytoplasm; male sex determination; nuclear speck; nucleus; positive regulation of male gonad development; positive regulation of transcription, DNA-dependent; sex differentiation
P63165	SUMO1_HUMAN	Small ubiquitin-related modifier (SUMO-1) (GAP-modifying protein 1) (GMP1) (SMT3 homolog 3) (Sentrin) (Ubiquitin-homology domain protein PIC1) (Ubiquitin-like protein SMT3C) (Smt3C) (Ubiquitin-like protein UBL1)	SUMO1 SMT3C SMT3H3 UBL1	Homo sapiens (Human)	101	DNA repair; SUMO ligase activity; cytoplasm; dendrite; interferon-gamma-mediated signaling pathway; negative regulation of DNA binding; negative regulation of sequence-specific DNA binding transcription factor activity; negative regulation of transcription, DNA-dependent; nuclear membrane; nuclear pore; nuclear speck; nucleoplasm; palate development; positive regulation of proteasomal ubiquitin-dependent protein catabolic process; positive regulation of protein complex assembly; protein sumoylation; regulation of interferon-gamma-mediated signaling pathway; regulation of protein localization; synaps
P25490	TYY1_HUMAN	Transcriptional repressor protein YY1 (Delta transcription factor) (INO80 complex subunit S) (NF-E1) (Yin and yang 1) (YY-1)	YY1 INO80S	Homo sapiens (Human)	414	Ino80 complex; PcG protein complex; RNA binding; RNA localization; anterior/posterior pattern specification; camera-type eye morphogenesis; cell differentiation; cellular response to UV; chromosome organization; double-strand break repair via homologous recombination; four-way junction DNA binding; negative regulation of transcription from RNA polymerase II promoter; nuclear matrix; plasma membrane; response to UV-C; sequence-specific DNA binding transcription factor activity; spermatogenesis; transcription coactivator activity; transcription corepressor activity; transcription factor compl transcription regulatory region DNA binding; transcription, DNA-dependent; zinc ion binding
P08670	VIME_HUMAN	Vimentin	VIM	Homo sapiens (Human)	466	cellular component disassembly involved in apoptotic process; cytosol; intermediate filament; interspecies interaction between organisms; muscle filament sliding; peroxisom structural constituent of cytoskeleton
O60315	ZEB2_HUMAN	Zinc finger E-box-binding homeobox 2 (Smad-interacting protein 1) (SMADIP1) (Zinc finger homeobox protein 1b)	ZEB2 KIAA0569 SIP1 ZFHX1B ZFX1B HRIHFB2411	Homo sapiens (Human)	1214	cell proliferation in forebrain; cytoplasm; hippocampus development; nervous system development; neural crest cell migration; neural tube closure; nucleolus; phosphatase regulator activity; positive regulation of JUN kinase activity; positive regulation of Wnt receptor signaling pathway; sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity; somitogenesis; transcription, DNA-dependent; zinc ion binding
Q15326	ZMY11_HUMAN	Zinc finger MYND domain-containing protein 11 (Adenovirus 5 E1A-binding protein) (Protein BS69)	ZMYND11 BS69	Homo sapiens (Human)	562	DNA binding; cell cycle; cell proliferation; cytoplasm; interspecies interaction between organisms; negative regulation of I-kappaB kinase/NF-kappaB cascade; negative regulation of JNK cascade; negative regulation of extrinsic apoptotic signaling pathway; negative regulation of transcription from RNA polymerase II promoter; nucleus; transcription, DNA-dependent; zinc ion binding
Q5RKT7	Q5RKT7_HUMAN	Ribosomal protein S27a	RPS27A	Homo sapiens (Human)	156	ribosome; structural constituent of ribosome; translation
Q9R0W0	Q9R0W0_RAT	Metabotropic glutamate receptor type 1 (Fragment)	Grm1 mGluR1a	Rattus norvegicus (Rat)	84	activation of MAPK activity; activation of MAPKK activity; cellular response to electrical stimulus; locomotory behavior; microsome; nucleus; postsynaptic density; receptor activity; regulation of MAPK cascade; regulation of sensory perception of pain; sensory perception of pain

SUPPLEMENTARY TABLE S7
Derivation of PTEN associated cancer hubs using a human cancer signaling map

+ activation
_ inhibition
0 physical interaction

From	**To**	**Link_Type**	
BRCA1	MRE11A	+	
BRCA1	MRE11A		0
BRCA1	FHL2	+	
BRCA1	ESR1		0
BRCA1	AKT1	+	
BRCA1	RAD50	+	
BRCA1	RAD50	+	
BRCA1	PRKG1		0
BRCA1	RBL2	+	
BRCA1	ATM	+	
BRCA1	ATM	+	
BRCA1	BARD1		0
BRCA1	BARD1	-	
BRCA1	CCND1	+	
BRCA1	XIST	+	
BRCA1	RBBP8	+	
BRCA1	RBBP8	+	
BRCA1	NBN		0
BRCA1	NBN	+	
BRCA1	H2AFX	-	
BRCA1	TFDP1		0
BRCA1	NFKB1		0
BRCA1	MDC1	+	
BRCA1	MDC1	+	
BRCA1	NPM1		0
BRCA1	CCNE1	+	
BRCA1	RPA2	+	
BRCA1	FANCI	+	
BRCA1	E2F4	+	
BRCA1	POLR2K	-	
BRCA1	POU2F1	-	
BRCA1	ATF2	+	
BRCA1	IGF1R	+	
BRCA1	BAP1	+	
BRCA1	MAPK3	+	
BRCA1	UBE2T	+	
BRCA1	EZH2		0
BRCA1	UBB		0
BRCA1	ATR	-	
BRCA1	LMO4	+	
BRCA1	PGR	+	
BRCA1	S100A7	+	
BRCA1	GADD45A	+	
BRCA1	CYP19A1	-	
BRCA1	E2F6		0
BRCA1	AR	-	
BRCA1	AR	-	
BRCA1	MAPK8	+	
BRCA1	TREX1	-	
BRCA1	KLK3	+	
BRCA1	CDKN1B		0
BRCA1	NF1		0
BRCA1	FANCD2	+	
BRCA1	MAP3K3		0
BRCA1	ECM1		0
BRCA1	TP53	+	
BRCA1	RBL1	+	
BRCA1	CHEK2	-	
BRCA1	PLK3	-	
BRCA1	TFDP2	-	
BRCA1	RAD51		0
BRCA1	TP53BP1	-	
BRCA1	SMAD3		0
BRCA1	CDK2	+	
DAXX	AKT1		0

