ADVANCED HEALTHCARE MATERIALS

Supporting Information

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Microneedle Patch for Painless Intradermal Collection of Interstitial Fluid Enabling Multianalyte Measurement of Small Molecules, SARS-CoV-2 Antibodies, and Protein Profiling

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Figure S1A illustrates the proposed alternative approach to standard blood sampling based on venipuncture. Firstly, a device is created to enable sampling at the PoC. Secondly, by drying the collected sample in a stable matrix such as analytical-grade paper, the logistics involved can be simplified. Finally, quality and versatility of the sample analysis are guaranteed by employing state-of-the-art equipment in clinical laboratory facilities.

To ensure correct insertion and operation of the disposable sampling device featuring the hollow microneedle, an applicator is required (Figure S1B-C). Both because penetration is not easily achieved manually when using microneedles, and because a driving pressure is then necessary after penetration to extract ISF from the skin. These two functions (insertion and pressure application) can be combined into a single device or be separated. Both solutions were successfully tested in sampling experiments. The applicator operation is based on a spring-loaded mechanism that applies a certain velocity (~3 m s^{-1}) to the disposable device, sufficient to reliably prick the epidermis upon impact and achieve intradermal insertion of the microneedle. Another prototype version of the applicator is illustrated in Figure S1D, where the system can be worn in the form of an armband. Optimized designs of the pressuring ring and the applicator are currently under development, to simultaneously maximize patient comfort and sampling speed. The microneedle size results in painless insertion and its size can be appreciated when compared side-to-side with a hypodermic needle used for venipuncture (Figure S1E). Optimized needle and device designs resulted in bleeding avoidance and thus enabled pure ISF sampling (Figure S1G).

Even for non-quantitative tests where a simple positive/negative answer to the presence of a certain analyte is sufficient (such as in the shown example of COVID-19 antibodies), the proposed color-based solution established for volume-metering (c.f. Figure 2B) and thus for quantitative analysis would still prove valuable. In fact, this would serve even as a simple filling confirmation, both for the patient to know that the procedure has succeeded and can be stopped, and subsequently for the laboratory as a visual quality control of the received sample. For non-quantitative tests (or when the concentration dynamics and magnitudes in the contaminating matrix are close enough to ISF), also the requirement of total absence of contamination by other body matrices becomes less important, while the one regarding exogenous contaminants (e.g. on the skin surface) remains valid.

Figure S2A shows the dilution curve for the measurement of SARS-CoV-2 spike IgG in the samples. Figure 2B-C show the results of the performed characterization using a proximity extension assay (Olink) in DBS and ISF, respectively. 147 of the analyzed targets were found in at least one of the volunteer's samples. Figure S2D show the sample correlation, rho, from different subjects for the detected targets.

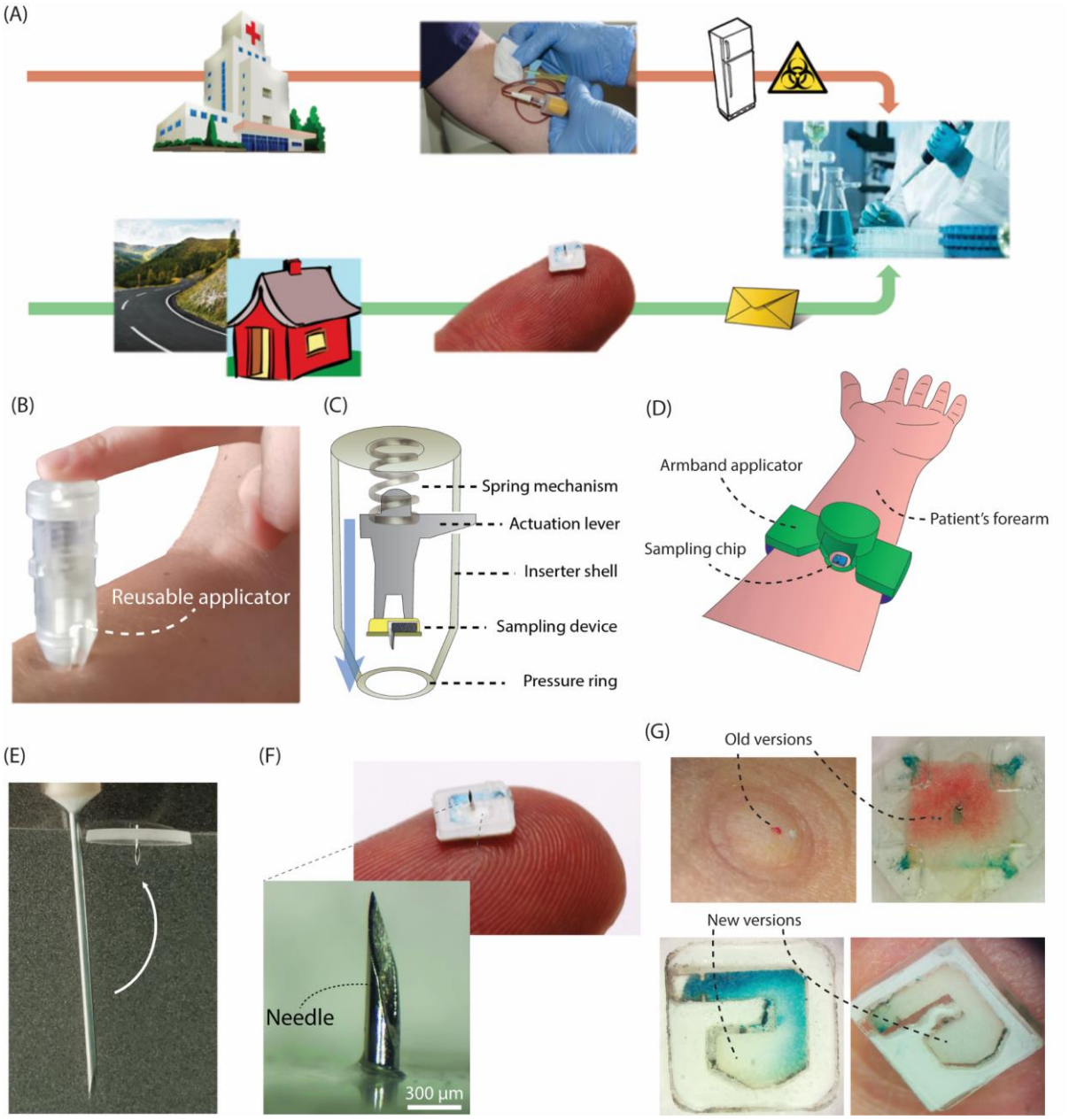

Figure S1. Operation flow and device implementation details. (A) Comparison of workflow between standard blood drawing and the proposed PoC device. (B) Prototype version of the reusable applicator, used to reliably apply the microneedle on the skin via a spring-loaded mechanism, as well as to apply the overpressure required to extract ISF. (C) Cross-section illustration of the spring-loaded applicator. (D) Illustration of a different version of the applicator in the form of an armband, applied to the forearm. The basic mechanism is the same of the applicator shown in Figure1B,C (pen-like format), but here the applied force can be made operator-independent by strapping the system around the forearm. (E) Side-to-side comparison between a hypodermic needle used for venipuncture and a microneedle used in our sampling device. (F) Zoomed-in picture of a microneedle, which can be obtained with conventional hypodermic needle processing and then assembled in the microfluidic device. (G) Effect of needle and device design optimization on avoiding bleeding.

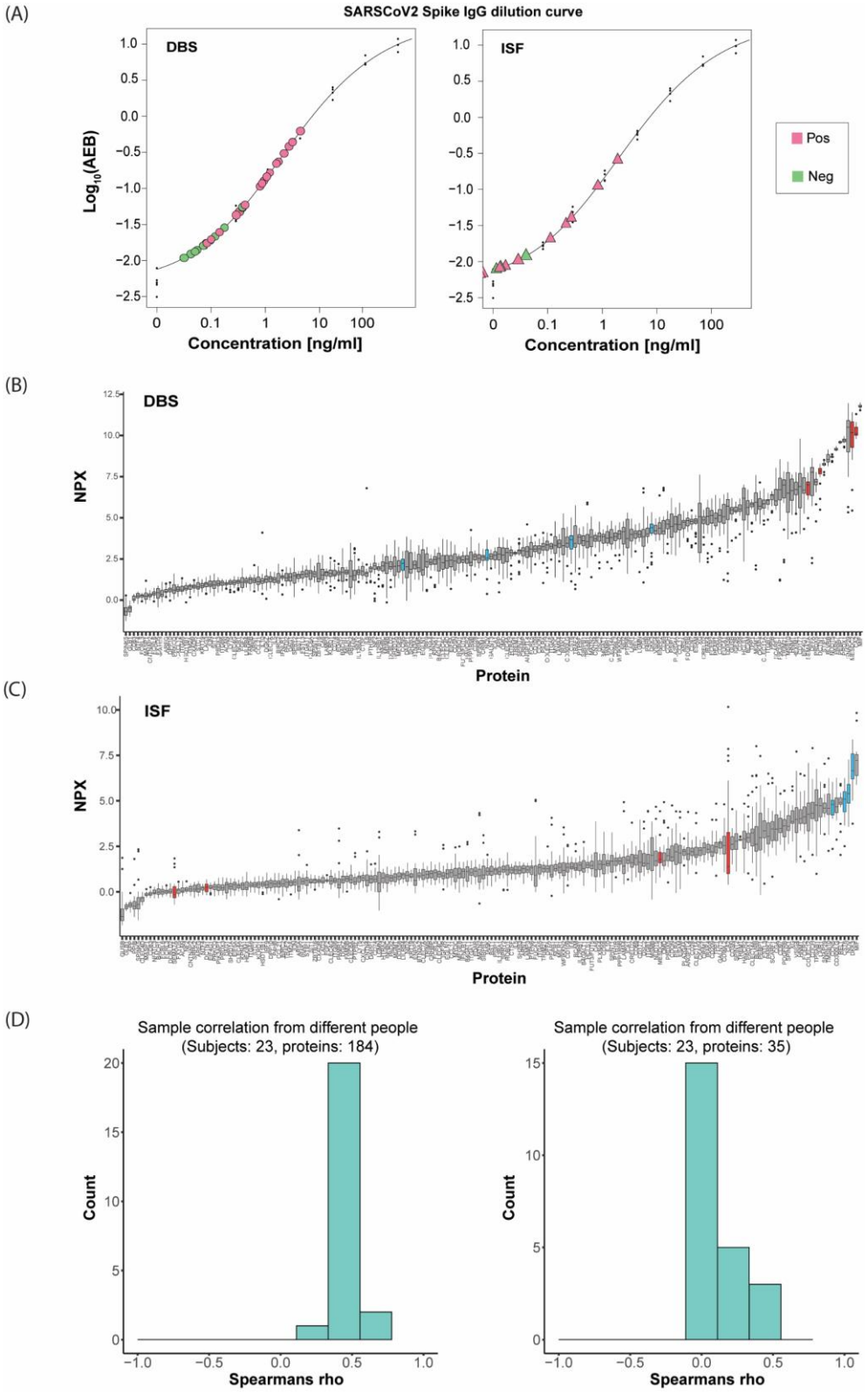

Figure S2. (A) SARS-CoV-2 Spike IgG calibrator curves with DBS samples (left) or ISF microsamples (right). Different colors indicate self-reported serostatus (Pos/Neg) for the sample. (B, C) Visualization of relative protein levels measured with Olink in (A) DBS and (B) ISF micro samples, respectively. The plot shows all the detected protein targets above LOD. The protein targets on the x-axis are sorted in ascending order. (D) Plots of the sample correlation, rho, from different subjects for all targets (left) and targets detected in >90% of the ISF samples (right).

Supporting Table S1

					ISF			DBS				
#	Panel	Assay	Uniprot ID	LOD (NPX)	median (NPX)	above_LOD counts	above_LOD freq (%)	median (NPX)	above_LOD counts	above_LOD freq (%)	Uniprot ID	Entry name
1	Olink Target 96 Development(v.3521)	MIF	P14174	1.25674	7.2496	26	100	11.761380	23	100	P14174	MIF_HUMAN
2	Olink Target 96 Development(v.3521)	DKK3	Q9UBP4	0.58263	6.79847	26	100	4.394830	23	100	Q9UBP4	DKK3_HUMAN
3	Olink Target 96 Development(v.3521)	NOV	P48745	-0.86381	5.534035	26	100	2.553360	23	100	P48745	CCN3_HUMAN
4	Olink Target 96 Development(v.3521)	CST6	Q15828	0.70613	5.111645	26	100	3.670850	23	100	Q15828	CYTM_HUMAN
5	Olink Target 96 Development(v.3521)	RELT	Q969Z4	0.66565	5.044745	26	100	4.046630	23	100	Q969Z4	TR19L_HUMAN
6	Olink Target 96 Development(v.3521)	CCN5	O76076	1.51191	4.922785	26	100	2.232230	19	83	O76076	CCN5_HUMAN
7	Olink Target 96 Development(v.3521)	LAIR1	Q6GTX8	1.97721	4.85102	26	100	3.990840	23	100	Q6GTX8	LAIR1_HUMAN
8	Olink Target 96 Development(v.3521)	TMSB10	P63313	1.68766	4.81259	26	100	6.495940	23	100	P63313	TYB10_HUMAN
9	Olink Target 96 Development(v.3521)	CD300LG	Q6UXG3	0.70142	4.81077	26	100	3.456210	23	100	Q6UXG3	CLM9_HUMAN
10	Olink Target 96 Immune Response(v.3204)	TPSAB1	Q15661	1.00675	4.660875	25	96	3.546030	23	100	Q15661	TRYB1_HUMAN
11	Olink Target 96 Development(v.3521)	SNAP29	O95721	2.39398	4.63025	26	100	10.509830	23	100	O95721	SNP29_HUMAN
12	Olink Target 96 Development(v.3521)	COCH	O43405	1.75772	4.4665	26	100	4.622290	23	100	O43405	COCH_HUMAN
13	Olink Target 96 Development(v.3521)	COLEC12	Q5KU26	1.99986	4.369785	26	100	3.348190	21	91	Q5KU26	COL12_HUMAN
14	Olink Target 96 Development(v.3521)	FCER2	P06734	2.40887	4.232035	25	96	5.123980	23	100	P06734	FCER2_HUMAN
15	Olink Target 96 Immune Response(v.3204)	HNMT	P50135	1.15928	4.17137	26	100	6.651750	23	100	P50135	HNMT_HUMAN
16	Olink Target 96 Development(v.3521)	VSIG4	Q9Y279	0.53604	4.16297	26	100	4.215590	23	100	Q9Y279	VSIG4_HUMAN
17	Olink Target 96 Development(v.3521)	XG	P55808	2.13062	3.997625	26	100	5.069960	23	100	P55808	XG_HUMAN
18	Olink Target 96 Development(v.3521)	SPINK1	P00995	0.54169	3.752935	26	100	2.529010	23	100	P00995	ISK1_HUMAN
19	Olink Target 96 Development(v.3521)	PDGFRB	P09619	1.45523	3.71501	26	100	4.821850	23	100	P09619	PGFRB_HUMAN
20	Olink Target 96 Development(v.3521)	CD97	P48960	2.98684	3.685785	23	88	4.790430	23	100	P48960	AGRE5_HUMAN
21	Olink Target 96 Development(v.3521)	CGA	P01215	0.55555	3.597395	26	100	3.839560	23	100	P01215	GLHA_HUMAN
22	Olink Target 96 Development(v.3521)	SCARF1	Q14162	0.90361	3.469925	25	96	6.025220	23	100	Q14162	SREC_HUMAN
23	Olink Target 96 Development(v.3521)	FSTL3	O95633	1.19873	3.45678	25	96	1.559250	19	83	O95633	FSTL3_HUMAN
24	Olink Target 96 Development(v.3521)	PARK7	Q99497	0.96524	3.33474	26	100	9.144080	23	100	Q99497	PARK7_HUMAN
25	Olink Target 96 Development(v.3521)	PEBP1	P30086	1.40092	3.321945	25	96	9.597420	23	100	P30086	PEBP1_HUMAN
26	Olink Target 96 Development(v.3521)	CLEC14A	Q86T13	0.628	3.31658	26	100	3.793490	23	100	Q86T13	CLC14_HUMAN
27	Olink Target 96 Immune Response(v.3204)	PRDX1	Q06830	0.19554	3.04892	26	100	9.709500	23	100	Q06830	PRDX1_HUMAN
28	Olink Target 96 Development(v.3521)	HAVCR2	Q8TDQ0	1.4805	2.99354	25	96	2.484530	23	100	Q8TDQ0	HAVR2_HUMAN
29	Olink Target 96 Development(v.3521)	SPINT2	O43291	0.55412	2.985535	26	100	2.981550	23	100	O43291	SPIT2_HUMAN
30	Olink Target 96 Immune Response(v.3204)	TREM1	Q9NP99	3.42186	2.847005	0	0	2.857100	0	0	Q9NP99	TREM1_HUMAN
31	Olink Target 96 Immune Response(v.3204)	GALNT3	Q14435	3.26588	2.64337	0	0	2.648210	0	0	Q14435	GALT3_HUMAN
32	Olink Target 96 Development(v.3521)	BLVRB	P30043	0.88696	2.626285	25	96	8.537070	23	100	P30043	BLVRB_HUMAN
33	Olink Target 96 Immune Response(v.3204)	CDSN	Q15517	2.53245	2.625885	16	62	2.365190	10	43	Q15517	CDSN_HUMAN
34	Olink Target 96 Development(v.3521)	CD99L2	Q8TCZ2	1.30242	2.575535	25	96	3.860110	23	100	Q8TCZ2	C99L2_HUMAN
35	Olink Target 96 Development(v.3521)	TPP1	O14773	1.60952	2.55503	25	96	5.827370	23	100	O14773	TPP1_HUMAN
36	Olink Target 96 Development(v.3521)	CRIM1	Q9NZV1	3.07092	2.44858	0	0	2.613900	1	4	Q9NZV1	CRIM1_HUMAN
37	Olink Target 96 Immune Response(v.3204)	IRAK4	Q9NWZ3	2.76266	2.34618	2	8	5.098950	21	91	Q9NWZ3	IRAK4_HUMAN
38	Olink Target 96 Development(v.3521)	PILRA	Q9UKJ1	1.04828	2.30595	25	96	3.247390	22	96	Q9UKJ1	PILRA_HUMAN

39	Olink Target 96 Immune Response(v.3204)	CKAP4	Q07065	2.65282	2.28338	4	15	5.703760	23	100	Q07065	CKAP4_HUMAN
40	Olink Target 96 Development(v.3521)	CD209	Q9NNX6	1.65318	2.26251	23	88	5.140290	23	100	Q9NNX6	CD209_HUMAN
41	Olink Target 96 Development(v.3521)	MSMB	P08118	-0.94299	2.233895	26	100	2.237120	23	100	P08118	MSMB_HUMAN
42	Olink Target 96 Development(v.3521)	PLA2G4A	P47712	3.39678	2.218445	0	0	4.606040	22	96	P47712	PA24A_HUMAN
43	Olink Target 96 Development(v.3521)	ESAM	Q96AP7	0.88027	2.19725	25	96	4.803560	23	100	Q96AP7	ESAM_HUMAN
44	Olink Target 96 Development(v.3521)	ANGPTL4	Q9BY76	1.84172	2.18556	18	69	2.947280	23	100	Q9BY76	ANGL4_HUMAN
45	Olink Target 96 Immune Response(v.3204)	CD28	P10747	2.22549	2.18234	12	46	2.665160	20	87	P10747	CD28_HUMAN
46	Olink Target 96 Development(v.3521)	CLEC11A	Q9Y240	1.22202	2.122195	25	96	5.838460	23	100	Q9Y240	CLC11_HUMAN
47	Olink Target 96 Development(v.3521)	CDON	Q4KMG0	2.16195	2.036795	11	42	3.122840	23	100	Q4KMG0	CDON_HUMAN
48	Olink Target 96 Development(v.3521)	MESDC2	Q14696	1.9723	2.02835	14	54	10.176610	23	100	Q14696	MESD_HUMAN
49	Olink Target 96 Immune Response(v.3204)	PRDX5	P30044	1.25608	1.93654	25	96	7.189020	23	100	P30044	PRDX5_HUMAN
50	Olink Target 96 Development(v.3521)	CD177	Q8N6Q3	1.50512	1.92597	15	58	6.899480	23	100	Q8N6Q3	CD177_HUMAN
51	Olink Target 96 Development(v.3521)	NUDT5	Q9UKK9	1.86471	1.868125	13	50	8.709860	23	100	Q9UKK9	NUDT5_HUMAN
52	Olink Target 96 Development(v.3521)	CD69	Q07108	2.53793	1.861215	0	0	4.192860	23	100	Q07108	CD69_HUMAN
53	Olink Target 96 Development(v.3521)	OMD	Q99983	1.37572	1.739935	21	81	2.739890	22	96	Q99983	OMD_HUMAN
54	Olink Target 96 Development(v.3521)	SPINT1	O43278	0.39954	1.714765	25	96	1.587390	23	100	O43278	SPIT1_HUMAN
55	Olink Target 96 Immune Response(v.3204)	ICA1	Q05084	2.12744	1.714055	3	12	2.731100	19	83	Q05084	ICA69_HUMAN
56	Olink Target 96 Development(v.3521)	CRELD2	Q6UXH1	1.3868	1.69701	20	77	4.864710	23	100	Q6UXH1	CREL2_HUMAN
57	Olink Target 96 Immune Response(v.3204)	PPP1R9B	Q96SB3	2.18812	1.67353	0	0	2.296710	13	57	Q96SB3	NEB2_HUMAN
58	Olink Target 96 Development(v.3521)	DSC2	Q02487	2.0469	1.66173	11	42	3.861040	22	96	Q02487	DSC2_HUMAN
59	Olink Target 96 Development(v.3521)	ITGB1	P05556	1.26745	1.64993	19	73	6.041870	23	100	P05556	ITB1_HUMAN
60	Olink Target 96 Immune Response(v.3204)	PTH1R	Q03431	2.1178	1.649775	2	8	1.911510	2	9	Q03431	PTH1R_HUMAN
61	Olink Target 96 Development(v.3521)	LAMA4	Q16363	1.15621	1.565905	18	69	3.441900	23	100	Q16363	LAMA4_HUMAN
62	Olink Target 96 Immune Response(v.3204)	IL10	P22301	2.1882	1.527065	0	0	1.146080	1	4	P22301	IL10_HUMAN
63	Olink Target 96 Development(v.3521)	CD58	P19256	0.60114	1.52617	24	92	5.530030	23	100	P19256	LFA3_HUMAN
64	Olink Target 96 Immune Response(v.3204)	PLXNA4	Q9HCM2	1.71577	1.522915	6	23	2.297460	22	96	Q9HCM2	PLXA4_HUMAN
65	Olink Target 96 Development(v.3521)	FUT3/FUT5	Q11128, P21217	2.67888	1.465655	0	0	2.445170	6	26	Q11128,P21217	FUT5_HUMAN
66	Olink Target 96 Immune Response(v.3204)	IL12RB1	P42701	1.82628	1.43986	1	4	1.933100	18	78	P42701	I12R1_HUMAN
67	Olink Target 96 Development(v.3521)	CD109	Q6YHK3	3.16451	1.41911	0	0	3.087190	8	35	Q6YHK3	CD109_HUMAN
68	Olink Target 96 Development(v.3521)	ITGA5	P08648	1.8611	1.418935	1	4	3.268710	23	100	P08648	ITA5_HUMAN
69	Olink Target 96 Immune Response(v.3204)	HCLS1	P14317	1.81006	1.416885	1	4	6.185740	23	100	P14317	HCLS1_HUMAN
70	Olink Target 96 Immune Response(v.3204)	IL6	P05231	1.76011	1.37292	4	15	1.604410	4	17	P05231	IL6_HUMAN
71	Olink Target 96 Development(v.3521)	BCAM	P50895	1.62528	1.37109	8	31	5.627980	23	100	P50895	BCAM_HUMAN
72	Olink Target 96 Immune Response(v.3204)	MILR1	Q7Z6M3	1.4044	1.348185	10	38	1.698560	20	87	Q7Z6M3	MILR1_HUMAN
73	Olink Target 96 Development(v.3521)	CA6	P23280	0.36957	1.335085	24	92	1.522630	23	100	P23280	CAH6_HUMAN
74	Olink Target 96 Development(v.3521)	B4GALT1	P15291	1.13917	1.33484	19	73	2.518140	21	91	P15291	B4GT1_HUMAN
75	Olink Target 96 Development(v.3521)	WFIKKN2	Q8TEU8	0.4612	1.31989	24	92	4.014920	23	100	Q8TEU8	WFKN2_HUMAN
76	Olink Target 96 Development(v.3521)	PTPN6	P29350	1.99527	1.30523	0	0	3.738260	21	91	P29350	PTN6_HUMAN
77	Olink Target 96 Immune Response(v.3204)	DFFA	O00273	1.00201	1.287205	22	85	7.767850	23	100	O00273	DFFA_HUMAN
78	Olink Target 96 Immune Response(v.3204)	ARNT	P27540	1.92105	1.277245	0	0	1.195100	1	4	P27540	ARNT_HUMAN
79	Olink Target 96 Development(v.3521)	ROBO1	Q9Y6N7	1.65457	1.258485	6	23	2.524220	23	100	Q9Y6N7	ROBO1_HUMAN
80	Olink Target 96 Immune Response(v.3204)	NCR1	O76036	0.92006	1.23822	24	92	1.131280	18	78	O76036	NCTR1_HUMAN

81	Olink Target 96 Development(v.3521)	CTSF	Q9UBX1	1.6618	1.233685	1	4	1.749390	15	65	Q9UBX1	CATF_HUMAN
82	Olink Target 96 Immune Response(v.3204)	TRIM21	P19474	1.61989	1.21965	1	4	6.997010	23	100	P19474	RO52_HUMAN
83	Olink Target 96 Immune Response(v.3204)	SPRY2	O43597	1.95713	1.21926	0	0	1.484740	4	17	O43597	SPY2_HUMAN
84	Olink Target 96 Development(v.3521)	IL13RA1	P78552	1.67584	1.207755	4	15	1.700020	12	52	P78552	I13R1_HUMAN
85	Olink Target 96 Immune Response(v.3204)	IL5	P05113	1.69867	1.181025	0	0	1.258680	1	4	P05113	IL5_HUMAN
86	Olink Target 96 Immune Response(v.3204)	SH2B3	Q9UQQ2	2.51949	1.170495	0	0	1.881810	7	30	Q9UQQ2	SH2B3_HUMAN
87	Olink Target 96 Immune Response(v.3204)	PSIP1	O75475	1.46836	1.17005	3	12	4.484110	23	100	O75475	PSIP1_HUMAN
88	Olink Target 96 Immune Response(v.3204)	LAMP3	Q9UQV4	1.47549	1.1626	3	12	1.675000	17	74	Q9UQV4	LAMP3_HUMAN
89	Olink Target 96 Development(v.3521)	MFGE8	Q08431	2.60631	1.155255	1	4	2.077920	3	13	Q08431	MFGM_HUMAN
90	Olink Target 96 Development(v.3521)	B4GAT1	O43505	0.65723	1.14835	16	62	3.856570	23	100	O43505	B4GA1_HUMAN
91	Olink Target 96 Development(v.3521)	CA2	P00918	1.33659	1.140265	12	46	10.112880	23	100	P00918	CAH2_HUMAN
92	Olink Target 96 Development(v.3521)	BST1	Q10588	1.59957	1.126025	1	4	1.481550	5	22	Q10588	BST1_HUMAN
93	Olink Target 96 Immune Response(v.3204)	EDAR	Q9UNE0	1.27721	1.112325	8	31	1.662910	21	91	Q9UNE0	EDAR_HUMAN
94	Olink Target 96 Immune Response(v.3204)	TANK	Q92844	2.18838	1.104385	0	0	1.501530	5	22	Q92844	TANK_HUMAN
95	Olink Target 96 Immune Response(v.3204)	IFNLR1	Q8IU57	1.13259	1.088095	11	42	1.414610	20	87	Q8IU57	INLR1_HUMAN
96	Olink Target 96 Development(v.3521)	FCRL5	Q96RD9	1.40186	1.08652	3	12	3.093820	23	100	Q96RD9	FCRL5_HUMAN
97	Olink Target 96 Development(v.3521)	MATN2	O00339	0.64391	1.08641	19	73	3.825710	23	100	O00339	MATN2_HUMAN
98	Olink Target 96 Development(v.3521)	MYOC	Q99972	1.03633	1.08027	14	54	3.327170	23	100	Q99972	MYOC_HUMAN
99	Olink Target 96 Immune Response(v.3204)	CCL11	P51671	1.14523	1.058165	9	35	4.586070	23	100	P51671	CCL11_HUMAN
100	Olink Target 96 Development(v.3521)	FUCA1	P04066	1.13268	1.047895	12	46	5.069530	23	100	P04066	FUCO_HUMAN
101	Olink Target 96 Immune Response(v.3204)	ITGA11	Q9UKX5	1.15251	1.035475	9	35	1.584870	21	91	Q9UKX5	ITA11_HUMAN
102	Olink Target 96 Development(v.3521)	CRHBP	P24387	1.31351	1.033895	4	15	3.005300	23	100	P24387	CRHBP_HUMAN
103	Olink Target 96 Development(v.3521)	PEAR1	Q5VY43	1.08394	1.029995	13	50	4.960450	23	100	Q5VY43	PEAR1_HUMAN
104	Olink Target 96 Development(v.3521)	SIRPB1	O00241	0.77883	1.01099	20	77	3.616170	23	100	O00241	SIRB1_HUMAN
105	Olink Target 96 Development(v.3521)	NID2	Q14112	1.38089	0.999605	2	8	4.157050	23	100	Q14112	NID2_HUMAN
106	Olink Target 96 Immune Response(v.3204)	EGLN1	Q9GZT9	1.35194	0.984405	4	15	1.843810	19	83	Q9GZT9	EGLN1_HUMAN
107	Olink Target 96 Immune Response(v.3204)	CLEC7A	Q9BXN2	0.76586	0.979635	16	62	1.302400	22	96	Q9BXN2	CLC7A_HUMAN
108	Olink Target 96 Immune Response(v.3204)	CLEC4C	Q8WTT0	1.44126	0.970095	1	4	2.280380	22	96	Q8WTT0	CLC4C_HUMAN
109	Olink Target 96 Immune Response(v.3204)	BTN3A2	P78410	1.04352	0.948125	9	35	2.143670	23	100	P78410	BT3A2_HUMAN
110	Olink Target 96 Immune Response(v.3204)	TRIM5	Q9C035	1.2291	0.94017	3	12	1.961840	22	96	Q9C035	TRIM5_HUMAN
111	Olink Target 96 Development(v.3521)	IGF2R	P11717	1.40614	0.916145	6	23	5.418750	23	100	P11717	MPRI_HUMAN
112	Olink Target 96 Immune Response(v.3204)	LILRB4	Q8NHJ6	0.95638	0.89308	11	42	1.142690	19	83	Q8NHJ6	LIRB4_HUMAN
113	Olink Target 96 Immune Response(v.3204)	DDX58	O95786	1.33517	0.84942	1	4	5.704870	22	96	O95786	DDX58_HUMAN
114	Olink Target 96 Immune Response(v.3204)	KRT19	P08727	1.02419	0.83901	5	19	0.866270	6	26	P08727	K1C19_HUMAN
115	Olink Target 96 Development(v.3521)	INHBC	P55103	1.00685	0.82679	5	19	2.081740	20	87	P55103	INHBC_HUMAN
116	Olink Target 96 Immune Response(v.3204)	MGMT	P16455	1.37403	0.815965	1	4	5.944100	23	100	P16455	MGMT_HUMAN
117	Olink Target 96 Development(v.3521)	ENPP2	Q13822	0.96876	0.807925	11	42	4.365280	23	100	Q13822	ENPP2_HUMAN
118	Olink Target 96 Development(v.3521)	HTRA2	O43464	1.27743	0.77893	0	0	2.885760	23	100	O43464	HTRA2_HUMAN
119	Olink Target 96 Immune Response(v.3204)	LY75	O60449	0.96247	0.7675	4	15	1.057050	17	74	O60449	LY75_HUMAN
120	Olink Target 96 Development(v.3521)	CD74	P04233	1.75006	0.746875	0	0	1.550710	8	35	P04233	HG2A_HUMAN
121	Olink Target 96 Immune Response(v.3204)	CXCL12	P48061	0.87701	0.74483	8	31	0.650130	3	13	P48061	SDF1_HUMAN
122	Olink Target 96 Immune Response(v.3204)	DAPP1	Q9UN19	1.5425	0.724845	0	0	2.021660	12	52	Q9UN19	DAPP1_HUMAN

