Supporting Information

Structure and Protein Interaction-based Gene Ontology Annotations Reveal Likely Functions of Uncharacterized Proteins on Human Chromosome 17

Chengxin Zhang, Xiaoqiong Wei, Gilbert S. Omenn, and Yang Zhang

Table of Contents

Text S1. SPARQL query for curating the list of uPE1 proteins from neXtProt database version 2018-01-17, which excluded six more GO terms (GO:0005524. ATP binding; GO:0000287 magnesium binding; GO:0003676 nucleic acid binding; GO:0003824 catalytic activity; GO:0007165 signal transduction; GO:0035556 intracellular signal transduction) in addition to the GO terms excluded by neXtProt 2017-08-01 (Text S2). Due to the exclusion of more GO terms, the number of uPE1 proteins has increased from 1218 in neXtProt version 2017-08-01 to 1260 in neXtProt version 2018-01-17.

```
select distinct ?entry where {
  ?entry :isoform ?iso.
  ?entry :existence :Evidence_at_protein_level.
  filter not exists { ?iso :functionInfo ?_ . }
  filter not exists { ?iso :function ?func .
                      optional {?func :term ?fterm1 .}
                      filter(!bound(?fterm1))        #eliminates
functions from pathways
                    }
  filter not exists {
                       ?iso :function / :term ?fterm .
                       filter(?fterm != cv:GO_0005524 && ?fterm
!=  cv:GO_0000287  &&  ?fterm  !=  cv:GO_0005515  &&  ?fterm  !=
cv:GO_0042802
                                  &&  ?fterm  !=  cv:GO_0008270  &&
?fterm != cv:GO_0051260 && ?fterm != cv:GO_0005509
                                  &&  ?fterm  !=  cv:GO_0003676  &&
?fterm != cv:GO_0003824 && ?fterm != cv:GO_0007165 && ?fterm !=
cv:GO_0035556)
                      #  eliminates  proteins  whose  ONLY  GO
functions  are  one  of  ATP-binding,  magnesium-binding,  calcium-
binding, zinc-binding,
                      # nucleic acid binding, protein-binding,
identical   protein   binding,   protein   homooligomerization,
catalytic activity, signal transduction,
                     }
 }
```

Text S2. SPARQL query for curating the initial list of unannotated proteins from neXtProt database. To curate the initial list of 66 uPE1 proteins, the following SPARQL query is used at neXtProt website version 2017-08-01 at https://www.nextprot.org/proteins/search?mode=advanced. The full list of 1232 uPE1 proteins is subsequently filtered by selecting proteins from chromosome 17. Due to the difference in database version, the same SPARQL query against the current neXtProt may return a slightly different list of uPE1 proteins. For example, as of neXtProt version 2018-01-17, the same SPARQL query retrieved 1218 entries. As an additional note, neXtProt version 2018-01-17 updated its definition of unannotated proteins by excluding in total 11 GO terms, including the 5 GO terms listed below (Text S1).

```
select distinct ?entry ?fterm where {
  ?entry :isoform ?iso.
  ?entry :existence :Evidence_at_protein_level .
  filter not exists { ?iso :functionInfo ?_ . }
  filter not exists { ?iso :function ?func .
                      optional {?func :term ?fterm1 .}
                      filter(!bound(?fterm1))         #eliminates
functions from pathways
                     }
  filter not exists {
                        ?iso :function / :term ?fterm .
                        filter(?fterm != cv:GO_0005515 && ?fterm
!= cv:GO_0042802 && ?fterm != cv:GO_0005509 && ?fterm !=
cv:GO_0008270 && ?fterm != cv:GO_0051260)
                       # eliminates proteins whose ONLY GO
function is one of calcium-binding, zinc-binding, protein-
binding, identical protein binding, protein homooligomerization
                      }
 }
```

Text S3. Benchmark set of 100 well annotated PE1 proteins randomly selected from chromosome 17. Only the canonical isoform listed by neXtProt is used for benchmark testing. The full list of benchmark proteins are: NX_P04626, NX_P04637, NX_Q9GZM8, NX_P02749, NX_P50616, NX_Q96GD4, NX_Q9GZT4, NX_Q9UKF7, NX_O75771, NX_Q13227, NX_Q9HC21, NX_Q96FM1, NX_P32322, NX_Q13829, NX_Q8N9F7, NX_Q15078, NX_P46108, NX_Q9UGN4, NX_Q9UH92, NX_Q9NRY6, NX_P14415, NX_Q07021, NX_Q9BXJ1, NX_Q9Y6N1, NX_P35232, NX_Q9Y5W9, NX_Q00169, NX_Q969T9, NX_Q9BZG1, NX_Q96H20, NX_Q86V81, NX_P62258, NX_P61289, NX_Q9H2A7, NX_Q8N2A8, NX_O95249, NX_Q07955, NX_Q8WVN6, NX_Q7Z4W1, NX_O95476, NX_Q8IW40, NX_Q13432, NX_P09564, NX_Q92988, NX_Q0VD86, NX_Q9UNK0, NX_O60248, NX_Q13253, NX_P60008, NX_Q9BYE0, NX_P16035, NX_Q86UA6, NX_P62993, NX_P01241, NX_P09629, NX_P51148, NX_Q9UKL6, NX_Q9BQB4, NX_Q16613, NX_Q14197, NX_Q96FZ7, NX_Q8TCD5, NX_P12829, NX_Q9Y584, NX_P60763, NX_Q86XA0, NX_Q9HD47, NX_P51452, NX_Q9NQ92, NX_Q9BRG1, NX_O60895, NX_P62253, NX_Q96F10, NX_O15273, NX_O75947, NX_P62750, NX_Q15649, NX_P63241, NX_P15531, NX_P61254, NX_O15392, NX_P07737, NX_P62829, NX_P84243, NX_P61353, NX_Q8IY31, NX_O14907, NX_Q9BRA2, NX_Q86WV5, NX_Q8WVK7, NX_O95166, NX_P63272, NX_P63027, NX_Q86UU9, NX_P41567, NX_P13500, NX_P61956, NX_P10147, NX_Q9NYG5, NX_A8MT69, NX_P63173, NX_O14610.

Table S2. Fmax of different programs for GO prediction using UniProt and neXtProt annotation as gold standard for the benchmark set of 100 chromosome 17 PE1 proteins.

	UniProt (EXP, IDA, IMP, IGI, IEP, TAS, IC)			neXtProt (Gold evidence)			neXtProt (Gold and Silver evidence)		
	MF	BP	CC	MF	BP	CC	MF	BP	CC
BLAST	0.225	0.206	0.312	0.320	0.235	0.340	0.312	0.234	0.351
PSIBLAST	0.253	0.188	0.314	0.332	0.230	0.348	0.334	0.243	0.359
GoFDR	0.355	0.341	0.447	0.472	0.376	0.476	0.447	0.364	0.479
GOtcha	0.251	0.195	0.414	0.321	0.219	0.444	0.454	0.219	0.454
Naïve	0.346	0.281	0.509	0.142	0.302	0.469	0.146	0.322	0.486
sequence	0.378	0.358	0.479	0.476	0.406	0.515	0.458	0.395	0.512
PPI	0.244	0.347	0.451	0.279	0.394	0.496	0.291	0.401	0.530
sequence+PPI	0.382	0.398	0.510	0.476	0.451	0.552	0.461	0.444	0.572
structure	0.498	0.431	0.499	0.647	0.490	0.547	0.648	0.512	0.571
COFACTOR	**0.545**	**0.497**	**0.599**	**0.693**	**0.573**	**0.669**	**0.689**	**0.591**	**0.688**

The upper block includes three different control methods (BLAST, PSIBLAST, Naïve) used as baseline algorithms in CAFA function annotation experiments and two top performing sequence-based function prediction methods. In the lower block, "sequence", "PPI", and "structure" are the three component methods of "COFACTOR", which combines these three components by weighted average. The program with the highest Fmax at each category is highlighted by bold. Both neXtProt and UniProt assigns GO terms to proteins using different evidence codes, with "gold" in neXtProt and "EXP, IDA, IMP, IGI, IEP, TAS, IC" in UniProt standing for confident function annotation with reliable literature references, typically with low throughput wet lab experiments.

Table S2. Fmax of "structure" component and the final consensus prediction in COFACTOR for a benchmark set of 59 proteins with experimental structure covering at least 30% of target sequence.