DAXX	CASP8	+	
DAXX	CASP8	+	
DAXX	STAT3	+	
DAXX	DFFA	+	
DAXX	HIPK1	+	
DAXX	TGFBR2	-	
DAXX	TGFBR2	+	
DAXX	MAP2K4		0
DAXX	MAP2K6		0
DAXX	MAP2K3	+	
DAXX	SLC9A1	+	
DAXX	RIPK1	+	
DAXX	SMAD4	-	
DAXX	TGFB1	+	
DAXX	CDK5	+	
DAXX	TNFRSF1A	+	
DAXX	TSG101	-	
DAXX	MDM2	-	
DAXX	CFLAR	+	
DAXX	RIPK2	+	
DAXX	USP7		0
DAXX	FLT1		0
DAXX	FADD	+	
DAXX	FADD	+	
DAXX	TGFBR1		0
DAXX	MAPKAPK5		0
DAXX	DMAP1		0
DAXX	AR		0
DAXX	PRKCZ		0
DAXX	FAF1		0
DAXX	FAF1		0
DAXX	TNNI3K		0
DAXX	PAK1		0
DAXX	S100B		0
DAXX	NR3C1	-	
DAXX	FAS	+	
DAXX	FAS		0
DAXX	FASLG		0
DAXX	HSPB1	-	
DAXX	MAP2K7	-	
DAXX	TP53	-	
DAXX	PRKACA	+	
DAXX	BID	+	
DAXX	CASP10		0
DAXX	CASP10	+	
DAXX	MAP3K5	+	
DAXX	MAP3K5	-	
DAXX	MAPK10	+	
DAXX	MAP3K7	+	
SMAD2	CREBBP		0
SMAD2	CREBBP		0
SMAD2	SMAD2		0
SMAD2	SMAD2	-	
SMAD2	KAT2B		0
SMAD2	KAT2B		0
SMAD2	DVL1	+	
SMAD2	ESR1		0
SMAD2	CTDSP2	+	
SMAD2	PARD3	+	
SMAD2	MYC	+	
SMAD2	RBL2		0
SMAD2	STAMBPL1	-	
SMAD2	CDKN2B		0
SMAD2	SP1		0
SMAD2	NUP153		0
SMAD2	MEF2C		0
SMAD2	INHBE	+	
SMAD2	INHBE	+	
SMAD2	CDC16		0
SMAD2	TGFB2	-	
SMAD2	TGFB2	-	
SMAD2	SNIP1	+	
SMAD2	SNIP1		0
SMAD2	PITX2	+	

SMAD2	CTBP1		0
SMAD2	NUP214		0
SMAD2	SAP18	-	
SMAD2	FOXO4		0
SMAD2	CSF2	+	
SMAD2	ACVR1	-	
SMAD2	SIN3A		0
SMAD2	SKIL	+	
SMAD2	TGFBR2	+	
SMAD2	TGFBR2		0
SMAD2	FKBP1A	+	
SMAD2	TFDP1		0
SMAD2	ZBTB17	+	
SMAD2	RBBP4	+	
SMAD2	ERBB2IP		0
SMAD2	ERBB2IP	-	
SMAD2	HDAC1		0
SMAD2	FOXG1		0
SMAD2	SKP1		0
SMAD2	CDKN1A		0
SMAD2	CTNNB1		0
SMAD2	E2F4		0
SMAD2	SMAD7	-	
SMAD2	SMAD7	-	
SMAD2	CTDSPL		0
SMAD2	GPC1		0
SMAD2	SMAD4		0
SMAD2	MAX		0
SMAD2	CUL1		0
SMAD2	ACVR1C	+	
SMAD2	ZFYVE9		0
SMAD2	ZFYVE9		0
SMAD2	RALB		0
SMAD2	SMAD6		0
SMAD2	ZEB1	-	
SMAD2	LEF1	-	
SMAD2	E2F5	-	
SMAD2	TGFB1	+	
SMAD2	TGFB1	-	
SMAD2	GSC	+	
SMAD2	PML	+	
SMAD2	PML		0
SMAD2	CDK1	-	
SMAD2	SIN3B	+	
SMAD2	EEF1A1		0
SMAD2	CEBPB	+	
SMAD2	NFYC		0
SMAD2	SAR1A		0
SMAD2	SKI	-	
SMAD2	SKI		0
SMAD2	PIAS3	+	
SMAD2	EP300		0
SMAD2	EP300	-	
SMAD2	RUNX2	+	
SMAD2	FOXO1	-	
SMAD2	dab2	+	
SMAD2	PPM1A		0
SMAD2	LOC728622	-	
SMAD2	GRIP1	-	
SMAD2	NCOR1	-	
SMAD2	UBE2D1	-	
SMAD2	SAP30		0
SMAD2	EPS8		0
SMAD2	NUCKS1		0
SMAD2	CALM3		0
SMAD2	TGFBR1	-	
SMAD2	TGFBR1	+	
SMAD2	HSPA8	-	
SMAD2	EID2	+	
SMAD2	FOXH1	-	
SMAD2	MAP3K1	+	
SMAD2	RBBP7	+	
SMAD2	CDC27	+	
SMAD2	HDAC2	-	