123	Olink Target 96 Development(v.3521)	CNTN4	Q8IWV2	0.71387	0.716645	13	50	3.718540	23	100	Q8IWV2	CNTN4_HUMAN
124	Olink Target 96 Immune Response(v.3204)	FAM3B	P58499	0.92411	0.711985	2	8	1.262470	18	78	P58499	FAM3B_HUMAN
125	Olink Target 96 Immune Response(v.3204)	CLEC6A	Q6EIG7	1.36841	0.702765	1	4	1.649800	16	70	Q6EIG7	CLC6A_HUMAN
126	Olink Target 96 Immune Response(v.3204)	PADI2	Q9Y2J8	0.7983	0.69838	9	35	1.349130	23	100	Q9Y2J8	PADI2_HUMAN
127	Olink Target 96 Development(v.3521)	LGMN	Q99538	0.35699	0.66131	15	58	3.985270	23	100	Q99538	LGMN_HUMAN
128	Olink Target 96 Immune Response(v.3204)	ZBTB16	Q05516	1.03546	0.653515	0	0	1.302530	20	87	Q05516	ZBT16_HUMAN
129	Olink Target 96 Immune Response(v.3204)	DGKZ	Q13574	1.14388	0.650395	1	4	1.268750	16	70	Q13574	DGKZ_HUMAN
130	Olink Target 96 Development(v.3521)	PTPRF	P10586	1.13398	0.644095	5	19	3.821100	23	100	P10586	PTPRF_HUMAN
131	Olink Target 96 Immune Response(v.3204)	ITGB6	P18564	1.08995	0.637855	0	0	1.039000	8	35	P18564	ITB6_HUMAN
132	Olink Target 96 Immune Response(v.3204)	CXADR	P78310	1.03855	0.61399	0	0	0.828000	3	13	P78310	CXAR_HUMAN
133	Olink Target 96 Immune Response(v.3204)	CLEC4G	Q6UXB4	1.00412	0.609205	3	12	1.063160	15	65	Q6UXB4	CLC4G_HUMAN
134	Olink Target 96 Immune Response(v.3204)	FGF2	P09038	0.99231	0.604365	0	0	1.091240	13	57	P09038	FGF2_HUMAN
135	Olink Target 96 Immune Response(v.3204)	LAG3	P18627	0.94335	0.575145	0	0	0.986240	13	57	P18627	LAG3_HUMAN
136	Olink Target 96 Immune Response(v.3204)	IRAK1	P51617	1.01493	0.574465	0	0	3.314140	23	100	P51617	IRAK1_HUMAN
137	Olink Target 96 Development(v.3521)	STIP1	P31948	1.19154	0.554265	1	4	8.256840	23	100	P31948	STIP1_HUMAN
138	Olink Target 96 Immune Response(v.3204)	SIT1	Q9Y3P8	0.89195	0.528095	1	4	0.923990	12	52	Q9Y3P8	SIT1_HUMAN
139	Olink Target 96 Development(v.3521)	CCL21	O00585	0.81527	0.52404	7	27	1.113290	21	91	O00585	CCL21_HUMAN
140	Olink Target 96 Immune Response(v.3204)	TRAF2	Q12933	0.82314	0.52366	3	12	3.447540	22	96	Q12933	TRAF2_HUMAN
141	Olink Target 96 Immune Response(v.3204)	ITM2A	O43736	0.84076	0.519015	2	8	0.841330	12	52	O43736	ITM2A_HUMAN
142	Olink Target 96 Immune Response(v.3204)	JUN	P05412	0.94077	0.500725	3	12	0.943610	12	52	P05412	JUN_HUMAN
143	Olink Target 96 Development(v.3521)	P4HB	P07237	0.97342	0.447105	1	4	4.023400	23	100	P07237	PDIA1_HUMAN
144	Olink Target 96 Immune Response(v.3204)	DPP10	Q8N608	0.86478	0.43003	0	0	0.633590	3	13	Q8N608	DPP10_HUMAN
145	Olink Target 96 Immune Response(v.3204)	KLRD1	Q13241	0.89155	0.42516	0	0	1.609420	21	91	Q13241	KLRD1_HUMAN
146	Olink Target 96 Immune Response(v.3204)	BIRC2	Q13490	0.70132	0.41833	6	23	1.139050	21	91	Q13490	BIRC2_HUMAN
147	Olink Target 96 Immune Response(v.3204)	EIF5A	P63241	1.22936	0.40968	0	0	2.431790	21	91	P63241	IF5A1_HUMAN
148	Olink Target 96 Development(v.3521)	PAMR1	Q6UXH9	0.55941	0.40304	11	42	3.763860	23	100	Q6UXH9	PAMR1_HUMAN
149	Olink Target 96 Immune Response(v.3204)	HSD11B1	P28845	0.78421	0.39605	1	4	0.711400	10	43	P28845	DHI1_HUMAN
150	Olink Target 96 Immune Response(v.3204)	STC1	P52823	0.7024	0.395555	2	8	0.800560	16	70	P52823	STC1_HUMAN
151	Olink Target 96 Development(v.3521)	DAG1	Q14118	0.89372	0.38402	0	0	1.404280	22	96	Q14118	DAG1_HUMAN
152	Olink Target 96 Immune Response(v.3204)	IRF9	Q00978	0.8248	0.38092	1	4	2.334420	21	91	Q00978	IRF9_HUMAN
153	Olink Target 96 Immune Response(v.3204)	ITGA6	P23229	0.8016	0.37855	0	0	0.628460	7	30	P23229	ITA6_HUMAN
154	Olink Target 96 Immune Response(v.3204)	KPNA1	P52294	1.00561	0.35488	0	0	2.462980	20	87	P52294	IMA5_HUMAN
155	Olink Target 96 Development(v.3521)	ARSA	P15289	0.78435	0.32375	9	35	4.727850	23	100	P15289	ARSA_HUMAN
156	Olink Target 96 Immune Response(v.3204)	CLEC4A	Q9UMR7	0.65442	0.31702	1	4	2.893240	23	100	Q9UMR7	CLC4A_HUMAN
157	Olink Target 96 Immune Response(v.3204)	SH2D1A	O60880	0.61201	0.28633	3	12	2.044460	23	100	O60880	SH21A_HUMAN
158	Olink Target 96 Immune Response(v.3204)	HEXIM1	O94992	0.41064	0.28456	11	42	6.716600	23	100	O94992	HEXI1_HUMAN
159	Olink Target 96 Immune Response(v.3204)	PRKCQ	Q04759	1.0699	0.27545	0	0	0.583920	4	17	Q04759	KPCT_HUMAN
160	Olink Target 96 Immune Response(v.3204)	PRDX3	P30048	0.41983	0.25079	4	15	0.990300	23	100	P30048	PRDX3_HUMAN
161	Olink Target 96 Immune Response(v.3204)	DCTN1	Q14203	0.23458	0.24265	13	50	7.844730	23	100	Q14203	DCTN1_HUMAN
162	Olink Target 96 Immune Response(v.3204)	EIF4G1	Q04637	0.4469	0.22871	2	8	6.684260	23	100	Q04637	IF4G1_HUMAN
163	Olink Target 96 Immune Response(v.3204)	PIK3AP1	Q6ZUJ8	0.41761	0.224695	5	19	6.704540	23	100	Q6ZUJ8	BCAP_HUMAN
164	Olink Target 96 Immune Response(v.3204)	NTF4	P34130	0.50255	0.219455	0	0	0.255140	1	4	P34130	NTF4_HUMAN

165	Olink Target 96 Immune Response(v.3204)	AREG	P15514	0.19635	0.155045	12	46	0.520410	22	96	P15514	AREG_HUMAN
166	Olink Target 96 Immune Response(v.3204)	SRPK2	P78362	0.29254	0.138915	8	31	1.442020	22	96	P78362	SRPK2_HUMAN
167	Olink Target 96 Immune Response(v.3204)	CNTNAP2	Q9UHC6	0.46689	0.138405	0	0	0.273180	3	13	Q9UHC6	CNTP2_HUMAN
168	Olink Target 96 Immune Response(v.3204)	FXYD5	Q96DB9	0.8255	0.096175	0	0	0.448440	1	4	Q96DB9	FXYD5_HUMAN
169	Olink Target 96 Immune Response(v.3204)	NF2	P35240	0.52878	0.086495	1	4	2.085800	20	87	P35240	MERL_HUMAN
170	Olink Target 96 Development(v.3521)	ACAN	P16112	0.2964	0.052285	6	23	1.002370	23	100	P16112	PGCA_HUMAN
171	Olink Target 96 Immune Response(v.3204)	DCBLD2	Q96PD2	0.45729	0.034165	1	4	2.025530	23	100	Q96PD2	DCBD2_HUMAN
172	Olink Target 96 Immune Response(v.3204)	FCRL3	Q96P31	0.34779	0.00805	1	4	0.271190	4	17	Q96P31	FCRL3_HUMAN
173	Olink Target 96 Immune Response(v.3204)	FCRL6	Q6DN72	0.29864	0.006195	2	8	0.395350	17	74	Q6DN72	FCRL6_HUMAN
174	Olink Target 96 Immune Response(v.3204)	BACH1	O14867	0.30138	-0.03738	1	4	1.693220	23	100	O14867	BACH1_HUMAN
175	Olink Target 96 Development(v.3521)	SEMA7A	O75326	0.52869	-0.03795	6	23	6.999390	23	100	O75326	SEM7A_HUMAN
176	Olink Target 96 Immune Response(v.3204)	NFATC3	Q12968	0.20245	-0.04836	1	4	0.346020	17	74	Q12968	NFAC3_HUMAN
177	Olink Target 96 Immune Response(v.3204)	CD83	Q01151	0.10243	-0.10753	3	12	0.069960	10	43	Q01151	CD83_HUMAN
178	Olink Target 96 Immune Response(v.3204)	MASP1	P48740	0.30084	-0.12779	0	0	0.234250	9	39	P48740	MASP1_HUMAN
179	Olink Target 96 Immune Response(v.3204)	CLEC4D	Q8WXI8	0.03691	-0.35782	0	0	2.379530	23	100	Q8WXI8	CLC4D_HUMAN
180	Olink Target 96 Development(v.3521)	SPINK5	Q9NQ38	-1.10447	-0.60487	24	92	-0.689170	20	87	Q9NQ38	ISK5_HUMAN
181	Olink Target 96 Development(v.3521)	PPIB	P23284	-0.63053	-0.7089	9	35	6.350530	23	100	P23284	PPIB_HUMAN
182	Olink Target 96 Development(v.3521)	APP	P05067	-0.3458	-0.71761	3	12	2.789630	23	100	P05067	A4_HUMAN
183	Olink Target 96 Immune Response(v.3204)	GLB1	P16278	-0.44964	-0.79779	0	0	-0.480620	11	48	P16278	BGAL_HUMAN
184	Olink Target 96 Development(v.3521)	GUSB	P08236	-0.39873	-1.26927	6	23	5.485860	23	100	P08236	BGLR_HUMAN

#	Protein names	Gene names	Length	Gene ontology (biological process)	Gene ontology (cellular component)	Gene ontology (molecular function)
1	Macrophage migration inhibitory factor (MIF) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) (L-dopachrome isomerase) (L-dopachrome tautomerase) (EC 5.3.3.12) (Phenylpyruvate tautomerase)	MIF GLIF MMIF	115	carboxylic acid metabolic process [GO:0019752]; cell surface receptor signaling pathway [GO:0007166]; inflammatory response [GO:0006954]; innate immune response [GO:0045087]; negative regulation of apoptotic process [GO:0043066]; negative regulation of cell aging [GO:0090344]; negative regulation of cell migration [GO:0030336]; negative regulation of DNA damage response, signal transduction by p53 class mediator [GO:0043518]; negative regulation of gene expression [GO:0010629]; negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator [GO:1902166]; negative regulation of macrophage chemotaxis [GO:0010760]; positive regulation of B cell proliferation [GO:0030890]; positive regulation of cytokine production [GO:0001819]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of fibroblast proliferation [GO:0048146]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of phosphorylation [GO:0042327]; positive regulation of protein kinase A signaling [GO:0010739]; positive regulation of tumor necrosis factor production [GO:0032760]; prostaglandin biosynthetic process [GO:0001516]; protein homotrimerization [GO:0070207]; regulation of cell cycle [GO:0051726]; regulation of macrophage activation [GO:0043030]	cell surface [GO:0009986]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; ficolin-1-rich granule lumen [GO:1904813]; nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; secretory granule lumen [GO:0034774]; vesicle [GO:0031982]	chemoattractant activity [GO:0042056]; cytokine activity [GO:0005125]; cytokine receptor binding [GO:0005126]; dopachrome isomerase activity [GO:0004167]; identical protein binding [GO:0042802]; phenylpyruvate tautomerase activity [GO:0050178]
2	Dickkopf-related protein 3 (Dickkopf-3) (Dkk-3) (hDkk-3)	DKK3 REIC UNQ258/PRO295	350	adrenal gland development [GO:0030325]; anatomical structure morphogenesis [GO:0009653]; negative regulation of aldosterone biosynthetic process [GO:0032348]; negative regulation of anti-Mullerian hormone signaling pathway [GO:1902613]; negative regulation of canonical Wnt signaling pathway [GO:0090090]; negative regulation of cortisol biosynthetic process [GO:2000065]; negative regulation of transcription, DNA-templated [GO:0045892]; regulation of transforming growth factor beta receptor signaling pathway [GO:0017015]; Wnt signaling pathway [GO:0016055]	extracellular space [GO:0005615]	co-receptor binding [GO:0039706]; receptor antagonist activity [GO:0048019]
3	CCN family member 3 (Cellular communication network factor 3) (Insulin-like growth factor-binding protein 9) (IBP-9) (IGF-binding protein 9) (IGFBP-9) (Nephroblastoma-overexpressed gene protein homolog) (Protein NOV homolog) (NovH)	CCN3 IGFBP9 NOV NOVH	357	angiogenesis [GO:0001525]; bone regeneration [GO:1990523]; cell adhesion [GO:0007155]; cell adhesion mediated by integrin [GO:0033627]; cell chemotaxis [GO:0060326]; chondrocyte differentiation [GO:0002062]; endothelial cell-cell adhesion [GO:0071603]; endothelial cell chemotaxis [GO:0035767]; fibroblast migration [GO:0010761]; hematopoietic stem cell homeostasis [GO:0061484]; negative regulation of cell death [GO:0060548]; negative regulation of cell growth [GO:0030308]; negative regulation of chondrocyte proliferation [GO:1902731]; negative regulation of inflammatory response [GO:0050728]; negative regulation of insulin secretion [GO:0046676]; negative regulation of monocyte chemotaxis [GO:0090027]; negative regulation of myotube differentiation [GO:0010832]; negative regulation of NIK/NF-kappaB signaling [GO:1901223]; negative regulation of sensory perception of pain [GO:1904057]; negative regulation of SMAD protein signal transduction [GO:0060392]; positive regulation of Notch signaling pathway [GO:0045747]; regulation of gene expression [GO:0010468]; signal transduction [GO:0007165]; smooth muscle cell migration [GO:0014909]; smooth muscle cell proliferation [GO:0048659]; type B pancreatic cell proliferation [GO:0044342]	axon [GO:0030424]; collagen-containing extracellular matrix [GO:0062023]; cytoplasm [GO:0005737]; dendrite [GO:0030425]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; gap junction [GO:0005921]; intracellular membrane-bounded organelle [GO:0043231]; neuronal cell body [GO:0043025]	growth factor activity [GO:0008083]; heparin binding [GO:0008201]; insulin-like growth factor binding [GO:0005520]; integrin binding [GO:0005178]; Notch binding [GO:0005112]
4	Cystatin-M (Cystatin-6) (Cystatin-E)	CST6	149	anatomical structure morphogenesis [GO:0009653]; epidermis development [GO:0008544]	cornified envelope [GO:0001533]; extracellular exosome [GO:0070062]	cysteine-type endopeptidase inhibitor activity [GO:0004869]
5	Tumor necrosis factor receptor superfamily member 19L (Receptor expressed in lymphoid tissues)	RELT TNFRSF19L	430	amelogenesis [GO:0097186]; apoptotic process [GO:0006915]	integral component of membrane [GO:0016021]; nucleoplasm [GO:0005654]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]	
6	CCN family member 5 (Connective tissue growth factor-like protein) (CTGF-L) (Connective tissue growth factor-related protein 58) (WNT1-inducible-signaling pathway protein 2) (WISP-2)	CCN5 CT58 CTGFL WISP2 UNQ228/PRO261	250	cell adhesion [GO:0007155]; cell-cell signaling [GO:0007267]; negative regulation of cell death [GO:0060548]; signal transduction [GO:0007165]	extracellular matrix [GO:0031012]; extracellular space [GO:0005615]; nucleus [GO:0005634]	heparin binding [GO:0008201]; insulin-like growth factor binding [GO:0005520]; integrin binding [GO:0005178]
7	Leukocyte-associated immunoglobulin-like receptor 1 (LAIR-1) (hLAIR1) (CD antigen CD305)	LAIR1 CD305	287	adaptive immune response [GO:0002250]	integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]; specific granule membrane [GO:0035579]; tertiary granule membrane [GO:0070821]	
8	Thymosin beta-10	TMSB10 PTMB10 THYB10	44	actin filament organization [GO:0007015]; regulation of cell migration [GO:0030334]; sequestering of actin monomers [GO:0042989]	cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]	actin monomer binding [GO:0003785]
9	CMRF35-like molecule 9 (CLM-9) (CD300 antigen-like family member G) (Triggering receptor expressed on myeloid cells 4) (TREM-4) (CD antigen CD300g)	CD300LG CLM9 TREM4 UNQ422/PRO846	332	immune system process [GO:0002376]	apical plasma membrane [GO:0016324]; basolateral plasma membrane [GO:0016323]; integral component of membrane [GO:0016021]; multivesicular body membrane [GO:0032585]; plasma membrane [GO:0005886]	transmembrane signaling receptor activity [GO:0004888]
10	Tryptase alpha/beta-1 (Tryptase-1) (EC 3.4.21.59) (Tryptase I) (Tryptase alpha-1)	TPSAB1 TPS1 TPS2 TPSB1	275	defense response [GO:0006952]; extracellular matrix disassembly [GO:0022617]; proteolysis [GO:0006508]	extracellular region [GO:0005576]; extracellular space [GO:0005615]	identical protein binding [GO:0042802]; serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]
11	Synaptosomal-associated protein 29 (SNAP-29) (Soluble 29 kDa NSF attachment protein) (Vesicle-membrane fusion protein SNAP-29)	SNAP29	258	autophagosome maturation [GO:0097352]; autophagosome membrane docking [GO:0016240]; cilium assembly [GO:0060271]; exocytosis [GO:0006887]; membrane fusion [GO:0061025]; protein transport [GO:0015031]; synaptic vesicle fusion to presynaptic active zone membrane [GO:0031629]; synaptic vesicle priming [GO:0016082]; vesicle fusion [GO:0006906]; vesicle targeting [GO:0006903]	autophagosome [GO:0005776]; autophagosome membrane [GO:0000421]; azurophil granule membrane [GO:0035577]; centrosome [GO:0005813]; ciliary pocket membrane [GO:0020018]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; Golgi membrane [GO:0000139]; nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; presynapse [GO:0098793]; SNARE complex [GO:0031201]	SNAP receptor activity [GO:0005484]; syntaxin binding [GO:0019905]
12	Cochlin (COCH-5B2)	COCH COCH5B2 UNQ257/PR	550	defense response to bacterium [GO:0042742]; positive regulation of innate immune response [GO:0045089]; regulation of cell shape [GO:0008360]; sensory perception of sound [GO:0007605]	collagen-containing extracellular matrix [GO:0062023]; extracellular region [GO:0005576]	collagen binding [GO:0005518]

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13	Collectin-12 (Collectin placenta protein 1) (CL-P1) (hCL-P1) (Nurse cell scavenger receptor 2) (Scavenger receptor class A member 4) (Scavenger receptor with C-type lectin)	COLEC12 CLP1 NSR2 SCARA4 SRCL	742	carbohydrate mediated signaling [GO:0009756]; cellular response to exogenous dsRNA [GO:0071360]; defense response [GO:0006952]; defense response to bacterium [GO:0042742]; innate immune response [GO:0045087]; phagocytosis, recognition [GO:0006910]; positive regulation of cell adhesion molecule production [GO:0060355]; toll-like receptor 3 signaling pathway [GO:0034138]	collagen trimer [GO:0005581]; endocytic vesicle membrane [GO:0030666]; extracellular matrix [GO:0031012]; extracellular space [GO:0005615]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	galactose binding [GO:0005534]; low-density lipoprotein particle binding [GO:0030169]; metal ion binding [GO:0046872]; pattern recognition receptor activity [GO:0038187]; scavenger receptor activity [GO:0005044]
14	Low affinity immunoglobulin epsilon Fc receptor (BLAST-2) (C-type lectin domain family 4 member J) (Fc-epsilon-RII) (Immunoglobulin E-binding factor) (Lymphocyte IgE receptor) (CD antigen CD23) [Cleaved into: Low affinity immunoglobulin epsilon Fc receptor membrane-bound form; Low affinity immunoglobulin epsilon Fc receptor soluble form]	FCER2 CD23A CLEC4J FCE2 IGEBF	321	positive regulation of humoral immune response mediated by circulating immunoglobulin [GO:0002925]; positive regulation of killing of cells of other organism [GO:0051712]; positive regulation of nitric-oxide synthase activity [GO:0051000]; positive regulation of nitric-oxide synthase biosynthetic process [GO:0051770]	external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	carbohydrate binding [GO:0030246]; IgE binding [GO:0019863]; integrin binding [GO:0005178]; metal ion binding [GO:0046872]
15	Histamine N-methyltransferase (HMT) (EC 2.1.1.8)	HNMT	292	brain development [GO:0007420]; histamine catabolic process [GO:0001695]; histamine metabolic process [GO:0001692]; histidine catabolic process [GO:0006548]; hyperosmotic response [GO:0006972]; methylation [GO:0032259]; respiratory gaseous exchange by respiratory system [GO:0007585]; response to amine [GO:0014075]; response to cocaine [GO:0042220]; response to glucocorticoid [GO:0051384]; response to immobilization stress [GO:0035902]; response to interleukin-1 [GO:0070555]; response to tumor cell [GO:0002347]	centrosome [GO:0005813]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; neuron projection [GO:0043005]; nucleoplasm [GO:0005654]	histamine N-methyltransferase activity [GO:0046539]
16	V-set and immunoglobulin domain-containing protein 4 (Protein Z39Ig)	VSIG4 CRIg Z39IG UNQ317/PRO362	399	complement activation, alternative pathway [GO:0006957]; negative regulation of complement activation, alternative pathway [GO:0045957]; negative regulation of interleukin-2 production [GO:0032703]; negative regulation of macrophage activation [GO:0043031]; negative regulation of T cell proliferation [GO:0042130]	integral component of membrane [GO:0016021]; protein-containing complex [GO:0032991]	complement component C3b binding [GO:0001851]
17	Glycoprotein Xg (Protein PBDX)	XG PBDX	180	homotypic cell-cell adhesion [GO:0034109]; positive regulation of neutrophil extravasation [GO:2000391]; T cell extravasation [GO:0072683]	integral component of plasma membrane [GO:0005887]	
18	Serine protease inhibitor Kazal-type 1 (Pancreatic secretory trypsin inhibitor) (Tumor-associated trypsin inhibitor) (TATI)	SPINK1 PSTI	79	negative regulation of calcium ion import [GO:0090281]; negative regulation of nitric oxide mediated signal transduction [GO:0010751]; negative regulation of peptidyl-tyrosine phosphorylation [GO:0050732]; negative regulation of serine-type endopeptidase activity [GO:1900004]; regulation of acrosome reaction [GO:0060046]; regulation of store-operated calcium entry [GO:2001256]; sperm capacitation [GO:0048240]	extracellular exosome [GO:0070062]	endopeptidase inhibitor activity [GO:0004866]; serine-type endopeptidase inhibitor activity [GO:0004867]
19	Platelet-derived growth factor receptor beta (PDGF-R-beta) (PDGFR-beta) (EC 2.7.10.1) (Beta platelet-derived growth factor receptor) (Beta-type platelet-derived growth factor receptor) (CD140 antigen-like family member B) (Platelet-derived growth factor receptor 1) (PDGFR-1) (CD antigen CD140b)	PDGFRB PDGFR PDGFR1	1106	aging [GO:0007568]; aorta morphogenesis [GO:0035909]; cardiac myofibril assembly [GO:0055003]; cell chemotaxis [GO:0060326]; cell migration [GO:0016477]; cell migration involved in coronary angiogenesis [GO:0060981]; cell migration involved in vasculogenesis [GO:0035441]; glycosaminoglycan biosynthetic process [GO:0006024]; inner ear development [GO:0048839]; lung growth [GO:0060437]; male gonad development [GO:0008584]; metanephric comma-shaped body morphogenesis [GO:0072278]; metanephric glomerular capillary formation [GO:0072277]; metanephric glomerular mesangial cell proliferation involved in metanephros development [GO:0072262]; metanephric mesenchymal cell migration [GO:0035789]; metanephric mesenchyme development [GO:0072075]; metanephric S-shaped body morphogenesis [GO:0072284]; negative regulation of apoptotic process [GO:0043066]; peptidyl-tyrosine phosphorylation [GO:0018108]; phosphatidylinositol-mediated signaling [GO:0048015]; phosphatidylinositol metabolic process [GO:0046488]; platelet-derived growth factor receptor-beta signaling pathway [GO:0035791]; platelet-derived growth factor receptor signaling pathway [GO:0048008]; positive regulation of apoptotic process [GO:0043065]; positive regulation of calcium ion import [GO:0090280]; positive regulation of cell migration [GO:0030335]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor signaling pathway [GO:0038091]; positive regulation of chemotaxis [GO:0050921]; positive regulation of collagen biosynthetic process [GO:0032967]; positive regulation of DNA biosynthetic process [GO:2000573]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of fibroblast proliferation [GO:0048146]; positive regulation of hepatic stellate cell activation [GO:2000491]; positive regulation of kinase activity [GO:0033674]; positive regulation of MAP kinase activity [GO:0043406]; positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway [GO:0035793]; positive regulation of mitotic nuclear division [GO:0045840]; positive regulation of phosphatidylinositol 3-kinase activity [GO:0043552]; positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; positive regulation of phospholipase C activity [GO:0010863]; positive regulation of phosphoprotein phosphatase activity [GO:0032516]; positive regulation of reactive oxygen species metabolic process [GO:2000379]; positive regulation of Rho protein signal transduction [GO:0035025]; positive regulation of smooth muscle cell migration [GO:0014911]; positive regulation of smooth muscle cell proliferation [GO:0048661]; protein autophosphorylation [GO:0046777]; regulation of actin cytoskeleton organization [GO:0032956]; response to estradiol [GO:0032355]; response to estrogen [GO:0043627]; response to fluid shear stress [GO:0034405]; response to hydrogen peroxide [GO:0042542]; response to hyperoxia [GO:0055093]; response to retinoic acid [GO:0032526]; response to toxic substance [GO:0009636]; retina vasculature development in camera-type eye [GO:0061298]; signal transduction [GO:0007165]; smooth muscle cell chemotaxis [GO:0071670]; transmembrane receptor protein tyrosine kinase signaling pathway [GO:0007169]; wound healing [GO:0042060]	apical plasma membrane [GO:0016324]; cell surface [GO:0009986]; cytoplasm [GO:0005737]; cytoplasmic vesicle [GO:0031410]; focal adhesion [GO:0005925]; Golgi apparatus [GO:0005794]; integral component of plasma membrane [GO:0005887]; intracellular membrane-bounded organelle [GO:0043231]; intrinsic component of plasma membrane [GO:0031226]; lysosomal lumen [GO:0043202]; membrane [GO:0016020]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]	ATP binding [GO:0005524]; enzyme binding [GO:0019899]; growth factor binding [GO:0019838]; phosphatidylinositol 3-kinase binding [GO:0043548]; platelet activating factor receptor activity [GO:0004992]; platelet-derived growth factor-activated receptor activity [GO:0005017]; platelet-derived growth factor beta-receptor activity [GO:0005019]; platelet-derived growth factor binding [GO:0048407]; platelet-derived growth factor receptor binding [GO:0005161]; protein kinase binding [GO:0019901]; protein tyrosine kinase activity [GO:0004713]; signaling receptor binding [GO:0005102]; transmembrane receptor protein tyrosine kinase activity [GO:0004714]; vascular endothelial growth factor binding [GO:0038085]
20	Adhesion G protein-coupled receptor E5 (Leukocyte antigen CD97) (CD antigen CD97) [Cleaved into: Adhesion G protein-	ADGRE5 CD97	835	adenylate cyclase-activating G protein-coupled receptor signaling pathway [GO:0007189]; cell adhesion [GO:0007155]; cell-cell signaling [GO:0007267]; cell surface receptor signaling pathway [GO:0007166]; G protein-coupled receptor signaling pathway [GO:0007186]; immune response [GO:0006955]; inflammatory response [GO:0006954]	extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; integral component of plasma membrane [GO:0005887]; membrane [GO:0016020]; plasma membrane [GO:0005886]; secretory granule	calcium ion binding [GO:0005509]; G protein-coupled receptor activity [GO:0004930]; transmembrane signaling receptor activity [GO:0004888]