neXtProt ID[a]	PDB chain ID[b]	Target coverage[c]	TM-score[d]	structure[e]			COFACTOR[f]		
				MF	BP	CC	MF	BP	CC
NX_O14907	2l4tA	1.000	0.659	1.000	0.861	0.800	1.000	0.805	0.815
NX_O95166	3wimA	1.000	0.957	0.941	0.892	0.784	0.941	0.921	0.779
NX_P15531	3l7uC	1.000	0.989	0.771	0.182	0.700	0.795	0.298	0.718
NX_P41567	2if1A	1.000	0.902	1.000	0.133	1.000	1.000	0.667	0.727
NX_P61956	2n9eB	1.000	0.697	0.941	0.860	0.762	0.941	0.860	1.000
NX_P63272	3h7hA	1.000	0.990	0.591	0.695	0.800	0.591	0.695	0.800
NX_Q7Z4W1	3d3wB	1.000	0.996	0.933	0.525	0.857	0.933	0.559	0.955
NX_Q9NYG5	5g05B	1.000	0.692	0.917	0.585	0.897	0.917	0.583	0.897
NX_P46108	2eyzA	0.997	0.996	0.667	0.483	0.800	0.615	0.474	0.750
NX_P07737	3chwP	0.993	0.980	0.258	0.611	0.423	0.404	0.662	0.730
NX_P61353	5t2cT	0.993	0.943	0.500	0.814	0.522	0.500	0.814	0.522
NX_P63173	5t2ce	0.986	0.877	1.000	0.857	0.944	1.000	0.897	0.971
NX_Q9BRG1	3cuqC	0.983	0.996	1.000	0.553	0.807	1.000	0.606	0.879
NX_O15392	3uedC	0.979	0.971	0.938	0.895	0.899	1.000	0.909	0.959
NX_P62993	1griB	0.972	0.982	0.800	0.565	0.824	0.849	0.631	0.873
NX_P51452	3f81B	0.968	0.985	0.923	0.968	0.811	0.960	0.943	0.878
NX_Q9BRA2	1wouA	0.968	0.926	1.000	1.000	1.000	0.900	0.698	1.000
NX_Q00169	1uw5C	0.967	0.995	0.552	1.000	0.250	0.552	1.000	0.421
NX_Q8TCD5	2i7dA	0.960	0.986	0.857	0.808	0.963	0.968	0.767	0.963
NX_Q86WV5	4joiD	0.959	0.987	0.750	0.730	0.750	0.750	0.811	0.900
NX_P62829	4v6xCV	0.950	0.954	1.000	0.623	0.546	1.000	0.623	0.600
NX_Q9UKL6	1ln1A	0.949	0.990	1.000	1.000	1.000	0.571	0.533	1.000
NX_Q9GZT4	3l6bA	0.944	0.951	1.000	0.790	0.800	0.979	0.793	0.800
NX_P02749	1c1zA	0.942	0.990	0.960	0.794	0.745	0.923	0.788	0.760
NX_A8MT69	4draH	0.938	0.946	0.833	0.756	1.000	1.000	0.829	1.000
NX_P61254	5t2cS	0.924	0.961	0.909	0.841	0.727	0.909	0.841	0.727
NX_Q96F10	2q4vB	0.924	0.891	0.941	1.000	0.870	0.875	0.732	0.714
NX_P60763	2ov2B	0.922	0.963	0.980	0.245	0.627	0.980	0.457	0.600
NX_P62258	3ualA	0.902	0.981	0.718	0.493	0.737	0.718	0.482	0.737
NX_Q8WVK7	4aj5T	0.901	0.825[d]	1.000	0.667	0.929	1.000	0.417	0.788
NX_P63241	5dlqF	0.890	0.948	0.783	0.815	0.913	0.783	0.800	0.958
NX_Q9BQB4	2k8pA	0.887	0.900	1.000	0.959	0.400	1.000	0.932	0.500
NX_P16035	1gxdD	0.873	0.922	0.929	0.722	0.900	0.929	0.880	0.957
NX_P32322	5uawE	0.862	0.988	0.909	0.933	0.333	0.909	0.933	0.933
NX_Q13253	1m4uA	0.858	0.969	0.800	0.770	1.000	0.727	0.782	1.000
NX_P01241	1bp3A	0.853	0.765	1.000	0.938	1.000	1.000	0.919	1.000
NX_Q96H20	3cuqA	0.849	0.989	1.000	0.852	0.949	0.889	0.887	0.963
NX_P62750	4v6xCX	0.776	0.898	0.737	0.957	0.558	0.737	0.971	0.640
NX_P13500	1donB	0.768	0.841	0.857	0.615	0.571	0.933	0.676	0.750
NX_P10147	5corJ	0.761	0.849	0.981	0.901	0.800	0.981	0.908	0.800
NX_P51148	4kyiH	0.755	0.973	1.000	0.516	0.702	1.000	0.564	0.849
NX_Q13432	3gqqD	0.738	0.968	1.000	0.829	0.938	0.154	0.815	0.769
NX_P84243	3wtpE	0.735	0.968	0.964	0.469	0.842	0.964	0.469	0.842
NX_Q96GD4	4af3A	0.733	0.905	0.941	0.746	0.892	0.968	0.693	0.941

NX_P62253	2awfA	0.677	0.952	1.000	0.857	0.846	1.000	0.857	0.846
NX_Q07021	1p32A	0.645	0.972	0.926	0.912	0.826	0.893	0.933	0.923
NX_Q14197	5oomp	0.617	0.919	0.867	1.000	0.839	0.867	1.000	0.973
NX_Q9Y5W9	4ikdA	0.526	0.729	0.750	0.667	0.346	0.857	0.947	0.900
NX_P04637	2fejA	0.519	0.873	0.914	0.868	0.901	0.953	0.873	0.932
NX_O15273	1ya5T	0.509	0.752	0.000	0.081	0.300	0.148	0.351	0.667
NX_Q15078	3o0gE	0.485	0.914	0.800	0.762	0.805	0.800	0.769	0.868
NX_P04626	3n85A	0.482	0.491	0.805	0.557	0.519	0.769	0.654	0.739
NX_Q15649	5l85A	0.458	0.469	0.353	0.000	0.182	0.462	0.522	0.600
NX_O60895	2xvtC	0.451	0.905	0.074	0.076	0.286	0.759	0.564	0.667
NX_Q07955	2o3dA	0.440	0.566	0.714	0.453	0.655	0.909	0.625	0.727
NX_Q9UGN4	2q87C	0.351	0.793	0.400	0.054	0.235	0.316	0.371	0.686
NX_P50616	2z15A	0.339	0.315	0.000	0.250	0.286	0.286	0.474	0.833
NX_Q9GZM8	2v66E	0.322	0.559	0.222	0.256	0.459	0.182	0.418	0.680
NX_Q86V81	3ulhA	0.319	0.684	0.727	0.443	0.450	1.000	0.683	0.597
Average		0.805	0.877	0.799	0.669	0.717	0.809	0.718	0.810
Pearson correlation to TM-score				0.435	0.400	0.432	0.286	0.249	0.161

[a] This set of 59 proteins is a subset from the benchmark set of 100 well annotated PE1 proteins from chromosome 17. The table is sorted in descending order of target coverage.

[b] Since the experimental structures do not necessarily cover the full length target sequence, if a target can be mapped to more than one experimental structure, only the structure that has the largest coverage to the target sequence is considered.

[c] "Target coverage" is the portion of query residues covered by corresponding experimental structure.

[d] "TM-score" is the TM-score between the first I-TASSER model and the corresponding experimental structures. I-TASSER model residues not solved in experimental structures are excluded in TM-score calculation.

[e] "structure" columns show the Fmax of structure-based component of COFACTOR pipeline.

[f] "COFACTOR" columns show the Fmax of final consensus COFACTOR function prediction.

Table S3. COFACTOR predicted functions for 66 uPE1 protein on chromosome 17 as of neXtProt 2017-08-01. General GO terms associated with more than 20% of annotated UniProt proteins are excluded. For each protein, only GO terms predicted with Cscore > 0.3 are included in the table, with Cscore > 0.5 highlighted in bold. Entries are sorted in descending order of the highest MF Cscore. The 30 uPE1 proteins with MF Cscore > 0.5 are shaded in grey. The first 13 proteins in this list have MF Cscore > 0.59, as reported in Table 1 in main text. Additionally, 33 and 49 proteins in this list have BP Cscore>0.55 and CC Cscore>0.59, respectively. NeXtProt does not use CC terms for classifying uPE1 proteins (see Text S2 for SPARQL query).

	NextProt Accession, Gene Name, and Common Name	Molecular Function (MF)	Biological Process (BP)	Cellular Component (CC)
1	NX_Q8TBR7-2, FAM57A. (FAM57A)	**GO:0016740 (1.00) transferase activity** **GO:0050291 (0.99) sphingosine N-acyltransferase activity**	**GO:0032502 (0.69) developmental process** **GO:0044767 (0.64) single-organism developmental process** **GO:0048856 (0.59) anatomical structure development** **GO:1901564 (0.57) organonitrogen compound metabolic process** **GO:0006629 (0.57) lipid metabolic process** **GO:0048869 (0.55) cellular developmental process** **GO:0016043 (0.54) cellular component organization** **GO:0007420 (0.54) brain development** **GO:0021952 (0.53) central nervous system projection neuron axonogenesis** **GO:0001654 (0.53) eye development** GO:0006672 (0.46) ceramide metabolic process GO:0046467 (0.42) membrane lipid biosynthetic process GO:0046513 (0.41) ceramide biosynthetic process GO:0048523 (0.31) negative regulation of cellular process	**GO:0005887 (1.00) integral component of plasma membrane** **GO:0005886 (1.00) plasma membrane** **GO:0005783 (0.98) endoplasmic reticulum** GO:0097458 (0.37) neuron part GO:0042995 (0.37) cell projection
2	NX_Q12767-1, TMEM94. (Transmembrane protein 94)	**GO:0043492 (0.91) ATPase activity, coupled to movement of substances** **GO:0022892 (0.91) substrate-specific transporter activity** **GO:0019829 (0.74) cation-transporting ATPase activity** **GO:0022890 (0.61) inorganic cation transmembrane transporter activity** **GO:0015662 (0.61) ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism** **GO:0046873 (0.57) metal ion transmembrane transporter activity**	**GO:0065008 (0.80) regulation of biological quality** **GO:0098771 (0.77) inorganic ion homeostasis** **GO:0030003 (0.77) cellular cation homeostasis** **GO:0006875 (0.72) cellular metal ion homeostasis** **GO:0006810 (0.71) transport** **GO:0006812 (0.68) cation transport** **GO:0034220 (0.66) ion transmembrane transport** **GO:0098662 (0.65) inorganic cation transmembrane transport** **GO:1902600 (0.64) hydrogen ion transmembrane transport** **GO:0090662 (0.60) ATP hydrolysis coupled transmembrane transport**	**GO:0005654 (1.00) nucleoplasm**

		GO:0015077 (0.41) monovalent inorganic cation transmembrane transporter activity GO:0005524 (0.37) ATP binding GO:0005391 (0.37) sodium:potassium-exchanging ATPase activity	**GO:0015988 (0.60) energy coupled proton transmembrane transport, against electrochemical gradient** **GO:0030004 (0.57) cellular monovalent inorganic cation homeostasis** **GO:0030001 (0.56) metal ion transport** **GO:0071805 (0.52) potassium ion transmembrane transport** **GO:0071436 (0.52) sodium ion export**	
3	NX_Q5BKU9-1, OXLD1. (Oxidoreductase-like domain-containing protein 1)	**GO:0016491 (0.87) oxidoreductase activity** **GO:0000166 (0.82) nucleotide binding** **GO:0071949 (0.73) FAD binding** **GO:0004128 (0.73) cytochrome-b5 reductase activity, acting on NAD(P)H** **GO:0016211 (0.52) ammonia ligase activity** GO:0035639 (0.33) purine ribonucleoside triphosphate binding GO:0032559 (0.33) adenyl ribonucleotide binding GO:0032550 (0.33) purine ribonucleoside binding	**GO:0015701 (0.90) bicarbonate transport** **GO:0009084 (0.53) glutamine family amino acid biosynthetic process** **GO:0008652 (0.53) cellular amino acid biosynthetic process** **GO:0006541 (0.53) glutamine metabolic process** GO:0071941 (0.34) nitrogen cycle metabolic process	**GO:0005739 (0.90) mitochondrion** **GO:0005737 (0.66) cytoplasm**
4	NX_A6NGC4-1, TLCD2. (TLC domain-containing protein 2)	**GO:0016740 (0.86) transferase activity** **GO:0050291 (0.76) sphingosine N-acyltransferase activity** **GO:0005216 (0.59) ion channel activity** **GO:0009881 (0.55) photoreceptor activity**	**GO:0006643 (0.76) membrane lipid metabolic process** **GO:0006672 (0.73) ceramide metabolic process** **GO:0044765 (0.61) single-organism transport** **GO:0006811 (0.60) ion transport** **GO:0034220 (0.58) ion transmembrane transport** **GO:0019538 (0.58) protein metabolic process** **GO:0044267 (0.56) cellular protein metabolic process** **GO:0050896 (0.55) response to stimulus** **GO:0006464 (0.54) cellular protein modification process** **GO:0018298 (0.53) protein-chromophore linkage** **GO:0007602 (0.53) phototransduction** **GO:0032502 (0.52) developmental process** **GO:0048856 (0.50) anatomical structure development** GO:0046467 (0.48) membrane lipid biosynthetic process GO:0046513 (0.46) ceramide biosynthetic process	**GO:0016021 (1.00) integral component of membrane** **GO:0016020 (1.00) membrane** **GO:0005783 (0.75) endoplasmic reticulum** **GO:0005886 (0.55) plasma membrane**
5	NX_O43934-1, MFSD11. (UNC93-like protein MFSD11)	**GO:0005215 (0.85) transporter activity** **GO:0022857 (0.84) transmembrane transporter activity** **GO:0022892 (0.78) substrate-specific transporter activity** **GO:0022891 (0.77) substrate-specific transmembrane transporter activity** **GO:0051119 (0.74) sugar transmembrane transporter activity** **GO:0015145 (0.72) monosaccharide transmembrane transporter**	**GO:0006810 (0.82) transport** **GO:0071702 (0.70) organic substance transport** **GO:0055085 (0.69) transmembrane transport** **GO:0008643 (0.68) carbohydrate transport** **GO:0015749 (0.67) monosaccharide transport** **GO:0008645 (0.66) hexose transport** **GO:0015758 (0.64) glucose transport** **GO:0034219 (0.61) carbohydrate transmembrane transport** **GO:0035428 (0.60) hexose transmembrane transport** GO:0046323 (0.47) glucose import	**GO:0016021 (1.00) integral component of membrane** **GO:0016020 (1.00) membrane** **GO:0005887 (0.77) integral component of plasma membrane** **GO:0005886 (0.70) plasma membrane**