SMAD2	ZEB2	+	
SMAD2	CITED1		0
SMAD2	NKX2-5	-	
SMAD2	SMURF1	+	
SMAD2	MYST2	+	
SMAD2	SNW1	-	
SMAD2	PTK6	+	
SMAD2	RBX1	+	
SMAD2	TP53	+	
SMAD2	STRAP	-	
SMAD2	STRAP	-	
SMAD2	CAMK2A	-	
SMAD2	CAMK2A	-	
SMAD2	RBL1	+	
SMAD2	CTDSP1	+	
SMAD2	CALM1	+	
SMAD2	TGIF1		0
SMAD2	TGIF1	+	
SMAD2	STK11	-	
SMAD2	UBE2D3	-	
SMAD2	TP73		0
SMAD2	DCP1A	+	
SMAD2	SMAD3		0
SMAD2	SMAD3	-	
SMAD2	FOXO3		0
SMAD2	NCOA2	+	
SMAD2	HGS	+	
SMAD2	DLG1	-	
SMAD2	PAX2	+	
SMAD2	MEF2A	+	
SMAD2	TGFB3	-	
SMAD2	TGFB3	+	
SMAD2	SMURF2	-	
SMAD2	UBE2D2	-	
SMAD3	CREBBP	+	
SMAD3	CREBBP	-	
SMAD3	SMAD2	+	
SMAD3	SMAD2	+	
SMAD3	KAT2B		0
SMAD3	KAT2B		0
SMAD3	CDK4	+	
SMAD3	DYRK1B		0
SMAD3	DVL1	+	
SMAD3	HDAC10	+	
SMAD3	ESR1	-	
SMAD3	CTDSP2		0
SMAD3	AKT1		0
SMAD3	IRF7		0
SMAD3	PARD3		0
SMAD3	CAMK1D		0
SMAD3	MYC	-	
SMAD3	CDK18		0
SMAD3	ATF3	-	
SMAD3	RBL2		0
SMAD3	AXIN2		0
SMAD3	PAX6		0
SMAD3	SPTBN1		0
SMAD3	CDKN2B	+	
SMAD3	SP1		0
SMAD3	NUP153		0
SMAD3	BRCA2		0
SMAD3	CDC16	-	
SMAD3	ARNT		0
SMAD3	TGFB2		0
SMAD3	TGFB2		0
SMAD3	SNIP1		0
SMAD3	PITX2	-	
SMAD3	HDAC6		0
SMAD3	SP3	+	
SMAD3	CTCF	-	
SMAD3	PRKAR2A	+	
SMAD3	ENG	+	
SMAD3	NEK8	-	
SMAD3	NUP214	-	

SMAD3	SAP18	-	
SMAD3	FOXO4		0
SMAD3	CSF2		0
SMAD3	ACVR1	+	
SMAD3	SIN3A		0
SMAD3	RNF111	+	
SMAD3	SKIL		0
SMAD3	ZNF217	-	
SMAD3	TGFBR2		0
SMAD3	TGFBR2	+	
SMAD3	FKBP1A	+	
SMAD3	MMS19		0
SMAD3	TFDP1	-	
SMAD3	ZBTB17	+	
SMAD3	HDAC8	+	
SMAD3	RBBP4	-	
SMAD3	ERBB2IP	-	
SMAD3	ERBB2IP		0
SMAD3	NR5A1	+	
SMAD3	RAP2A		0
SMAD3	BTK		0
SMAD3	HDAC1		0
SMAD3	RUNX1		0
SMAD3	HNF4A	+	
SMAD3	FOXG1	-	
SMAD3	ACHE	+	
SMAD3	HDAC5		0
SMAD3	PPP2CA	-	
SMAD3	CDKN1A		0
SMAD3	CTNNB1	-	
SMAD3	E2F4		0
SMAD3	E2F4	+	
SMAD3	SMAD7		0
SMAD3	SMAD7	+	
SMAD3	NR0B2		0
SMAD3	CTDSPL	-	
SMAD3	SMAD4	-	
SMAD3	SMAD4		0
SMAD3	E2F1		0
SMAD3	MAX		0
SMAD3	CUL1		0
SMAD3	CUL1		0
SMAD3	ACVR1C	-	
SMAD3	ACVR1C	+	
SMAD3	HR		0
SMAD3	HIF1A	-	
SMAD3	ZFYVE9		0
SMAD3	ZFYVE9	-	
SMAD3	SMAD6	+	
SMAD3	TERT	+	
SMAD3	ZEB1	+	
SMAD3	LEF1		0
SMAD3	E2F5	+	
SMAD3	E2F5	+	
SMAD3	HDAC11	+	
SMAD3	MAPK1		0
SMAD3	TGFB1	+	
SMAD3	TGFB1		0
SMAD3	RUNX3	-	
SMAD3	GSC	-	
SMAD3	CDK5	+	
SMAD3	SFTPB	+	
SMAD3	ATF2		0
SMAD3	PML		0
SMAD3	PML	+	
SMAD3	BRCA1		0
SMAD3	TCF4		0
SMAD3	SIN3B	+	
SMAD3	TFE3		0
SMAD3	GATA3	+	
SMAD3	HDAC7		0
SMAD3	FGF11	+	
SMAD3	EEF1A1	+	
SMAD3	CEBPB	-	