	coupled receptor E5 subunit alpha; Adhesion G protein-coupled receptor E5 subunit beta]				membrane [GO:0030667]	
21	Glycoprotein hormones alpha chain (Anterior pituitary glycoprotein hormones common subunit alpha) (Choriogonadotropin alpha chain) (Chorionic gonadotrophin subunit alpha) (CG-alpha) (Follicle-stimulating hormone alpha chain) (FSH-alpha) (Follitropin alpha chain) (Luteinizing hormone alpha chain) (LSH-alpha) (Lutropin alpha chain) (Thyroid-stimulating hormone alpha chain) (TSH-alpha) (Thyrotropin alpha chain)	CGA	116	cellular response to hormone stimulus [GO:0032870]; developmental growth [GO:0048589]; follicle-stimulating hormone secretion [GO:0046884]; gonad development [GO:0008406]; G protein-coupled receptor signaling pathway [GO:0007186]; luteinizing hormone secretion [GO:0032275]; negative regulation of organ growth [GO:0046621]; positive regulation of cell migration [GO:0030335]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of steroid biosynthetic process [GO:0010893]; positive regulation of transcription by RNA polymerase II [GO:0045944]; regulation of signaling receptor activity [GO:0010469]; thyroid gland development [GO:0030878]; thyroid hormone generation [GO:0006590]	extracellular region [GO:0005576]; extracellular space [GO:0005615]; follicle-stimulating hormone complex [GO:0016914]; Golgi lumen [GO:0005796]	follicle-stimulating hormone activity [GO:0016913]; hormone activity [GO:0005179]
22	Scavenger receptor class F member 1 (Acetyl LDL receptor) (Scavenger receptor expressed by endothelial cells 1) (SREC-I)	SCARF1 KIAA0149 SREC	830	cell adhesion [GO:0007155]; cholesterol catabolic process [GO:0006707]; dendrite development [GO:0016358]; neuron remodeling [GO:0016322]; positive regulation of axon regeneration [GO:0048680]; positive regulation of neuron projection development [GO:0010976]; receptor-mediated endocytosis [GO:0006898]	endocytic vesicle membrane [GO:0030666]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	low-density lipoprotein particle binding [GO:0030169]; scavenger receptor activity [GO:0005044]; transmembrane signaling receptor activity [GO:0004888]
23	Follistatin-related protein 3 (Follistatin-like protein 3) (Follistatin-related gene protein)	FSTL3 FLRG UNQ674/PRO1308	263	adrenal gland development [GO:0030325]; cell differentiation [GO:0030154]; cellular response to metal ion [GO:0071248]; hematopoietic progenitor cell differentiation [GO:0002244]; kidney development [GO:0001822]; lung development [GO:0030324]; male gonad development [GO:0008584]; negative regulation of activin receptor signaling pathway [GO:0032926]; negative regulation of BMP signaling pathway [GO:0030514]; negative regulation of osteoclast differentiation [GO:0045671]; negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway [GO:0090101]; ossification [GO:0001503]; positive regulation of cell-cell adhesion [GO:0022409]; positive regulation of transcription by RNA polymerase II [GO:0045944]; regulation of BMP signaling pathway [GO:0030510]; regulation of transcription by RNA polymerase II [GO:0006357]; spermatogenesis [GO:0007283]	endoplasmic reticulum lumen [GO:0005788]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]; neuron projection terminus [GO:0044306]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; secretory granule [GO:0030141]	activin binding [GO:0048185]; fibronectin binding [GO:0001968]
24	Parkinson disease protein 7 (Maillard deglycase) (Oncogene DJ1) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1) (Protein/nucleic acid deglycase DJ-1) (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124)	PARK7	189	activation of protein kinase B activity [GO:0032148]; adult locomotory behavior [GO:0008344]; autophagy [GO:0006914]; cellular detoxification of aldehyde [GO:0110095]; cellular detoxification of methylglyoxal [GO:0140041]; cellular response to glyoxal [GO:0036471]; cellular response to hydrogen peroxide [GO:0070301]; cellular response to oxidative stress [GO:0034599]; detection of oxidative stress [GO:0070994]; detoxification of copper ion [GO:0010273]; detoxification of mercury ion [GO:0050787]; DNA repair [GO:0006281]; dopamine uptake involved in synaptic transmission [GO:0051583]; glucose homeostasis [GO:0042593]; glutathione deglycation [GO:0036531]; glycolate biosynthetic process [GO:0046295]; glyoxal metabolic process [GO:1903189]; guanine deglycation [GO:0106044]; guanine deglycation, glyoxal removal [GO:0106046]; guanine deglycation, methylglyoxal removal [GO:0106045]; histone modification [GO:0016570]; hydrogen peroxide metabolic process [GO:0042743]; inflammatory response [GO:0006954]; insulin secretion [GO:0030073]; lactate biosynthetic process [GO:0019249]; membrane depolarization [GO:0051899]; membrane hyperpolarization [GO:0060081]; methylglyoxal catabolic process to lactate [GO:0061727]; methylglyoxal metabolic process [GO:0009438]; mitochondrion organization [GO:0007005]; negative regulation of apoptotic process [GO:0043066]; negative regulation of cell death [GO:0060548]; negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway [GO:2001268]; negative regulation of death-inducing signaling complex assembly [GO:1903073]; negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway [GO:1902236]; negative regulation of extrinsic apoptotic signaling pathway [GO:2001237]; negative regulation of gene expression [GO:0010629]; negative regulation of hydrogen peroxide-induced cell death [GO:1903206]; negative regulation of hydrogen peroxide-induced neuron death [GO:1903208]; negative regulation of hydrogen peroxide-induced neuron intrinsic apoptotic signaling pathway [GO:1903384]; negative regulation of neuron apoptotic process [GO:0043524]; negative regulation of neuron death [GO:1901215]; negative regulation of nitrosative stress-induced intrinsic apoptotic signaling pathway [GO:1905259]; negative regulation of oxidative stress-induced cell death [GO:1903202]; negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway [GO:1903377]; negative regulation of proteasomal ubiquitin-dependent protein catabolic process [GO:0032435]; negative regulation of protein acetylation [GO:1901984]; negative regulation of protein binding [GO:0032091]; negative regulation of protein export from nucleus [GO:0046826]; negative regulation of protein K48-linked deubiquitination [GO:1903094]; negative regulation of protein kinase activity [GO:0006469]; negative regulation of protein phosphorylation [GO:0001933]; negative regulation of protein sumoylation [GO:0033234]; negative regulation of protein ubiquitination [GO:0031397]; negative regulation of reactive oxygen species biosynthetic process [GO:1903427]; negative regulation of TRAIL-activated apoptotic signaling pathway [GO:1903122]; negative regulation of ubiquitin-protein transferase activity [GO:0051444]; negative regulation of ubiquitin-specific protease activity [GO:2000157]; peptidyl-arginine deglycation [GO:0036527]; peptidyl-cysteine deglycation [GO:0036526]; peptidyl-lysine deglycation [GO:0036528]; positive regulation of acute inflammatory response to antigenic stimulus [GO:0002866]; positive regulation of androgen receptor activity [GO:2000825]; positive regulation of autophagy of mitochondrion [GO:1903599]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of dopamine biosynthetic process [GO:1903181]; positive regulation of gene expression [GO:0010628]; positive regulation of interleukin-8 production [GO:0032757]; positive regulation of L-dopa biosynthetic process [GO:1903197]; positive regulation of L-dopa decarboxylase activity [GO:1903200]; positive regulation of mitochondrial electron	adherens junction [GO:0005912]; axon [GO:0030424]; cell body [GO:0044297]; chromatin [GO:0000785]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; membrane raft [GO:0045121]; mitochondrial intermembrane space [GO:0005758]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; PML body [GO:0016605]; presynapse [GO:0098793]	androgen receptor binding [GO:0050681]; cadherin binding [GO:0045296]; copper ion binding [GO:0005507]; cupric ion binding [GO:1903135]; cuprous ion binding [GO:1903136]; cytokine binding [GO:0019955]; DNA-binding transcription factor binding [GO:0140297]; enzyme binding [GO:0019899]; glyoxalase (glycolic acid-forming) activity [GO:1990422]; identical protein binding [GO:0042802]; kinase binding [GO:0019900]; L-dopa decarboxylase activator activity [GO:0036478]; mercury ion binding [GO:0045340]; mRNA binding [GO:0003729]; oxidoreductase activity, acting on peroxide as acceptor [GO:0016684]; oxygen sensor activity [GO:0019826]; peptidase activity [GO:0008233]; peroxiredoxin activity [GO:0051920]; protein-containing complex binding [GO:0044877]; protein deglycase activity [GO:0036524]; protein homodimerization activity [GO:0042803]; scaffold protein binding [GO:0097110]; signaling receptor binding [GO:0005102]; small protein activating enzyme binding [GO:0044388]; superoxide dismutase copper chaperone activity [GO:0016532]; transcription coactivator activity [GO:0003713]; transcription factor binding [GO:0008134]; tyrosine 3-monooxygenase activator activity [GO:0036470]; ubiquitin-like protein conjugating enzyme binding [GO:0044390]; ubiquitin-specific protease binding [GO:1990381]

				transport, NADH to ubiquinone [GO:1902958]; positive regulation of NAD(P)H oxidase activity [GO:0033864]; positive regulation of oxidative phosphorylation uncoupler activity [GO:2000277]; positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway [GO:1902177]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; positive regulation of protein-containing complex assembly [GO:0031334]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of protein localization to nucleus [GO:1900182]; positive regulation of pyrroline-5-carboxylate reductase activity [GO:1903168]; positive regulation of reactive oxygen species biosynthetic process [GO:1903428]; positive regulation of superoxide dismutase activity [GO:1901671]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of transcription regulatory region DNA binding [GO:2000679]; positive regulation of tyrosine 3-monooxygenase activity [GO:1903178]; protein deglycation, glyoxal removal [GO:0036529]; protein deglycation, methylglyoxal removal [GO:0036530]; protein deglycosylation [GO:0006517]; protein stabilization [GO:0050821]; Ras protein signal transduction [GO:0007265]; regulation of androgen receptor signaling pathway [GO:0060765]; regulation of histone acetylation [GO:0035065]; regulation of histone ubiquitination [GO:0033182]; regulation of inflammatory response [GO:0050727]; regulation of mitochondrial membrane potential [GO:0051881]; regulation of neuron apoptotic process [GO:0043523]; regulation of supramolecular fiber organization [GO:1902903]; single fertilization [GO:0007338]		
25	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1 PBP PEBP	187	negative regulation of MAPK cascade [GO:0043409]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; nucleus [GO:0005634]	ATP binding [GO:0005524]; enzyme binding [GO:0019899]; phosphatidylethanolamine binding [GO:0008429]; protein kinase binding [GO:0019901]; RNA binding [GO:0003723]; serine-type endopeptidase inhibitor activity [GO:0004867]
26	C-type lectin domain family 14 member A (Epidermal growth factor receptor 5) (EGFR-5)	CLEC14A C14orf27 EGFR5 UNQ236/PRO269	490	cell migration [GO:0016477]; cell migration involved in sprouting angiogenesis [GO:0002042]; lymphangiogenesis [GO:0001946]; vascular endothelial growth factor receptor-2 signaling pathway [GO:0036324]; vascular endothelial growth factor receptor-3 signaling pathway [GO:0036325]	collagen-containing extracellular matrix [GO:0062023]; external side of plasma membrane [GO:0009897]; integral component of membrane [GO:0016021]	carbohydrate binding [GO:0030246]; extracellular matrix binding [GO:0050840]; extracellular matrix protein binding [GO:1990430]
27	Peroxiredoxin-1 (EC 1.11.1.24) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Thioredoxin-dependent peroxiredoxin 1)	PRDX1 PAGA PAGB TDPX2	199	cell population proliferation [GO:0008283]; cell redox homeostasis [GO:0045454]; erythrocyte homeostasis [GO:0034101]; hydrogen peroxide catabolic process [GO:0042744]; leukocyte activation [GO:0045321]; natural killer cell activation [GO:0030101]; natural killer cell mediated cytotoxicity [GO:0042267]; regulation of NIK/NF-kappaB signaling [GO:1901222]; regulation of stress-activated MAPK cascade [GO:0032872]; removal of superoxide radicals [GO:0019430]; retina homeostasis [GO:0001895]; skeletal system development [GO:0001501]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; melanosome [GO:0042470]; nucleus [GO:0005634]	cadherin binding [GO:0045296]; identical protein binding [GO:0042802]; peroxidase activity [GO:0004601]; RNA binding [GO:0003723]; thioredoxin peroxidase activity [GO:0008379]
28	Hepatitis A virus cellular receptor 2 (HAVcr-2) (T-cell immunoglobulin and mucin domain-containing protein 3) (TIMD-3) (T-cell immunoglobulin mucin receptor 3) (TIM-3) (T-cell membrane protein 3) (CD antigen CD366)	HAVCR2 TIM3 TIMD3	301	adaptive immune response [GO:0002250]; cellular response to lipopolysaccharide [GO:0071222]; defense response to Gram-positive bacterium [GO:0050830]; inflammatory response [GO:0006954]; innate immune response [GO:0045087]; macrophage activation involved in immune response [GO:0002281]; maternal process involved in female pregnancy [GO:0060135]; natural killer cell tolerance induction [GO:0002519]; negative regulation of defense response to bacterium [GO:1900425]; negative regulation of gene expression [GO:0010629]; negative regulation of granulocyte colony-stimulating factor production [GO:0071656]; negative regulation of immunological synapse formation [GO:2000521]; negative regulation of interferon-alpha production [GO:0032687]; negative regulation of interferon-gamma production [GO:0032689]; negative regulation of interleukin-2 production [GO:0032703]; negative regulation of interleukin-3 production [GO:0032712]; negative regulation of interleukin-6 production [GO:0032715]; negative regulation of myeloid dendritic cell activation [GO:0030886]; negative regulation of natural killer cell activation [GO:0032815]; negative regulation of natural killer cell mediated cytotoxicity directed against tumor cell target [GO:0002859]; negative regulation of NF-kappaB transcription factor activity [GO:0032088]; negative regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell [GO:2001189]; negative regulation of T cell proliferation [GO:0042130]; negative regulation of T-helper 1 type immune response [GO:0002826]; negative regulation of tumor necrosis factor production [GO:0032720]; positive regulation of chemokine production [GO:0032722]; positive regulation of defense response to bacterium [GO:1900426]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of innate immune response [GO:0045089]; positive regulation of interferon-gamma production [GO:0032729]; positive regulation of interleukin-1 production [GO:0032732]; positive regulation of interleukin-4 production [GO:0032753]; positive regulation of macrophage activation [GO:0043032]; positive regulation of NIK/NF-kappaB signaling [GO:1901224]; positive regulation of T cell proliferation [GO:0042102]; positive regulation of tumor necrosis factor production [GO:0032760]; regulation of tolerance induction dependent upon immune response [GO:0002652]; toll-like receptor 3 signaling pathway [GO:0034138]; toll-like receptor 7 signaling pathway [GO:0034154]; toll-like receptor 9 signaling pathway [GO:0034162]	cell junction [GO:0030054]; cell surface [GO:0009986]; early endosome [GO:0005769]; immunological synapse [GO:0001772]; integral component of membrane [GO:0016021]	metal ion binding [GO:0046872]
29	Kunitz-type protease inhibitor 2 (Hepatocyte growth factor activator inhibitor type 2) (HAI-2) (Placental bikunin)	SPINT2 HAI2 KOP	252	basement membrane organization [GO:0071711]; cellular response to BMP stimulus [GO:0071773]; epithelial cell morphogenesis involved in placental branching [GO:0060672]; establishment or maintenance of cell polarity [GO:0007163]; negative regulation of cell-cell adhesion [GO:0022408]; negative regulation of cell motility [GO:2000146]; negative regulation of neural precursor cell proliferation [GO:2000178]; neural tube closure [GO:0001843]	cytoplasm [GO:0005737]; extracellular region [GO:0005576]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	endopeptidase inhibitor activity [GO:0004866]; serine-type endopeptidase inhibitor activity [GO:0004867]
30	Triggering receptor expressed on myeloid cells 1 (TREM-1) (Triggering receptor	TREM1	234	acute inflammatory response [GO:0002526]; adaptive immune response [GO:0002250]; humoral immune response [GO:0006959]; innate immune response [GO:0045087]; intracellular signal transduction [GO:0035556]	extracellular region [GO:0005576]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	scaffold protein binding [GO:0097110]; signaling receptor activity [GO:0038023]

	expressed on monocytes 1) (CD antigen CD354)					
31	Polypeptide N-acetylgalactosaminyltransferase 3 (EC 2.4.1.41) (Polypeptide GalNAc transferase 3) (GalNAc-T3) (pp-GaNTase 3) (Protein-UDP acetylgalactosaminyltransferase 3) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 3)	GALNT3	633	carbohydrate metabolic process [GO:0005975]; fibroblast growth factor receptor signaling pathway [GO:0008543]; O-glycan processing [GO:0016266]; protein O-linked glycosylation via serine [GO:0018242]; protein O-linked glycosylation via threonine [GO:0018243]	extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; Golgi cisterna membrane [GO:0032580]; Golgi membrane [GO:0000139]; integral component of membrane [GO:0016021]; membrane [GO:0016020]; perinuclear region of cytoplasm [GO:0048471]	calcium ion binding [GO:0005509]; carbohydrate binding [GO:0030246]; manganese ion binding [GO:0030145]; polypeptide N-acetylgalactosaminyltransferase activity [GO:0004653]
32	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB FLR	206	heme catabolic process [GO:0042167]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; intracellular membrane-bounded organelle [GO:0043231]; nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; terminal bouton [GO:0043195]	biliverdin reductase NAD+ activity [GO:0106276]; biliverdin reductase (NAD(P)+) activity [GO:0004074]; biliverdin reductase (NADP+) activity [GO:0106277]; riboflavin reductase (NADPH) activity [GO:0042602]
33	Corneodesmosin (S protein)	CDSN	529	cell adhesion [GO:0007155]; cell-cell adhesion [GO:0098609]; corneocyte desquamation [GO:0003336]; epidermis development [GO:0008544]; keratinocyte differentiation [GO:0030216]; negative regulation of cornification [GO:1905716]; skin morphogenesis [GO:0043589]	cell-cell junction [GO:0005911]; cornified envelope [GO:0001533]; desmosome [GO:0030057]; extracellular region [GO:0005576]; plasma membrane [GO:0005886]	protein homodimerization activity [GO:0042803]
34	CD99 antigen-like protein 2 (MIC2-like protein 1) (CD antigen CD99)	CD99L2 MIC2L1 UNQ1964/PRO4486	262	cell adhesion [GO:0007155]	focal adhesion [GO:0005925]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	
35	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPIC) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1 CLN2 GIG1 UNQ267/PRO304	563	bone resorption [GO:0045453]; central nervous system development [GO:0007417]; epithelial cell differentiation [GO:0030855]; lipid metabolic process [GO:0006629]; lysosomal protein catabolic process [GO:1905146]; lysosome organization [GO:0007040]; nervous system development [GO:0007399]; neuromuscular process controlling balance [GO:0050885]; peptide catabolic process [GO:0043171]; protein catabolic process [GO:0030163]; protein localization to chromosome, telomeric region [GO:0070198]; proteolysis [GO:0006508]	extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; lysosomal lumen [GO:0043202]; lysosome [GO:0005764]; melanosome [GO:0042470]; membrane raft [GO:0045121]; recycling endosome [GO:0055037]	endopeptidase activity [GO:0004175]; lysophosphatidic acid binding [GO:0035727]; metal ion binding [GO:0046872]; peptidase activity [GO:0008233]; peptide binding [GO:0042277]; serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]; sulfatide binding [GO:0120146]; tripeptidyl-peptidase activity [GO:0008240]
36	Cysteine-rich motor neuron 1 protein (CRIM-1) (Cysteine-rich repeat-containing protein S52) [Cleaved into: Processed cysteine-rich motor neuron 1 protein]	CRIM1 S52 UNQ1886/PRO4330	1036	negative regulation of BMP signaling pathway [GO:0030514]; negative regulation of osteoblast differentiation [GO:0045668]; nervous system development [GO:0007399]	extracellular region [GO:0005576]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	insulin-like growth factor-activated receptor activity [GO:0005010]; insulin-like growth factor binding [GO:0005520]; PDZ domain binding [GO:0030165]; serine-type endopeptidase inhibitor activity [GO:0004867]
37	Interleukin-1 receptor-associated kinase 4 (IRAK-4) (EC 2.7.11.1) (Renal carcinoma antigen NY-REN-64)	IRAK4	460	cytokine-mediated signaling pathway [GO:0019221]; innate immune response [GO:0045087]; interleukin-1-mediated signaling pathway [GO:0070498]; intracellular signal transduction [GO:0035556]; JNK cascade [GO:0007254]; MyD88-dependent toll-like receptor signaling pathway [GO:0002755]; neutrophil mediated immunity [GO:0002446]; neutrophil migration [GO:1990266]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of smooth muscle cell proliferation [GO:0048661]; toll-like receptor 9 signaling pathway [GO:0034162]; toll-like receptor signaling pathway [GO:0002224]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; endosome membrane [GO:0010008]; extracellular space [GO:0005615]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	ATP binding [GO:0005524]; interleukin-1 receptor binding [GO:0005149]; magnesium ion binding [GO:0000287]; protein kinase binding [GO:0019901]; protein serine/threonine kinase activity [GO:0004674]; protein serine kinase activity [GO:0106310]; protein threonine kinase activity [GO:0106311]
38	Paired immunoglobulin-like type 2 receptor alpha (Cell surface receptor FDF03) (Inhibitory receptor PILR-alpha)	PILRA	303	signal transduction [GO:0007165]	extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	MHC class I protein binding [GO:0042288]
39	Cytoskeleton-associated protein 4 (63-kDa cytoskeleton-linking membrane protein) (Climp-63) (p63)	CKAP4	602		azurophil granule membrane [GO:0035577]; cytoplasmic ribonucleoprotein granule [GO:0036464]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]; endoplasmic reticulum membrane [GO:0005789]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; lamellar body [GO:0042599]; lipid droplet [GO:0005811]; membrane [GO:0016020]; nuclear speck [GO:0016607]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; rough endoplasmic reticulum [GO:0005791]; specific granule membrane [GO:0035579]	RNA binding [GO:0003723]
40	CD209 antigen (C-type lectin domain	CD209 CLEC	404	adaptive immune response [GO:0002250]; antigen processing and presentation [GO:0019882]; B cell adhesion [GO:0097323]; cell-cell recognition [GO:0009988];	cell surface [GO:0009986]; cytoplasm [GO:0005737]; external side of plasma	carbohydrate binding [GO:0030246]; mannose binding [GO:0005537]; metal