		activity **GO:0015149 (0.71) hexose transmembrane transporter activity** **GO:0005355 (0.70) glucose transmembrane transporter activity** **GO:0008324 (0.67) cation transmembrane transporter activity** **GO:0005351 (0.66) sugar:proton symporter activity** GO:0051183 (0.34) vitamin transporter activity GO:0048029 (0.33) monosaccharide binding GO:0015146 (0.33) pentose transmembrane transporter activity GO:0015148 (0.32) D-xylose transmembrane transporter activity	GO:0050896 (0.38) response to stimulus GO:0006820 (0.38) anion transport GO:0051716 (0.35) cellular response to stimulus GO:0042221 (0.34) response to chemical GO:1901700 (0.33) response to oxygen-containing compound	
6	NX_Q9P298-1, HIGD1B. (HIG1 domain family member 1B)	**GO:0016740 (0.79) transferase activity** **GO:0061630 (0.71) ubiquitin protein ligase activity**	GO:0043066 (0.32) negative regulation of apoptotic process GO:0043623 (0.31) cellular protein complex assembly	**GO:0043234 (0.88) protein complex** **GO:0005634 (0.71) nucleus** **GO:0044429 (0.53) mitochondrial part** GO:0005737 (0.46) cytoplasm GO:0044428 (0.45) nuclear part GO:0044427 (0.45) chromosomal part GO:0005739 (0.42) mitochondrion GO:0016020 (0.38) membrane GO:0043232 (0.37) intracellular non-membrane-bounded organelle GO:0016021 (0.36) integral component of membrane GO:0097249 (0.32) mitochondrial respiratory chain supercomplex GO:0031305 (0.32) integral component of mitochondrial inner membrane GO:0031090 (0.30) organelle membrane
7	NX_Q2TAL5-1, SMTNL2. (Smoothelin-like protein 2)	**GO:0008092 (0.77) cytoskeletal protein binding** GO:0003779 (0.42) actin binding GO:1901363 (0.40) heterocyclic compound binding GO:0097159 (0.40) organic cyclic compound binding GO:0050660 (0.37) flavin adenine dinucleotide binding GO:0046983 (0.30) protein dimerization activity GO:0042802 (0.30) identical protein binding	**GO:0016043 (0.70) cellular component organization** **GO:0032502 (0.69) developmental process** **GO:0044767 (0.63) single-organism developmental process** **GO:0048856 (0.59) anatomical structure development** GO:0006996 (0.47) organelle organization GO:0007010 (0.45) cytoskeleton organization GO:1902589 (0.42) single-organism organelle organization GO:0048869 (0.41) cellular developmental process GO:0030029 (0.41) actin filament-based process GO:0030036 (0.39) actin cytoskeleton organization GO:0048519 (0.32) negative regulation of biological process GO:0031032 (0.31) actomyosin structure organization GO:0048523 (0.30) negative regulation of cellular process	**GO:0005737 (0.66) cytoplasm** **GO:0016020 (0.52) membrane** **GO:0043232 (0.51) intracellular non-membrane-bounded organelle** **GO:0044430 (0.50) cytoskeletal part** GO:0005856 (0.43) cytoskeleton GO:0005886 (0.42) plasma membrane GO:0042995 (0.38) cell projection GO:0043234 (0.37) protein complex GO:0044459 (0.36) plasma membrane part GO:0030054 (0.36) cell junction GO:0030055 (0.32) cell-substrate junction GO:0005912 (0.31) adherens junction GO:0044449 (0.30) contractile fiber part

			GO:0048468 (0.30) cell development	
8	NX_Q9BQS6-1, HSPB9. (Heat shock protein beta-9)	**GO:0042802 (0.76) identical protein binding** **GO:0042803 (0.63) protein homodimerization activity** **GO:0051082 (0.52) unfolded protein binding** **GO:0005212 (0.50) structural constituent of eye lens** GO:0032182 (0.39) ubiquitin-like protein binding GO:0030291 (0.39) protein serine/threonine kinase inhibitor activity GO:0019900 (0.39) kinase binding GO:0003723 (0.37) RNA binding GO:0043169 (0.35) cation binding	**GO:0050896 (0.82) response to stimulus** **GO:0006950 (0.80) response to stress** **GO:0009628 (0.71) response to abiotic stimulus** **GO:0042221 (0.60) response to chemical** **GO:0009408 (0.60) response to heat** **GO:0016043 (0.56) cellular component organization** **GO:0044767 (0.52) single-organism developmental process** **GO:0048523 (0.51) negative regulation of cellular process** **GO:0042981 (0.51) regulation of apoptotic process** **GO:0006457 (0.51) protein folding** **GO:0043066 (0.50) negative regulation of apoptotic process** GO:0022607 (0.49) cellular component assembly GO:1901700 (0.48) response to oxygen-containing compound GO:0048856 (0.48) anatomical structure development GO:0031323 (0.48) regulation of cellular metabolic process	**GO:0005634 (0.97) nucleus** **GO:0005737 (0.96) cytoplasm**
9	NX_Q96LD4-1, TRIM47. (Tripartite motif-containing protein 47)	**GO:0004842 (0.76) ubiquitin-protein transferase activity** GO:0061630 (0.31) ubiquitin protein ligase activity	**GO:0031323 (0.54) regulation of cellular metabolic process** **GO:0019538 (0.54) protein metabolic process** **GO:0060255 (0.53) regulation of macromolecule metabolic process** **GO:0080090 (0.52) regulation of primary metabolic process** **GO:0048518 (0.50) positive regulation of biological process** **GO:0006464 (0.50) cellular protein modification process** GO:0032446 (0.48) protein modification by small protein conjugation GO:0048522 (0.47) positive regulation of cellular process GO:0016567 (0.47) protein ubiquitination GO:0065008 (0.46) regulation of biological quality GO:0044764 (0.46) multi-organism cellular process GO:0051715 (0.43) cytolysis in other organism GO:0010468 (0.41) regulation of gene expression GO:2001141 (0.40) regulation of RNA biosynthetic process GO:2000112 (0.40) regulation of cellular macromolecule biosynthetic process	**GO:0005737 (0.57) cytoplasm** GO:0016020 (0.41) membrane GO:0005634 (0.41) nucleus GO:0005576 (0.41) extracellular region GO:0043232 (0.38) intracellular non-membrane-bounded organelle GO:0043234 (0.35) protein complex GO:0044428 (0.32) nuclear part
10	NX_Q8N7B9-1, EFCAB3. (EF-hand calcium-binding domain-containing protein 3)	**GO:0043169 (0.74) cation binding** GO:0005509 (0.47) calcium ion binding	**GO:0019538 (0.58) protein metabolic process** **GO:0044267 (0.52) cellular protein metabolic process** GO:0007165 (0.46) signal transduction GO:0050896 (0.43) response to stimulus GO:0035556 (0.43) intracellular signal transduction GO:0006796 (0.42) phosphate-containing compound metabolic process GO:0006464 (0.41) cellular protein modification process GO:0051179 (0.40) localization GO:0006468 (0.40) protein phosphorylation	**GO:0016020 (0.82) membrane** **GO:0005737 (0.68) cytoplasm** **GO:0005886 (0.66) plasma membrane** **GO:0005634 (0.62) nucleus** GO:0043234 (0.45) protein complex GO:0044459 (0.44) plasma membrane part GO:0005829 (0.39) cytosol GO:0044430 (0.38) cytoskeletal part GO:0097458 (0.33) neuron part GO:0031090 (0.31) organelle membrane GO:0042995 (0.30) cell projection