SMAD3	NFYC		0
SMAD3	JAK2		0
SMAD3	SKI	-	
SMAD3	SKI	+	
SMAD3	INTS6	-	
SMAD3	PIAS3	-	
SMAD3	EP300	-	
SMAD3	EP300	+	
SMAD3	JUND	-	
SMAD3	RPS6KA2	-	
SMAD3	RUNX2	-	
SMAD3	FOXO1	+	
SMAD3	dab2	-	
SMAD3	MBD2		0
SMAD3	JUNB	+	
SMAD3	FOSB	+	
SMAD3	PPM1A	+	
SMAD3	LOC728622	-	
SMAD3	GRIP1	-	
SMAD3	NCOR1	-	
SMAD3	CDKN2A	-	
SMAD3	SAP30		0
SMAD3	HDAC4	-	
SMAD3	EPS8	-	
SMAD3	KAT2A		0
SMAD3	MUC5AC		0
SMAD3	TGFBR1	+	
SMAD3	TGFBR1		0
SMAD3	HSPA8		0
SMAD3	POLR2C	+	
SMAD3	SOX9	+	
SMAD3	ITGB5		0
SMAD3	POLR2J	+	
SMAD3	AR	-	
SMAD3	AR	-	
SMAD3	MAPK8		0
SMAD3	EID2	-	
SMAD3	FOXH1		0
SMAD3	IL10	-	
SMAD3	PIAS4	-	
SMAD3	PIAS4	-	
SMAD3	ETS1	+	
SMAD3	RBBP7	+	
SMAD3	SNAI1		0
SMAD3	BTRC	-	
SMAD3	PAK1	-	
SMAD3	HDAC3	+	
SMAD3	CDC27	+	
SMAD3	NCOA1		0
SMAD3	CD44	-	
SMAD3	CD44	-	
SMAD3	NR3C1	+	
SMAD3	NR3C1		0
SMAD3	HDAC2	-	
SMAD3	CDKN1B	+	
SMAD3	VDR		0
SMAD3	ZEB2	+	
SMAD3	CITED1		0
SMAD3	MAPK14	+	
SMAD3	SMO		0
SMAD3	SMURF1	-	
SMAD3	KDM5C	+	
SMAD3	COL1A2		0
SMAD3	CBX5	+	
SMAD3	CDH1	-	
SMAD3	MYST2		0
SMAD3	SNW1	-	
SMAD3	RBX1	-	
SMAD3	JAG1	-	
SMAD3	STRAP		0
SMAD3	STRAP		0
SMAD3	CAMK2A	-	
SMAD3	RBL1	+	
SMAD3	CTDSP1		0

SMAD3	BMPR1B	+	
SMAD3	CBFB	+	
SMAD3	IFNB1	-	
SMAD3	PRKY	-	
SMAD3	POFUT1	+	
SMAD3	FOS		0
SMAD3	FZD2		0
SMAD3	FCGR3A	-	
SMAD3	HDAC9	-	
SMAD3	HDAC9	+	
SMAD3	JUN		0
SMAD3	JUN	-	
SMAD3	CDC25A	+	
SMAD3	COL17A1	+	
SMAD3	APC		0
SMAD3	CYP7A1	-	
SMAD3	INTS3	-	
SMAD3	LAMC1	+	
SMAD3	TNC	+	
SMAD3	SMAD3		0
SMAD3	SMAD3		0
SMAD3	KPNB1	-	
SMAD3	SERPINE1		0
SMAD3	INPPL1		0
SMAD3	IGHA1	+	
SMAD3	CDK2		0
SMAD3	FOXO3		0
SMAD3	MAP3K7	+	
SMAD3	NCOA2	-	
SMAD3	NOTCH1	-	
SMAD3	HGS	-	
SMAD3	RCHY1	-	
SMAD3	DLG1	+	
SMAD3	MUC2	-	
SMAD3	PAX2	-	
SMAD3	TGFB3	-	
SMAD3	TGFB3	+	
SMAD3	NRIP1		0
SMAD3	POLR2B	+	
SMAD3	MSTN		0
SMAD3	BAG4	+	
SMAD3	PRKAR1B	-	
SMAD3	IL5	-	
MDM2	KAT2B	-	
MDM2	KAT2B	+	
MDM2	PRG1	-	
MDM2	PPM1D	-	
MDM2	RELA	+	
MDM2	NUP210	-	
MDM2	AKT1	-	
MDM2	PAK6	+	
MDM2	PIAS2	-	
MDM2	ATM		0
MDM2	SRPK2	-	
MDM2	ARRB1	-	
MDM2	NUP153	+	
MDM2	STK17A	-	
MDM2	HIPK2	-	
MDM2	NUP214	-	
MDM2	PSMD10		0
MDM2	ACVR1	+	
MDM2	PIAS1	+	
MDM2	HEXIM1	-	
MDM2	DLAT	+	
MDM2	TGFBR2		0
MDM2	JMY	-	
MDM2	TP63	-	
MDM2	TP63	-	
MDM2	TAF1	+	
MDM2	LOC652799	-	
MDM2	UBXN6		0
MDM2	CCNG1	+	
MDM2	BTK	+	
MDM2	HDAC1	-	

MDM2	PPP2CA	-	
MDM2	CSF1R	+	
MDM2	CDKN1A	-	
MDM2	DNAJB1	+	
MDM2	E2F1	-	
MDM2	PPP2R4	-	
MDM2	HIF1A	-	
MDM2	HIF1A	-	
MDM2	KIT	-	
MDM2	MAPK1	+	
MDM2	RASSF1	-	
MDM2	FGFR3	-	
MDM2	TGFB1	-	
MDM2	CDK5	+	
MDM2	SSRP1	-	
MDM2	PNCK	+	
MDM2	PDPK1	-	
MDM2	PML	+	
MDM2	TSG101	+	
MDM2	RB1	+	
MDM2	RB1		0
MDM2	IGF1R	+	
MDM2	FGFR4	+	
MDM2	MAPKAPK2	+	
MDM2	RPL11	+	
MDM2	RANBP2	-	
MDM2	MTBP	+	
MDM2	TBK1		0
MDM2	MDM4	+	
MDM2	MDM4	+	
MDM2	YY1	-	
MDM2	PDGFRA	+	
MDM2	CASP3	-	
MDM2	DYRK2	+	
MDM2	NCL	+	
MDM2	DHFR	+	
MDM2	EP300	+	
MDM2	UBB	+	
MDM2	RPS6KA2	+	
MDM2	FOXO1	+	
MDM2	ATR	+	
MDM2	USP7		0
MDM2	FLT1	-	
MDM2	UBE2I	+	
MDM2	NEK3	+	
MDM2	CDKN2A	+	
MDM2	CDKN2A	+	
MDM2	CCNA2	-	
MDM2	CCNA2		0
MDM2	UBE2D1	-	
MDM2	TRIM28	-	
MDM2	ABL1	+	
MDM2	FGFR2	+	
MDM2	SENP8	+	
MDM2	PRKCI	-	
MDM2	TERC	+	
MDM2	RFFL	+	
MDM2	ARHGAP24	+	
MDM2	MAPKAPK5	+	
MDM2	NEDD8	+	
MDM2	AR	+	
MDM2	AR	+	
MDM2	CDKN2D	-	
MDM2	CDKN2D	-	
MDM2	TREX1	+	
MDM2	AKT3	-	
MDM2	TNNI3K	+	
MDM2	PRKAA2	+	
MDM2	RPS6KA4	+	
MDM2	BUB1	+	
MDM2	KLK3	+	
MDM2	NEK9	-	
MDM2	HDAC2	+	
MDM2	LNCR1		0