	family 4 member L) (Dendritic cell-specific ICAM-3-grabbing non-integrin 1) (DC-SIGN) (DC-SIGN1) (CD antigen CD209)	4L		endocytosis [GO:0006897]; heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules [GO:0007157]; innate immune response [GO:0045087]; intracellular signal transduction [GO:0035556]; intracellular transport of virus [GO:0075733]; leukocyte cell-cell adhesion [GO:0007159]; modulation by virus of host process [GO:0019048]; peptide antigen transport [GO:0046968]; positive regulation of T cell proliferation [GO:0042102]; positive regulation of viral life cycle [GO:1903902]; regulation of T cell proliferation [GO:0042129]; viral entry into host cell [GO:0046718]; viral genome replication [GO:0019079]; virion attachment to host cell [GO:0019062]	membrane [GO:0009897]; extracellular region [GO:0005576]; host cell [GO:0043657]; integral component of membrane [GO:0016021]; membrane [GO:0016020]; plasma membrane [GO:0005886]	ion binding [GO:0046872]; peptide antigen binding [GO:0042605]; virion binding [GO:0046790]; virus receptor activity [GO:0001618]
41	Beta-microseminoprotein (Immunoglobulin-binding factor) (IGBF) (PN44) (Prostate secreted seminal plasma protein) (Prostate secretory protein of 94 amino acids) (PSP-94) (PSP94) (Seminal plasma beta-inhibin)	MSMB PRSP	114		extracellular space [GO:0005615]; nucleus [GO:0005634]	
42	Cytosolic phospholipase A2 (cPLA2) (Phospholipase A2 group IVA) [Includes: Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase (EC 3.1.1.5)]	PLA2G4A CPLA2 PLA2G4	749	arachidonic acid metabolic process [GO:0019369]; arachidonic acid secretion [GO:0050482]; cellular response to antibiotic [GO:0071236]; glycerol metabolic process [GO:0006071]; glycerophospholipid catabolic process [GO:0046475]; icosanoid metabolic process [GO:0006690]; leukotriene biosynthetic process [GO:0019370]; monoacylglycerol biosynthetic process [GO:0006640]; phosphatidylcholine acyl-chain remodeling [GO:0036151]; phosphatidylcholine catabolic process [GO:0034638]; phosphatidylglycerol catabolic process [GO:0034478]; platelet activating factor biosynthetic process [GO:0006663]; positive regulation of macrophage activation [GO:0043032]; positive regulation of platelet activation [GO:0010572]; positive regulation of prostaglandin secretion [GO:0032308]; positive regulation of T-helper 1 type immune response [GO:0002827]; prostaglandin biosynthetic process [GO:0001516]; regulation of cell population proliferation [GO:0042127]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]; Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]; intracellular membrane-bounded organelle [GO:0043231]; mitochondrial inner membrane [GO:0005743]; nuclear envelope [GO:0005635]; nucleus [GO:0005634]	calcium-dependent phospholipase A2 activity [GO:0047498]; calcium-dependent phospholipid binding [GO:0005544]; calcium-independent phospholipase A2 activity [GO:0047499]; calcium ion binding [GO:0005509]; ceramide 1-phosphate binding [GO:1902387]; lysophospholipase activity [GO:0004622]; O-acyltransferase activity [GO:0008374]; phosphatidylinositol-3-phosphate binding [GO:0032266]; phosphatidylinositol-4-phosphate binding [GO:0070273]; phosphatidylinositol-5-phosphate binding [GO:0010314]; phosphatidyl phospholipase B activity [GO:0102545]; phospholipase A2 activity [GO:0004623]; phospholipase A2 activity (consuming 1,2-dipalmitoylphosphatidylcholine) [GO:0102567]; phospholipase A2 activity consuming 1,2-dioleoylphosphatidylethanolamine) [GO:0102568]
43	Endothelial cell-selective adhesion molecule	ESAM UNQ220/PRO246	390	bicellular tight junction assembly [GO:0070830]; cell-cell adhesion [GO:0098609]; cellular protein localization [GO:0034613]; homophilic cell adhesion via plasma membrane adhesion molecules [GO:0007156]; maintenance of blood-brain barrier [GO:0035633]; regulation of actin cytoskeleton reorganization [GO:2000249]; regulation of actin filament polymerization [GO:0030833]	adherens junction [GO:0005912]; bicellular tight junction [GO:0005923]; cell-cell junction [GO:0005911]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]; protein-containing complex [GO:0032991]	cell-cell adhesion mediator activity [GO:0098632]
44	Angiopoietin-related protein 4 (Angiopoietin-like protein 4) (Hepatic fibrinogen/angiopoietin-related protein) (HFARP) [Cleaved into: ANGPTL4 N-terminal chain; ANGPTL4 C-terminal chain]	ANGPTL4 ARP4 HFARP PGARP PP1158 PSEC0166 UNQ171/PRO197	406	angiogenesis [GO:0001525]; lipid metabolic process [GO:0006629]; negative regulation of apoptotic process [GO:0043066]; negative regulation of endothelial cell apoptotic process [GO:2000352]; negative regulation of lipoprotein lipase activity [GO:0051005]; positive regulation of angiogenesis [GO:0045766]; protein unfolding [GO:0043335]; response to hypoxia [GO:0001666]; triglyceride homeostasis [GO:0070328]	blood microparticle [GO:0072562]; collagen-containing extracellular matrix [GO:0062023]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	enzyme inhibitor activity [GO:0004857]; identical protein binding [GO:0042802]; signaling receptor binding [GO:0005102]
45	T-cell-specific surface glycoprotein CD28 (TP44) (CD antigen CD28)	CD28	220	apoptotic signaling pathway [GO:0097190]; cell surface receptor signaling pathway [GO:0007166]; humoral immune response [GO:0006959]; negative regulation of apoptotic process [GO:0043066]; negative regulation of gene expression [GO:0010629]; negative thymic T cell selection [GO:0045060]; positive regulation of alpha-beta T cell proliferation [GO:0046641]; positive regulation of cytokine production [GO:0001819]; positive regulation of gene expression [GO:0010628]; positive regulation of inflammatory response to antigenic stimulus [GO:0002863]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-2 production [GO:0032743]; positive regulation of interleukin-4 production [GO:0032753]; positive regulation of isotype switching to IgG isotypes [GO:0048304]; positive regulation of mitotic nuclear division [GO:0045840]; positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of T cell proliferation [GO:0042102]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of translation [GO:0045727]; positive regulation of viral genome replication [GO:0045070]; regulation of regulatory T cell differentiation [GO:0045589]; regulatory T cell differentiation [GO:0045066]; T cell activation [GO:0042110]; T cell costimulation [GO:0031295]; T cell receptor signaling pathway [GO:0050852]	cell surface [GO:0009986]; cytosol [GO:0005829]; external side of plasma membrane [GO:0009897]; immunological synapse [GO:0001772]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]; protein complex involved in cell adhesion [GO:0098636]	coreceptor activity [GO:0015026]; identical protein binding [GO:0042802]; protease binding [GO:0002020]; protein kinase binding [GO:0019901]
46	C-type lectin domain family 11 member A (C-type lectin superfamily member 3) (Lymphocyte secreted C-type lectin) (Osteolectin) (Stem cell growth factor) (p47)	CLEC11A CLECSF3 LSLCL SCGF	323	ossification [GO:0001503]; positive regulation of cell population proliferation [GO:0008284]	cytoplasm [GO:0005737]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	carbohydrate binding [GO:0030246]; growth factor activity [GO:0008083]
47	Cell adhesion molecule-related/down-regulated by oncogenes	CDON CDO	1287	cell adhesion [GO:0007155]; embryonic morphogenesis [GO:0048598]; positive regulation of myoblast differentiation [GO:0045663]; regulation of neuron differentiation [GO:0045664]; smoothened signaling pathway [GO:0007224]	integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	
4	LRP chaperone	MESD	234	mesoderm development [GO:0007498]; ossification [GO:0001503]; phagocytosis	endoplasmic reticulum [GO:0005783];	identical protein binding [GO:0042802];

8	MESD (LDLR chaperone MESD) (Mesoderm development LRP chaperone MESD) (Mesoderm development candidate 2) (Mesoderm development protein) (Renal carcinoma antigen NY-REN-61)	KIAA0081 MESDC2 MESDM UNQ1911/PRO4369		[GO:0006909]; positive regulation of skeletal muscle acetylcholine-gated channel clustering [GO:1904395]; protein folding [GO:0006457]; protein localization to cell surface [GO:0034394]; Wnt signaling pathway [GO:0016055]	plasma membrane [GO:0005886]	low-density lipoprotein particle receptor binding [GO:0050750]
49	Peroxiredoxin-5, mitochondrial (EC 1.11.1.24) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 71B) (PLP) (Peroxiredoxin V) (Prx-V) (Peroxisomal antioxidant enzyme) (TPx type VI) (Thioredoxin peroxidase PMP20) (Thioredoxin-dependent peroxiredoxin 5)	PRDX5 ACR1 SBBI10	214	cell redox homeostasis [GO:0045454]; cellular response to oxidative stress [GO:0034599]; cellular response to reactive oxygen species [GO:0034614]; hydrogen peroxide catabolic process [GO:0042744]; inflammatory response [GO:0006954]; NADPH oxidation [GO:0070995]; negative regulation of apoptotic process [GO:0043066]; negative regulation of oxidoreductase activity [GO:0051354]; negative regulation of transcription by RNA polymerase III [GO:0016480]; positive regulation of collagen biosynthetic process [GO:0032967]; reactive nitrogen species metabolic process [GO:2001057]; regulation of apoptosis involved in tissue homeostasis [GO:0060785]; response to oxidative stress [GO:0006979]	cytoplasm [GO:0005737]; cytoplasmic vesicle [GO:0031410]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; intracellular membrane-bounded organelle [GO:0043231]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; peroxisomal matrix [GO:0005782]; peroxisome [GO:0005777]	antioxidant activity [GO:0016209]; cysteine-type endopeptidase inhibitor activity involved in apoptotic process [GO:0043027]; peroxidase activity [GO:0004601]; peroxiredoxin activity [GO:0051920]; peroxynitrite reductase activity [GO:0072541]; RNA polymerase III transcription regulatory region sequence-specific DNA binding [GO:0001016]; signaling receptor binding [GO:0005102]; thioredoxin peroxidase activity [GO:0008379]
50	CD177 antigen (Human neutrophil alloantigen 2a) (HNA-2a) (NB1 glycoprotein) (NB1 GP) (Polycythemia rubra vera protein 1) (PRV-1) (CD antigen CD177)	CD177 NB1 PRV1 UNQ595/PRO1181	437	cell adhesion [GO:0007155]; cell-cell adhesion via plasma-membrane adhesion molecules [GO:0098742]; cell-cell junction maintenance [GO:0045217]; innate immune response [GO:0045087]; leukocyte cell-cell adhesion [GO:0007159]; neutrophil extravasation [GO:0072672]; neutrophil migration [GO:1990266]; positive regulation of neutrophil degranulation [GO:0043315]; positive regulation of superoxide anion generation [GO:0032930]; protein localization to cell surface [GO:0034394]; regulation of endocytosis [GO:0030100]; regulation of integrin-mediated signaling pathway [GO:2001044]	anchored component of plasma membrane [GO:0046658]; extracellular exosome [GO:0070062]; lamellipodium [GO:0030027]; plasma membrane [GO:0005886]; plasma membrane raft [GO:0044853]; secretory granule membrane [GO:0030667]; specific granule membrane [GO:0035579]; tertiary granule membrane [GO:0070821]	calcium-dependent protein binding [GO:0048306]; integrin binding [GO:0005178]; protease binding [GO:0002020]
51	ADP-sugar pyrophosphatase (EC 3.6.1.13) (8-oxo-dGDP phosphatase) (EC 3.6.1.58) (Nuclear ATP-synthesis protein NUDIX5) (EC 2.7.7.96) (Nucleoside diphosphate-linked moiety X motif 5) (Nudix motif 5) (hNUDT5) (YSA1H)	NUDT5 NUDIX5 HSPC115	219	ATP generation from poly-ADP-D-ribose [GO:1990966]; chromatin remodeling [GO:0006338]; D-ribose catabolic process [GO:0019303]; nucleobase-containing small molecule metabolic process [GO:0055086]; nucleoside phosphate metabolic process [GO:0006753]; nucleotide metabolic process [GO:0009117]; ribonucleoside diphosphate catabolic process [GO:0009191]; ribose phosphate metabolic process [GO:0019693]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; nucleus [GO:0005634]	8-oxo-dGDP phosphatase activity [GO:0044715]; 8-oxo-GDP phosphatase activity [GO:0044716]; ADP-ribose diphosphatase activity [GO:0047631]; ADP-sugar diphosphatase activity [GO:0019144]; identical protein binding [GO:0042802]; magnesium ion binding [GO:0000287]; nucleotidyltransferase activity [GO:0016779]; protein homodimerization activity [GO:0042803]; snoRNA binding [GO:0030515]
52	Early activation antigen CD69 (Activation inducer molecule) (AIM) (BL-AC/P26) (C-type lectin domain family 2 member C) (EA1) (Early T-cell activation antigen p60) (GP32/28) (Leukocyte surface antigen Leu-23) (MLR-3) (CD antigen CD69)	CD69 CLEC2C	199		external side of plasma membrane [GO:0009897]; integral component of plasma membrane [GO:0005887]; protein-containing complex [GO:0032991]	calcium ion binding [GO:0005509]; carbohydrate binding [GO:0030246]; identical protein binding [GO:0042802]; transmembrane signaling receptor activity [GO:0004888]
53	Osteomodulin (Keratan sulfate proteoglycan osteomodulin) (KSPG osteomodulin) (Osteoadherin) (OSAD)	OMD SLRR2C UNQ190/PRO216	421	cell adhesion [GO:0007155]; regulation of bone mineralization [GO:0030500]	collagen-containing extracellular matrix [GO:0062023]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]	
54	Kunitz-type protease inhibitor 1 (Hepatocyte growth factor activator inhibitor type 1) (HAI-1)	SPINT1 HAI1 UNQ223/PRO256	529	branching involved in labyrinthine layer morphogenesis [GO:0060670]; cellular response to BMP stimulus [GO:0071773]; extracellular matrix organization [GO:0030198]; negative regulation of neural precursor cell proliferation [GO:2000178]; neural tube closure [GO:0001843]; placenta blood vessel development [GO:0060674]; positive regulation of glial cell differentiation [GO:0045687]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; membrane [GO:0016020]; plasma membrane [GO:0005886]	serine-type endopeptidase inhibitor activity [GO:0004867]
55	Islet cell autoantigen 1 (69 kDa islet cell autoantigen) (ICA69) (Islet cell autoantigen p69) (ICAp69) (p69)	ICA1	483	neurotransmitter transport [GO:0006836]; regulation of insulin secretion [GO:0050796]; regulation of transport [GO:0051049]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]; intracellular membrane-bounded organelle [GO:0043231]; secretory granule membrane [GO:0030667]; synaptic vesicle membrane [GO:0030672]	membrane curvature sensor activity [GO:0140090]; protein domain specific binding [GO:0019904]
56	Protein disulfide isomerase CRELD2 (EC 5.3.4.1) (Cysteine-rich with EGF-like domain protein 2)	CRELD2 UNQ185/PRO211	353		endoplasmic reticulum [GO:0005783]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]	calcium ion binding [GO:0005509]; protein disulfide isomerase activity [GO:0003756]
57	Neurabin-2 (Neurabin-II) (Protein phosphatase 1 regulatory subunit 9B) (Spinophilin)	PPP1R9B PPP1R6	817	actin filament depolymerization [GO:0030042]; actin filament organization [GO:0007015]; aging [GO:0007568]; calcium-mediated signaling [GO:0019722]; cell migration [GO:0016477]; cellular response to drug [GO:0035690]; cellular response to epidermal growth factor stimulus [GO:0071364]; cellular response to estradiol stimulus [GO:0071392]; cellular response to morphine [GO:0071315]; cellular response to peptide [GO:1901653]; cerebral cortex development [GO:0021987]; dendrite development [GO:0016358]; developmental process involved in reproduction	actin cytoskeleton [GO:0015629]; adherens junction [GO:0005912]; cortical actin cytoskeleton [GO:0030864]; cytoplasm [GO:0005737]; cytoplasmic side of dendritic spine plasma membrane [GO:1990780]; dendrite [GO:0030425];	actin filament binding [GO:0051015]; D2 dopamine receptor binding [GO:0031749]; kinase binding [GO:0019900]; protein C-terminus binding [GO:0008022]; protein kinase activity [GO:0004672]; protein phosphatase 1 binding [GO:0008157];

				[GO:0003006]; filopodium assembly [GO:0046847]; hippocampus development [GO:0021766]; learning [GO:0007612]; male mating behavior [GO:0060179]; modulation of chemical synaptic transmission [GO:0050804]; negative regulation of cell growth [GO:0030308]; negative regulation of phosphoprotein phosphatase activity [GO:0032515]; neuron projection development [GO:0031175]; positive regulation of protein localization to actin cortical patch [GO:1904372]; positive regulation of protein localization to plasma membrane [GO:1903078]; protein localization to actin cytoskeleton [GO:1903119]; protein localization to cell periphery [GO:1990778]; regulation of cell cycle [GO:0051726]; regulation of cell growth by extracellular stimulus [GO:0001560]; regulation of cell population proliferation [GO:0042127]; regulation of exit from mitosis [GO:0007096]; regulation of opioid receptor signaling pathway [GO:2000474]; regulation of protein phosphorylation [GO:0001932]; reproductive system development [GO:0061458]; response to amphetamine [GO:0001975]; response to clozapine [GO:0097338]; response to immobilization stress [GO:0035902]; response to kainic acid [GO:1904373]; response to L-phenylalanine derivative [GO:1904386]; response to nicotine [GO:0035094]; response to prostaglandin E [GO:0034695]; response to steroid hormone [GO:0048545]; RNA splicing [GO:0008380]	dendritic spine head [GO:0044327]; dendritic spine neck [GO:0044326]; filopodium [GO:0030175]; growth cone [GO:0030426]; lamellipodium [GO:0030027]; neuronal cell body [GO:0043025]; nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; postsynaptic density [GO:0014069]; protein phosphatase type 1 complex [GO:0000164]; ruffle membrane [GO:0032587]	protein phosphatase inhibitor activity [GO:0004864]; transmembrane transporter binding [GO:0044325]
58	Desmocollin-2 (Cadherin family member 2) (Desmocollin-3) (Desmosomal glycoprotein II) (Desmosomal glycoprotein III)	DSC2 CDHF2 DSC3	901	bundle of His cell-Purkinje myocyte adhesion involved in cell communication [GO:0086073]; cardiac muscle cell-cardiac muscle cell adhesion [GO:0086042]; cell adhesion [GO:0007155]; cell-cell adhesion [GO:0098609]; homophilic cell adhesion via plasma membrane adhesion molecules [GO:0007156]; regulation of heart rate by cardiac conduction [GO:0086091]; regulation of ventricular cardiac muscle cell action potential [GO:0098911]	cell-cell junction [GO:0005911]; cornified envelope [GO:0001533]; cytoplasmic vesicle [GO:0031410]; desmosome [GO:0030057]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; intercalated disc [GO:0014704]; plasma membrane [GO:0005886]	calcium ion binding [GO:0005509]; cell adhesive protein binding involved in bundle of His cell-Purkinje myocyte communication [GO:0086083]
59	Integrin beta-1 (Fibronectin receptor subunit beta) (Glycoprotein IIa) (GPIIA) (VLA-4 subunit beta) (CD antigen CD29)	ITGB1 FNRB MDF2 MSK12	798	axon extension [GO:0048675]; basement membrane organization [GO:0071711]; B cell differentiation [GO:0030183]; calcium-independent cell-matrix adhesion [GO:0007161]; cardiac muscle cell differentiation [GO:0055007]; CD40 signaling pathway [GO:0023035]; cell adhesion [GO:0007155]; cell adhesion mediated by integrin [GO:0033627]; cell-cell adhesion mediated by integrin [GO:0033631]; cell fate specification [GO:0001708]; cell-matrix adhesion [GO:0007160]; cell migration [GO:0016477]; cell migration involved in sprouting angiogenesis [GO:0002042]; cell projection organization [GO:0030030]; cell-substrate adhesion [GO:0031589]; cellular defense response [GO:0006968]; cellular response to low-density lipoprotein particle stimulus [GO:0071404]; dendrite morphogenesis [GO:0048813]; establishment of mitotic spindle orientation [GO:0000132]; formation of radial glial scaffolds [GO:0021943]; G1/S transition of mitotic cell cycle [GO:0000082]; germ cell migration [GO:0008354]; heterotypic cell-cell adhesion [GO:0034113]; homophilic cell adhesion via plasma membrane adhesion molecules [GO:0007156]; integrin-mediated signaling pathway [GO:0007229]; in utero embryonic development [GO:0001701]; lamellipodium assembly [GO:0030032]; leukocyte cell-cell adhesion [GO:0007159]; leukocyte tethering or rolling [GO:0050901]; maintenance of blood-brain barrier [GO:0035633]; mesodermal cell differentiation [GO:0048333]; negative regulation of anoikis [GO:2000811]; negative regulation of cell differentiation [GO:0045596]; negative regulation of Rho protein signal transduction [GO:0035024]; phagocytosis [GO:0006909]; positive regulation of angiogenesis [GO:0045766]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cell migration [GO:0030335]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of fibroblast migration [GO:0010763]; positive regulation of glutamate uptake involved in transmission of nerve impulse [GO:0051951]; positive regulation of GTPase activity [GO:0043547]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of protein localization to plasma membrane [GO:1903078]; positive regulation of signaling receptor activity [GO:2000273]; positive regulation of wound healing [GO:0090303]; reactive gliosis [GO:0150103]; receptor internalization [GO:0031623]; regulation of cell cycle [GO:0051726]; regulation of collagen catabolic process [GO:0010710]; regulation of inward rectifier potassium channel activity [GO:1901979]; regulation of spontaneous synaptic transmission [GO:0150003]; sarcomere organization [GO:0045214]; visual learning [GO:0008542]	cell surface [GO:0009986]; cleavage furrow [GO:0032154]; cytoplasm [GO:0005737]; dendritic spine [GO:0043197]; endosome membrane [GO:0010008]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; filopodium [GO:0030175]; focal adhesion [GO:0005925]; glial cell projection [GO:0097386]; glutamatergic synapse [GO:0098978]; integral component of synaptic membrane [GO:0099699]; integrin alpha10-beta1 complex [GO:0034680]; integrin alpha11-beta1 complex [GO:0034681]; integrin alpha1-beta1 complex [GO:0034665]; integrin alpha2-beta1 complex [GO:0034666]; integrin alpha3-beta1 complex [GO:0034667]; integrin alpha4-beta1 complex [GO:0034668]; integrin alpha5-beta1 complex [GO:0034674]; integrin alpha7-beta1 complex [GO:0034677]; integrin alpha8-beta1 complex [GO:0034678]; intercalated disc [GO:0014704]; lamellipodium [GO:0030027]; melanosome [GO:0042470]; membrane [GO:0016020]; membrane raft [GO:0045121]; myelin sheath abaxonal region [GO:0035748]; neuromuscular junction [GO:0031594]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]; recycling endosome [GO:0055037]; ruffle [GO:0001726]; ruffle membrane [GO:0032587]; sarcolemma [GO:0042383]; Schaffer collateral - CA1 synapse [GO:0098685]	actin binding [GO:0003779]; cadherin binding [GO:0045296]; cell adhesion molecule binding [GO:0050839]; collagen binding involved in cell-matrix adhesion [GO:0098639]; coreceptor activity [GO:0015026]; fibronectin binding [GO:0001968]; integrin binding [GO:0005178]; laminin binding [GO:0043236]; metal ion binding [GO:0046872]; protease binding [GO:0002020]; protein-containing complex binding [GO:0044877]; protein heterodimerization activity [GO:0046982]; protein tyrosine kinase binding [GO:1990782]; virus receptor activity [GO:0001618]
60	Parathyroid hormone/parathyroid hormone-related peptide receptor (PTH/PTHrP type I receptor) (PTH/PTHr receptor) (Parathyroid hormone 1 receptor) (PTH1 receptor)	PTH1R PTHR PTHR1	593	adenylate cyclase-activating G protein-coupled receptor signaling pathway [GO:0007189]; adenylate cyclase-modulating G protein-coupled receptor signaling pathway [GO:0007188]; aging [GO:0007568]; bone mineralization [GO:0030282]; bone resorption [GO:0045453]; cell maturation [GO:0048469]; cell surface receptor signaling pathway [GO:0007166]; cellular calcium ion homeostasis [GO:0006874]; chondrocyte differentiation [GO:0002062]; G protein-coupled receptor signaling pathway [GO:0007186]; G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger [GO:0007187]; in utero embryonic development [GO:0001701]; negative regulation of cell population proliferation [GO:0008285]; osteoblast development [GO:0002076]; phospholipase C-activating G protein-coupled receptor signaling pathway [GO:0007200]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of cytosolic calcium ion concentration [GO:0007204]; positive regulation of inositol phosphate biosynthetic process [GO:0060732]; skeletal system development [GO:0001501]	apical plasma membrane [GO:0016324]; basolateral plasma membrane [GO:0016323]; brush border membrane [GO:0031526]; cytoplasm [GO:0005737]; integral component of plasma membrane [GO:0005887]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]	G protein-coupled peptide receptor activity [GO:0008528]; parathyroid hormone receptor activity [GO:0004991]; peptide hormone binding [GO:0017046]; protein homodimerization activity [GO:0042803]; protein self-association [GO:0043621]
61	Laminin subunit alpha-4 (Laminin-14 subunit alpha) (Laminin-8 subunit alpha) (Laminin-9 subunit alpha)	LAMA4	1823	cell adhesion [GO:0007155]; negative regulation of cold-induced thermogenesis [GO:0120163]; regulation of cell adhesion [GO:0030155]; regulation of cell migration [GO:0030334]; regulation of embryonic development [GO:0045995]	basement membrane [GO:0005604]; collagen-containing extracellular matrix [GO:0062023]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]	extracellular matrix structural constituent [GO:0005201]; signaling receptor binding [GO:0005102]
62	Interleukin-10 (IL-10) (Cytokine synthesis inhibitory factor) (CSIF)	IL10	178	aging [GO:0007568]; B cell differentiation [GO:0030183]; B cell proliferation [GO:0042100]; branching involved in labyrinthine layer morphogenesis [GO:0060670]; cellular response to estradiol stimulus [GO:0071392]; cellular response to hepatocyte growth factor stimulus [GO:0035729]; cellular response to lipopolysaccharide [GO:0071222]; cytoplasmic sequestering of NF-kappaB [GO:0007253]; defense response to bacterium [GO:0042742]; defense response to protozoan [GO:0042832]; endothelial cell apoptotic process [GO:0072577]; hemopoiesis [GO:0030097]; leukocyte chemotaxis [GO:0030595]; liver regeneration [GO:0097421]; negative regulation of apoptotic process [GO:0043066]; negative regulation of autophagy [GO:0010507]; negative regulation of B cell proliferation [GO:0030889]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of chemokine (C-C motif) ligand 5 production [GO:0071650]; negative regulation of chronic inflammatory response to antigenic stimulus [GO:0002875]; negative regulation of cytokine activity [GO:0060302]; negative regulation of cytokine production [GO:0001818]; negative regulation of cytokine production involved in immune response [GO:0002719]; negative regulation of	extracellular region [GO:0005576]; extracellular space [GO:0005615]	cytokine activity [GO:0005125]; growth factor activity [GO:0008083]; interleukin-10 receptor binding [GO:0005141]; protein dimerization activity [GO:0046983]