			GO:0046777 (0.39) protein autophosphorylation GO:0042221 (0.39) response to chemical GO:0018105 (0.39) peptidyl-serine phosphorylation GO:0051234 (0.38) establishment of localization GO:0010038 (0.37) response to metal ion GO:0009738 (0.34) abscisic acid-activated signaling pathway	
11	NX_Q6AI12-1, ANKRD40. (Ankyrin repeat domain-containing protein 40)	**GO:0019899 (0.64) enzyme binding** **GO:0044389 (0.62) ubiquitin-like protein ligase binding** **GO:0008092 (0.62) cytoskeletal protein binding** **GO:0030507 (0.57) spectrin binding** **GO:0008093 (0.57) cytoskeletal adaptor activity** **GO:0044877 (0.51) macromolecular complex binding** **GO:0008134 (0.51) transcription factor binding** **GO:0005048 (0.50) signal sequence binding** GO:0005200 (0.49) structural constituent of cytoskeleton GO:0051117 (0.48) ATPase binding GO:0016740 (0.30) transferase activity	**GO:0060255 (0.62) regulation of macromolecule metabolic process** **GO:0007165 (0.62) signal transduction** **GO:0080090 (0.61) regulation of primary metabolic process** **GO:0031323 (0.61) regulation of cellular metabolic process** **GO:0051179 (0.60) localization** **GO:0048522 (0.60) positive regulation of cellular process** **GO:0016043 (0.60) cellular component organization** **GO:0065008 (0.58) regulation of biological quality** **GO:0050896 (0.58) response to stimulus** **GO:0048519 (0.58) negative regulation of biological process** **GO:0006355 (0.58) regulation of transcription, DNA-templated** **GO:0048523 (0.57) negative regulation of cellular process** **GO:0010604 (0.57) positive regulation of macromolecule metabolic process** **GO:0006810 (0.57) transport** **GO:0031325 (0.56) positive regulation of cellular metabolic process**	**GO:0005737 (0.77) cytoplasm** **GO:0005634 (0.65) nucleus** **GO:0016020 (0.63) membrane** **GO:0005886 (0.55) plasma membrane** **GO:0044459 (0.51) plasma membrane part** **GO:0043234 (0.51) protein complex** GO:0016021 (0.46) integral component of membrane GO:0005829 (0.43) cytosol GO:0097458 (0.34) neuron part
12	NX_Q6UX52-1, C17orf99. (Uncharacterized protein C17orf99)	**GO:0004872 (0.63) receptor activity** **GO:0004888 (0.56) transmembrane signaling receptor activity** **GO:0004672 (0.53) protein kinase activity** **GO:0019199 (0.50) transmembrane receptor protein kinase activity** GO:0097367 (0.49) carbohydrate derivative binding GO:0035639 (0.47) purine ribonucleoside triphosphate binding GO:0032559 (0.47) adenyl ribonucleotide binding GO:0032550 (0.47) purine ribonucleoside binding GO:0046983 (0.39) protein dimerization activity	**GO:0032502 (0.68) developmental process** **GO:0044767 (0.67) single-organism developmental process** **GO:0048869 (0.61) cellular developmental process** **GO:0016043 (0.61) cellular component organization** **GO:0009653 (0.60) anatomical structure morphogenesis** **GO:0006928 (0.58) movement of cell or subcellular component** **GO:0048856 (0.54) anatomical structure development** **GO:0030030 (0.54) cell projection organization** **GO:0032989 (0.53) cellular component morphogenesis** **GO:0048812 (0.52) neuron projection morphogenesis** **GO:0016477 (0.52) cell migration** **GO:0006796 (0.51) phosphate-containing compound metabolic process** **GO:0006464 (0.51) cellular protein modification process** **GO:0016310 (0.50) phosphorylation** GO:0061564 (0.48) axon development	**GO:0031224 (1.00) intrinsic component of membrane** **GO:0016020 (1.00) membrane** **GO:0016021 (0.95) integral component of membrane** **GO:0005886 (0.90) plasma membrane** **GO:0044459 (0.75) plasma membrane part** **GO:0005887 (0.63) integral component of plasma membrane** GO:0031982 (0.42) vesicle GO:0097458 (0.41) neuron part GO:0042995 (0.40) cell projection GO:0031988 (0.38) membrane-bounded vesicle GO:0009986 (0.38) cell surface GO:0043005 (0.35) neuron projection GO:0030054 (0.35) cell junction GO:0030424 (0.34) axon GO:0044421 (0.32) extracellular region part
13	NX_Q3MHD2-1, LSM12. (Protein LSM12 homolog)	**GO:0003723 (0.59) RNA binding**	**GO:0090304 (0.79) nucleic acid metabolic process** **GO:0016070 (0.73) RNA metabolic process** GO:0022618 (0.39) ribonucleoprotein complex assembly GO:0000387 (0.32) spliceosomal snRNP	**GO:0005576 (0.55) extracellular region** GO:0005829 (0.47) cytosol GO:0005634 (0.33) nucleus GO:0036464 (0.31) cytoplasmic ribonucleoprotein granule

			assembly	
14	NX_A8MVW0-1, FAM171A2. (FAM171A2)	**GO:1901363 (0.58) heterocyclic compound binding** **GO:0097159 (0.58) organic cyclic compound binding** **GO:0003676 (0.56) nucleic acid binding** **GO:0019899 (0.54) enzyme binding** **GO:0017016 (0.52) Ras GTPase binding** GO:0022892 (0.47) substrate-specific transporter activity	**GO:0016043 (0.52) cellular component organization** GO:0051179 (0.49) localization GO:0006810 (0.46) transport GO:0060255 (0.42) regulation of macromolecule metabolic process GO:0006996 (0.42) organelle organization GO:0080090 (0.41) regulation of primary metabolic process GO:0031323 (0.41) regulation of cellular metabolic process GO:0048519 (0.40) negative regulation of biological process GO:0019538 (0.40) protein metabolic process GO:0051171 (0.39) regulation of nitrogen compound metabolic process GO:0050896 (0.39) response to stimulus GO:0048523 (0.39) negative regulation of cellular process GO:0032879 (0.39) regulation of localization GO:0016192 (0.39) vesicle-mediated transport GO:0010468 (0.39) regulation of gene expression	**GO:0005737 (0.66) cytoplasm** **GO:0043234 (0.64) protein complex** **GO:0031982 (0.53) vesicle** **GO:0031988 (0.52) membrane-bounded vesicle** **GO:0044421 (0.51) extracellular region part** GO:0070062 (0.48) extracellular exosome GO:0005634 (0.48) nucleus GO:0044428 (0.40) nuclear part GO:0016020 (0.40) membrane GO:0005829 (0.35) cytosol GO:0031090 (0.34) organelle membrane
15	NX_Q0P5P2-1, C17orf67. (Uncharacterized protein C17orf67)	**GO:0043169 (0.58) cation binding** **GO:0004112 (0.58) cyclic-nucleotide phosphodiesterase activity** GO:0032561 (0.48) guanyl ribonucleotide binding GO:0030551 (0.48) cyclic nucleotide binding	GO:0046068 (0.48) cGMP metabolic process GO:0009214 (0.48) cyclic nucleotide catabolic process GO:0009154 (0.48) purine ribonucleotide catabolic process GO:2000243 (0.37) positive regulation of reproductive process GO:1900542 (0.37) regulation of purine nucleotide metabolic process GO:0090075 (0.37) relaxation of muscle GO:0071902 (0.37) positive regulation of protein serine/threonine kinase activity GO:0060281 (0.37) regulation of oocyte development GO:0055117 (0.37) regulation of cardiac muscle contraction GO:0050868 (0.37) negative regulation of T cell activation GO:0050672 (0.37) negative regulation of lymphocyte proliferation GO:0045988 (0.37) negative regulation of striated muscle contraction GO:0045822 (0.37) negative regulation of heart contraction GO:0043902 (0.37) positive regulation of multi-organism process GO:0043410 (0.37) positive regulation of MAPK cascade	**GO:0005829 (0.53) cytosol** GO:0005737 (0.47) cytoplasm GO:0016020 (0.33) membrane
16	NX_Q9BQA9-1, C17orf62. (Uncharacterized protein C17orf62)	**GO:0035639 (0.57) purine ribonucleoside triphosphate binding** **GO:0032559 (0.57) adenyl ribonucleotide binding** **GO:0032550 (0.57) purine ribonucleoside binding** GO:0051427 (0.37) hormone receptor binding GO:0031701 (0.37) angiotensin receptor binding GO:0005126 (0.37) cytokine receptor binding GO:0004672 (0.37) protein	**GO:0044351 (0.83) macropinocytosis** GO:0048870 (0.32) cell motility GO:0048869 (0.32) cellular developmental process GO:0046777 (0.32) protein autophosphorylation GO:0018108 (0.32) peptidyl-tyrosine phosphorylation GO:0008283 (0.32) cell proliferation GO:0007165 (0.32) signal transduction GO:0006955 (0.32) immune response GO:0006952 (0.32) defense response	**GO:0043232 (0.79) intracellular non-membrane-bounded organelle** **GO:0044430 (0.74) cytoskeletal part** **GO:0005856 (0.74) cytoskeleton** **GO:0005737 (0.74) cytoplasm** **GO:0005874 (0.68) microtubule** **GO:0005829 (0.68) cytosol** **GO:0005871 (0.63) kinesin complex** **GO:0016020 (0.53) membrane** **GO:0005634 (0.53) nucleus** GO:0005815 (0.42) microtubule organizing center

		kinase activity		GO:0005819 (0.37) spindle GO:0005876 (0.32) spindle microtubule
17	NX_Q96T59-1, CDRT15. (CMT1A duplicated region transcript 15 protein)	**GO:0030234 (0.57) enzyme regulator activity** **GO:0016887 (0.55) ATPase activity** **GO:0003777 (0.55) microtubule motor activity** GO:0043178 (0.49) alcohol binding GO:0032934 (0.49) sterol binding GO:0015248 (0.49) sterol transporter activity GO:0008047 (0.49) enzyme activator activity GO:0071814 (0.40) protein-lipid complex binding GO:0070405 (0.40) ammonium ion binding GO:0042277 (0.40) peptide binding GO:0070325 (0.30) lipoprotein particle receptor binding GO:0034190 (0.30) apolipoprotein receptor binding GO:0004857 (0.30) enzyme inhibitor activity	**GO:0006810 (0.68) transport** **GO:0016043 (0.57) cellular component organization** **GO:0071702 (0.55) organic substance transport** **GO:0006928 (0.55) movement of cell or subcellular component** **GO:0007165 (0.54) signal transduction** **GO:0065008 (0.53) regulation of biological quality** **GO:0044707 (0.53) single-multicellular organism process** **GO:0051239 (0.52) regulation of multicellular organismal process** GO:0055092 (0.49) sterol homeostasis GO:0045940 (0.49) positive regulation of steroid metabolic process GO:0042157 (0.49) lipoprotein metabolic process GO:0034645 (0.49) cellular macromolecule biosynthetic process GO:0034377 (0.49) plasma lipoprotein particle assembly GO:0016101 (0.49) diterpenoid metabolic process GO:0015914 (0.49) phospholipid transport	**GO:0016020 (0.79) membrane** **GO:0043234 (0.54) protein complex** **GO:0016021 (0.54) integral component of membrane** GO:0044430 (0.47) cytoskeletal part GO:0005886 (0.47) plasma membrane GO:0005871 (0.44) kinesin complex GO:0070062 (0.35) extracellular exosome GO:0005829 (0.33) cytosol GO:0005634 (0.33) nucleus
18	NX_Q8N2U0-1, TMEM256. (Transmembrane protein 256)	**GO:0022892 (0.57) substrate-specific transporter activity** **GO:0017128 (0.55) phospholipid scramblase activity** GO:0008865 (0.45) fructokinase activity GO:0004454 (0.45) ketohexokinase activity	**GO:0046835 (0.57) carbohydrate phosphorylation** GO:0006810 (0.46) transport GO:0044351 (0.43) macropinocytosis	**GO:0070062 (0.51) extracellular exosome** GO:0016020 (0.41) membrane
19	NX_Q7RTS6-1, OTOP2. (Otopetrin-2)	**GO:0046983 (0.55) protein dimerization activity** **GO:0046873 (0.55) metal ion transmembrane transporter activity** **GO:0042802 (0.55) identical protein binding** **GO:0031420 (0.55) alkali metal ion binding** **GO:0015077 (0.55) monovalent inorganic cation transmembrane transporter activity** GO:0009678 (0.39) hydrogen-translocating pyrophosphatase activity GO:0004427 (0.39) inorganic diphosphatase activity	**GO:0042472 (1.00) inner ear morphogenesis** **GO:0009590 (0.51) detection of gravity** GO:0045299 (0.49) otolith mineralization GO:0032475 (0.49) otolith formation GO:0098662 (0.41) inorganic cation transmembrane transport GO:0030001 (0.41) metal ion transport	**GO:0016020 (0.86) membrane** **GO:0016021 (0.61) integral component of membrane** GO:0005886 (0.35) plasma membrane GO:0043234 (0.31) protein complex
20	NX_A6NFU0-1, FAM187A. (Ig-like V-type domain-containing protein FAM187A)	**GO:0004872 (0.55) receptor activity** **GO:0042802 (0.50) identical protein binding** GO:0046983 (0.48) protein dimerization activity GO:0004888 (0.46) transmembrane signaling receptor activity GO:0097367 (0.42) carbohydrate derivative binding GO:0098632 (0.30) protein binding involved in cell-cell adhesion	**GO:0006928 (0.64) movement of cell or subcellular component** **GO:0032502 (0.63) developmental process** **GO:0044767 (0.60) single-organism developmental process** **GO:0007411 (0.59) axon guidance** **GO:0048856 (0.55) anatomical structure development** **GO:0048869 (0.53) cellular developmental process** **GO:0016043 (0.53) cellular component organization** **GO:0051239 (0.52) regulation of**	**GO:0031224 (0.93) intrinsic component of membrane** **GO:0016020 (0.92) membrane** **GO:0016021 (0.82) integral component of membrane** **GO:0005886 (0.71) plasma membrane** **GO:0044459 (0.66) plasma membrane part** **GO:0097458 (0.59) neuron part** **GO:0044421 (0.55) extracellular region part** **GO:0043005 (0.53) neuron projection**