MDM2	TEP1	+	
MDM2	SRPK1		0
MDM2	EGFR	+	
MDM2	MET	+	
MDM2	DAXX	+	
MDM2	RET	+	
MDM2	RPS6KB1	+	
MDM2	PSMB6	+	
MDM2	UBE2A	+	
MDM2	PLK1	+	
MDM2	NTRK1	-	
MDM2	TP53	+	
MDM2	TP53	+	
MDM2	RBL1	+	
MDM2	STK38	+	
MDM2	SCYL2	+	
MDM2	SYK	+	
MDM2	PRKDC	-	
MDM2	RANGAP1	+	
MDM2	TRRAP	-	
MDM2	NPR2	+	
MDM2	ERBB3	-	
MDM2	CLK2	+	
MDM2	TNK2	+	
MDM2	CHEK2	+	
MDM2	CHEK2	+	
MDM2	KDR	+	
MDM2	TP73	-	
MDM2	WEE1	+	
MDM2	MAPK9	+	
MDM2	ERBB4	+	
MDM2	ERBB4	+	
MDM2	TP53BP1	+	
MDM2	CSNK1A1	+	
MDM2	AKT2	-	
MDM2	CDK2	-	
MDM2	MAPK10	+	
MDM2	SUMO1	+	
MDM2	SUMO1	+	
MDM2	NUP62	+	
MDM2	DBT	+	
MDM2	NR4A1	+	
TP53	CREBBP	-	
TP53	SMAD2		0
TP53	EPHA2	-	
TP53	KAT2B	+	
TP53	KAT2B	+	
TP53	UBE3A	-	
TP53	IFRD1	+	
TP53	FHL2	+	
TP53	HIPK4	-	
TP53	PRG1	+	
TP53	PRG1	+	
TP53	PPM1D	+	
TP53	BAG1	-	
TP53	BIK	+	
TP53	PCBP4	-	
TP53	BAX	+	
TP53	AEN	+	
TP53	BMP4	+	
TP53	SNORA62	-	
TP53	RECQL4	-	
TP53	ESR1	+	
TP53	CDCA8	+	
TP53	POLR1B	+	
TP53	DUSP1	+	
TP53	SKP2	-	
TP53	DKK1	+	
TP53	GPX1	-	
TP53	IFI16	+	
TP53	BCL2L14	+	
TP53	CSNK1E	+	
TP53	TNFRSF10D	+	
TP53	ZMAT3		0

TP53	GADD45G	+
TP53	MYC	+
TP53	TOPBP1	+
TP53	RRM2B	+
TP53	RRM2B	+
TP53	TRAF6	+
TP53	TP53BP2	+
TP53	CASP8	+
TP53	ATF3	+
TP53	CXCL1	+
TP53	RBL2	+
TP53	ATM	+
TP53	ATM	-
TP53	DDX5	+
TP53	PDGFRB	-
TP53	CARM1	-
TP53	RNF144B	+
TP53	PRKAB1	+
TP53	COL18A1	+
TP53	ORC1L	+
TP53	CKS2	-
TP53	ARHGEF2	+
TP53	SP1	+
TP53	C13orf15	+
TP53	BARD1	+
TP53	BARD1	+
TP53	TGFA	+
TP53	AXIN1	-
TP53	CSNK2B	-
TP53	HSPA1A	+
TP53	CCNG2	+
TP53	HIPK2	-
TP53	UBE4A	+
TP53	FLI1	+
TP53	ARID3A	+
TP53	PPM1J	+
TP53	PHB	+
TP53	MYST1	+
TP53	SIRT1	-
TP53	BTG2	+
TP53	PSMD10	+
TP53	PIAS1	+
TP53	DLAT	+
TP53	TP63	+
TP53	CTSD	+
TP53	DDB2	-
TP53	CSNK1G1	-
TP53	IRF1	+
TP53	CSNK1D	+
TP53	MLH1	+
TP53	TRIAP1	+
TP53	PRDX3	+
TP53	NFKB1	-
TP53	NFKB1	+
TP53	RRM2	-
TP53	SOX4	+
TP53	BDKRB2	+
TP53	TAF1	+
TP53	TAF1	-
TP53	NGFR	+
TP53	STEAP3	+
TP53	HNRNPUL1	+
TP53	SORT1	-
TP53	LTB	+
TP53	CCNG1	+
TP53	CCNG1	+
TP53	SCN3B	+
TP53	NPM1	+
TP53	CCNE1	-
TP53	BAK1	+
TP53	BBC3	+
TP53	BBC3	+
TP53	SIK1	+
TP53	BCKDHB	+