				heterotypic cell-cell adhesion [GO:0034115]; negative regulation of hydrogen peroxide-induced neuron death [GO:1903208]; negative regulation of inflammatory response [GO:0050728]; negative regulation of interferon-alpha production [GO:0032687]; negative regulation of interferon-gamma production [GO:0032689]; negative regulation of interleukin-12 production [GO:0032695]; negative regulation of interleukin-18 production [GO:0032701]; negative regulation of interleukin-1 production [GO:0032692]; negative regulation of interleukin-6 production [GO:0032715]; negative regulation of interleukin-8 production [GO:0032717]; negative regulation of membrane protein ectodomain proteolysis [GO:0051045]; negative regulation of MHC class II biosynthetic process [GO:0045347]; negative regulation of mitotic cell cycle [GO:0045930]; negative regulation of myeloid dendritic cell activation [GO:0030886]; negative regulation of neuron apoptotic process [GO:0043524]; negative regulation of nitric oxide biosynthetic process [GO:0045019]; negative regulation of sensory perception of pain [GO:1904057]; negative regulation of T cell proliferation [GO:0042130]; negative regulation of tumor necrosis factor production [GO:0032720]; negative regulation of vascular associated smooth muscle cell proliferation [GO:1904706]; positive regulation of B cell apoptotic process [GO:0002904]; positive regulation of cell cycle [GO:0045787]; positive regulation of cytokine production [GO:0001819]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of endothelial cell proliferation [GO:0001938]; positive regulation of heterotypic cell-cell adhesion [GO:0034116]; positive regulation of immunoglobulin production [GO:0002639]; positive regulation of macrophage activation [GO:0043032]; positive regulation of MHC class II biosynthetic process [GO:0045348]; positive regulation of plasma cell differentiation [GO:1900100]; positive regulation of pri-miRNA transcription by RNA polymerase II [GO:1902895]; positive regulation of receptor signaling pathway via JAK-STAT [GO:0046427]; positive regulation of signaling receptor activity [GO:2000273]; positive regulation of sprouting angiogenesis [GO:1903672]; positive regulation of transcription, DNA-templated [GO:0045893]; positive regulation of vascular associated smooth muscle cell proliferation [GO:1904707]; regulation of gene expression [GO:0010468]; regulation of isotype switching [GO:0045191]; regulation of response to wounding [GO:1903034]; regulation of synapse organization [GO:0050807]; response to activity [GO:0014823]; response to carbon monoxide [GO:0034465]; response to drug [GO:0042493]; response to glucocorticoid [GO:0051384]; response to inactivity [GO:0014854]; response to insulin [GO:0032868]; response to molecule of bacterial origin [GO:0002237]; type 2 immune response [GO:0042092]		
63	Lymphocyte function-associated antigen 3 (Ag3) (Surface glycoprotein LFA-3) (CD antigen CD58)	CD58 LFA3	250	cell-cell adhesion [GO:0098609]; cellular response to interferon-gamma [GO:0071346]; cellular response to tumor necrosis factor [GO:0071356]; heterotypic cell-cell adhesion [GO:0034113]; positive regulation of interleukin-8 production [GO:0032757]	cell surface [GO:0009986]; extracellular exosome [GO:0070062]; ficolin-1-rich granule membrane [GO:0101003]; integral component of plasma membrane [GO:0005887]; membrane [GO:0016020]; plasma membrane [GO:0005886]; secretory granule membrane [GO:0030667]	signaling receptor binding [GO:0005102]
64	Plexin-A4	PLXNA4 KIAA1550 PLXNA4A PLXNA4B UNQ2820/PRO34003	1894	anterior commissure morphogenesis [GO:0021960]; chemorepulsion of branchiomotor axon [GO:0021793]; facial nerve structural organization [GO:0021612]; glossopharyngeal nerve morphogenesis [GO:0021615]; negative regulation of cell adhesion [GO:0007162]; positive regulation of axonogenesis [GO:0050772]; postganglionic parasympathetic fiber development [GO:0021784]; regulation of axon extension involved in axon guidance [GO:0048841]; regulation of cell migration [GO:0030334]; regulation of cell shape [GO:0008360]; regulation of GTPase activity [GO:0043087]; regulation of negative chemotaxis [GO:0050923]; semaphorin-plexin signaling pathway [GO:0071526]; semaphorin-plexin signaling pathway involved in axon guidance [GO:1902287]; sympathetic nervous system development [GO:0048485]; trigeminal nerve structural organization [GO:0021637]; vagus nerve morphogenesis [GO:0021644]	integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]; semaphorin receptor complex [GO:0002116]	semaphorin receptor activity [GO:0017154]
65	4-galactosyl-N-acetylglucosaminide 3-alpha-L-fucosyltransferase FUT5 (EC 2.4.1.152) (3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase FUT5) (EC 2.4.1.65) (Fucosyltransferase 5) (Fucosyltransferase V) (Fuc-TV) (FucT-V) (Galactoside 3-L-fucosyltransferase)	FUT5	374	carbohydrate metabolic process [GO:0005975]; ceramide metabolic process [GO:0006672]; fucosylation [GO:0036065]; L-fucose catabolic process [GO:0042355]; oligosaccharide biosynthetic process [GO:0009312]; oligosaccharide metabolic process [GO:0009311]; protein glycosylation [GO:0006486]	Golgi apparatus [GO:0005794]; Golgi cisterna membrane [GO:0032580]; Golgi membrane [GO:0000139]; integral component of membrane [GO:0016021]	3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity [GO:0017060]; 4-galactosyl-N-acetylglucosaminide 3-alpha-L-fucosyltransferase activity [GO:0017083]; alpha-(1->3)-fucosyltransferase activity [GO:0046920]; fucosyltransferase activity [GO:0008417]
66	Interleukin-12 receptor subunit beta-1 (IL-12 receptor subunit beta-1) (IL-12R subunit beta-1) (IL-12R-beta-1) (IL-12RB1) (IL-12 receptor beta component) (CD antigen CD212)	IL12RB1 IL12RB	662	cellular response to interferon-gamma [GO:0071346]; cytokine-mediated signaling pathway [GO:0019221]; interleukin-12-mediated signaling pathway [GO:0035722]; interleukin-23-mediated signaling pathway [GO:0038155]; positive regulation of activated T cell proliferation [GO:0042104]; positive regulation of defense response to virus by host [GO:0002230]; positive regulation of interferon-gamma production [GO:0032729]; positive regulation of memory T cell differentiation [GO:0043382]; positive regulation of T cell mediated cytotoxicity [GO:0001916]; positive regulation of T-helper 17 cell lineage commitment [GO:2000330]; positive regulation of T-helper 17 type immune response [GO:2000318]; positive regulation of T-helper 1 type immune response [GO:0002827]; signal transduction [GO:0007165]	external side of plasma membrane [GO:0009897]; interleukin-12 receptor complex [GO:0042022]; interleukin-23 receptor complex [GO:0072536]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]	cytokine binding [GO:0019955]; cytokine receptor activity [GO:0004896]
67	CD109 antigen (150 kDa TGF-beta-1-binding protein) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 7) (Platelet-specific Gov antigen) (p180) (r150) (CD antigen CD109)	CD109 CPAMD7	1445	hair follicle development [GO:0001942]; negative regulation of keratinocyte proliferation [GO:0010839]; negative regulation of protein phosphorylation [GO:0001933]; negative regulation of transforming growth factor beta receptor signaling pathway [GO:0030512]; negative regulation of wound healing [GO:0061045]; osteoclast fusion [GO:0072675]; regulation of keratinocyte differentiation [GO:0045616]	anchored component of membrane [GO:0031225]; cell surface [GO:0009986]; cytosol [GO:0005829]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]; platelet alpha granule membrane [GO:0031092]	serine-type endopeptidase inhibitor activity [GO:0004867]; transforming growth factor beta binding [GO:0050431]
68	Integrin alpha-5 (CD49 antigen-like family member E) (Fibronectin receptor subunit alpha) (Integrin alpha-F) (VLA-5) (CD antigen CD49e) [Cleaved into: Integrin alpha-5	ITGA5 FNRA	1049	angiogenesis [GO:0001525]; CD40 signaling pathway [GO:0023035]; cell adhesion [GO:0007155]; cell adhesion mediated by integrin [GO:0033627]; cell-substrate adhesion [GO:0031589]; endodermal cell differentiation [GO:0035987]; heterotypic cell-cell adhesion [GO:0034113]; integrin-mediated signaling pathway [GO:0007229]; negative regulation of anoikis [GO:2000811]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of sprouting angiogenesis [GO:1903672]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0030949]; wound healing, spreading of epidermal cells [GO:0035313]	alphav-beta3 integrin-vitronectin complex [GO:0071062]; cell surface [GO:0009986]; focal adhesion [GO:0005925]; integrin alpha5-beta1 complex [GO:0034674]; integrin complex [GO:0008305]; plasma membrane [GO:0005886]; ruffle [GO:0001726]	metal ion binding [GO:0046872]; platelet-derived growth factor receptor binding [GO:0005161]; vascular endothelial growth factor receptor 2 binding [GO:0043184]; virus receptor activity [GO:0001618]

	heavy chain; Integrin alpha-5 light chain]					
69	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1 HS1	486	actin filament polymerization [GO:0030041]; cellular response to cytokine stimulus [GO:0071345]; erythrocyte differentiation [GO:0030218]; intracellular signal transduction [GO:0035556]; negative regulation of leukocyte apoptotic process [GO:2000107]; negative regulation of transcription by RNA polymerase II [GO:0000122]; positive regulation of actin cytoskeleton reorganization [GO:2000251]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of granulocyte differentiation [GO:0030854]; positive regulation of macrophage differentiation [GO:0045651]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; positive regulation of protein import into nucleus [GO:0042307]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of tyrosine phosphorylation of STAT protein [GO:0042531]; regulation of actin filament polymerization [GO:0030833]; regulation of transcription, DNA-templated [GO:0006355]; response to hormone [GO:0009725]	cortical actin cytoskeleton [GO:0030864]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; site of polarized growth [GO:0030427]; transcription regulator complex [GO:0005667]	actin filament binding [GO:0051015]; protein kinase binding [GO:0019901]; RNA polymerase II-specific DNA-binding transcription factor binding [GO:0061629]; SH3 domain binding [GO:0017124]
70	Interleukin-6 (IL-6) (B-cell stimulatory factor 2) (BSF-2) (CTL differentiation factor) (CDF) (Hybridoma growth factor) (Interferon beta-2) (IFN-beta-2)	IL6 IFNB2	212	acute-phase response [GO:0006953]; cellular response to hydrogen peroxide [GO:0070301]; cellular response to lipopolysaccharide [GO:0071222]; cellular response to virus [GO:0098586]; cytokine-mediated signaling pathway [GO:0019221]; defense response to Gram-negative bacterium [GO:0050829]; defense response to Gram-positive bacterium [GO:0050830]; defense response to virus [GO:0051607]; endocrine pancreas development [GO:0031018]; germinal center B cell differentiation [GO:0002314]; glucagon secretion [GO:0070091]; glucose homeostasis [GO:0042593]; hepatic immune response [GO:0002384]; hepatocyte proliferation [GO:0072574]; humoral immune response [GO:0006959]; inflammatory response [GO:0006954]; interleukin-6-mediated signaling pathway [GO:0070102]; liver regeneration [GO:0097421]; maintenance of blood-brain barrier [GO:0035633]; monocyte chemotaxis [GO:0002548]; negative regulation of apoptotic process [GO:0043066]; negative regulation of bone resorption [GO:0045779]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of chemokine production [GO:0032682]; negative regulation of collagen biosynthetic process [GO:0032966]; negative regulation of fat cell differentiation [GO:0045599]; negative regulation of interleukin-1-mediated signaling pathway [GO:2000660]; negative regulation of lipid storage [GO:0010888]; negative regulation of neurogenesis [GO:0050768]; negative regulation of primary miRNA processing [GO:2000635]; neuron cellular homeostasis [GO:0070050]; neuron projection development [GO:0031175]; neutrophil apoptotic process [GO:0001781]; neutrophil mediated immunity [GO:0002446]; platelet activation [GO:0030168]; positive regulation of acute inflammatory response [GO:0002675]; positive regulation of apoptotic DNA fragmentation [GO:1902512]; positive regulation of apoptotic process [GO:0043065]; positive regulation of B cell activation [GO:0050871]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of chemokine production [GO:0032722]; positive regulation of cytokine production involved in inflammatory response [GO:1900017]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of epithelial to mesenchymal transition [GO:0010718]; positive regulation of extracellular matrix disassembly [GO:0090091]; positive regulation of gene expression [GO:0010628]; positive regulation of glial cell proliferation [GO:0060252]; positive regulation of immunoglobulin production [GO:0002639]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-17 production [GO:0032740]; positive regulation of interleukin-1 beta production [GO:0032731]; positive regulation of interleukin-21 production [GO:0032745]; positive regulation of interleukin-6 production [GO:0032755]; positive regulation of interleukin-8 production [GO:0032757]; positive regulation of leukocyte adhesion to vascular endothelial cell [GO:1904996]; positive regulation of leukocyte chemotaxis [GO:0002690]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of neuroinflammatory response [GO:0150078]; positive regulation of osteoblast differentiation [GO:0045669]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of platelet aggregation [GO:1901731]; positive regulation of production of miRNAs involved in gene silencing by miRNA [GO:1903800]; positive regulation of receptor signaling pathway via JAK-STAT [GO:0046427]; positive regulation of receptor signaling pathway via STAT [GO:1904894]; positive regulation of smooth muscle cell proliferation [GO:0048661]; positive regulation of T cell proliferation [GO:0042102]; positive regulation of T-helper 2 cell cytokine production [GO:2000553]; positive regulation of transcription, DNA-templated [GO:0045893]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of translation [GO:0045727]; positive regulation of tumor necrosis factor production [GO:0032760]; positive regulation of type B pancreatic cell apoptotic process [GO:2000676]; positive regulation of tyrosine phosphorylation of STAT protein [GO:0042531]; positive regulation of vascular endothelial growth factor production [GO:0010575]; regulation of angiogenesis [GO:0045765]; regulation of astrocyte activation [GO:0061888]; regulation of glucagon secretion [GO:0070092]; regulation of insulin secretion [GO:0050796]; regulation of microglial cell activation [GO:1903978]; regulation of neuroinflammatory response [GO:0150077]; regulation of vascular endothelial growth factor production [GO:0010574]; response to activity [GO:0014823]; response to glucocorticoid [GO:0051384]; response to peptidoglycan [GO:0032494]; T follicular helper cell differentiation [GO:0061470]; T-helper 17 cell lineage commitment [GO:0072540]; vascular endothelial growth factor production [GO:0010573]	endoplasmic reticulum lumen [GO:0005788]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; interleukin-6 receptor complex [GO:0005896]	cytokine activity [GO:0005125]; growth factor activity [GO:0008083]; interleukin-6 receptor binding [GO:0005138]
71	Basal cell adhesion molecule (Auberger B antigen) (B-CAM cell surface glycoprotein) (F8/G253 antigen) (Lutheran antigen) (Lutheran blood group glycoprotein) (CD antigen CD239)	BCAM LU MSK19	628	cell adhesion [GO:0007155]; cell-matrix adhesion [GO:0007160]; signal transduction [GO:0007165]	collagen-containing extracellular matrix [GO:0062023]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	laminin binding [GO:0043236]; laminin receptor activity [GO:0005055]; protein C-terminus binding [GO:0008022]; transmembrane signaling receptor activity [GO:0004888]
72	Allergin-1 (Allergy inhibitory receptor 1) (Mast cell antigen 32) (MCA-32) (Mast cell immunoglobulin-like receptor 1)	MILR1 C17orf60 MCA32	343	cell-cell adhesion via plasma-membrane adhesion molecules [GO:0098742]; cell surface receptor signaling pathway [GO:0007166]; mast cell degranulation [GO:0043303]; negative regulation of mast cell activation [GO:0033004]	integral component of plasma membrane [GO:0005887]	transmembrane signaling receptor activity [GO:0004888]
73	Carbonic anhydrase 6 (EC 4.2.1.1) (Carbonate dehydratase VI) (Carbonic anhydrase	CA6	308	detection of chemical stimulus involved in sensory perception of bitter taste [GO:0001580]; one-carbon metabolic process [GO:0006730]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	carbonate dehydratase activity [GO:0004089]; hydro-lyase activity [GO:0016836]; zinc ion binding [GO:0008270]

	VI) (CA-VI) (Salivary carbonic anhydrase) (Secreted carbonic anhydrase)					
74	Beta-1,4-galactosyltransferase 1 (Beta-1,4-GalTase 1) (Beta4Gal-T1) (b4Gal-T1) (EC 2.4.1.-) (Beta-N-acetylglucosaminyl-glycolipid beta-1,4-galactosyltransferase) (Beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase) (EC 2.4.1.38) (Lactose synthase A protein) (EC 2.4.1.22) (N-acetyllactosamine synthase) (EC 2.4.1.90) (Nal synthase) (Neolactotriaosylceramide beta-1,4-galactosyltransferase) (EC 2.4.1.275) (UDP-Gal:beta-GlcNAc beta-1,4-galactosyltransferase 1) (UDP-galactose:beta-N-acetylglucosamine beta-1,4-galactosyltransferase 1) [Cleaved into: Processed beta-1,4-galactosyltransferase 1]	B4GALT1 GGTB2	398	acute inflammatory response [GO:0002526]; angiogenesis involved in wound healing [GO:0060055]; binding of sperm to zona pellucida [GO:0007339]; cell adhesion [GO:0007155]; development of secondary sexual characteristics [GO:0045136]; epithelial cell development [GO:0002064]; extracellular matrix organization [GO:0030198]; galactose metabolic process [GO:0006012]; glycosylation [GO:0070085]; lactose biosynthetic process [GO:0005989]; leukocyte migration [GO:0050900]; negative regulation of cell population proliferation [GO:0008285]; oligosaccharide biosynthetic process [GO:0009312]; penetration of zona pellucida [GO:0007341]; positive regulation of apoptotic process [GO:0043065]; positive regulation of epithelial cell proliferation involved in wound healing [GO:0060054]; protein N-linked glycosylation [GO:0006487]; regulation of acrosome reaction [GO:0060046]	azurophil granule membrane [GO:0035577]; basolateral plasma membrane [GO:0016323]; brush border membrane [GO:0031526]; desmosome [GO:0030057]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; filopodium [GO:0030175]; Golgi apparatus [GO:0005794]; Golgi cisterna membrane [GO:0032580]; Golgi membrane [GO:0000139]; Golgi trans cisterna [GO:0000138]; integral component of membrane [GO:0016021]; membrane [GO:0016020]; plasma membrane [GO:0005886]; secretory granule membrane [GO:0030667]	alpha-tubulin binding [GO:0043014]; beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase activity [GO:0003831]; beta-tubulin binding [GO:0048487]; cytoskeletal protein binding [GO:0008092]; galactosyltransferase activity [GO:0008378]; identical protein binding [GO:0042802]; lactose synthase activity [GO:0004461]; manganese ion binding [GO:0030145]; N-acetyllactosamine synthase activity [GO:0003945]; UDP-galactosyltransferase activity [GO:0035250]
75	WAP, Kazal, immunoglobulin, Kunitz and NTR domain-containing protein 2 (Growth and differentiation factor-associated serum protein 1) (GASP-1) (hGASP-1) (WAP, follistatin, immunoglobulin, Kunitz and NTR domain-containing-related protein) (WFIKKN-related protein)	WFIKKN2 GASP1 WFIKKNRP UNQ9235/PRO31996	576	muscle cell development [GO:0055001]; negative regulation of DNA binding [GO:0043392]; negative regulation of protein binding [GO:0032091]; negative regulation of transforming growth factor beta receptor signaling pathway [GO:0030512]; roof of mouth development [GO:0060021]; skeletal system development [GO:0001501]; transforming growth factor beta receptor signaling pathway [GO:0007179]	extracellular space [GO:0005615]	metalloendopeptidase inhibitor activity [GO:0008191]; receptor antagonist activity [GO:0048019]; serine-type endopeptidase inhibitor activity [GO:0004867]; transforming growth factor beta binding [GO:0050431]
76	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Hematopoietic cell protein-tyrosine phosphatase) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Protein-tyrosine phosphatase SHP-1) (SH-PTP1)	PTPN6 HCP PTP1C	595	abortive mitotic cell cycle [GO:0033277]; B cell receptor signaling pathway [GO:0050853]; cell differentiation [GO:0030154]; cytokine-mediated signaling pathway [GO:0019221]; epididymis development [GO:1905867]; G protein-coupled receptor signaling pathway [GO:0007186]; hematopoietic progenitor cell differentiation [GO:0002244]; intracellular signal transduction [GO:0035556]; megakaryocyte development [GO:0035855]; natural killer cell mediated cytotoxicity [GO:0042267]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of humoral immune response mediated by circulating immunoglobulin [GO:0002924]; negative regulation of interleukin-6 production [GO:0032715]; negative regulation of MAP kinase activity [GO:0043407]; negative regulation of peptidyl-tyrosine phosphorylation [GO:0050732]; negative regulation of T cell proliferation [GO:0042130]; negative regulation of T cell receptor signaling pathway [GO:0050860]; negative regulation of tumor necrosis factor production [GO:0032720]; peptidyl-tyrosine dephosphorylation [GO:0035335]; peptidyl-tyrosine phosphorylation [GO:0018108]; platelet aggregation [GO:0070527]; platelet formation [GO:0030220]; positive regulation of cell adhesion mediated by integrin [GO:0033630]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; protein dephosphorylation [GO:0006470]; regulation of apoptotic process [GO:0042981]; regulation of B cell differentiation [GO:0045577]; regulation of ERK1 and ERK2 cascade [GO:0070372]; regulation of G1/S transition of mitotic cell cycle [GO:2000045]; regulation of release of sequestered calcium ion into cytosol [GO:0051279]; regulation of type I interferon-mediated signaling pathway [GO:0060338]; T cell costimulation [GO:0031295]	alpha-beta T cell receptor complex [GO:0042105]; cell-cell junction [GO:0005911]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; membrane [GO:0016020]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; protein-containing complex [GO:0032991]; specific granule lumen [GO:0035580]; tertiary granule lumen [GO:1904724]	cell adhesion molecule binding [GO:0050839]; phosphorylation-dependent protein binding [GO:0140031]; phosphotyrosine residue binding [GO:0001784]; protein kinase binding [GO:0019901]; protein tyrosine phosphatase activity [GO:0004725]; SH2 domain binding [GO:0042169]; SH3 domain binding [GO:0017124]; transmembrane receptor protein tyrosine phosphatase activity [GO:0005001]
77	DNA fragmentation factor subunit alpha (DNA fragmentation factor 45 kDa subunit) (DFF-45) (Inhibitor of CAD) (ICAD)	DFFA DFF1 DFF45 H13	331	apoptotic DNA fragmentation [GO:0006309]; chaperone-mediated protein folding [GO:0061077]; negative regulation of apoptotic DNA fragmentation [GO:1902511]; negative regulation of deoxyribonuclease activity [GO:0032076]; negative regulation of execution phase of apoptosis [GO:1900118]; positive regulation of apoptotic process [GO:0043065]; regulation of apoptotic process [GO:0042981]; thymocyte apoptotic process [GO:0070242]	chromatin [GO:0000785]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; protein-containing complex [GO:0032991]	deoxyribonuclease inhibitor activity [GO:0060703]; protein domain specific binding [GO:0019904]; protein folding chaperone [GO:0044183]
78	Aryl hydrocarbon receptor nuclear translocator (ARNT protein) (Class E basic helix-loop-helix protein 2) (bHLHe2) (Dioxin receptor, nuclear translocator) (Hypoxia-inducible factor 1-beta) (HIF-1-beta) (HIF1-beta)	ARNT BHLHE2	789	cell differentiation [GO:0030154]; embryonic placenta development [GO:0001892]; positive regulation of endothelial cell proliferation [GO:0001938]; positive regulation of erythrocyte differentiation [GO:0045648]; positive regulation of glycolytic process [GO:0045821]; positive regulation of hormone biosynthetic process [GO:0046886]; positive regulation of protein sumoylation [GO:0033235]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of vascular endothelial growth factor production [GO:0010575]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0030949]; regulation of transcription by RNA polymerase II [GO:0006357]; regulation of transcription from RNA polymerase II promoter in response to oxidative stress [GO:0043619]; response to hypoxia [GO:0001666]	aryl hydrocarbon receptor complex [GO:0034751]; chromatin [GO:0000785]; cytoplasm [GO:0005737]; nuclear body [GO:0016604]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; RNA polymerase II transcription regulator complex [GO:0090575]	aryl hydrocarbon receptor binding [GO:0017162]; cis-regulatory region sequence-specific DNA binding [GO:0000987]; DNA-binding transcription factor activity [GO:0003700]; DNA-binding transcription factor activity, RNA polymerase II-specific [GO:0000981]; nuclear receptor activity [GO:0004879]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]; sequence-specific DNA binding [GO:0043565];

						sequence-specific double-stranded DNA binding [GO:1990837]; transcription factor binding [GO:0008134]
79	Roundabout homolog 1 (Deleted in U twenty twenty) (H-Robo-1)	ROBO1 DUTT1	1651	activation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0006919]; aorta development [GO:0035904]; aortic valve morphogenesis [GO:0003180]; axon midline choice point recognition [GO:0016199]; cell adhesion [GO:0007155]; cell migration involved in sprouting angiogenesis [GO:0002042]; chemorepulsion involved in postnatal olfactory bulb interneuron migration [GO:0021836]; endocardial cushion formation [GO:0003272]; homophilic cell adhesion via plasma membrane adhesion molecules [GO:0007156]; negative regulation of cell migration [GO:0030336]; negative regulation of chemokine-mediated signaling pathway [GO:0070100]; negative regulation of gene expression [GO:0010629]; negative regulation of mammary gland epithelial cell proliferation [GO:0033600]; negative regulation of negative chemotaxis [GO:0050925]; nervous system development [GO:0007399]; outflow tract septum morphogenesis [GO:0003148]; positive regulation of axonogenesis [GO:0050772]; positive regulation of gene expression [GO:0010628]; positive regulation of MAP kinase activity [GO:0043406]; positive regulation of Notch signaling pathway involved in heart induction [GO:0035481]; positive regulation of Rho protein signal transduction [GO:0035025]; positive regulation of vascular endothelial growth factor signaling pathway [GO:1900748]; pulmonary valve morphogenesis [GO:0003184]; Roundabout signaling pathway [GO:0035385]; ventricular septum morphogenesis [GO:0060412]	axon [GO:0030424]; cell surface [GO:0009986]; cytoplasm [GO:0005737]; endoplasmic reticulum-Golgi intermediate compartment membrane [GO:0033116]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	axon guidance receptor activity [GO:0008046]; identical protein binding [GO:0042802]; LRR domain binding [GO:0030275]
80	Natural cytotoxicity triggering receptor 1 (Lymphocyte antigen 94 homolog) (NK cell-activating receptor) (Natural killer cell p46-related protein) (NK-p46) (NKp46) (hNKp46) (CD antigen CD335)	NCR1 LY94	304	cellular defense response [GO:0006968]; natural killer cell activation [GO:0030101]; regulation of natural killer cell mediated cytotoxicity [GO:0042269]; signal transduction [GO:0007165]	integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]; SWI/SNF complex [GO:0016514]	
81	Cathepsin F (CATSF) (EC 3.4.22.41)	CTSF	484	antigen processing and presentation of exogenous peptide antigen via MHC class II [GO:0019886]; proteolysis [GO:0006508]; proteolysis involved in cellular protein catabolic process [GO:0051603]	collagen-containing extracellular matrix [GO:0062023]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; lysosomal lumen [GO:0043202]; lysosome [GO:0005764]	cysteine-type endopeptidase activity [GO:0004197]
82	E3 ubiquitin-protein ligase TRIM21 (EC 2.3.2.27) (52 kDa Ro protein) (52 kDa ribonucleoprotein autoantigen Ro/SS-A) (RING finger protein 81) (RING-type E3 ubiquitin transferase TRIM21) (Ro(SS-A)) (Sjoegren syndrome type A antigen) (SS-A) (Tripartite motif-containing protein 21)	TRIM21 RNF81 RO52 SSA1	475	cell cycle [GO:0007049]; innate immune response [GO:0045087]; negative regulation of innate immune response [GO:0045824]; negative regulation of NF-kappaB transcription factor activity [GO:0032088]; negative regulation of protein deubiquitination [GO:0090086]; negative regulation of viral release from host cell [GO:1902187]; negative regulation of viral transcription [GO:0032897]; positive regulation of autophagy [GO:0010508]; positive regulation of cell cycle [GO:0045787]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of protein binding [GO:0032092]; positive regulation of viral entry into host cell [GO:0046598]; protein autoubiquitination [GO:0051865]; protein destabilization [GO:0031648]; protein K63-linked ubiquitination [GO:0070534]; protein monoubiquitination [GO:0006513]; protein polyubiquitination [GO:0000209]; protein ubiquitination [GO:0016567]; regulation of gene expression [GO:0010468]; regulation of protein localization [GO:0032880]; regulation of type I interferon production [GO:0032479]; regulation of viral entry into host cell [GO:0046596]; response to interferon-gamma [GO:0034341]	autophagosome [GO:0005776]; cytoplasm [GO:0005737]; cytoplasmic vesicle [GO:0031410]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; P-body [GO:0000932]; ribonucleoprotein complex [GO:1990904]	DNA binding [GO:0003677]; identical protein binding [GO:0042802]; protein homodimerization activity [GO:0042803]; protein kinase binding [GO:0019901]; RNA binding [GO:0003723]; transcription coactivator activity [GO:0003713]; ubiquitin protein ligase activity [GO:0061630]; ubiquitin-protein transferase activity [GO:0004842]; zinc ion binding [GO:0008270]
83	Protein sprouty homolog 2 (Spry-2)	SPRY2	315	animal organ development [GO:0048513]; bud elongation involved in lung branching [GO:0060449]; cell fate commitment [GO:0045165]; cellular response to leukemia inhibitory factor [GO:1990830]; cellular response to vascular endothelial growth factor stimulus [GO:0035924]; establishment of mitotic spindle orientation [GO:0000132]; inner ear morphogenesis [GO:0042472]; lung growth [GO:0060437]; negative regulation of angiogenesis [GO:0016525]; negative regulation of apoptotic process [GO:0043066]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of cell projection organization [GO:0031345]; negative regulation of epithelial to mesenchymal transition [GO:0010719]; negative regulation of ERK1 and ERK2 cascade [GO:0070373]; negative regulation of fibroblast growth factor receptor signaling pathway [GO:0040037]; negative regulation of GTPase activity [GO:0034260]; negative regulation of lens fiber cell differentiation [GO:1902747]; negative regulation of MAP kinase activity [GO:0043407]; negative regulation of neurotrophin TRK receptor signaling pathway [GO:0051387]; negative regulation of peptidyl-threonine phosphorylation [GO:0010801]; negative regulation of protein ubiquitination [GO:0031397]; negative regulation of Ras protein signal transduction [GO:0046580]; negative regulation of transforming growth factor beta receptor signaling pathway [GO:0030512]; negative regulation of vascular endothelial growth factor signaling pathway [GO:1900747]; positive regulation of cell migration [GO:0030335]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of gene expression [GO:0010628]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; positive regulation of protein kinase B signaling [GO:0051897]; sensory perception of sound [GO:0007605]	actin cytoskeleton [GO:0015629]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; membrane [GO:0016020]; microtubule cytoskeleton [GO:0015630]; microtubule end [GO:1990752]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; ruffle membrane [GO:0032587]	protein kinase binding [GO:0019901]; protein serine/threonine kinase activator activity [GO:0043539]; protein serine/threonine kinase inhibitor activity [GO:0030291]
84	Interleukin-13 receptor subunit alpha-1 (IL-13 receptor subunit alpha-1) (IL-13R subunit alpha-1) (IL-13R-alpha-1) (IL-13RA1) (Cancer/testis antigen 19) (CT19) (CD antigen CD213a1)	IL13RA1 IL13RA	427	cell surface receptor signaling pathway [GO:0007166]; cytokine-mediated signaling pathway [GO:0019221]; oncostatin-M-mediated signaling pathway [GO:0038165]; positive regulation of cell population proliferation [GO:0008284]	external side of plasma membrane [GO:0009897]; interleukin-13 receptor complex [GO:0005898]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]	ciliary neurotrophic factor receptor binding [GO:0005127]; cytokine binding [GO:0019955]; cytokine receptor activity [GO:0004896]; leukemia inhibitory factor receptor activity [GO:0004923]
85	Interleukin-5 (IL-5) (B-cell differentiation factor I) (Eosinophil differentiation factor) (T-cell replacing factor) (TRF)	IL5	134	cytokine-mediated signaling pathway [GO:0019221]; immune response [GO:0006955]; inflammatory response [GO:0006954]; positive regulation of B cell proliferation [GO:0030890]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of eosinophil differentiation [GO:0045645]; positive regulation of immunoglobulin production [GO:0002639]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of podosome assembly [GO:0071803]; positive regulation of receptor signaling pathway via JAK-STAT [GO:0046427]; positive regulation of transcription, DNA-templated [GO:0045893]	extracellular region [GO:0005576]; extracellular space [GO:0005615]	cytokine activity [GO:0005125]; growth factor activity [GO:0008083]; interleukin-5 receptor binding [GO:0005137]
86	SH2B adapter protein 3 (Lymphocyte adapter protein)	SH2B3 LNK	575	cellular response to chemokine [GO:1990869]; cellular response to interleukin-3 [GO:0036016]; embryonic hemopoiesis [GO:0035162]; erythrocyte development [GO:0048821]; intracellular signal transduction [GO:0035556]; megakaryocyte	cytosol [GO:0005829]; plasma membrane [GO:0005886]	protein tyrosine kinase binding [GO:1990782]; signaling receptor complex adaptor activity