			multicellular organismal process **GO:0007155 (0.52) cell adhesion** **GO:0048518 (0.51) positive regulation of biological process** **GO:0050793 (0.50) regulation of developmental process** **GO:0048583 (0.50) regulation of response to stimulus** **GO:0009653 (0.50) anatomical structure morphogenesis** GO:2000026 (0.49) regulation of multicellular organismal development GO:0098609 (0.49) cell-cell adhesion	**GO:0030424 (0.52) axon** **GO:0031226 (0.51) intrinsic component of plasma membrane** **GO:0005887 (0.50) integral component of plasma membrane** GO:0030054 (0.43) cell junction GO:0043025 (0.40) neuronal cell body GO:0005737 (0.32) cytoplasm GO:0005576 (0.32) extracellular region
21	NX_Q5M775-1, SPECC1. (Cytospin-B)	**GO:0008092 (0.53) cytoskeletal protein binding** GO:0046983 (0.45) protein dimerization activity GO:0042802 (0.45) identical protein binding GO:0019899 (0.45) enzyme binding GO:0003779 (0.43) actin binding GO:0042805 (0.42) actinin binding GO:0005198 (0.41) structural molecule activity GO:1901363 (0.40) heterocyclic compound binding GO:0097367 (0.40) carbohydrate derivative binding GO:0097159 (0.40) organic cyclic compound binding GO:0032403 (0.40) protein complex binding GO:0051015 (0.38) actin filament binding GO:0044389 (0.38) ubiquitin-like protein ligase binding GO:0003676 (0.38) nucleic acid binding GO:0001948 (0.38) glycoprotein binding	**GO:0016043 (0.67) cellular component organization** **GO:0032502 (0.62) developmental process** **GO:0044767 (0.60) single-organism developmental process** **GO:0006996 (0.55) organelle organization** **GO:0048856 (0.51) anatomical structure development** GO:1902589 (0.49) single-organism organelle organization GO:0007010 (0.48) cytoskeleton organization GO:0048869 (0.46) cellular developmental process GO:0051179 (0.45) localization GO:0006928 (0.43) movement of cell or subcellular component GO:0030029 (0.42) actin filament-based process GO:0009653 (0.42) anatomical structure morphogenesis GO:0030036 (0.41) actin cytoskeleton organization GO:0051641 (0.39) cellular localization GO:0022607 (0.37) cellular component assembly	**GO:0044430 (0.66) cytoskeletal part** **GO:0016020 (0.59) membrane** **GO:0043232 (0.54) intracellular non-membrane-bounded organelle** **GO:0030054 (0.51) cell junction** **GO:0005856 (0.51) cytoskeleton** GO:0005886 (0.48) plasma membrane GO:0044459 (0.47) plasma membrane part GO:0042995 (0.45) cell projection GO:0005912 (0.45) adherens junction GO:0005737 (0.42) cytoplasm GO:0030055 (0.41) cell-substrate junction GO:0005924 (0.38) cell-substrate adherens junction GO:0005911 (0.36) cell-cell junction GO:0044449 (0.35) contractile fiber part GO:0044448 (0.34) cell cortex part
22	NX_O43149-1, ZZEF1. (Zinc finger ZZ-type and EF-hand domain-containing protein 1)	**GO:0016740 (0.53) transferase activity** GO:0004842 (0.32) ubiquitin-protein transferase activity	**GO:0019538 (0.61) protein metabolic process** **GO:0006464 (0.50) cellular protein modification process** GO:0032446 (0.36) protein modification by small protein conjugation GO:0016567 (0.35) protein ubiquitination	GO:0005634 (0.47) nucleus GO:0005737 (0.46) cytoplasm
23	NX_Q7Z5L0-1, VMO1. (Vitelline membrane outer layer protein 1 homolog)	**GO:0016787 (0.53) hydrolase activity** GO:0008061 (0.36) chitin binding GO:0004568 (0.36) chitinase activity	GO:0048856 (0.35) anatomical structure development	**GO:0070062 (1.00) extracellular exosome**
24	NX_A8MSI8-1, LYRM9. (LYR motif-containing protein 9)	**GO:0008137 (0.52) NADH dehydrogenase (ubiquinone) activity**	GO:0022607 (0.41) cellular component assembly GO:0043623 (0.36) cellular protein complex assembly GO:0070271 (0.32) protein complex biogenesis GO:0033108 (0.32) mitochondrial respiratory chain complex assembly	**GO:0005737 (0.56) cytoplasm** **GO:0005739 (0.53) mitochondrion** GO:0044421 (0.42) extracellular region part GO:0070062 (0.40) extracellular exosome GO:0016020 (0.40) membrane GO:0005576 (0.40) extracellular region
25	NX_Q8WU58-1, FAM222B. (FAM222B)	**GO:0003676 (0.52) nucleic acid binding** GO:0043169 (0.32) cation binding	GO:0019222 (0.33) regulation of metabolic process GO:0060255 (0.32) regulation of macromolecule metabolic process GO:0031323 (0.32) regulation of cellular metabolic process	**GO:0005654 (1.00) nucleoplasm**

			GO:0080090 (0.30) regulation of primary metabolic process GO:0010468 (0.30) regulation of gene expression	
26	NX_Q8TC99-1, FNDC8. (Fibronectin type III domain-containing protein 8)	**GO:0097367 (0.51) carbohydrate derivative binding** **GO:1901363 (0.50) heterocyclic compound binding** **GO:0097159 (0.50) organic cyclic compound binding** GO:0035639 (0.49) purine ribonucleoside triphosphate binding GO:0032559 (0.49) adenyl ribonucleotide binding GO:0032550 (0.49) purine ribonucleoside binding GO:0016740 (0.37) transferase activity GO:0004872 (0.37) receptor activity GO:0016787 (0.35) hydrolase activity GO:0004888 (0.35) transmembrane signaling receptor activity GO:0004672 (0.35) protein kinase activity GO:0008186 (0.31) RNA-dependent ATPase activity GO:0008026 (0.31) ATP-dependent helicase activity GO:0003724 (0.31) RNA helicase activity	**GO:0032502 (0.67) developmental process** **GO:0044767 (0.63) single-organism developmental process** **GO:0048856 (0.54) anatomical structure development** **GO:0048869 (0.52) cellular developmental process** GO:0006928 (0.40) movement of cell or subcellular component GO:0016043 (0.39) cellular component organization GO:0019538 (0.36) protein metabolic process GO:0006464 (0.35) cellular protein modification process GO:0009653 (0.34) anatomical structure morphogenesis GO:0006796 (0.34) phosphate-containing compound metabolic process GO:0051239 (0.32) regulation of multicellular organismal process GO:0007411 (0.32) axon guidance GO:2000026 (0.30) regulation of multicellular organismal development GO:0051128 (0.30) regulation of cellular component organization GO:0016310 (0.30) phosphorylation	**GO:0005634 (0.96) nucleus**
27	NX_Q9C073-1, FAM117A. (FAM117A)	**GO:0022891 (0.51) substrate-specific transmembrane transporter activity** GO:0005459 (0.40) UDP-galactose transmembrane transporter activity	GO:0032501 (0.48) multicellular organismal process GO:0044767 (0.46) single-organism developmental process GO:0048856 (0.44) anatomical structure development GO:0048869 (0.42) cellular developmental process GO:0003008 (0.40) system process GO:0051179 (0.37) localization GO:0072015 (0.36) glomerular visceral epithelial cell development GO:0006810 (0.36) transport GO:0003094 (0.36) glomerular filtration	**GO:0005737 (0.57) cytoplasm**
28	NX_O14894-1, TM4SF5. (Transmembrane 4 L6 family member 5)	**GO:0015370 (0.50) solute:sodium symporter activity** **GO:0005326 (0.50) neurotransmitter transporter activity**	**GO:0048856 (1.00) anatomical structure development** **GO:0044767 (1.00) single-organism developmental process** **GO:2000227 (0.64) negative regulation of pancreatic A cell differentiation** **GO:2000077 (0.64) negative regulation of type B pancreatic cell development** **GO:0090104 (0.64) pancreatic epsilon cell differentiation** **GO:0031018 (0.64) endocrine pancreas development** GO:0042246 (0.36) tissue regeneration GO:0044765 (0.34) single-organism transport	**GO:0016021 (1.00) integral component of membrane**
29	NX_Q96MC4-1, CEP295NL. (CEP295 N-terminal-like protein)	**GO:0016740 (0.50) transferase activity** GO:0036094 (0.45) small molecule binding GO:1901981 (0.44) phosphatidylinositol phosphate	**GO:0051128 (0.64) regulation of cellular component organization** **GO:0048518 (0.63) positive regulation of biological process** **GO:0048522 (0.62) positive regulation of cellular process**	**GO:0043234 (0.63) protein complex** **GO:0044430 (0.58) cytoskeletal part** **GO:0005737 (0.53) cytoplasm** GO:0016020 (0.44) membrane