TP53	ING5	+	
TP53	PTTG1	+	
TP53	STK40	+	
TP53	ZNF274	+	
TP53	PRG2	+	
TP53	MAPK12	+	
TP53	TRAF2	-	
TP53	CDKN1A	+	
TP53	CDKN1A	+	
TP53	EIF4E	-	
TP53	RPL23	-	
TP53	IRF5	-	
TP53	FBXO11	-	
TP53	PIN1	+	
TP53	GDF15	+	
TP53	DNAJB1P	+	
TP53	E2F1	-	
TP53	E2F1	+	
TP53	HNRNPK	+	
TP53	MAX	+	
TP53	LIF	+	
TP53	S100A2	+	
TP53	PSEN1	+	
TP53	DAPK1	+	
TP53	HIF1A	-	
TP53	HIF1A	+	
TP53	NDRG1	+	
TP53	TIMP3	+	
TP53	TERT	+	
TP53	PTK2B	-	
TP53	SPP1	+	
TP53	CSNK1G3	-	
TP53	PLAGL1	+	
TP53	MXD1	+	
TP53	RPRM	+	
TP53	MAPK1	-	
TP53	ADRBK1	+	
TP53	TGFB1	-	
TP53	RFWD2	+	
TP53	CDK5	+	
TP53	SH2D1A	+	
TP53	STC1	+	
TP53	YEATS4	+	
TP53	LATS2	+	
TP53	PRMT1	+	
TP53	GTF2A1	-	
TP53	CDK9	+	
TP53	NDN	-	
TP53	SP100	-	
TP53	TGM1		0
TP53	BHLHE40	+	
TP53	GSTP1	+	
TP53	FDXR	-	
TP53	GTSE1	+	
TP53	MAPK11	-	
TP53	MYO6	-	
TP53	PML	+	
TP53	PML	+	
TP53	PCNA	+	
TP53	TYRP1	+	
TP53	ING1	+	
TP53	BRCA1	+	
TP53	INGX	+	
TP53	RB1	+	
TP53	RB1	+	
TP53	C12orf5	+	
TP53	IGF1R	+	
TP53	IGKV1-6	-	
TP53	SFN	-	
TP53	PARK2	-	
TP53	MDM2	+	
TP53	MDM2	+	
TP53	HSP90AA1	+	
TP53	HMMR	+	

TP53	TAP1	+	
TP53	MDM4	+	
TP53	MDM4	+	
TP53	AREG	+	
TP53	TP53INP1	+	
TP53	CFLAR	+	
TP53	YY1	+	
TP53	UNC5D	+	
TP53	REEP5	+	
TP53	PAK4	+	
TP53	PTEN	+	
TP53	CREB1	-	
TP53	HIC1	+	
TP53	SERPINB5	+	
TP53	NFE2L2	+	
TP53	DYRK2	+	
TP53	CAV1	+	
TP53	PYCARD	-	
TP53	ING2	+	
TP53	LRDD	-	
TP53	DUSP4	+	
TP53	GADD45B	+	
TP53	ATF1	+	
TP53	CSNK1G2	-	
TP53	MAPK3	+	
TP53	SHISA5	+	
TP53	GSK3B	-	
TP53	CASP1	+	
TP53	EP300	+	
TP53	EP300	+	
TP53	E4F1	+	
TP53	ZNF420		0
TP53	EIF2AK2	-	
TP53	EIF2AK2	+	
TP53	H19	-	
TP53	EZH2	+	
TP53	PRB3	+	
TP53	IGFBP2		0
TP53	UBB	+	
TP53	HECW1	+	
TP53	CDKN3	+	
TP53	CDC6	+	
TP53	VRK1	+	
TP53	VRK1	+	
TP53	NUMB	+	
TP53	ATR	+	
TP53	USP7	+	
TP53	IER3	-	
TP53	PLK4	-	
TP53	BCL6	+	
TP53	BCL6	+	
TP53	SNAI2	-	
TP53	CLCA2	+	
TP53	HGF	+	
TP53	KAT5	+	
TP53	BNIP3L	+	
TP53	SPAG5	-	
TP53	THBS1	-	
TP53	MMP2	+	
TP53	MSH2	-	
TP53	CSNK2A2	-	
TP53	EIF5A	+	
TP53	VCAN	+	
TP53	CDKN2A	+	
TP53	CDKN2A	-	
TP53	CCNA2	+	
TP53	UBE2D1	+	
TP53	SMYD2	+	
TP53	TRIM28	-	
TP53	CCNK	+	
TP53	MED1	+	
TP53	FADD	+	
TP53	APAF1	+	
TP53	DDB1	-	

TP53	PTP4A3	+	
TP53	RPS27L		0
TP53	MEG3	-	
TP53	LASP1	+	
TP53	DUSP5	-	
TP53	EI24	-	
TP53	PRL		0
TP53	DEK	-	
TP53	DEK	-	
TP53	SMARCA4	-	
TP53	LOC731751	+	
TP53	ARHGAP24	+	
TP53	GADD45A	-	
TP53	FGFR1OP	+	
TP53	MAPKAPK5	+	
TP53	TNFRSF10A	+	
TP53	NEDD8	-	
TP53	RPA4		0
TP53	LOC651610	+	
TP53	BACE2	+	
TP53	PRMT5	+	
TP53	HTT	+	
TP53	AURKA	+	
TP53	AURKA	+	
TP53	AR	+	
TP53	MAPK8	+	
TP53	TREX1		0
TP53	ICAM1	+	
TP53	S100A9	+	
TP53	CSNK2A1	+	
TP53	S100B	+	
TP53	RAD23A	+	
TP53	GLI1	+	
TP53	GLI1	+	
TP53	S100A4	+	
TP53	VRK2	-	
TP53	BAI1	-	
TP53	BUB1	+	
TP53	CD44	+	
TP53	NR3C1	+	
TP53	NR3C1	+	
TP53	CCNB1	-	
TP53	SESN3	+	
TP53	TNFRSF10C	+	
TP53	FAS	+	
TP53	FAS	+	
TP53	RAC1		0
TP53	RAC1	+	
TP53	AFP	+	
TP53	VDR	+	
TP53	DNAJA3	-	
TP53	PRC1	-	
TP53	ERCC2	+	
TP53	NF1		0
TP53	MAPK14	-	
TP53	DDIT4	+	
TP53	BCL2	-	
TP53	BCL2	-	
TP53	WRN	+	
TP53	WRN	+	
TP53	EGFR	+	
TP53	ALK	+	
TP53	TP53AIP1	-	
TP53	MET	+	
TP53	DAXX	+	
TP53	WT1	+	
TP53	PLA2G6	+	
TP53	FASLG	+	
TP53	PTP4A1	+	
TP53	TSC2	+	
TP53	HSPB1	+	
TP53	FLII	-	
TP53	MYB	-	
TP53	MTA2	-	