	(Lymphocyte-specific adapter protein Lnk) (Signal transduction protein Lnk)			development [GO:0035855]; monocyte homeostasis [GO:0035702]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of chemokine-mediated signaling pathway [GO:0070100]; negative regulation of Kit signaling pathway [GO:1900235]; negative regulation of MAP kinase activity [GO:0043407]; negative regulation of platelet aggregation [GO:0090331]; negative regulation of protein kinase B signaling [GO:0051898]; negative regulation of receptor signaling pathway via JAK-STAT [GO:0046426]; negative regulation of response to cytokine stimulus [GO:0060761]; negative regulation of tyrosine phosphorylation of STAT protein [GO:0042532]; neutrophil homeostasis [GO:0001780]; thrombopoietin-mediated signaling pathway [GO:0038163]		[GO:0030159]; stem cell factor receptor binding [GO:0005173]; transmembrane receptor protein tyrosine kinase adaptor activity [GO:0005068]
87	PC4 and SFRS1-interacting protein (CLL-associated antigen KW-7) (Dense fine speckles 70 kDa protein) (DFS 70) (Lens epithelium-derived growth factor) (Transcriptional coactivator p75/p52)	PSIP1 DFS70 LEDGF PSIP2	530	mRNA 5'-splice site recognition [GO:0000395]; positive regulation of transcription by RNA polymerase II [GO:0045944]; regulation of transcription by RNA polymerase II [GO:0006357]; response to heat [GO:0009408]; response to oxidative stress [GO:0006979]	cytosol [GO:0005829]; heterochromatin [GO:0000792]; nuclear periphery [GO:0034399]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; transcriptionally active chromatin [GO:0035327]	chromatin binding [GO:0003682]; DNA-binding transcription factor binding [GO:0140297]; double-stranded DNA binding [GO:0003690]; RNA binding [GO:0003723]; supercoiled DNA binding [GO:0097100]; transcription coactivator activity [GO:0003713]; transcription coregulator activity [GO:0003712]
88	Lysosome-associated membrane glycoprotein 3 (LAMP-3) (Lysosomal-associated membrane protein 3) (DC-lysosome-associated membrane glycoprotein) (DC LAMP) (Protein TSC403) (CD antigen CD208)	LAMP3 DCLAMP TSC403	416	adaptive immune response [GO:0002250]; establishment of protein localization to organelle [GO:0072594]; negative regulation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0043154]; negative regulation of proteasomal protein catabolic process [GO:1901799]; positive regulation of gene expression [GO:0010628]; regulation of autophagy [GO:0010506]; regulation of viral life cycle [GO:1903900]; response to interferon-alpha [GO:0035455]	alveolar lamellar body membrane [GO:0097233]; early endosome [GO:0005769]; integral component of membrane [GO:0016021]; intracellular membrane-bounded organelle [GO:0043231]; late endosome membrane [GO:0031902]; lysosomal membrane [GO:0005765]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; vesicle [GO:0031982]	
89	Lactadherin (Breast epithelial antigen BA46) (HMFG) (MFGM) (Milk fat globule-EGF factor 8) (MFG-E8) (SED1) [Cleaved into: Lactadherin short form; Medin]	MFGE8	387	angiogenesis [GO:0001525]; apoptotic cell clearance [GO:0043277]; cell adhesion [GO:0007155]; phagocytosis, engulfment [GO:0006911]; phagocytosis, recognition [GO:0006910]; positive regulation of phagocytosis [GO:0050766]; single fertilization [GO:0007338]	acrosomal membrane [GO:0002080]; collagen-containing extracellular matrix [GO:0062023]; endoplasmic reticulum lumen [GO:0005788]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; extrinsic component of plasma membrane [GO:0019897]; membrane [GO:0016020]	integrin binding [GO:0005178]; phosphatidylethanolamine binding [GO:0008429]; phosphatidylserine binding [GO:0001786]
90	Beta-1,4-glucuronyltransferase 1 (EC 2.4.1.-) (I-beta-1,3-N-acetylglucosaminyltransferase) (iGnT) (N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase) (Poly-N-acetyllactosamine extension enzyme) (UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1)	B4GAT1 B3GNT1 B3GNT6	415	keratan sulfate biosynthetic process [GO:0018146]; protein O-linked mannosylation [GO:0035269]	extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]; integral component of Golgi membrane [GO:0030173]	glucuronosyltransferase activity [GO:0015020]; metal ion binding [GO:0046872]; N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase activity [GO:0008532]
91	Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonate dehydratase II) (Carbonic anhydrase C) (CAC) (Carbonic anhydrase II) (CA-II)	CA2	260	angiotensin-activated signaling pathway [GO:0038166]; carbon dioxide transport [GO:0015670]; cellular response to fluid shear stress [GO:0071498]; kidney development [GO:0001822]; odontogenesis of dentin-containing tooth [GO:0042475]; one-carbon metabolic process [GO:0006730]; positive regulation of bone resorption [GO:0045780]; positive regulation of cellular pH reduction [GO:0032849]; positive regulation of dipeptide transmembrane transport [GO:2001150]; positive regulation of osteoclast differentiation [GO:0045672]; regulation of anion transport [GO:0044070]; regulation of intracellular pH [GO:0051453]; response to estrogen [GO:0043627]; response to pH [GO:0009268]; response to steroid hormone [GO:0048545]; response to zinc ion [GO:0010043]	apical part of cell [GO:0045177]; axon [GO:0030424]; basolateral plasma membrane [GO:0016323]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; microvillus [GO:0005902]; plasma membrane [GO:0005886]	arylesterase activity [GO:0004064]; carbonate dehydratase activity [GO:0004089]; hydro-lyase activity [GO:0016836]; zinc ion binding [GO:0008270]
92	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2 (EC 3.2.2.6) (ADP-ribosyl cyclase 2) (Bone marrow stromal antigen 1) (BST-1) (Cyclic ADP-ribose hydrolase 2) (cADPr hydrolase 2) (CD antigen CD157)	BST1	318	humoral immune response [GO:0006959]; positive regulation of B cell proliferation [GO:0030890]; positive regulation of cell population proliferation [GO:0008284]; regulation of actin cytoskeleton organization [GO:0032956]; regulation of calcium-mediated signaling [GO:0050848]; regulation of cell-matrix adhesion [GO:0001952]; regulation of cellular extravasation [GO:0002691]; regulation of inflammatory response [GO:0050727]; regulation of integrin-mediated signaling pathway [GO:2001044]; regulation of neutrophil chemotaxis [GO:0090022]; regulation of peptidyl-tyrosine phosphorylation [GO:0050730]; regulation of superoxide metabolic process [GO:0090322]; signal transduction [GO:0007165]	anchored component of membrane [GO:0031225]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extrinsic component of membrane [GO:0019898]; plasma membrane [GO:0005886]; specific granule membrane [GO:0035579]; uropod [GO:0001931]	ADP-ribosyl cyclase activity [GO:0061811]; cyclic ADP-ribose hydrolase [GO:0061812]; NAD(P)+ nucleosidase activity [GO:0050135]; NAD+ nucleosidase activity [GO:0003953]; NAD+ nucleotidase, cyclic ADP-ribose generating [GO:0061809]; phosphorus-oxygen lyase activity [GO:0016849]; transferase activity [GO:0016740]
93	Tumor necrosis factor receptor superfamily member EDAR (Anhidrotic ectodysplasin receptor 1) (Downless homolog) (EDA-A1 receptor) (Ectodermal dysplasia receptor) (Ectodysplasin-A receptor)	EDARDL	448	apoptotic process [GO:0006915]; cell differentiation [GO:0030154]; epidermis development [GO:0008544]; hair follicle development [GO:0001942]; odontogenesis of dentin-containing tooth [GO:0042475]; pigmentation [GO:0043473]; positive regulation of gene expression [GO:0010628]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of JNK cascade [GO:0046330]; positive regulation of NIK/NF-kappaB signaling [GO:1901224]; salivary gland cavitation [GO:0060662]	apical part of cell [GO:0045177]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	signaling receptor activity [GO:0038023]; transmembrane signaling receptor activity [GO:0004888]
94	TRAF family member-associated NF-kappa-B activator (TRAF-interacting protein) (I-TRAF)	TANKITRAF TRAF2	425	cellular response to DNA damage stimulus [GO:0006974]; cellular response to interleukin-1 [GO:0071347]; cellular response to ionizing radiation [GO:0071479]; cellular response to tumor necrosis factor [GO:0071356]; I-kappaB kinase/NF-kappaB signaling [GO:0007249]; negative regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043124]; positive regulation of protein deubiquitination [GO:1903003]; positive	cytosol [GO:0005829]; protein-containing complex [GO:0032991]	deubiquitinase activator activity [GO:0035800]; metal ion binding [GO:0046872]; ubiquitin protein ligase binding [GO:0031625]

				regulation of ubiquitin-specific protease activity [GO:2000158]; proteolysis [GO:0006508]; signal transduction [GO:0007165]		
95	Interferon lambda receptor 1 (IFN-lambda receptor 1) (IFN-lambda-R1) (Cytokine receptor class-II member 12) (Cytokine receptor family 2 member 12) (CRF2-12) (Interleukin-28 receptor subunit alpha) (IL-28 receptor subunit alpha) (IL-28R-alpha) (IL-28RA) (Likely interleukin or cytokine receptor 2) (LICR2)	IFNLR1 IL28RA LICR2	520	cytokine-mediated signaling pathway [GO:0019221]; defense response to virus [GO:0051607]; mucosal immune response [GO:0002385]; negative regulation of cell population proliferation [GO:0008285]; positive regulation of cellular respiration [GO:1901857]; regulation of defense response to virus by host [GO:0050691]; response to type III interferon [GO:0034342]	integral component of membrane [GO:0016021]; interleukin-28 receptor complex [GO:0032002]; plasma membrane [GO:0005886]	cytokine receptor activity [GO:0004896]
96	Fc receptor-like protein 5 (FcR-like protein 5) (FcRL5) (BXMAS1) (Fc receptor homolog 5) (FcRH5) (Immune receptor translocation-associated protein 2) (CD antigen CD307e)	FCRL5 FCRH5 IRTA2 UNQ503/PRO820	977	cell surface receptor signaling pathway [GO:0007166]	cell surface [GO:0009986]; integral component of plasma membrane [GO:0005887]; receptor complex [GO:0043235]	transmembrane signaling receptor activity [GO:0004888]
97	Matrilin-2	MATN2 UNQ193/PRO219	956		collagen-containing extracellular matrix [GO:0062023]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]	calcium ion binding [GO:0005509]; extracellular matrix structural constituent [GO:0005201]
98	Myocilin (Myocilin 55 kDa subunit) (Trabecular meshwork-induced glucocorticoid response protein) [Cleaved into: Myocilin, N-terminal fragment (Myocilin 20 kDa N-terminal fragment); Myocilin, C-terminal fragment (Myocilin 35 kDa N-terminal fragment)]	MYOC GLC1A TIGR	504	bone development [GO:0060348]; clustering of voltage-gated sodium channels [GO:0045162]; ERBB2-ERBB3 signaling pathway [GO:0038133]; myelination in peripheral nervous system [GO:0022011]; negative regulation of cell-matrix adhesion [GO:0001953]; negative regulation of Rho protein signal transduction [GO:0035024]; negative regulation of stress fiber assembly [GO:0051497]; neuron projection development [GO:0031175]; non-canonical Wnt signaling pathway via JNK cascade [GO:0038031]; osteoblast differentiation [GO:0001649]; positive regulation of cell migration [GO:0030335]; positive regulation of focal adhesion assembly [GO:0051894]; positive regulation of mitochondrial depolarization [GO:0051901]; positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of stress fiber assembly [GO:0051496]; positive regulation of substrate adhesion-dependent cell spreading [GO:1900026]; regulation of MAPK cascade [GO:0043408]; skeletal muscle hypertrophy [GO:0014734]	cilium [GO:0005929]; collagen-containing extracellular matrix [GO:0062023]; cytoplasmic vesicle [GO:0031410]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]; mitochondrial inner membrane [GO:0005743]; mitochondrial intermembrane space [GO:0005758]; mitochondrial outer membrane [GO:0005741]; node of Ranvier [GO:0033268]; rough endoplasmic reticulum [GO:0005791]	fibronectin binding [GO:0001968]; frizzled binding [GO:0005109]; metal ion binding [GO:0046872]; myosin light chain binding [GO:0032027]; receptor tyrosine kinase binding [GO:0030971]
99	Eotaxin (C-C motif chemokine 11) (Eosinophil chemotactic protein) (Small-inducible cytokine A11)	CCL11 SCYA11	97	actin filament organization [GO:0007015]; antimicrobial humoral immune response mediated by antimicrobial peptide [GO:0061844]; branching involved in mammary gland duct morphogenesis [GO:0060444]; cell adhesion [GO:0007155]; cellular calcium ion homeostasis [GO:0006874]; cellular response to interferon-gamma [GO:0071346]; cellular response to interleukin-1 [GO:0071347]; cellular response to tumor necrosis factor [GO:0071356]; chemokine-mediated signaling pathway [GO:0070098]; chemotaxis [GO:0006935]; chronic inflammatory response [GO:0002544]; cytoskeleton organization [GO:0007010]; eosinophil chemotaxis [GO:0048245]; ERK1 and ERK2 cascade [GO:0070371]; G protein-coupled receptor signaling pathway [GO:0007186]; inflammatory response [GO:0006954]; killing of cells of other organism [GO:0031640]; learning or memory [GO:0007611]; lymphocyte chemotaxis [GO:0048247]; mammary duct terminal end bud growth [GO:0060763]; mast cell chemotaxis [GO:0002551]; modulation of age-related behavioral decline [GO:0090647]; monocyte chemotaxis [GO:0002548]; negative regulation of neurogenesis [GO:0050768]; neutrophil chemotaxis [GO:0030593]; positive regulation of actin filament polymerization [GO:0030838]; positive regulation of angiogenesis [GO:0045766]; positive regulation of cell migration [GO:0030335]; positive regulation of endothelial cell proliferation [GO:0001938]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of GTPase activity [GO:0043547]; protein phosphorylation [GO:0006468]; regulation of cell shape [GO:0008360]; response to interleukin-13 [GO:0035962]; response to interleukin-4 [GO:0070670]; response to radiation [GO:0009314]; response to virus [GO:0009615]; signal transduction [GO:0007165]	extracellular region [GO:0005576]; extracellular space [GO:0005615]	CCR3 chemokine receptor binding [GO:0031728]; CCR chemokine receptor binding [GO:0048020]; chemokine activity [GO:0008009]; protein dimerization activity [GO:0046983]; receptor ligand activity [GO:0048018]
100	Tissue alpha-L-fucosidase (EC 3.2.1.51) (Alpha-L-fucosidase I) (Alpha-L-fucoside fucohydrolase 1) (Alpha-L-fucosidase 1)	FUCA1 Nbla10230	466	fucose metabolic process [GO:0006004]; glycolipid catabolic process [GO:0019377]; glycosaminoglycan catabolic process [GO:0006027]; glycoside catabolic process [GO:0016139]	azurophil granule lumen [GO:0035578]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; lysosomal lumen [GO:0043202]; lysosome [GO:0005764]	alpha-L-fucosidase activity [GO:0004560]
101	Integrin alpha-11	ITGA11 MSTP018	1188	cell adhesion [GO:0007155]; cell adhesion mediated by integrin [GO:0033627]; cell-matrix adhesion [GO:0007160]; collagen-activated signaling pathway [GO:0038065]; integrin-mediated signaling pathway [GO:0007229]; muscle organ development [GO:0007517]; osteoblast differentiation [GO:0001649]; substrate-dependent cell migration [GO:0006929]	focal adhesion [GO:0005925]; integrin alpha11-beta1 complex [GO:0034681]; integrin complex [GO:0008305]; membrane [GO:0016020]; plasma membrane [GO:0005886]	collagen binding [GO:0005518]; collagen binding involved in cell-matrix adhesion [GO:0098639]; collagen receptor activity [GO:0038064]; metal ion binding [GO:0046872]
102	Corticotropin-releasing factor-binding protein (CRF-BP) (CRF-binding protein) (Corticotropin-releasing hormone-binding protein) (CRH-BP)	CRHBP CRFBP	322	behavioral response to ethanol [GO:0048149]; cellular response to calcium ion [GO:0071277]; cellular response to cAMP [GO:0071320]; cellular response to cocaine [GO:0071314]; cellular response to drug [GO:0035690]; cellular response to estradiol stimulus [GO:0071392]; cellular response to estrogen stimulus [GO:0071391]; cellular response to gonadotropin-releasing hormone [GO:0097211]; cellular response to potassium ion [GO:0035865]; cellular response to tumor necrosis factor [GO:0071356]; female pregnancy [GO:0007565]; hormone-mediated signaling pathway [GO:0009755]; inflammatory response [GO:0006954]; learning or memory [GO:0007611]; negative regulation of corticotropin-releasing hormone receptor activity [GO:1900011]; negative regulation of corticotropin secretion [GO:0051460]; regulated exocytosis [GO:0045055]; regulation of cellular response to stress [GO:0080135]; regulation of corticotropin secretion [GO:0051459]; regulation of NMDA receptor activity [GO:2000310]; signal transduction [GO:0007165]; synaptic transmission, dopaminergic [GO:0001963]	axon terminus [GO:0043679]; dendrite [GO:0030425]; dense core granule [GO:0031045]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; microtubule [GO:0005874]; multivesicular body [GO:0005771]; nucleus [GO:0005634]; perikaryon [GO:0043204]; secondary lysosome [GO:0005767]; secretory granule [GO:0030141]; varicosity [GO:0043196]	corticotropin-releasing hormone binding [GO:0051424]; peptide binding [GO:0042277]
10	Platelet endothelial aggregation receptor	PEAR1	1037	phosphatidylinositol 3-kinase signaling [GO:0014065]; platelet aggregation [GO:0070527]; protein kinase B signaling [GO:0043491]; recognition of apoptotic cell	integral component of membrane [GO:0016021]; membrane	signaling receptor activity [GO:0038023]

3	1 (hPEAR1) (Multiple epidermal growth factor-like domains protein 12) (Multiple EGF-like domains protein 12)	MEGF12		[GO:0043654]	[GO:0016020]; phagocytic cup [GO:0001891]	
104	Signal-regulatory protein beta-1 (SIRP-beta-1) (CD172 antigen-like family member B) (CD antigen CD172b)	SIRPB1	398	cell surface receptor signaling pathway [GO:0007166]; positive regulation of phagocytosis [GO:0050766]; positive regulation of T cell activation [GO:0050870]; signal transduction [GO:0007165]	cell surface [GO:0009986]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]; secretory granule membrane [GO:0030667]	
105	Nidogen-2 (NID-2) (Osteonidogen)	NID2	1375	basement membrane organization [GO:0071711]; cell adhesion [GO:0007155]; cell-matrix adhesion [GO:0007160]	basement membrane [GO:0005604]; collagen-containing extracellular matrix [GO:0062023]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]	calcium ion binding [GO:0005509]; collagen binding [GO:0005518]; extracellular matrix structural constituent [GO:0005201]
106	Egl nine homolog 1 (EC 1.14.11.29) (Hypoxia-inducible factor prolyl hydroxylase 2) (HIF-PH2) (HIF-prolyl hydroxylase 2) (HPH-2) (Prolyl hydroxylase domain-containing protein 2) (PHD2) (SM-20)	EGLN1 C1orf12 PNAS-118 PNAS-137	426	cellular response to hypoxia [GO:0071456]; negative regulation of cyclic-nucleotide phosphodiesterase activity [GO:0051344]; negative regulation of DNA-binding transcription factor activity [GO:0043433]; oxygen homeostasis [GO:0032364]; peptidyl-proline hydroxylation to 4-hydroxy-L-proline [GO:0018401]; regulation of angiogenesis [GO:0045765]; response to hypoxia [GO:0001666]; response to nitric oxide [GO:0071731]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleus [GO:0005634]	2-oxoglutarate-dependent dioxygenase activity [GO:0016706]; enzyme binding [GO:0019899]; ferrous iron binding [GO:0008198]; L-ascorbic acid binding [GO:0031418]; peptidyl-proline 4-dioxygenase activity [GO:0031545]; peptidyl-proline dioxygenase activity [GO:0031543]
107	C-type lectin domain family 7 member A (Beta-glucan receptor) (C-type lectin superfamily member 12) (Dendritic cell-associated C-type lectin 1) (DC-associated C-type lectin 1) (Dectin-1) (CD antigen CD369)	CLEC7A BGR CLECSF12 DECTIN1 UNQ539/PRO1082	247	antifungal innate immune response [GO:0061760]; carbohydrate mediated signaling [GO:0009756]; cell activation [GO:0001775]; cell recognition [GO:0008037]; cellular response to molecule of fungal origin [GO:0071226]; defense response to protozoan [GO:0042832]; detection of fungus [GO:0016046]; detection of molecule of fungal origin [GO:0032491]; detection of yeast [GO:0001879]; inflammatory response [GO:0006954]; leukocyte activation involved in immune response [GO:0002366]; phagocytosis, recognition [GO:0006910]; positive regulation of calcium-mediated signaling [GO:0050850]; positive regulation of cell maturation [GO:1903431]; positive regulation of cell migration [GO:0030335]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0043280]; positive regulation of cytokine production involved in inflammatory response [GO:1900017]; positive regulation of dendritic cell cytokine production [GO:0002732]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of gene expression [GO:0010628]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of interferon-gamma production [GO:0032729]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-12 production [GO:0032735]; positive regulation of interleukin-1 beta production [GO:0032731]; positive regulation of interleukin-23 production [GO:0032747]; positive regulation of interleukin-2 production [GO:0032743]; positive regulation of interleukin-6 production [GO:0032755]; positive regulation of interleukin-8 production [GO:0032757]; positive regulation of killing of cells of other organism [GO:0051712]; positive regulation of lymphocyte activation [GO:0051251]; positive regulation of monocyte chemotactic protein-1 production [GO:0071639]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of nitric oxide biosynthetic process [GO:0045429]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of phagocytosis [GO:0050766]; positive regulation of protein-containing complex assembly [GO:0031334]; positive regulation of respiratory burst [GO:0060267]; positive regulation of stress-activated MAPK cascade [GO:0032874]; positive regulation of superoxide anion generation [GO:0032930]; positive regulation of T-helper 17 type immune response [GO:2000318]; positive regulation of tumor necrosis factor production [GO:0032760]; positive regulation of wound healing [GO:0090303]; regulation of calcineurin-NFAT signaling cascade [GO:0070884]; regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043122]; response to yeast [GO:0001878]; stimulatory C-type lectin receptor signaling pathway [GO:0002223]; T cell activation [GO:0042110]	cell surface [GO:0009986]; cytoplasm [GO:0005737]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	(1->3)-beta-D-glucan binding [GO:0001872]; carbohydrate binding [GO:0030246]; identical protein binding [GO:0042802]; metal ion binding [GO:0046872]; MHC protein binding [GO:0042287]; pattern recognition receptor activity [GO:0038187]
108	C-type lectin domain family 4 member C (Blood dendritic cell antigen 2) (BDCA-2) (C-type lectin superfamily member 7) (Dendritic lectin) (CD antigen CD303)	CLEC4C BDCA2 CLECSF11 CLECSF7 DLECHECL UNQ9361/PRO34150	213	adaptive immune response [GO:0002250]; innate immune response [GO:0045087]	ficolin-1-rich granule membrane [GO:0101003]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]; secretory granule membrane [GO:0030667]; tertiary granule membrane [GO:0070821]	carbohydrate binding [GO:0030246]; metal ion binding [GO:0046872]
109	Butyrophilin subfamily 3 member A2	BTN3A2 BT3.2 BTF3 BTF4	334	positive regulation of interferon-gamma production [GO:0032729]; regulation of cytokine production [GO:0001817]; T cell mediated immunity [GO:0002456]; T cell receptor signaling pathway [GO:0050852]	external side of plasma membrane [GO:0009897]; integral component of membrane [GO:0016021]; membrane [GO:0016020]; plasma membrane [GO:0005886]	signaling receptor binding [GO:0005102]
110	Tripartite motif-containing protein 5 (EC 2.3.2.27) (RING finger protein 88) (RING-type E3 ubiquitin transferase TRIM5)	TRIM5 RNF88	493	activation of innate immune response [GO:0002218]; autophagy [GO:0006914]; defense response to virus [GO:0051607]; innate immune response [GO:0045087]; negative regulation of viral entry into host cell [GO:0046597]; negative regulation of viral release from host cell [GO:1902187]; positive regulation of autophagy [GO:0010508]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; protein K63-linked ubiquitination [GO:0070534]; protein polyubiquitination [GO:0000209]; protein ubiquitination [GO:0016567]; regulation of gene expression [GO:0010468]; regulation of lipopolysaccharide-mediated signaling pathway [GO:0031664]; regulation of protein localization [GO:0032880]; regulation of viral entry into host cell [GO:0046596]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; P-body [GO:0000932]	identical protein binding [GO:0042802]; pattern recognition receptor activity [GO:0038187]; protein homodimerization activity [GO:0042803]; protein kinase binding [GO:0019901]; protein-macromolecule adaptor activity [GO:0030674]; transcription coactivator activity [GO:0003713]; ubiquitin protein ligase activity [GO:0061630]; ubiquitin-protein transferase activity [GO:0004842]; zinc ion binding [GO:0008270]
111	Cation-independent mannose-6-phosphate	IGF2RMPRI	2491	animal organ regeneration [GO:0031100]; G protein-coupled receptor signaling pathway [GO:0007186]; liver development [GO:0001889]; lysosomal transport	cell surface [GO:0009986]; clathrin coat [GO:0030118]; clathrin-coated	enzyme binding [GO:0019899]; G-protein alpha-subunit binding