		binding GO:0030234 (0.44) enzyme regulator activity GO:0033218 (0.43) amide binding GO:0030246 (0.43) carbohydrate binding GO:0010485 (0.43) H4 histone acetyltransferase activity GO:0008375 (0.43) acetylglucosaminyltransferase activity	**GO:0033043 (0.61) regulation of organelle organization** **GO:0010638 (0.58) positive regulation of organelle organization** **GO:0016043 (0.55) cellular component organization** **GO:0032502 (0.51) developmental process** GO:0044767 (0.49) single-organism developmental process GO:0051179 (0.48) localization GO:0006996 (0.48) organelle organization GO:0048856 (0.47) anatomical structure development GO:0065008 (0.44) regulation of biological quality GO:0051641 (0.44) cellular localization GO:0022607 (0.44) cellular component assembly GO:0044267 (0.43) cellular protein metabolic process	GO:0005829 (0.43) cytosol GO:0043232 (0.42) intracellular non-membrane-bounded organelle GO:0044428 (0.33) nuclear part GO:0005634 (0.33) nucleus GO:0044450 (0.30) microtubule organizing center part
30	NX_Q9Y2Y6-1, TMEM98. (Transmembrane protein 98)	**GO:0046914 (0.50) transition metal ion binding** **GO:0046906 (0.50) tetrapyrrole binding** **GO:0016676 (0.50) oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor** **GO:0015078 (0.50) hydrogen ion transmembrane transporter activity** **GO:0015002 (0.50) heme-copper terminal oxidase activity** **GO:0009055 (0.50) electron carrier activity**	**GO:0098662 (0.50) inorganic cation transmembrane transport** **GO:0046034 (0.50) ATP metabolic process** **GO:0045333 (0.50) cellular respiration** **GO:0016310 (0.50) phosphorylation** **GO:0015672 (0.50) monovalent inorganic cation transport** **GO:0006818 (0.50) hydrogen transport**	**GO:0005634 (0.52) nucleus** GO:0005783 (0.48) endoplasmic reticulum
31	NX_Q8IZD0-1, SAMD14. (Sterile alpha motif domain-containing protein 14)	GO:0044877 (0.48) macromolecular complex binding GO:0032403 (0.47) protein complex binding GO:0051015 (0.45) actin filament binding GO:1901363 (0.43) heterocyclic compound binding GO:0097159 (0.43) organic cyclic compound binding GO:0043169 (0.42) cation binding GO:0097367 (0.41) carbohydrate derivative binding GO:0017076 (0.41) purine nucleotide binding GO:0035639 (0.40) purine ribonucleoside triphosphate binding GO:0032559 (0.40) adenyl ribonucleotide binding GO:0032550 (0.40) purine ribonucleoside binding GO:0016879 (0.40) ligase activity, forming carbon-nitrogen bonds	**GO:0016043 (0.64) cellular component organization** **GO:0007165 (0.61) signal transduction** GO:0030030 (0.49) cell projection organization GO:0035556 (0.47) intracellular signal transduction GO:0019932 (0.46) second-messenger-mediated signaling GO:0031175 (0.45) neuron projection development GO:0019722 (0.45) calcium-mediated signaling GO:0007015 (0.44) actin filament organization GO:0044710 (0.30) single-organism metabolic process	**GO:0005737 (0.81) cytoplasm** **GO:0043232 (0.61) intracellular non-membrane-bounded organelle** **GO:0097458 (0.53) neuron part** **GO:0042995 (0.51) cell projection** **GO:0044456 (0.50) synapse part** **GO:0043005 (0.50) neuron projection** **GO:0016020 (0.50) membrane** **GO:0005856 (0.50) cytoskeleton** GO:0015629 (0.42) actin cytoskeleton GO:0014069 (0.42) postsynaptic density GO:0030425 (0.38) dendrite GO:0005829 (0.33) cytosol GO:0005739 (0.30) mitochondrion
32	NX_A8MV24-1, C17orf98. (Uncharacterized protein C17orf98)	GO:0015926 (0.48) glucosidase activity	GO:0051275 (0.37) beta-glucan catabolic process GO:0030243 (0.37) cellulose metabolic process	**GO:0005576 (0.75) extracellular region**
33	NX_Q8IYN6-1, UBALD2. (UBA-like domain-containing protein	GO:1901363 (0.46) heterocyclic compound binding GO:0097159 (0.46) organic cyclic compound binding	**GO:0044248 (0.53) cellular catabolic process** GO:0050896 (0.44) response to stimulus GO:0044710 (0.41) single-organism	**GO:0005576 (0.55) extracellular region** GO:0043234 (0.44) protein complex GO:0005634 (0.43) nucleus

	2)	GO:0043169 (0.41) cation binding GO:0016491 (0.40) oxidoreductase activity GO:0046906 (0.39) tetrapyrrole binding GO:0016684 (0.39) oxidoreductase activity, acting on peroxide as acceptor GO:0016209 (0.39) antioxidant activity	metabolic process GO:0006950 (0.41) response to stress GO:1990748 (0.39) cellular detoxification GO:0042743 (0.39) hydrogen peroxide metabolic process GO:0016043 (0.38) cellular component organization	GO:0044428 (0.42) nuclear part GO:0044451 (0.36) nucleoplasm part GO:0005737 (0.31) cytoplasm GO:0005829 (0.30) cytosol
34	NX_Q86X02-1, CDR2L. (Cerebellar degeneration-related protein 2-like)	GO:0016787 (0.46) hydrolase activity GO:0017111 (0.45) nucleoside-triphosphatase activity GO:0008092 (0.37) cytoskeletal protein binding GO:1901363 (0.35) heterocyclic compound binding GO:0097159 (0.35) organic cyclic compound binding GO:0035639 (0.33) purine ribonucleoside triphosphate binding GO:0032559 (0.33) adenyl ribonucleotide binding GO:0032550 (0.33) purine ribonucleoside binding	**GO:0016043 (0.52) cellular component organization** GO:0006996 (0.44) organelle organization GO:0022607 (0.37) cellular component assembly GO:0007010 (0.36) cytoskeleton organization GO:0070925 (0.33) organelle assembly GO:0043933 (0.31) macromolecular complex subunit organization GO:0043623 (0.30) cellular protein complex assembly	**GO:0044430 (0.87) cytoskeletal part** **GO:0005737 (0.80) cytoplasm** **GO:0043234 (0.64) protein complex** **GO:0043232 (0.61) intracellular non-membrane-bounded organelle** **GO:0016459 (0.54) myosin complex** GO:0016020 (0.49) membrane GO:0042995 (0.32) cell projection GO:0032982 (0.31) myosin filament GO:0031988 (0.30) membrane-bounded vesicle
35	NX_B2RV13-1, C17orf105. (Uncharacterized protein C17orf105)	GO:0016740 (0.44) transferase activity GO:0004842 (0.41) ubiquitin-protein transferase activity GO:0004185 (0.36) serine-type carboxypeptidase activity GO:0004181 (0.36) metallocarboxypeptidase activity	**GO:0019538 (0.94) protein metabolic process** **GO:0006464 (0.51) cellular protein modification process** GO:0042787 (0.49) protein ubiquitination involved in ubiquitin-dependent protein catabolic process GO:1901564 (0.47) organonitrogen compound metabolic process GO:0043603 (0.47) cellular amide metabolic process GO:0016485 (0.44) protein processing GO:0006518 (0.44) peptide metabolic process	**GO:0005737 (0.88) cytoplasm** **GO:0005634 (0.81) nucleus** **GO:0005829 (0.76) cytosol** **GO:0044428 (0.54) nuclear part** **GO:0016020 (0.51) membrane** **GO:0005654 (0.51) nucleoplasm** GO:0044421 (0.48) extracellular region part GO:0044454 (0.45) nuclear chromosome part GO:0005615 (0.44) extracellular space GO:0000790 (0.41) nuclear chromatin
36	NX_Q2TAC2-1, CCDC57. (Coiled-coil domain-containing protein 57)	GO:0097367 (0.44) carbohydrate derivative binding GO:0035639 (0.41) purine ribonucleoside triphosphate binding GO:0032559 (0.41) adenyl ribonucleotide binding GO:0032550 (0.41) purine ribonucleoside binding GO:0052813 (0.31) phosphatidylinositol bisphosphate kinase activity GO:0052742 (0.31) phosphatidylinositol kinase activity GO:0035004 (0.31) phosphatidylinositol 3-kinase activity GO:0016307 (0.31) phosphatidylinositol phosphate kinase activity	**GO:0016043 (0.56) cellular component organization** **GO:0048518 (0.50) positive regulation of biological process** GO:0060255 (0.48) regulation of macromolecule metabolic process GO:0010604 (0.46) positive regulation of macromolecule metabolic process GO:0035556 (0.43) intracellular signal transduction GO:0010468 (0.43) regulation of gene expression GO:0048017 (0.41) inositol lipid-mediated signaling GO:1901576 (0.34) organic substance biosynthetic process GO:0044249 (0.34) cellular biosynthetic process GO:0032502 (0.34) developmental process GO:0044767 (0.33) single-organism developmental process GO:0006796 (0.33) phosphate-containing compound metabolic process GO:0044710 (0.32) single-organism metabolic process GO:0016310 (0.32) phosphorylation GO:0046834 (0.31) lipid phosphorylation	**GO:0016020 (1.00) membrane** **GO:0043234 (0.90) protein complex** **GO:0005942 (0.85) phosphatidylinositol 3-kinase complex** **GO:0005737 (0.74) cytoplasm** **GO:0005886 (0.69) plasma membrane** **GO:0005829 (0.60) cytosol** GO:0044430 (0.47) cytoskeletal part GO:0044421 (0.35) extracellular region part GO:0005773 (0.34) vacuole GO:0044428 (0.33) nuclear part GO:0043232 (0.32) intracellular non-membrane-bounded organelle GO:0042995 (0.32) cell projection GO:0031982 (0.32) vesicle GO:0031988 (0.31) membrane-bounded vesicle GO:0005634 (0.30) nucleus
37	NX_Q8N3J3-1,	GO:0016787 (0.43) hydrolase	**GO:0016043 (0.62) cellular component**	**GO:0005576 (0.91) extracellular**