TP53	CD82	+	
TP53	UBE2A	+	
TP53	ANKRD11		0
TP53	PLK1	+	
TP53	EAF2		0
TP53	SESN1	-	
TP53	LGALS3	-	
TP53	SETD2	+	
TP53	RBM38	+	
TP53	TP53	+	
TP53	TP53	+	
TP53	CABLES2	+	
TP53	IGFBP3	+	
TP53	EDN2	+	
TP53	PTGS2		0
TP53	KLF4	-	
TP53	PRKDC	+	
TP53	CX3CL1	-	
TP53	TRRAP	+	
TP53	MAPK13	-	
TP53	CABIN1	-	
TP53	FANCC	-	
TP53	BCL2L1	+	
TP53	BCL2L1	-	
TP53	SIAH1	+	
TP53	SETD7	-	
TP53	UIMC1	+	
TP53	FOS	+	
TP53	ABCB1	-	
TP53	ABCB1	+	
TP53	SESN2	+	
TP53	STK11	+	
TP53	CHEK2	+	
TP53	GH1	-	
TP53	PMS2	+	
TP53	SOD2	+	
TP53	CD40	+	
TP53	SETD8	+	
TP53	PRKCD	-	
TP53	FGF2	+	
TP53	CD40LG		0
TP53	XIAP	+	
TP53	XIAP	-	
TP53	TP73	+	
TP53	PMAIP1	-	
TP53	ZNF148	-	
TP53	PLK3	-	
TP53	PLK3	+	
TP53	GNL3	+	
TP53	TOPORS	+	
TP53	HMGB1	-	
TP53	HMGB1	+	
TP53	JUN	+	
TP53	MAPK9	-	
TP53	BDNF	-	
TP53	RAD51	+	
TP53	PPP1R13L	+	
TP53	APC	-	
TP53	BID	+	
TP53	PERP	+	
TP53	MAP4K4	+	
TP53	ECT2	+	
TP53	TCEAL1	+	
TP53	S100A6	-	
TP53	TTC5	+	
TP53	CHEK1	+	
TP53	CASP10	+	
TP53	CASP10	+	
TP53	ELAVL1	+	
TP53	CSNK1A1	+	
TP53	TNFRSF10B	+	
TP53	TP53I3	+	
TP53	NCKAP1L	-	
TP53	SERPINE1	+	

TP53	MORC3	-	
TP53	CDK2	+	
TP53	CDK2	-	
TP53	AIFM2	+	
TP53	NLRC4	-	
TP53	NLRC4	+	
TP53	MAPK10	+	
TP53	FBXO42	-	
TP53	SUMO1	+	
TP53	SUMO1	+	
TP53	C8orf4	-	
TP53	NOTCH1		0
TP53	RCHY1	+	
TP53	RCHY1	+	
TP53	MUC2	+	
TP53	PRDM1	-	
TP53	IRF3	+	
TP53	CASP6	+	
TP53	DBT	+	
TP53	MSX1	+	
TP53	NR4A1	+	
TP53	HSPA1B	-	
SUMO1	UBE3A	+	
SUMO1	XPO1	+	
SUMO1	NUP210	+	
SUMO1	GATA4	-	
SUMO1	PIAS2	+	
SUMO1	NUP153	+	
SUMO1	NUP153	+	
SUMO1	HIPK2	+	
SUMO1	HDAC6	-	
SUMO1	RAN	+	
SUMO1	CTBP1	+	
SUMO1	CTBP1		0
SUMO1	NUP214		0
SUMO1	NUP214	+	
SUMO1	PIAS1	+	
SUMO1	HDAC1	+	
SUMO1	HDAC1		0
SUMO1	MKL1	+	
SUMO1	UBE2L6	+	
SUMO1	SMAD4	+	
SUMO1	UBE2G2	+	
SUMO1	LEF1	+	
SUMO1	TGFB1		0
SUMO1	UBE2F	+	
SUMO1	SP100		0
SUMO1	PML	-	
SUMO1	MDM2	+	
SUMO1	MDM2	+	
SUMO1	UBE2G1		0
SUMO1	RANBP2	+	
SUMO1	ATF7	+	
SUMO1	SHC1	+	
SUMO1	UBA1		0
SUMO1	UBE2L3	+	
SUMO1	PRAM1		0
SUMO1	UBB	+	
SUMO1	UBB	-	
SUMO1	CR2		0
SUMO1	TCF7L2		0
SUMO1	UBE2I	+	
SUMO1	CDKN2A	+	
SUMO1	HDAC4		0
SUMO1	HDAC4		0
SUMO1	PGR	+	
SUMO1	MAPK8		0
SUMO1	NR3C1		0
SUMO1	DLD		0
SUMO1	NFKBIA		0
SUMO1	HSF1	+	
SUMO1	CDH1	+	
SUMO1	UBE2A		0
SUMO1	TP53	+	