1	receptor (CI Man-6-P receptor) (CI-MPR) (M6PR) (300 kDa mannose 6-phosphate receptor) (MPR 300) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (CD antigen CD222)			[GO:0007041]; positive regulation by host of viral process [GO:0044794]; positive regulation of apoptotic process [GO:0043065]; post-embryonic development [GO:0009791]; receptor-mediated endocytosis [GO:0006898]; response to retinoic acid [GO:0032526]; response to tetrachloromethane [GO:1904772]; signal transduction [GO:0007165]; spermatogenesis [GO:0007283]	endocytic vesicle membrane [GO:0030669]; early endosome [GO:0005769]; endocytic vesicle [GO:0030139]; endosome [GO:0005768]; endosome membrane [GO:0010008]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; Golgi apparatus [GO:0005794]; integral component of plasma membrane [GO:0005887]; late endosome [GO:0005770]; membrane [GO:0016020]; nuclear envelope lumen [GO:0005641]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; secretory granule membrane [GO:0030667]; trans-Golgi network [GO:0005802]; trans-Golgi network membrane [GO:0032588]; trans-Golgi network transport vesicle [GO:0030140]; transport vesicle [GO:0030133]	[GO:0001965]; identical protein binding [GO:0042802]; insulin-like growth factor-activated receptor activity [GO:0005010]; insulin-like growth factor binding [GO:0005520]; insulin-like growth factor II binding [GO:0031995]; mannose binding [GO:0005537]; phosphoprotein binding [GO:0051219]; retinoic acid binding [GO:0001972]; retromer complex binding [GO:1905394]; signaling receptor activity [GO:0038023]
1 1 2	Leukocyte immunoglobulin-like receptor subfamily B member 4 (CD85 antigen-like family member K) (Immunoglobulin-like transcript 3) (ILT-3) (Leukocyte immunoglobulin-like receptor 5) (LIR-5) (Monocyte inhibitory receptor HM18) (CD antigen CD85k)	LILRB4 ILT3 LIR5	448	adaptive immune response [GO:0002250]; Fc receptor mediated inhibitory signaling pathway [GO:0002774]; interleukin-10-mediated signaling pathway [GO:0140105]; negative regulation of activated T cell proliferation [GO:0046007]; negative regulation of chemokine production [GO:0032682]; negative regulation of cytokine production involved in inflammatory response [GO:1900016]; negative regulation of cytotoxic T cell differentiation [GO:0045584]; negative regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043124]; negative regulation of interferon-gamma production [GO:0032689]; negative regulation of interleukin-10 production [GO:0032693]; negative regulation of interleukin-1 beta production [GO:0032691]; negative regulation of interleukin-2 production [GO:0032703]; negative regulation of interleukin-5 production [GO:0032714]; negative regulation of interleukin-6 production [GO:0032715]; negative regulation of IP-10 production [GO:0071659]; negative regulation of MAPK cascade [GO:0043409]; negative regulation of monocyte activation [GO:0150102]; negative regulation of osteoclast differentiation [GO:0045671]; negative regulation of pri-miRNA transcription by RNA polymerase II [GO:1902894]; negative regulation of protein localization to nucleus [GO:1900181]; negative regulation of protein tyrosine kinase activity [GO:0061099]; negative regulation of signaling receptor activity [GO:2000272]; negative regulation of T cell costimulation [GO:2000524]; negative regulation of T cell cytokine production [GO:0002725]; negative regulation of T cell proliferation [GO:0042130]; negative regulation of T cell receptor signaling pathway [GO:0050860]; positive regulation of CD8-positive, alpha-beta T cell differentiation [GO:0043378]; positive regulation of regulatory T cell differentiation [GO:0045591]; positive regulation of T cell anergy [GO:0002669]; receptor internalization [GO:0031623]; tolerance induction [GO:0002507]	cell surface [GO:0009986]; extracellular exosome [GO:0070062]; integral component of the cytoplasmic side of the plasma membrane [GO:0098752]; plasma membrane [GO:0005886]	protein phosphatase binding [GO:0019903]; signaling receptor inhibitor activity [GO:0030547]; transmembrane receptor protein tyrosine kinase inhibitor activity [GO:0030293]
1 1 3	Antiviral innate immune response receptor RIG-I (DEAD box protein 58) (Probable ATP-dependent RNA helicase DDX58) (EC 3.6.4.13) (RIG-I-like receptor 1) (RLR-1) (Retinoic acid-inducible gene 1 protein) (RIG-1) (Retinoic acid-inducible gene I protein) (RIG-I)	DDX58	925	antiviral innate immune response [GO:0140374]; cellular response to exogenous dsRNA [GO:0071360]; cytoplasmic pattern recognition receptor signaling pathway in response to virus [GO:0039528]; defense response to virus [GO:0051607]; detection of virus [GO:0009597]; innate immune response [GO:0045087]; positive regulation of defense response to virus by host [GO:0002230]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of gene expression [GO:0010628]; positive regulation of granulocyte macrophage colony-stimulating factor production [GO:0032725]; positive regulation of interferon-alpha production [GO:0032727]; positive regulation of interferon-beta production [GO:0032728]; positive regulation of interleukin-6 production [GO:0032755]; positive regulation of interleukin-8 production [GO:0032757]; positive regulation of myeloid dendritic cell cytokine production [GO:0002735]; positive regulation of response to cytokine stimulus [GO:0060760]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of tumor necrosis factor production [GO:0032760]; regulation of cell migration [GO:0030334]; regulation of type III interferon production [GO:0034344]; response to exogenous dsRNA [GO:0043330]; response to virus [GO:0009615]; RIG-I signaling pathway [GO:0039529]	actin cytoskeleton [GO:0015629]; bicellular tight junction [GO:0005923]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; plasma membrane [GO:0005886]; ribonucleoprotein complex [GO:1990904]; ruffle membrane [GO:0032587]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0140603]; double-stranded RNA binding [GO:0003725]; identical protein binding [GO:0042802]; RNA helicase activity [GO:0003724]; single-stranded RNA binding [GO:0003727]; ubiquitin protein ligase binding [GO:0031625]; zinc ion binding [GO:0008270]
1 1 4	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19	400	cell differentiation involved in embryonic placenta development [GO:0060706]; Notch signaling pathway [GO:0007219]; response to estrogen [GO:0043627]; sarcomere organization [GO:0045214]	apicolateral plasma membrane [GO:0016327]; cell periphery [GO:0071944]; costamere [GO:0043034]; cytosol [GO:0005829]; dystrophin-associated glycoprotein complex [GO:0016010]; extracellular exosome [GO:0070062]; intermediate filament [GO:0005882]; plasma membrane [GO:0005886]; sarcolemma [GO:0042383]; terminal web [GO:1990357]; Z disc [GO:0030018]	protein-containing complex binding [GO:0044877]; structural constituent of cytoskeleton [GO:0005200]; structural constituent of muscle [GO:0008307]
1 1 5	Inhibin beta C chain (Activin beta-C chain)	INHBC	352	positive regulation of pathway-restricted SMAD protein phosphorylation [GO:0010862]; SMAD protein signal transduction [GO:0060395]	extracellular region [GO:0005576]; extracellular space [GO:0005615]	cytokine activity [GO:0005125]; growth factor activity [GO:0008083]; hormone activity [GO:0005179]; transforming growth factor beta receptor binding [GO:0005160]
1 1 6	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (MGMT) (O-6-methylguanine-DNA-alkyltransferase)	MGMT	207	cellular response to ionizing radiation [GO:0071479]; cellular response to organic cyclic compound [GO:0071407]; cellular response to oxidative stress [GO:0034599]; DNA dealkylation involved in DNA repair [GO:0006307]; DNA ligation [GO:0006266]; DNA repair [GO:0006281]; mammary gland epithelial cell differentiation [GO:0060644]; negative regulation of apoptotic process [GO:0043066]; positive regulation of double-strand break repair [GO:2000781]; regulation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0043281]; response to drug [GO:0042493]; response to ethanol [GO:0045471]; response to folic acid [GO:0051593]; response to toxic substance [GO:0009636]	membrane [GO:0016020]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	calcium ion binding [GO:0005509]; DNA binding [GO:0003677]; DNA-methyltransferase activity [GO:0009008]; methylated-DNA-[protein]-cysteine S-methyltransferase activity [GO:0003908]; methyltransferase activity [GO:0008168]
1 1 7	Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 (E-NPP 2) (EC 3.1.4.39) (Autotaxin) (Extracellular lysophospholipase D) (LysoPLD)	ENPP2 ATX PDNP2	863	cell motility [GO:0048870]; chemotaxis [GO:0006935]; immune response [GO:0006955]; phosphatidylcholine catabolic process [GO:0034638]; phospholipid catabolic process [GO:0009395]; positive regulation of epithelial cell migration [GO:0010634]; positive regulation of lamellipodium morphogenesis [GO:2000394]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; regulation of angiogenesis [GO:0045765]; regulation of cell migration [GO:0030334]; sphingolipid catabolic process [GO:0030149]	extracellular space [GO:0005615]; plasma membrane [GO:0005886]	alkylglycerophosphoethanolamine phosphodiesterase activity [GO:0047391]; calcium ion binding [GO:0005509]; hydrolase activity [GO:0016787]; lysophospholipase activity [GO:0004622]; nucleic acid binding [GO:0003676]; nucleotide diphosphatase activity [GO:0004551]; phosphodiesterase I activity [GO:0004528]; polysaccharide binding [GO:0030247]; scavenger receptor activity [GO:0005044]; transcription factor binding [GO:0008134]; zinc ion binding [GO:0008270]

118	Serine protease HTRA2, mitochondrial (EC 3.4.21.108) (High temperature requirement protein A2) (HtrA2) (Omi stress-regulated endoprotease) (Serine protease 25) (Serine proteinase OMI)	HTRA2 OMI PRSS25	458	adult walking behavior [GO:0007628]; aging [GO:0007568]; cellular protein catabolic process [GO:0044257]; cellular response to growth factor stimulus [GO:0071363]; cellular response to heat [GO:0034605]; cellular response to interferon-beta [GO:0035458]; cellular response to oxidative stress [GO:0034599]; cellular response to retinoic acid [GO:0071300]; ceramide metabolic process [GO:0006672]; execution phase of apoptosis [GO:0097194]; forebrain development [GO:0030900]; intrinsic apoptotic signaling pathway in response to DNA damage [GO:0008630]; mitochondrion organization [GO:0007005]; negative regulation of cell cycle [GO:0045786]; negative regulation of mitophagy in response to mitochondrial depolarization [GO:1904924]; negative regulation of neuron death [GO:1901215]; negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway [GO:1902176]; neuron development [GO:0048666]; pentacyclic triterpenoid metabolic process [GO:0019742]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0043280]; positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway [GO:2001269]; positive regulation of extrinsic apoptotic signaling pathway in absence of ligand [GO:2001241]; positive regulation of mitochondrion organization [GO:0010822]; positive regulation of protein targeting to mitochondrion [GO:1903955]; programmed cell death [GO:0012501]; protein autoprocessing [GO:0016540]; proteolysis [GO:0006508]; regulation of autophagy of mitochondrion [GO:1903146]; regulation of multicellular organism growth [GO:0040014]; response to herbicide [GO:0009635]	CD40 receptor complex [GO:0035631]; chromatin [GO:0000785]; cytoplasmic side of plasma membrane [GO:0009898]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]; membrane [GO:0016020]; mitochondrial intermembrane space [GO:0005758]; mitochondrial membrane [GO:0031966]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; serine-type endopeptidase complex [GO:1905370]	identical protein binding [GO:0042802]; peptidase activity [GO:0008233]; serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]; unfolded protein binding [GO:0051082]
119	Lymphocyte antigen 75 (Ly-75) (C-type lectin domain family 13 member B) (DEC-205) (gp200-MR6) (CD antigen CD205)	LY75 CD205 CLEC13B	1722	endocytosis [GO:0006897]; immune response [GO:0006955]; inflammatory response [GO:0006954]	external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; integral component of plasma membrane [GO:0005887]	carbohydrate binding [GO:0030246]; signaling receptor activity [GO:0038023]
120	HLA class II histocompatibility antigen gamma chain (HLA-DR antigens-associated invariant chain) (Ia antigen-associated invariant chain) (Ii) (CD antigen CD74) [Cleaved into: Class-II-associated invariant chain peptide (CLIP)]	CD74 DHLAG	296	activation of MAPK activity [GO:0000187]; antigen processing and presentation [GO:0019882]; antigen processing and presentation of endogenous antigen [GO:0019883]; antigen processing and presentation of exogenous peptide antigen via MHC class II [GO:0019886]; cell population proliferation [GO:0008283]; chaperone cofactor-dependent protein refolding [GO:0051085]; immunoglobulin mediated immune response [GO:0016064]; intracellular protein transport [GO:0006886]; macrophage migration inhibitory factor signaling pathway [GO:0035691]; negative regulation of apoptotic process [GO:0043066]; negative regulation of cell migration [GO:0030336]; negative regulation of DNA damage response, signal transduction by p53 class mediator [GO:0043518]; negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator [GO:1902166]; negative regulation of mature B cell apoptotic process [GO:0002906]; negative regulation of peptide secretion [GO:0002792]; negative regulation of T cell differentiation [GO:0045581]; negative regulation of viral entry into host cell [GO:0046597]; negative thymic T cell selection [GO:0045060]; positive regulation of B cell proliferation [GO:0030890]; positive regulation of chemokine (C-X-C motif) ligand 2 production [GO:2000343]; positive regulation of chemokine production [GO:0032722]; positive regulation of cytokine-mediated signaling pathway [GO:0001961]; positive regulation of dendritic cell antigen processing and presentation [GO:0002606]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of fibroblast proliferation [GO:0048146]; positive regulation of gene expression [GO:0010628]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of interleukin-6 production [GO:0032755]; positive regulation of interleukin-8 production [GO:0032757]; positive regulation of kinase activity [GO:0033674]; positive regulation of macrophage cytokine production [GO:0060907]; positive regulation of macrophage migration inhibitory factor signaling pathway [GO:2000448]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of monocyte differentiation [GO:0045657]; positive regulation of neutrophil chemotaxis [GO:0090023]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of prostaglandin biosynthetic process [GO:0031394]; positive regulation of protein phosphorylation [GO:0001934]; positive regulation of T cell differentiation [GO:0045582]; positive regulation of transcription, DNA-templated [GO:0045893]; positive regulation of type 2 immune response [GO:0002830]; positive regulation of viral entry into host cell [GO:0046598]; positive thymic T cell selection [GO:0045059]; prostaglandin biosynthetic process [GO:0001516]; protein-containing complex assembly [GO:0065003]; protein stabilization [GO:0050821]; protein trimerization [GO:0070206]; regulation of macrophage activation [GO:0043030]; response to interferon-gamma [GO:0034341]; T cell activation involved in immune response [GO:0002286]; T cell selection [GO:0045058]	cell surface [GO:0009986]; clathrin-coated endocytic vesicle membrane [GO:0030669]; cytoplasm [GO:0005737]; endocytic vesicle membrane [GO:0030666]; ER to Golgi transport vesicle membrane [GO:0012507]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; Golgi membrane [GO:0000139]; integral component of lumenal side of endoplasmic reticulum membrane [GO:0071556]; integral component of membrane [GO:0016021]; late endosome [GO:0005770]; lysosomal lumen [GO:0043202]; lysosomal membrane [GO:0005765]; lysosome [GO:0005764]; macrophage migration inhibitory factor receptor complex [GO:0035692]; membrane [GO:0016020]; MHC class II protein complex [GO:0042613]; multivesicular body [GO:0005771]; NOS2-CD74 complex [GO:0035693]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; protein-containing complex [GO:0032991]; trans-Golgi network membrane [GO:0032588]; transport vesicle membrane [GO:0030658]; vacuole [GO:0005773]	amyloid-beta binding [GO:0001540]; CD4 receptor binding [GO:0042609]; cytokine binding [GO:0019955]; cytokine receptor activity [GO:0004896]; identical protein binding [GO:0042802]; macrophage migration inhibitory factor binding [GO:0035718]; MHC class II protein binding [GO:0042289]; MHC class II protein binding, via antigen binding groove [GO:0042658]; MHC class II protein complex binding [GO:0023026]; nitric-oxide synthase binding [GO:0050998]; protein folding chaperone [GO:0044183]
121	Stromal cell-derived factor 1 (SDF-1) (hSDF-1) (C-X-C motif chemokine 12) (Intercrine reduced in hepatomas) (IRH) (hIRH) (Pre-B cell growth-stimulating factor) (PBSF) [Cleaved into: SDF-1-beta(3-72); SDF-1-alpha(3-67)]	CXCL12 SDF1 SDF1A SDF1B	93	adult locomotory behavior [GO:0008344]; animal organ regeneration [GO:0031100]; antimicrobial humoral immune response mediated by antimicrobial peptide [GO:0061844]; axon guidance [GO:0007411]; blood circulation [GO:0008015]; cell adhesion [GO:0007155]; cell chemotaxis [GO:0060326]; cellular calcium ion homeostasis [GO:0006874]; cellular response to chemokine [GO:1990869]; chemokine (C-X-C motif) ligand 12 signaling pathway [GO:0038146]; chemokine-mediated signaling pathway [GO:0070098]; chemotaxis [GO:0006935]; defense response [GO:0006952]; detection of mechanical stimulus involved in sensory perception of pain [GO:0050966]; detection of temperature stimulus involved in sensory perception of pain [GO:0050965]; G protein-coupled receptor signaling pathway [GO:0007186]; immune response [GO:0006955]; induction of positive chemotaxis [GO:0050930]; integrin activation [GO:0033622]; killing of cells of other organism [GO:0031640]; negative regulation of dendritic cell apoptotic process [GO:2000669]; negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage [GO:1902230]; negative regulation of leukocyte tethering or rolling [GO:1903237]; neuron migration [GO:0001764]; positive regulation of axon extension involved in axon guidance [GO:0048842]; positive regulation of calcium ion import [GO:0090280]; positive regulation of cell adhesion [GO:0045785]; positive regulation of cell migration [GO:0030335]; positive regulation of dopamine secretion [GO:0033603]; positive regulation of endothelial cell proliferation [GO:0001938]; positive regulation of monocyte chemotaxis [GO:0090026]; positive regulation of neuron differentiation [GO:0045666]; positive regulation of T cell migration [GO:2000406]; regulation of actin polymerization or depolymerization [GO:0008064]; response to heat [GO:0009408]; response to hypoxia [GO:0001666]; response to peptide hormone [GO:0043434]; response to radiation [GO:0009314]; response to ultrasound [GO:1990478]; response to virus [GO:0009615]; signal transduction [GO:0007165]; T cell chemotaxis [GO:0010818]; telencephalon cell migration [GO:0022029]	collagen-containing extracellular matrix [GO:0062023]; cytoplasm [GO:0005737]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; nucleus [GO:0005634]	chemokine activity [GO:0008009]; chemokine receptor binding [GO:0042379]; CXCR chemokine receptor binding [GO:0045236]; growth factor activity [GO:0008083]; integrin binding [GO:0005178]; signaling receptor binding [GO:0005102]
122	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide (hDAPP1) (B	DAPP1 BAM32 HSPC066	280	protein dephosphorylation [GO:0006470]; signal transduction [GO:0007165]	cytosol [GO:0005829]; plasma membrane [GO:0005886]	phosphatidylinositol-3,4,5-trisphosphate binding [GO:0005547]; phosphatidylinositol-3,4-bisphosphate binding [GO:0043325]; phospholipid binding [GO:0005543]

	lymphocyte adapter protein Bam32) (B-cell adapter molecule of 32 kDa)					
123	Contactin-4 (Brain-derived immunoglobulin superfamily protein 2) (BIG-2)	CNTN4	1026	axonal fasciculation [GO:0007413]; axon guidance [GO:0007411]; axonogenesis [GO:0007409]; brain development [GO:0007420]; dendrite self-avoidance [GO:0070593]; homophilic cell adhesion via plasma membrane adhesion molecules [GO:0007156]; negative regulation of neuron differentiation [GO:0045665]; nervous system development [GO:0007399]; neuron cell-cell adhesion [GO:0007158]; neuron projection development [GO:0031175]; regulation of synaptic plasticity [GO:0048167]	anchored component of membrane [GO:0031225]; axon [GO:0030424]; extracellular region [GO:0005576]; plasma membrane [GO:0005886]	cell-cell adhesion mediator activity [GO:0098632]
124	Protein FAM3B (Cytokine-like protein 2-21) (Pancreatic-derived factor) (PANDER)	FAM3B C21orf11 C21orf76 PRED44 UNQ320/PRO365	235	apoptotic process [GO:0006915]; glucose homeostasis [GO:0042593]; insulin secretion [GO:0030073]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	cytokine activity [GO:0005125]
125	C-type lectin domain family 6 member A (C-type lectin superfamily member 10) (Dendritic cell-associated C-type lectin 2) (DC-associated C-type lectin 2) (Dectin-2)	CLEC6A CLECSF10 DECTIN2	209	adaptive immune response [GO:0002250]; antifungal innate immune response [GO:0061760]; defense response to fungus [GO:0050832]; detection of yeast [GO:0001879]; innate immune response [GO:0045087]; positive regulation of cytokine production [GO:0001819]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of intracellular signal transduction [GO:1902533]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of T-helper 17 type immune response [GO:2000318]; response to yeast [GO:0001878]; stimulatory C-type lectin receptor signaling pathway [GO:0002223]	integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	calcium ion binding [GO:0005509]; carbohydrate binding [GO:0030246]; mannose binding [GO:0005537]; pattern recognition receptor activity [GO:0038187]; phospholipase binding [GO:0043274]
126	Protein-arginine deiminase type-2 (EC 3.5.3.15) (PAD-H19) (Peptidylarginine deiminase II) (Protein-arginine deiminase type II)	PADI2 KIAA0994 PAD2 PDI2	665	cellular response to leukemia inhibitory factor [GO:1990830]; chromatin-mediated maintenance of transcription [GO:0048096]; histone citrullination [GO:0036414]; histone H3-R26 citrullination [GO:0036413]; intracellular estrogen receptor signaling pathway [GO:0030520]; negative regulation of chemokine-mediated signaling pathway [GO:0070100]; negative regulation of lymphocyte chemotaxis [GO:1901624]; protein citrullination [GO:0018101]; regulation of chromatin disassembly [GO:0010848]; substantia nigra development [GO:0021762]	azurophil granule lumen [GO:0035578]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; nucleus [GO:0005634]; transcriptionally active chromatin [GO:0035327]	calcium ion binding [GO:0005509]; estrogen receptor binding [GO:0030331]; protein-arginine deiminase activity [GO:0004668]; protein homodimerization activity [GO:0042803]
127	Legumain (EC 3.4.22.34) (Asparaginyl endopeptidase) (Protease, cysteine 1)	LGMN PRSC1	433	activation of cysteine-type endopeptidase activity [GO:0097202]; antigen processing and presentation of exogenous peptide antigen via MHC class II [GO:0019886]; associative learning [GO:0008306]; cellular response to amyloid-beta [GO:1904646]; cellular response to calcium ion [GO:0071277]; cellular response to hepatocyte growth factor stimulus [GO:0035729]; dendritic spine organization [GO:0097061]; memory [GO:0007613]; negative regulation of ERBB signaling pathway [GO:1901185]; negative regulation of gene expression [GO:0010629]; negative regulation of multicellular organism growth [GO:0040015]; negative regulation of neuron apoptotic process [GO:0043524]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of endothelial cell chemotaxis [GO:2001028]; positive regulation of long-term synaptic potentiation [GO:1900273]; positive regulation of mitotic cell cycle [GO:0045931]; positive regulation of monocyte chemotaxis [GO:0090026]; proteolysis [GO:0006508]; proteolysis involved in cellular protein catabolic process [GO:0051603]; receptor catabolic process [GO:0032801]; renal system process [GO:0003014]; response to acidic pH [GO:0010447]; self proteolysis [GO:0097264]; vacuolar protein processing [GO:0006624]; vitamin D metabolic process [GO:0042359]	apical part of cell [GO:0045177]; cytoplasm [GO:0005737]; endolysosome lumen [GO:0036021]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; late endosome [GO:0005770]; lysosomal lumen [GO:0043202]; lysosome [GO:0005764]; perinuclear region of cytoplasm [GO:0048471]	cysteine-type endopeptidase activity [GO:0004197]; peptidase activity [GO:0008233]; tau protein binding [GO:0048156]
128	Zinc finger and BTB domain-containing protein 16 (Promyelocytic leukemia zinc finger protein) (Zinc finger protein 145) (Zinc finger protein PLZF)	ZBTB16 PLZF ZNF145	673	anterior/posterior pattern specification [GO:0009952]; apoptotic process [GO:0006915]; cartilage development [GO:0051216]; central nervous system development [GO:0007417]; embryonic digit morphogenesis [GO:0042733]; embryonic hindlimb morphogenesis [GO:0035116]; embryonic pattern specification [GO:0009880]; forelimb morphogenesis [GO:0035136]; hemopoiesis [GO:0030097]; male germ-line stem cell asymmetric division [GO:0048133]; mesonephros development [GO:0001823]; myeloid cell differentiation [GO:0030099]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of myeloid cell differentiation [GO:0045638]; negative regulation of transcription, DNA-templated [GO:0045892]; negative regulation of transcription by RNA polymerase II [GO:0000122]; ossification involved in bone maturation [GO:0043931]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cartilage development [GO:0061036]; positive regulation of chondrocyte differentiation [GO:0032332]; positive regulation of fat cell differentiation [GO:0045600]; positive regulation of NK T cell differentiation [GO:0051138]; positive regulation of ossification [GO:0045778]; positive regulation of transcription, DNA-templated [GO:0045893]; protein localization to nucleus [GO:0034504]; protein ubiquitination [GO:0016567]; regulation of transcription by RNA polymerase II [GO:0006357]	cytosol [GO:0005829]; nuclear body [GO:0016604]; nuclear speck [GO:0016607]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; PML body [GO:0016605]; protein-containing complex [GO:0032991]; transcription repressor complex [GO:0017053]	DNA binding [GO:0003677]; DNA-binding transcription activator activity, RNA polymerase II-specific [GO:0001228]; DNA-binding transcription repressor activity, RNA polymerase II-specific [GO:0001227]; identical protein binding [GO:0042802]; metal ion binding [GO:0046872]; protein C-terminus binding [GO:0008022]; protein domain specific binding [GO:0019904]; protein homodimerization activity [GO:0042803]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]; transcription corepressor binding [GO:0001222]
129	Diacylglycerol kinase zeta (DAG kinase zeta) (EC 2.7.1.107) (Diglyceride kinase zeta) (DGK-zeta)	DGKZ DAGK6	928	cell migration [GO:0016477]; diacylglycerol metabolic process [GO:0046339]; glycerolipid metabolic process [GO:0046486]; intracellular signal transduction [GO:0035556]; lipid phosphorylation [GO:0046834]; mitotic G1 DNA damage checkpoint signaling [GO:0031571]; negative regulation of mitotic cell cycle [GO:0045930]; negative regulation of T cell receptor signaling pathway [GO:0050860]; phosphatidic acid biosynthetic process [GO:0006654]; platelet activation [GO:0030168]; positive regulation of 1-phosphatidylinositol-4-phosphate 5-kinase activity [GO:0090216]; protein kinase C-activating G protein-coupled receptor signaling pathway [GO:0007205]; regulation of synaptic transmission, glutamatergic [GO:0051966]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; glutamatergic synapse [GO:0098978]; lamellipodium [GO:0030027]; nuclear speck [GO:0016607]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; postsynaptic density [GO:0014069]	ATP binding [GO:0005524]; diacylglycerol kinase activity [GO:0004143]; kinase activity [GO:0016301]; lipid kinase activity [GO:0001727]; metal ion binding [GO:0046872]; NAD+ kinase activity [GO:0003951]; protein C-terminus binding [GO:0008022]
130	Receptor-type tyrosine-protein phosphatase F (EC 3.1.3.48) (Leukocyte common antigen related) (LAR)	PTPRF LAR	1907	cell adhesion [GO:0007155]; cell migration [GO:0016477]; negative regulation of receptor binding [GO:1900121]; neuron projection regeneration [GO:0031102]; peptidyl-tyrosine dephosphorylation [GO:0035335]; protein dephosphorylation [GO:0006470]; regulation of axon regeneration [GO:0048679]; synaptic membrane adhesion [GO:0099560]; transmembrane receptor protein tyrosine phosphatase signaling pathway [GO:0007185]	extracellular exosome [GO:0070062]; integral component of plasma membrane [GO:0005887]; neuronal cell body [GO:0043025]; neuron projection [GO:0043005]; plasma membrane [GO:0005886]	cell adhesion molecule binding [GO:0050839]; chondroitin sulfate proteoglycan binding [GO:0035373]; heparin binding [GO:0008201]; protein-containing complex binding [GO:0044877]; protein tyrosine phosphatase activity [GO:0004725]; transmembrane receptor protein tyrosine phosphatase activity [GO:0005001]
131	Integrin beta-6	ITGB6	788	bone development [GO:0060348]; bronchiole development [GO:0060435]; cell adhesion [GO:0007155]; cell adhesion mediated by integrin [GO:0033627]; cell-matrix adhesion [GO:0007160]; cell migration [GO:0016477]; cell morphogenesis [GO:0000902]; cellular response to ionizing radiation [GO:0071479]; enamel mineralization [GO:0070166]; hard palate development [GO:0060022]; immune response [GO:0006955]; inflammatory response [GO:0006954]; integrin-mediated signaling pathway [GO:0007229]; Langerhans cell differentiation [GO:0061520]; lung alveolus development [GO:0048286]; phospholipid homeostasis [GO:0055091]; regulation of transforming growth factor beta activation [GO:1901388]; response to virus [GO:0009615]; skin development [GO:0043588]; SMAD protein signal	cell junction [GO:0030054]; centrosome [GO:0005813]; external side of plasma membrane [GO:0009897]; focal adhesion [GO:0005925]; integrin alphav-beta6 complex [GO:0034685]; integrin complex [GO:0008305]; nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]	integrin binding [GO:0005178]; signaling receptor activity [GO:0038023]; virus receptor activity [GO:0001618]