	C17orf53. (Uncharacterized protein C17orf53)	activity GO:0004175 (0.37) endopeptidase activity GO:0004252 (0.36) serine-type endopeptidase activity	**organization** **GO:0048518 (0.60) positive regulation of biological process** **GO:0051179 (0.58) localization** **GO:0048519 (0.58) negative regulation of biological process** **GO:0065008 (0.57) regulation of biological quality** **GO:0048523 (0.57) negative regulation of cellular process** **GO:0006810 (0.57) transport** **GO:0051239 (0.54) regulation of multicellular organismal process** **GO:0048583 (0.54) regulation of response to stimulus** **GO:1902578 (0.53) single-organism localization** **GO:0048584 (0.52) positive regulation of response to stimulus** **GO:0044765 (0.52) single-organism transport** **GO:0016192 (0.52) vesicle-mediated transport** **GO:0051240 (0.51) positive regulation of multicellular organismal process** **GO:0042127 (0.51) regulation of cell proliferation**	**region** **GO:0044421 (0.70) extracellular region part** **GO:0005615 (0.67) extracellular space** **GO:0031982 (0.55) vesicle** **GO:0031988 (0.54) membrane-bounded vesicle** **GO:0070062 (0.53) extracellular exosome** **GO:0016020 (0.53) membrane** GO:0005886 (0.36) plasma membrane GO:0005737 (0.30) cytoplasm
38	NX_Q9BSJ5-1, C17orf80. (Uncharacterized protein C17orf80)	GO:1901363 (0.43) heterocyclic compound binding GO:0097159 (0.43) organic cyclic compound binding GO:0097367 (0.40) carbohydrate derivative binding GO:0035639 (0.39) purine ribonucleoside triphosphate binding GO:0032559 (0.39) adenyl ribonucleotide binding GO:0032550 (0.39) purine ribonucleoside binding GO:0008092 (0.35) cytoskeletal protein binding GO:0003676 (0.35) nucleic acid binding GO:0043169 (0.30) cation binding	GO:0032501 (0.47) multicellular organismal process GO:0044767 (0.46) single-organism developmental process GO:0016043 (0.46) cellular component organization GO:0065008 (0.44) regulation of biological quality GO:0044707 (0.37) single-multicellular organism process GO:0006996 (0.33) organelle organization GO:0051239 (0.30) regulation of multicellular organismal process	**GO:0070062 (0.97) extracellular exosome**
39	NX_Q96N21-1, TEPSIN. (AP-4 complex accessory subunit Tepsin)	GO:0043167 (0.43) ion binding GO:0043169 (0.42) cation binding		**GO:0043234 (0.63) protein complex** **GO:0005737 (0.60) cytoplasm** GO:0016020 (0.41) membrane GO:0044428 (0.38) nuclear part GO:0043232 (0.33) intracellular non-membrane-bounded organelle GO:1902494 (0.32) catalytic complex GO:1990234 (0.31) transferase complex GO:0005634 (0.30) nucleus
40	NX_Q71RG4-1, TMUB2. (Transmembrane and ubiquitin-like domain-containing protein 2)	GO:1990841 (0.41) promoter-specific chromatin binding GO:0051718 (0.41) DNA (cytosine-5-)-methyltransferase activity, acting on CpG substrates GO:0045322 (0.41) unmethylated CpG binding GO:0042826 (0.41) histone deacetylase binding GO:0030331 (0.41) estrogen receptor binding GO:0019904 (0.41) protein	**GO:0019538 (0.78) protein metabolic process** **GO:0019941 (0.63) modification-dependent protein catabolic process** **GO:0006511 (0.62) ubiquitin-dependent protein catabolic process** **GO:0043412 (0.56) macromolecule modification** **GO:0071840 (0.54) cellular component organization or biogenesis** **GO:0016043 (0.53) cellular component organization**	**GO:0005634 (1.00) nucleus** **GO:0044428 (0.89) nuclear part** **GO:0005737 (0.81) cytoplasm** **GO:0005654 (0.79) nucleoplasm** **GO:0043234 (0.64) protein complex** GO:0044427 (0.44) chromosomal part GO:0043025 (0.44) neuronal cell body GO:0005721 (0.43) pericentric heterochromatin

		domain specific binding GO:0008327 (0.41) methyl-CpG binding GO:0008270 (0.41) zinc ion binding GO:0003723 (0.41) RNA binding GO:0003690 (0.41) double-stranded DNA binding	GO:0048519 (0.49) negative regulation of biological process GO:0080090 (0.48) regulation of primary metabolic process GO:0060255 (0.48) regulation of macromolecule metabolic process GO:0090304 (0.47) nucleic acid metabolic process GO:0051246 (0.47) regulation of protein metabolic process GO:0050896 (0.47) response to stimulus GO:0048523 (0.47) negative regulation of cellular process GO:0043161 (0.47) proteasome-mediated ubiquitin-dependent protein catabolic process GO:0031323 (0.47) regulation of cellular metabolic process	GO:0005657 (0.43) replication fork
41	NX_P84157-1, MXRA7. (Matrix-remodeling-associated protein 7)	GO:0003676 (0.40) nucleic acid binding	GO:0050896 (0.43) response to stimulus GO:0051716 (0.37) cellular response to stimulus GO:0006950 (0.31) response to stress	**GO:0005634 (0.59) nucleus** **GO:0044428 (0.53) nuclear part** GO:0009986 (0.30) cell surface
42	NX_Q86X59-1, C17orf82. (Putative uncharacterized protein C17orf82)	GO:0015926 (0.39) glucosidase activity GO:0003676 (0.34) nucleic acid binding	**GO:0016043 (0.55) cellular component organization** **GO:0032502 (0.52) developmental process** GO:0048856 (0.48) anatomical structure development GO:0051179 (0.45) localization GO:0006810 (0.44) transport GO:0043933 (0.42) macromolecular complex subunit organization GO:0022607 (0.42) cellular component assembly GO:0065003 (0.39) macromolecular complex assembly GO:0051641 (0.39) cellular localization GO:0051649 (0.38) establishment of localization in cell GO:0048731 (0.38) system development GO:0006139 (0.38) nucleobase-containing compound metabolic process GO:0090304 (0.37) nucleic acid metabolic process GO:0034622 (0.37) cellular macromolecular complex assembly GO:0046907 (0.36) intracellular transport	**GO:0005576 (0.53) extracellular region** GO:0016020 (0.48) membrane GO:0005737 (0.44) cytoplasm GO:0043234 (0.39) protein complex GO:0005886 (0.33) plasma membrane
43	NX_Q8WXE0-1, CASKIN2. (Caskin-2)	GO:0016740 (0.39) transferase activity GO:0019899 (0.31) enzyme binding	GO:0007165 (0.41) signal transduction	**GO:0005737 (0.60) cytoplasm** GO:0005634 (0.36) nucleus
44	NX_O43760-1, SYNGR2. (Synaptogyrin-2)	GO:0043169 (0.37) cation binding	**GO:0006810 (0.66) transport** **GO:0051649 (0.64) establishment of localization in cell** **GO:0051641 (0.64) cellular localization** **GO:0006605 (0.52) protein targeting** GO:0051049 (0.31) regulation of transport	**GO:0031594 (1.00) neuromuscular junction** **GO:0030672 (1.00) synaptic vesicle membrane**
45	NX_Q8NAA5-1, LRRC75A. (Leucine-rich repeat-containing protein 75A)	GO:0030234 (0.37) enzyme regulator activity GO:0004857 (0.36) enzyme inhibitor activity	GO:0044767 (0.48) single-organism developmental process GO:0065009 (0.45) regulation of molecular function GO:0050790 (0.44) regulation of catalytic activity GO:0051239 (0.43) regulation of multicellular organismal process GO:0019222 (0.40) regulation of metabolic process GO:0048518 (0.39) positive regulation of	**GO:0005737 (0.69) cytoplasm** **GO:0043234 (0.58) protein complex** **GO:0016020 (0.57) membrane** GO:0005886 (0.45) plasma membrane GO:0044421 (0.38) extracellular region part GO:0005634 (0.37) nucleus GO:0031988 (0.36) membrane-bounded vesicle

			biological process GO:0044092 (0.39) negative regulation of molecular function GO:0009057 (0.39) macromolecule catabolic process GO:0060255 (0.38) regulation of macromolecule metabolic process GO:0050793 (0.38) regulation of developmental process GO:0031323 (0.38) regulation of cellular metabolic process GO:2000026 (0.37) regulation of multicellular organismal development GO:0090304 (0.37) nucleic acid metabolic process GO:0044265 (0.37) cellular macromolecule catabolic process GO:0080090 (0.36) regulation of primary metabolic process	GO:0070062 (0.35) extracellular exosome GO:0031224 (0.32) intrinsic component of membrane GO:0044428 (0.31) nuclear part
46	NX_P34910-1, EVI2B. (EVI2B)	GO:0005198 (0.37) structural molecule activity	GO:0051179 (0.43) localization GO:0051234 (0.42) establishment of localization GO:0006810 (0.41) transport GO:0051649 (0.39) establishment of localization in cell GO:0051641 (0.39) cellular localization GO:0046907 (0.37) intracellular transport GO:0071702 (0.34) organic substance transport GO:0051169 (0.33) nuclear transport GO:0050658 (0.32) RNA transport GO:0045184 (0.32) establishment of protein localization	**GO:0005887 (1.00) integral component of plasma membrane**
47	NX_Q96A25-1, TMEM106A. (Transmembrane protein 106A)	GO:0008236 (0.36) serine-type peptidase activity GO:0004175 (0.36) endopeptidase activity	**GO:0048813 (1.00) dendrite morphogenesis** **GO:0032418 (1.00) lysosome localization** **GO:0007041 (0.93) lysosomal transport** **GO:0007040 (0.93) lysosome organization**	**GO:0016020 (0.97) membrane**
48	NX_Q8NEP4-1, C17orf47. (Uncharacterized protein C17orf47)	GO:1901363 (0.37) heterocyclic compound binding GO:0097159 (0.37) organic cyclic compound binding GO:0003676 (0.35) nucleic acid binding		**GO:0043234 (0.68) protein complex** GO:0005737 (0.41) cytoplasm GO:1990234 (0.34) transferase complex GO:0043232 (0.33) intracellular non-membrane-bounded organelle GO:0016020 (0.33) membrane
49	NX_Q9NWM3-1, CUEDC1. (CUE domain-containing protein 1)	GO:0022892 (0.35) substrate-specific transporter activity GO:0019899 (0.32) enzyme binding	**GO:0006796 (0.55) phosphate-containing compound metabolic process** **GO:0016310 (0.52) phosphorylation**	**GO:0005634 (0.85) nucleus** **GO:0005737 (0.75) cytoplasm** **GO:0044428 (0.66) nuclear part** **GO:0016020 (0.60) membrane** **GO:0043234 (0.58) protein complex** **GO:0070062 (0.56) extracellular exosome** **GO:0005643 (0.54) nuclear pore** GO:0005829 (0.36) cytosol GO:0005654 (0.30) nucleoplasm
50	NX_Q96QE4-1, LRRC37B. (Leucine-rich repeat-containing protein 37B)	GO:0005215 (0.35) transporter activity GO:0022892 (0.34) substrate-specific transporter activity	GO:0007165 (0.45) signal transduction GO:0032502 (0.42) developmental process GO:0044767 (0.41) single-organism developmental process GO:0051179 (0.35) localization GO:0016043 (0.35) cellular component organization GO:0051641 (0.34) cellular localization GO:0006810 (0.34) transport GO:0051649 (0.33) establishment of localization in cell GO:0008104 (0.33) protein localization	GO:0005737 (0.49) cytoplasm GO:0044421 (0.30) extracellular region part