SUMO1	TP53		0
SUMO1	RANGAP1		0
SUMO1	HDAC9		0
SUMO1	HDAC9		0
SUMO1	TOPORS	+	
SUMO1	SUMO1		0
SUMO1	SUMO1	+	
SUMO1	UBE2E2		0
SUMO1	NUP62	-	
PTEN	MAGI3	-	
PTEN	AKT1	-	
PTEN	INPP5J	-	
PTEN	PRKCA	-	
PTEN	PDGFRB		0
PTEN	CD79A	+	
PTEN	CD28	+	
PTEN	PIK3CG	+	
PTEN	BMP2	+	
PTEN	TNF	-	
PTEN	ROCK2	-	
PTEN	NEDD4	-	
PTEN	PTK2	-	
PTEN	BCR		0
PTEN	SLC9A3R1	-	
PTEN	TFAP2A	-	
PTEN	IGF2	-	
PTEN	IGF2	-	
PTEN	PIK3CA	-	
PTEN	PIK3CA	-	
PTEN	PPP2R4	+	
PTEN	NDRG1	+	
PTEN	C11orf2	+	
PTEN	TERT	-	
PTEN	RETN	-	
PTEN	TGFB1	+	
PTEN	INPP5A	-	
PTEN	IGF1R	-	
PTEN	ERVK2	-	
PTEN	HSP90AA1		0
PTEN	ITGB1	-	
PTEN	SHC1	-	
PTEN	CASP3	+	
PTEN	CAV1	+	
PTEN	ADM	-	
PTEN	IGFBP2	+	
PTEN	PIK3R1	-	
PTEN	SLC9A3R2	+	
PTEN	HGF	+	
PTEN	BMI1	+	
PTEN	SOS1	+	
PTEN	FGFR2	+	
PTEN	CD79B	-	
PTEN	TNKS	+	
PTEN	AR	+	
PTEN	AR		0
PTEN	AKT3	-	
PTEN	RSL1D1	+	
PTEN	GLTSCR2	+	
PTEN	TEP1	+	
PTEN	ROCK1	+	
PTEN	EGFR	-	
PTEN	TP53	+	
PTEN	FOS	+	
PTEN	HPCX	-	
PTEN	MAGI2	+	
PTEN	XIAP	+	
PTEN	JUN	+	
PTEN	AKT2	+	
PTEN	NOTCH1	+	
PTEN	GRB2		0
PTEN	SMAD2		0
PTEN	SMAD3		0
PTEN	WWP2		0
PTEN	AR		0

PTEN	Thioredoxin	0
PTEN	PCAF	0
PTEN	ARRB1	0
PTEN	ARRB2	0
PTEN	BMI-1	0
PTEN	Prdx-1	0
PTEN	RAK	0
PTEN	p53	0
PTEN	CAV	0
PTEN	STK11	0
PTEN	MVP	0
PTEN	PICT-1	0
PTEN	NEP	0
PTEN	Myo5a	0
PTEN	Myo5b	0
PTEN	Myo5c	0
PTEN	MSP58	0
PTEN	PREX 2	0
PTEN	APC 3	0
PTEN	APC 4	0
PTEN	APC 5	0
PTEN	APC 7	0
PTEN	Cenpc 1	0
PTEN	PDGFRB	0
PTEN	DLG1	0
PTEN	MAGI1	0
PTEN	MAGI2	0
PTEN	MAGI3	0
PTEN	Mast1	0
PTEN	Mast2	0
PTEN	Mast3	0
PTEN	NHERF 1	0
PTEN	NHERF2	0
PTEN	Par3	0
PTEN	5-HTR2C	0
PTEN	Sharpin	0

Topological Analysis of Network

Gene name	Protein name	Centrality Score
TP53	TP53	0.503
SMAD3	SMAD3	0.267
MDM2	MDM2	0.175
SMAD2	SMAD2	0.148
PTEN	PTEN	0.119
BRCA1	BRCA1	0.073
SUMO1	SUMO1	0.067
DAXX	DAXX	0.056
TGFB1	TGFB1	0.009
AR	AR	0.008

SUPPLEMENTARY TABLE S8
DISORDER SCORES FOR KINASES THAT PHOSPHORYLATE PTEN

Uniprot ID	Name of Kinase	Total no. of amino acids	No. of disordered amino acids	No. of disordered stretches >30	Disordered or Ordered	Position of disordered amino acids	Kinase domain
P12931	Src	536	86	1	D	1-64; 68-75; 77-78; 522; 526-536	270-523
P68400	Casein Kinase II subnit α	391	80	1	D	1-18; 77-78; 332-391	39-324
P19784	Casein Kinase II subunit α'	350	25	0	O	1-14; 77-81; 345-350	40-325
P67870	Casein Kinase II subunit β	215	41	0	O	1-14; 59-75; 206-215	Not applicable (Interacts with α subunit)
P42685	RAK	505	30	0	O	1-13; 89-92; 493-505	234-491
P49841	GSK 3β	420	101	2	D	1-54; 56; 376-420	56-340
Q9H4B4	PLK3	646	156	2	D	1-64; 354-428; 632-646	62-314
Q9R1L5	MAST1	1570	960	7	D	23-28; 33-80; 89-125; 134; 138-170; 173-174; 339-370; 373-374; 681-683; 686-704; 717-967; 1016-1020; 1022; 1027-1029; 1033; 1036-1037; 1054-1104; 1107-1570	375-648
Q60592	MAST2	1734	1049	10	D	24; 30-31; 38-40; 64-66; 70-78; 85-96; 103-104; 112-114; 118-160; 167; 169-201; 203-205; 209-210; 212-245; 264-267; 272; 274-279; 335-336; 418-447; 451-452; 690-691; 696-697; 699; 703; 752-754; 756-778; 800-834; 847-962; 964-985; 1004-1032; 1080-1083; 1086-1101; 1109-1110; 1122; 1126-1177; 1180-1559; 1565-1567; 1570; 1575-1586; 1590-1600; 1603-1734	453-726
O60307	MAST3	1309	676	7	D	1-63; 70-72; 86-120; 129-130; 136-163; 182; 250-252; 333; 335-358; 627; 670-696; 719-740; 757-786; 788-896; 898-904; 908; 911-950; 990; 996-1000; 1035-1039; 1041-1084; 1086-1309	367-640
O15021	MAST4	2626	1922	15	D	1-81; 86-174; 178; 181-184; 186-223; 225-277; 286-319; 321-323; 343-361; 385; 394; 538-561; 799; 803; 805-811; 816-817; 872-899; 919-1086; 1106; 1108-1144; 1193; 1228-1277; 1281-1288; 1291-1502;1503-1505; 1507-1535; 1537-1568; 1581-1677; 1692-1694; 1702-1714; 1716-1747; 1749; 1756; 1758; 1761-1793; 1795-1798; 1810-1867; 1871; 1873-1874; 1876-1882; 1884-2626	573-846
Q15831	STK11	433	82	1	D	212; 215-218; 312-329; 331-334; 365-418; 421	49-309
P48729	Casein Kinase I subunit α	337	33	0	O	172-173; 175; 235; 309-337	17-285