			GO:0048583 (0.32) regulation of response to stimulus GO:0006886 (0.32) intracellular protein transport GO:0007166 (0.31) cell surface receptor signaling pathway GO:0031323 (0.30) regulation of cellular metabolic process	
51	NX_Q8N6N6-1, NATD1. (NATD1)	GO:0004402 (0.33) histone acetyltransferase activity	**GO:0006473 (0.68) protein acetylation** GO:0018393 (0.44) internal peptidyl-lysine acetylation GO:0001702 (0.37) gastrulation with mouth forming second GO:0016573 (0.35) histone acetylation GO:0006474 (0.35) N-terminal protein amino acid acetylation	**GO:0043234 (0.64) protein complex** **GO:0031248 (0.55) protein acetyltransferase complex** GO:0005737 (0.36) cytoplasm GO:0044428 (0.33) nuclear part GO:0044427 (0.33) chromosomal part GO:0005634 (0.30) nucleus
52	NX_Q71RC9-1, SMIM5. (Small integral membrane protein 5)	GO:0051015 (0.33) actin filament binding GO:0030274 (0.33) LIM domain binding GO:0017166 (0.33) vinculin binding GO:0005200 (0.33) structural constituent of cytoskeleton GO:0005178 (0.33) integrin binding	GO:0098876 (0.48) vesicle-mediated transport to the plasma membrane GO:0071702 (0.48) organic substance transport GO:0051278 (0.48) fungal-type cell wall polysaccharide biosynthetic process GO:0045184 (0.48) establishment of protein localization GO:0030010 (0.48) establishment of cell polarity GO:0006892 (0.48) post-Golgi vesicle-mediated transport GO:0006038 (0.48) cell wall chitin biosynthetic process GO:0000281 (0.48) mitotic cytokinesis GO:0070527 (0.33) platelet aggregation GO:0030866 (0.33) cortical actin cytoskeleton organization GO:0007044 (0.33) cell-substrate junction assembly GO:0007016 (0.33) cytoskeletal anchoring at plasma membrane	**GO:0016020 (0.93) membrane** **GO:0043234 (0.60) protein complex** **GO:0044431 (0.53) Golgi apparatus part** **GO:0005794 (0.53) Golgi apparatus** GO:0031988 (0.47) membrane-bounded vesicle GO:0005737 (0.47) cytoplasm GO:0070062 (0.40) extracellular exosome GO:0044430 (0.40) cytoskeletal part GO:0034044 (0.40) exomer complex GO:0005925 (0.40) focal adhesion GO:0005886 (0.40) plasma membrane GO:0005856 (0.40) cytoskeleton GO:0032587 (0.33) ruffle membrane GO:0009986 (0.33) cell surface GO:0005815 (0.33) microtubule organizing center
53	NX_Q96GE4-1, CEP95. (Centrosomal protein of 95 kDa)	GO:0035639 (0.32) purine ribonucleoside triphosphate binding GO:0032559 (0.32) adenyl ribonucleotide binding GO:0032550 (0.32) purine ribonucleoside binding GO:0003676 (0.32) nucleic acid binding	GO:0016043 (0.38) cellular component organization	**GO:0005813 (1.00) centrosome** **GO:0000922 (1.00) spindle pole**
54	NX_Q9BU68-1, PRR15L. (Proline-rich protein 15-like protein)	GO:0044877 (0.31) macromolecular complex binding GO:0005524 (0.31) ATP binding GO:0004672 (0.31) protein kinase activity	GO:0018108 (0.42) peptidyl-tyrosine phosphorylation GO:0008283 (0.42) cell proliferation GO:0006955 (0.42) immune response GO:0006952 (0.42) defense response GO:2001236 (0.31) regulation of extrinsic apoptotic signaling pathway GO:2001234 (0.31) negative regulation of apoptotic signaling pathway GO:0043068 (0.31) positive regulation of programmed cell death GO:0022610 (0.31) biological adhesion	**GO:0005737 (0.84) cytoplasm** **GO:0016020 (0.74) membrane** **GO:0044459 (0.58) plasma membrane part** **GO:0005829 (0.58) cytosol** GO:0098590 (0.37) plasma membrane region GO:0005886 (0.37) plasma membrane GO:0043234 (0.32) protein complex GO:0005634 (0.32) nucleus
55	NX_A8MU93-1, C17orf100. (Uncharacterized protein C17orf100)		**GO:0030308 (0.84) negative regulation of cell growth**	**GO:0005737 (0.88) cytoplasm** **GO:0005634 (0.81) nucleus** **GO:0043234 (0.77) protein complex** **GO:0016459 (0.76) myosin complex** **GO:0031988 (0.60) membrane-bounded vesicle** **GO:0016020 (0.59) membrane** GO:0042995 (0.44) cell projection

				GO:0016023 (0.44) cytoplasmic, membrane-bounded vesicle GO:0044421 (0.30) extracellular region part GO:0030139 (0.30) endocytic vesicle GO:0005886 (0.30) plasma membrane
56	NX_Q969W3-1, FAM104A. (FAM104A)		**GO:0006950 (0.81) response to stress** **GO:0042276 (0.80) error-prone translesion synthesis**	**GO:0043234 (0.85) protein complex** **GO:0005634 (0.84) nucleus** **GO:0061695 (0.81) transferase complex, transferring phosphorus-containing groups** **GO:0016035 (0.80) zeta DNA polymerase complex** **GO:0005829 (0.68) cytosol** **GO:0016020 (0.57) membrane** **GO:0005737 (0.57) cytoplasm** **GO:0031982 (0.51) vesicle** **GO:0005886 (0.51) plasma membrane** GO:0043232 (0.45) intracellular non-membrane-bounded organelle GO:0031410 (0.45) cytoplasmic vesicle GO:0030054 (0.45) cell junction GO:0044459 (0.40) plasma membrane part GO:0031988 (0.40) membrane-bounded vesicle GO:0005773 (0.40) vacuole
57	NX_P0DI83-1, RAB34. (Ras-related protein Rab-34, isoform NARR)		**GO:0032502 (0.51) developmental process** GO:0016043 (0.32) cellular component organization GO:0080090 (0.31) regulation of primary metabolic process GO:0060255 (0.31) regulation of macromolecule metabolic process GO:0031323 (0.31) regulation of cellular metabolic process GO:0031326 (0.30) regulation of cellular biosynthetic process	GO:0016020 (0.46) membrane GO:0043234 (0.43) protein complex GO:0031224 (0.36) intrinsic component of membrane GO:0016021 (0.31) integral component of membrane
58	NX_O60309-1, LRRC37A3. (Leucine-rich repeat-containing protein 37A3)		GO:0007165 (0.47) signal transduction GO:0032502 (0.45) developmental process GO:0044767 (0.44) single-organism developmental process GO:0016043 (0.35) cellular component organization GO:0048583 (0.34) regulation of response to stimulus GO:0007166 (0.32) cell surface receptor signaling pathway GO:0009653 (0.31) anatomical structure morphogenesis GO:0019222 (0.30) regulation of metabolic process	GO:0005737 (0.38) cytoplasm
59	NX_A6NM11-1, LRRC37A2. (Leucine-rich repeat-containing protein 37A2)		GO:0007165 (0.45) signal transduction GO:0032502 (0.44) developmental process GO:0044767 (0.42) single-organism developmental process GO:0016043 (0.35) cellular component organization GO:0048583 (0.32) regulation of response to stimulus GO:0007166 (0.30) cell surface receptor signaling pathway	GO:0005737 (0.37) cytoplasm
60	NX_Q96MW1-1, CCDC43. (Coiled-coil		GO:0006810 (0.44) transport GO:0046907 (0.41) intracellular transport GO:0006886 (0.38) intracellular protein	**GO:0005829 (0.70) cytosol** **GO:0044428 (0.66) nuclear part** **GO:0005737 (0.53) cytoplasm**

	domain-containing protein 43)		transport GO:0006606 (0.35) protein import into nucleus GO:0006607 (0.32) NLS-bearing protein import into nucleus	**GO:0005654 (0.51) nucleoplasm** **GO:0016020 (0.50) membrane** GO:0043234 (0.43) protein complex GO:0043228 (0.37) non-membrane-bounded organelle GO:0031090 (0.37) organelle membrane GO:0005643 (0.35) nuclear pore GO:0044463 (0.33) cell projection part GO:0043232 (0.32) intracellular non-membrane-bounded organelle GO:0030054 (0.31) cell junction
61	NX_A6NMS7-1, LRRC37A. (Leucine-rich repeat-containing protein 37A)		GO:0032502 (0.44) developmental process GO:0007165 (0.44) signal transduction GO:0044767 (0.42) single-organism developmental process GO:0016043 (0.35) cellular component organization GO:0048583 (0.32) regulation of response to stimulus GO:0007166 (0.30) cell surface receptor signaling pathway	GO:0005737 (0.38) cytoplasm
62	NX_Q9H0J4-1, QRICH2. (Glutamine-rich protein 2)		GO:0016043 (0.43) cellular component organization GO:0006996 (0.31) organelle organization GO:0007017 (0.30) microtubule-based process	GO:0044430 (0.40) cytoskeletal part GO:0043234 (0.36) protein complex
63	NX_A4FU69-1, EFCAB5. (EF-hand calcium-binding domain-containing protein 5)		GO:0016043 (0.40) cellular component organization GO:0032502 (0.32) developmental process GO:0044767 (0.31) single-organism developmental process	
64	NX_Q2M2W7-1, C17orf58. (UPF0450 protein C17orf58)		GO:0052548 (0.37) regulation of endopeptidase activity GO:0010466 (0.37) negative regulation of peptidase activity	**GO:0005615 (0.67) extracellular space** **GO:0005576 (0.67) extracellular region** **GO:0031988 (0.60) membrane-bounded vesicle** **GO:0070062 (0.53) extracellular exosome** GO:0016020 (0.33) membrane
65	NX_Q0P670-1, SPEM2. (Uncharacterized protein SPEM2)		GO:0044767 (0.36) single-organism developmental process	**GO:0043234 (0.57) protein complex** **GO:0005737 (0.53) cytoplasm** GO:0044428 (0.31) nuclear part GO:0043232 (0.31) intracellular non-membrane-bounded organelle GO:0016020 (0.31) membrane
66	NX_Q8WW18-1, C17orf50. (Uncharacterized protein C17orf50)			**GO:0005737 (1.00) cytoplasm** **GO:0043657 (0.90) host cell** **GO:0070062 (0.77) extracellular exosome** **GO:0016020 (0.77) membrane** **GO:0005829 (0.77) cytosol** **GO:0005634 (0.77) nucleus** **GO:0044428 (0.56) nuclear part** GO:0072372 (0.37) primary cilium GO:0034399 (0.37) nuclear periphery GO:0031965 (0.37) nuclear membrane GO:0015630 (0.37) microtubule cytoskeleton GO:0005739 (0.37) mitochondrion GO:0005694 (0.37) chromosome GO:0000775 (0.37) chromosome, centromeric region GO:0000159 (0.37) protein

				phosphatase type 2A complex