				transduction [GO:0060395]; surfactant homeostasis [GO:0043129]; transforming growth factor beta production [GO:0071604]; transforming growth factor beta receptor signaling pathway [GO:0007179]; wound healing [GO:0042060]		
132	Coxsackievirus and adenovirus receptor (CAR) (hCAR) (CVB3-binding protein) (Coxsackievirus B-adenovirus receptor) (HCVADR)	CXADR CAR	365	actin cytoskeleton reorganization [GO:0031532]; AV node cell-bundle of His cell adhesion involved in cell communication [GO:0086072]; AV node cell to bundle of His cell communication [GO:0086067]; cardiac muscle cell development [GO:0055013]; cell-cell junction organization [GO:0045216]; defense response to virus [GO:0051607]; epithelial structure maintenance [GO:0010669]; gamma-delta T cell activation [GO:0046629]; germ cell migration [GO:0008354]; heart development [GO:0007507]; heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules [GO:0007157]; homotypic cell-cell adhesion [GO:0034109]; mitochondrion organization [GO:0007005]; neutrophil chemotaxis [GO:0030593]; regulation of AV node cell action potential [GO:0098904]; transepithelial transport [GO:0070633]	acrosomal vesicle [GO:0001669]; adherens junction [GO:0005912]; apicolateral plasma membrane [GO:0016327]; basolateral plasma membrane [GO:0016323]; bicellular tight junction [GO:0005923]; cell body [GO:0044297]; cell-cell junction [GO:0005911]; cell junction [GO:0030054]; cytoplasm [GO:0005737]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; filopodium [GO:0030175]; growth cone [GO:0030426]; integral component of plasma membrane [GO:0005887]; intercalated disc [GO:0014704]; membrane raft [GO:0045121]; neuromuscular junction [GO:0031594]; neuron projection [GO:0043005]; nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; protein-containing complex [GO:0032991]	beta-catenin binding [GO:0008013]; cell adhesion molecule binding [GO:0050839]; cell adhesive protein binding involved in AV node cell-bundle of His cell communication [GO:0086082]; connexin binding [GO:0071253]; identical protein binding [GO:0042802]; integrin binding [GO:0005178]; PDZ domain binding [GO:0030165]; signaling receptor binding [GO:0005102]; virus receptor activity [GO:0001618]
133	C-type lectin domain family 4 member G (Liver and lymph node sinusoidal endothelial cell C-type lectin) (LSECtin)	CLEC4G UNQ431/PRO792	293	negative regulation of T cell mediated immunity [GO:0002710]; negative regulation of T cell proliferation [GO:0042130]; positive regulation of viral life cycle [GO:1903902]; viral entry into host cell [GO:0046718]	integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	carbohydrate derivative binding [GO:0097367]; fructose binding [GO:0070061]; glycosylated region protein binding [GO:0140081]; mannose binding [GO:0005537]; polysaccharide binding [GO:0030247]; virus coreceptor activity [GO:0120274]; virus receptor activity [GO:0001618]
134	Fibroblast growth factor 2 (FGF-2) (Basic fibroblast growth factor) (bFGF) (Heparin-binding growth factor 2) (HBGF-2)	FGF2 FGFB	288	activation of MAPK activity [GO:0000187]; aging [GO:0007568]; angiogenesis involved in coronary vascular morphogenesis [GO:0060978]; animal organ morphogenesis [GO:0009887]; branching involved in ureteric bud morphogenesis [GO:0001658]; cell differentiation [GO:0030154]; cell migration involved in sprouting angiogenesis [GO:0002042]; chemotaxis [GO:0006935]; chondroblast differentiation [GO:0060591]; corticotropin hormone secreting cell differentiation [GO:0060128]; embryo development ending in birth or egg hatching [GO:0009792]; embryonic morphogenesis [GO:0048598]; fibroblast growth factor receptor signaling pathway [GO:0008543]; glial cell differentiation [GO:0010001]; growth factor dependent regulation of skeletal muscle satellite cell proliferation [GO:0014843]; hyaluronan catabolic process [GO:0030214]; inositol phosphate biosynthetic process [GO:0032958]; lung development [GO:0030324]; mammary gland epithelial cell differentiation [GO:0060644]; negative regulation of blood vessel endothelial cell migration [GO:0043537]; negative regulation of cell death [GO:0060548]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of fibroblast growth factor receptor signaling pathway [GO:0040037]; negative regulation of fibroblast migration [GO:0010764]; negative regulation of gene expression [GO:0010629]; negative regulation of wound healing [GO:0061045]; nervous system development [GO:0007399]; organ induction [GO:0001759]; paracrine signaling [GO:0038001]; phosphatidylinositol biosynthetic process [GO:0006661]; positive regulation of angiogenesis [GO:0045766]; positive regulation of blood vessel endothelial cell migration [GO:0043536]; positive regulation of canonical Wnt signaling pathway [GO:0090263]; positive regulation of cardiac muscle cell proliferation [GO:0060045]; positive regulation of cell division [GO:0051781]; positive regulation of cell fate specification [GO:0042660]; positive regulation of cell migration involved in sprouting angiogenesis [GO:0090050]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of cerebellar granule cell precursor proliferation [GO:0021940]; positive regulation of DNA biosynthetic process [GO:2000573]; positive regulation of endothelial cell chemotaxis [GO:2001028]; positive regulation of endothelial cell chemotaxis to fibroblast growth factor [GO:2000546]; positive regulation of endothelial cell migration [GO:0010595]; positive regulation of endothelial cell proliferation [GO:0001938]; positive regulation of epithelial cell proliferation [GO:0050679]; positive regulation of epithelial tube formation [GO:1905278]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of gene expression [GO:0010628]; positive regulation of lens fiber cell differentiation [GO:1902748]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of MAP kinase activity [GO:0043406]; positive regulation of osteoblast differentiation [GO:0045669]; positive regulation of phosphatidylinositol 3-kinase activity [GO:0043552]; positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; positive regulation of phospholipase C activity [GO:0010863]; positive regulation of pri-miRNA transcription by RNA polymerase II [GO:1902895]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of protein phosphorylation [GO:0001934]; positive regulation of sprouting angiogenesis [GO:1903672]; positive regulation of transcription, DNA-templated [GO:0045893]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of vascular associated smooth muscle cell proliferation [GO:1904707]; positive regulation of vascular endothelial cell proliferation [GO:1905564]; Ras protein signal transduction [GO:0007265]; regulation of angiogenesis [GO:0045765]; regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis [GO:1903587]; regulation of cell cycle [GO:0051726]; regulation of cell migration [GO:0030334]; regulation of cell migration involved in sprouting angiogenesis [GO:0090049]; regulation of endothelial cell chemotaxis to fibroblast growth factor [GO:2000544]; regulation of retinal cell programmed cell death [GO:0046668]; release of sequestered calcium ion into cytosol [GO:0051209]; response to axon injury [GO:0048678]; signal transduction [GO:0007165]; stem cell development [GO:0048864]; stem cell proliferation [GO:0072089]; substantia nigra development [GO:0021762]; thyroid-stimulating hormone-secreting cell differentiation [GO:0060129]; wound healing [GO:0042060]	cytoplasm [GO:0005737]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; nucleus [GO:0005634]	chemoattractant activity [GO:0042056]; chemokine binding [GO:0019956]; cytokine activity [GO:0005125]; fibroblast growth factor receptor binding [GO:0005104]; growth factor activity [GO:0008083]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; integrin binding [GO:0005178]; nuclear receptor coactivator activity [GO:0030374]; receptor-receptor interaction [GO:0090722]
135	Lymphocyte activation gene 3 protein (LAG-3) (CD antigen CD223) [Cleaved into: Secreted lymphocyte activation gene 3 protein (sLAG-3)]	LAG3 FDC	525	adaptive immune response [GO:0002250]; cell surface receptor signaling pathway [GO:0007166]; negative regulation of interleukin-2 production [GO:0032703]; negative regulation of regulatory T cell differentiation [GO:0045590]; plasmacytoid dendritic cell activation [GO:0002270]; positive regulation of natural killer cell mediated cytotoxicity [GO:0045954]; regulation of immune response [GO:0050776]	external side of plasma membrane [GO:0009897]; extracellular region [GO:0005576]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	antigen binding [GO:0003823]; MHC class II protein binding [GO:0042289]; transmembrane signaling receptor activity [GO:0004888]
13	Interleukin-1 receptor-associated	IRAK1 IRAK	712	activation of NF-kappaB-inducing kinase activity [GO:0007250]; aging [GO:0007568]; cellular response to heat [GO:0034605]; cellular response to hypoxia	cytoplasm [GO:0005737]; cytosol [GO:0005829]; endosome membrane	ATP binding [GO:0005524]; heat shock protein binding [GO:0031072]; identical

6	kinase 1 (IRAK-1) (EC 2.7.11.1)			[GO:0071456]; cellular response to lipopolysaccharide [GO:0071222]; cytokine-mediated signaling pathway [GO:0019221]; innate immune response [GO:0045087]; interleukin-1-mediated signaling pathway [GO:0070498]; intracellular signal transduction [GO:0035556]; JNK cascade [GO:0007254]; lipopolysaccharide-mediated signaling pathway [GO:0031663]; MyD88-dependent toll-like receptor signaling pathway [GO:0002755]; negative regulation of NF-kappaB transcription factor activity [GO:0032088]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of leukocyte adhesion to vascular endothelial cell [GO:1904996]; positive regulation of MAP kinase activity [GO:0043406]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of NIK/NF-kappaB signaling [GO:1901224]; positive regulation of smooth muscle cell proliferation [GO:0048661]; positive regulation of type I interferon production [GO:0032481]; protein autophosphorylation [GO:0046777]; protein phosphorylation [GO:0006468]; regulation of cytokine-mediated signaling pathway [GO:0001959]; response to interleukin-1 [GO:0070555]; response to lipopolysaccharide [GO:0032496]; toll-like receptor 2 signaling pathway [GO:0034134]; toll-like receptor 4 signaling pathway [GO:0034142]; toll-like receptor 9 signaling pathway [GO:0034162]; toll-like receptor signaling pathway [GO:0002224]; type I interferon signaling pathway [GO:0060337]	[GO:0010008]; lipid droplet [GO:0005811]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; protein-containing complex [GO:0032991]	protein binding [GO:0042802]; kinase activity [GO:0016301]; NF-kappaB-inducing kinase activity [GO:0004704]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; protein kinase activity [GO:0004672]; protein kinase binding [GO:0019901]; protein serine/threonine kinase activity [GO:0004674]; protein serine kinase activity [GO:0106310]; protein threonine kinase activity [GO:0106311]
137	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Renal carcinoma antigen NY-REN-11) (Transformation-sensitive protein IEF SSP 3521)	STIP1	543	cellular response to interleukin-7 [GO:0098761]	chaperone complex [GO:0101031]; cytosol [GO:0005829]; dynein axonemal particle [GO:0120293]; Golgi apparatus [GO:0005794]; nucleus [GO:0005634]; protein-containing complex [GO:0032991]	chaperone binding [GO:0051087]; Hsp70 protein binding [GO:0030544]; Hsp90 protein binding [GO:0051879]; protein C-terminus binding [GO:0008022]; RNA binding [GO:0003723]
138	Signaling threshold-regulating transmembrane adapter 1 (SHP2-interacting transmembrane adapter protein) (Suppression-inducing transmembrane adapter 1) (gp30/40)	SIT1 SIT	196	adaptive immune response [GO:0002250]; regulation of T cell activation [GO:0050863]; signal transduction [GO:0007165]; T cell homeostasis [GO:0043029]	extracellular exosome [GO:0070062]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	kinase binding [GO:0019900]; SH2 domain binding [GO:0042169]
139	C-C motif chemokine 21 (6Ckine) (Beta-chemokine exodus-2) (Secondary lymphoid-tissue chemokine) (SLC) (Small-inducible cytokine A21)	CCL21 SCYA 21 UNQ7 84/PR O1600	134	activation of GTPase activity [GO:0090630]; antimicrobial humoral immune response mediated by antimicrobial peptide [GO:0061844]; cell-cell signaling [GO:0007267]; cell chemotaxis [GO:0060326]; cell maturation [GO:0048469]; cellular response to chemokine [GO:1990869]; cellular response to interferon-gamma [GO:0071346]; cellular response to interleukin-1 [GO:0071347]; cellular response to tumor necrosis factor [GO:0071356]; chemokine (C-C motif) ligand 21 signaling pathway [GO:0038116]; chemokine-mediated signaling pathway [GO:0070098]; dendritic cell chemotaxis [GO:0002407]; dendritic cell dendrite assembly [GO:0097026]; eosinophil chemotaxis [GO:0048245]; establishment of T cell polarity [GO:0001768]; G protein-coupled receptor signaling pathway [GO:0007186]; immune response [GO:0006955]; immunological synapse formation [GO:0001771]; inflammatory response [GO:0006954]; killing of cells of other organism [GO:0031640]; lymphocyte chemotaxis [GO:0048247]; mesangial cell-matrix adhesion [GO:0035759]; monocyte chemotaxis [GO:0002548]; negative regulation of dendritic cell apoptotic process [GO:2000669]; negative regulation of dendritic cell dendrite assembly [GO:2000548]; negative regulation of leukocyte tethering or rolling [GO:1903237]; neutrophil chemotaxis [GO:0030593]; positive regulation of actin filament polymerization [GO:0030838]; positive regulation of cell adhesion mediated by integrin [GO:0033630]; positive regulation of cell-matrix adhesion [GO:0001954]; positive regulation of cell motility [GO:2000147]; positive regulation of chemotaxis [GO:0050921]; positive regulation of dendritic cell antigen processing and presentation [GO:0002606]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of filopodium assembly [GO:0051491]; positive regulation of glycoprotein biosynthetic process [GO:0010560]; positive regulation of GTPase activity [GO:0043547]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of JNK cascade [GO:0046330]; positive regulation of myeloid dendritic cell chemotaxis [GO:2000529]; positive regulation of neutrophil chemotaxis [GO:0090023]; positive regulation of phosphatidylinositol 3-kinase activity [GO:0043552]; positive regulation of protein kinase activity [GO:0045860]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of pseudopodium assembly [GO:0031274]; positive regulation of receptor-mediated endocytosis [GO:0048260]; positive regulation of T cell chemotaxis [GO:0010820]; positive regulation of T cell migration [GO:2000406]; release of sequestered calcium ion into cytosol [GO:0051209]; response to prostaglandin E [GO:0034695]; ruffle organization [GO:0031529]; T cell costimulation [GO:0031295]	extracellular region [GO:0005576]; extracellular space [GO:0005615]	CCR7 chemokine receptor binding [GO:0031732]; CCR chemokine receptor binding [GO:0048020]; chemokine activity [GO:0008009]; chemokine receptor binding [GO:0042379]
140	TNF receptor-associated factor 2 (EC 2.3.2.27) (E3 ubiquitin-protein ligase TRAF2) (RING-type E3 ubiquitin transferase TRAF2) (Tumor necrosis factor type 2 receptor-associated protein 3)	TRAF 2 TRAP 3	501	activation of NF-kappaB-inducing kinase activity [GO:0007250]; cellular protein-containing complex assembly [GO:0034622]; cellular response to nitric oxide [GO:0071732]; interleukin-17-mediated signaling pathway [GO:0097400]; intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress [GO:0070059]; mRNA stabilization [GO:0048255]; negative regulation of glial cell apoptotic process [GO:0034351]; negative regulation of neuron death [GO:1901215]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of extrinsic apoptotic signaling pathway [GO:2001238]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of I-kappaB phosphorylation [GO:1903721]; positive regulation of interleukin-2 production [GO:0032743]; positive regulation of JNK cascade [GO:0046330]; positive regulation of JUN kinase activity [GO:0043507]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of T cell cytokine production [GO:0002726]; positive regulation of tumor necrosis factor-mediated signaling pathway [GO:1903265]; programmed necrotic cell death [GO:0097300]; protein autoubiquitination [GO:0051865]; protein catabolic process [GO:0030163]; protein-containing complex assembly [GO:0065003]; protein K63-linked ubiquitination [GO:0070534]; regulation of apoptotic process [GO:0042981]; regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043122]; regulation of immunoglobulin production [GO:0002637]; regulation of protein-containing complex assembly [GO:0043254]; response to endoplasmic reticulum stress [GO:0034976]; signal transduction [GO:0007165]; signal transduction involved in regulation of gene expression [GO:0023019]; tumor necrosis factor-mediated signaling pathway [GO:0033209]	CD40 receptor complex [GO:0035631]; cell cortex [GO:0005938]; cytoplasmic side of plasma membrane [GO:0009898]; cytosol [GO:0005829]; IRE1-TRAF2-ASK1 complex [GO:1990604]; membrane raft [GO:0045121]; nucleoplasm [GO:0005654]; TRAF2-GSTP1 complex [GO:0097057]; tumor necrosis factor receptor superfamily complex [GO:0002947]; ubiquitin ligase complex [GO:0000151]; vesicle membrane [GO:0012506]	CD40 receptor binding [GO:0005174]; enzyme binding [GO:0019899]; identical protein binding [GO:0042802]; mitogen-activated protein kinase kinase kinase binding [GO:0031435]; protein-containing complex binding [GO:0044877]; protein kinase binding [GO:0019901]; protein-macromolecule adaptor activity [GO:0030674]; protein phosphatase binding [GO:0019903]; sphingolipid binding [GO:0046625]; thioesterase binding [GO:0031996]; tumor necrosis factor binding [GO:0043120]; tumor necrosis factor receptor binding [GO:0005164]; ubiquitin protein ligase binding [GO:0031625]; ubiquitin-protein transferase activity [GO:0004842]; zinc ion binding [GO:0008270]
14	Integral membrane protein 2A (Protein	ITM2 A	263	negative regulation of amyloid precursor protein biosynthetic process [GO:0042985]; plasma cell differentiation [GO:0002317]	Golgi apparatus [GO:0005794]; integral component of membrane [GO:0016021];	amyloid-beta binding [GO:0001540]

1	E25)	UNQ603/PRO1189			plasma membrane [GO:0005886]	
142	Transcription factor AP-1 (Activator protein 1) (AP1) (Proto-oncogene c-Jun) (V-jun avian sarcoma virus 17 oncogene homolog) (p39)	JUN	331	aging [GO:0007568]; angiogenesis [GO:0001525]; cellular response to cadmium ion [GO:0071276]; cellular response to potassium ion starvation [GO:0051365]; cellular response to reactive oxygen species [GO:0034614]; circadian rhythm [GO:0007623]; learning [GO:0007612]; membrane depolarization [GO:0051899]; negative regulation by host of viral transcription [GO:0043922]; negative regulation of DNA binding [GO:0043392]; negative regulation of transcription, DNA-templated [GO:0045892]; negative regulation of transcription by RNA polymerase II [GO:0000122]; negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress [GO:1990441]; positive regulation by host of viral transcription [GO:0043923]; positive regulation of apoptotic process [GO:0043065]; positive regulation of DNA replication [GO:0045740]; positive regulation of DNA-templated transcription, initiation [GO:2000144]; positive regulation of monocyte differentiation [GO:0045657]; positive regulation of neuron apoptotic process [GO:0043525]; positive regulation of pri-miRNA transcription by RNA polymerase II [GO:1902895]; positive regulation of transcription, DNA-templated [GO:0045893]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of vascular associated smooth muscle cell proliferation [GO:1904707]; Ras protein signal transduction [GO:0007265]; regulation of cell cycle [GO:0051726]; regulation of cell population proliferation [GO:0042127]; regulation of transcription by RNA polymerase II [GO:0006357]; release of cytochrome c from mitochondria [GO:0001836]; response to cAMP [GO:0051591]; response to cytokine [GO:0034097]; response to drug [GO:0042493]; response to hydrogen peroxide [GO:0042542]; response to lipopolysaccharide [GO:0032496]; response to mechanical stimulus [GO:0009612]; response to radiation [GO:0009314]; SMAD protein signal transduction [GO:0060395]; transcription by RNA polymerase II [GO:0006366]; transforming growth factor beta receptor signaling pathway [GO:0007179]	chromatin [GO:0000785]; cytosol [GO:0005829]; euchromatin [GO:0000791]; nuclear chromosome [GO:0000228]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; transcription factor AP-1 complex [GO:0035976]; transcription regulator complex [GO:0005667]	cAMP response element binding [GO:0035497]; DNA binding [GO:0003677]; DNA-binding transcription activator activity, RNA polymerase II-specific [GO:0001228]; DNA-binding transcription factor activity [GO:0003700]; DNA-binding transcription factor activity, RNA polymerase II-specific [GO:0000981]; DNA-binding transcription repressor activity, RNA polymerase II-specific [GO:0001227]; enzyme binding [GO:0019899]; GTPase activator activity [GO:0005096]; HMG box domain binding [GO:0071837]; identical protein binding [GO:0042802]; protein-containing complex binding [GO:0044877]; RNA binding [GO:0003723]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]; RNA polymerase II-specific DNA-binding transcription factor binding [GO:0061629]; R-SMAD binding [GO:0070412]; sequence-specific double-stranded DNA binding [GO:1990837]; transcription cis-regulatory region binding [GO:0000976]; transcription factor binding [GO:0008134]; ubiquitin-like protein ligase binding [GO:0044389]; ubiquitin protein ligase binding [GO:0031625]
143	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB ERBA2L PDI PDIA1 PO4DB	508	cellular response to hypoxia [GO:0071456]; cellular response to interleukin-7 [GO:0098761]; interleukin-12-mediated signaling pathway [GO:0035722]; interleukin-23-mediated signaling pathway [GO:0038155]; peptidyl-proline hydroxylation to 4-hydroxy-L-proline [GO:0018401]; positive regulation of cell adhesion [GO:0045785]; positive regulation of substrate adhesion-dependent cell spreading [GO:1900026]; positive regulation of viral entry into host cell [GO:0046598]; protein folding [GO:0006457]; protein folding in endoplasmic reticulum [GO:0034975]; regulation of oxidative stress-induced intrinsic apoptotic signaling pathway [GO:1902175]; response to endoplasmic reticulum stress [GO:0034976]	cytoskeleton [GO:0005856]; cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum chaperone complex [GO:0034663]; endoplasmic reticulum-Golgi intermediate compartment [GO:0005793]; endoplasmic reticulum lumen [GO:0005788]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; focal adhesion [GO:0005925]; lamellipodium [GO:0030027]; melanosome [GO:0042470]; procollagen-proline 4-dioxygenase complex [GO:0016222]; protein-containing complex [GO:0032991]	actin binding [GO:0003779]; enzyme binding [GO:0019899]; integrin binding [GO:0005178]; procollagen-proline 4-dioxygenase activity [GO:0004656]; protein disulfide isomerase activity [GO:0003756]; protein-disulfide reductase activity [GO:0015035]; protein heterodimerization activity [GO:0046982]; RNA binding [GO:0003723]; thiol oxidase activity [GO:0016972]
144	Inactive dipeptidyl peptidase 10 (Dipeptidyl peptidase IV-related protein 3) (DPRP-3) (Dipeptidyl peptidase X) (DPP X) (Dipeptidyl peptidase-like protein 2) (DPL2)	DPP10 DPRP3 KIAA1492	796	positive regulation of protein localization to plasma membrane [GO:1903078]; protein localization to plasma membrane [GO:0072659]; regulation of potassium ion transmembrane transport [GO:1901379]	membrane [GO:0016020]; plasma membrane [GO:0005886]; voltage-gated potassium channel complex [GO:0008076]	potassium channel regulator activity [GO:0015459]; serine-type peptidase activity [GO:0008236]; transmembrane transporter binding [GO:0044325]
145	Natural killer cells antigen CD94 (KP43) (Killer cell lectin-like receptor subfamily D member 1) (NK cell receptor) (CD antigen CD94)	KLRD1 CD94	179	adaptive immune response [GO:0002250]; cell surface receptor signaling pathway [GO:0007166]; natural killer cell mediated immunity [GO:0002228]; negative regulation of natural killer cell mediated cytotoxicity [GO:0045953]; negative regulation of T cell mediated cytotoxicity [GO:0001915]; positive regulation of natural killer cell mediated cytotoxicity [GO:0045954]; stimulatory C-type lectin receptor signaling pathway [GO:0002223]	integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]	carbohydrate binding [GO:0030246]; HLA-E specific inhibitory MHC class Ib receptor activity [GO:0062082]; MHC class Ib protein binding, via antigen binding groove [GO:0023030]; MHC class I protein complex binding [GO:0023024]; protein antigen binding [GO:1990405]; transmembrane signaling receptor activity [GO:0004888]
146	Baculoviral IAP repeat-containing protein 2 (EC 2.3.2.27) (Cellular inhibitor of apoptosis 1) (C-IAP1) (IAP homolog B) (Inhibitor of apoptosis protein 2) (hIAP-2) (hIAP2) (RING finger protein 48) (RING-type E3 ubiquitin transferase BIRC2) (TNFR2-TRAF-signaling complex protein 2)	BIRC2 API1 MIHB RNF48	618	cell surface receptor signaling pathway [GO:0007166]; I-kappaB kinase/NF-kappaB signaling [GO:0007249]; necroptotic process [GO:0070266]; negative regulation of apoptotic process [GO:0043066]; negative regulation of necroptotic process [GO:0060546]; negative regulation of ripoptosome assembly involved in necroptotic process [GO:1902443]; NIK/NF-kappaB signaling [GO:0038061]; placenta development [GO:0001890]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of protein K48-linked ubiquitination [GO:1902524]; positive regulation of protein K63-linked ubiquitination [GO:1902523]; positive regulation of protein monoubiquitination [GO:1902527]; positive regulation of protein ubiquitination [GO:0031398]; proteasome-mediated ubiquitin-dependent protein catabolic process [GO:0043161]; protein polyubiquitination [GO:0000209]; regulation of apoptotic process [GO:0042981]; regulation of cell cycle [GO:0051726]; regulation of cell differentiation [GO:0045595]; regulation of cell population proliferation [GO:0042127]; regulation of cysteine-type endopeptidase activity [GO:2000116]; regulation of inflammatory response [GO:0050727]; regulation of innate immune response [GO:0045088]; regulation of necroptotic process [GO:0060544]; regulation of NIK/NF-kappaB signaling [GO:1901222]; regulation of nucleotide-binding oligomerization domain containing signaling pathway [GO:0070424]; regulation of reactive oxygen species metabolic process [GO:2000377]; regulation of RIG-I signaling pathway [GO:0039535]; regulation of toll-like receptor signaling pathway [GO:0034121]; response to cAMP [GO:0051591]; response to ethanol [GO:0045471]; response to hypoxia [GO:0001666]; tumor necrosis factor-mediated signaling pathway [GO:0033209]	CD40 receptor complex [GO:0035631]; cytoplasm [GO:0005737]; cytoplasmic side of plasma membrane [GO:0009898]; cytosol [GO:0005829]; membrane raft [GO:0045121]; nucleus [GO:0005634]; XY body [GO:0001741]	chaperone binding [GO:0051087]; cysteine-type endopeptidase inhibitor activity involved in apoptotic process [GO:0043027]; FBXO family protein binding [GO:0098770]; identical protein binding [GO:0042802]; protein-containing complex binding [GO:0044877]; protein N-terminus binding [GO:0047485]; transcription coactivator activity [GO:0003713]; transferase activity [GO:0016740]; ubiquitin binding [GO:0043130]; ubiquitin protein ligase activity [GO:0061630]; ubiquitin-protein transferase activity [GO:0004842]; zinc ion binding [GO:0008270]
147	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-	EIF5A	154	cellular response to virus [GO:0098586]; mRNA transport [GO:0051028]; positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator [GO:1902255]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of translational elongation [GO:0045901]; positive regulation of translational termination [GO:0045905]; protein transport [GO:0015031]; tumor necrosis factor-mediated signaling pathway [GO:0033209]	annulate lamellae [GO:0005642]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; endoplasmic reticulum membrane [GO:0005789]; membrane [GO:0016020]; nuclear pore [GO:0005643]; nucleus [GO:0005634]	protein N-terminus binding [GO:0047485]; ribosome binding [GO:0043022]; RNA binding [GO:0003723]; translation elongation factor activity [GO:0003746]; U6 snRNA binding [GO:0017070]

	4D)					
148	Inactive serine protease PAMR1 (Peptidase domain-containing protein associated with muscle regeneration 1) (Regeneration-associated muscle protease homolog)	PAMR1 RAMP FP938 UNQ699/PRO1344	720		extracellular region [GO:0005576]	calcium ion binding [GO:0005509]
149	Corticosteroid 11-beta-dehydrogenase isozyme 1 (EC 1.1.1.146) (11-beta-hydroxysteroid dehydrogenase 1) (11-DH) (11-beta-HSD1) (Short chain dehydrogenase/reductase family 26C member 1)	HSD11B1 HSD11 HSD11L SDR26C1	292	lung development [GO:0030324]; steroid catabolic process [GO:0006706]	endoplasmic reticulum membrane [GO:0005789]; integral component of endoplasmic reticulum membrane [GO:0030176]; membrane [GO:0016020]	11-beta-hydroxysteroid dehydrogenase (NADP+) activity [GO:0070524]; 11-beta-hydroxysteroid dehydrogenase [NAD(P)] activity [GO:0003845]; NADP binding [GO:0050661]; protein homodimerization activity [GO:0042803]; steroid binding [GO:0005496]
150	Stanniocalcin-1 (STC-1)	STC1 STC	247	bone development [GO:0060348]; cellular calcium ion homeostasis [GO:0006874]; cellular response to cAMP [GO:0071320]; cellular response to glucocorticoid stimulus [GO:0071385]; cellular response to hypoxia [GO:0071456]; chondrocyte proliferation [GO:0035988]; decidualization [GO:0046697]; embryo implantation [GO:0007566]; endothelial cell morphogenesis [GO:0001886]; growth plate cartilage axis specification [GO:0003421]; negative regulation of calcium ion transport [GO:0051926]; negative regulation of cell migration [GO:0030336]; negative regulation of endothelial cell migration [GO:0010596]; negative regulation of renal phosphate excretion [GO:1903403]; ossification [GO:0001503]; positive regulation of calcium ion import [GO:0090280]; regulation of anion transport [GO:0044070]; regulation of cardiac muscle cell contraction [GO:0086004]; response to vitamin D [GO:0033280]	apical plasma membrane [GO:0016324]; cytoplasm [GO:0005737]; extracellular space [GO:0005615]; nucleus [GO:0005634]	hormone activity [GO:0005179]; identical protein binding [GO:0042802]
151	Dystroglycan 1 (Dystroglycan) (Dystrophin-associated glycoprotein 1) [Cleaved into: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta-DG)]	DAG1	895	aging [GO:0007568]; angiogenesis involved in wound healing [GO:0060055]; axon guidance [GO:0007411]; axon regeneration [GO:0031103]; basement membrane organization [GO:0071711]; branching involved in salivary gland morphogenesis [GO:0060445]; calcium-dependent cell-matrix adhesion [GO:0016340]; cellular response to cholesterol [GO:0071397]; cellular response to mechanical stimulus [GO:0071260]; commissural neuron axon guidance [GO:0071679]; epithelial tube branching involved in lung morphogenesis [GO:0060441]; membrane protein ectodomain proteolysis [GO:0006509]; microtubule anchoring [GO:0034453]; modulation by virus of host process [GO:0019048]; morphogenesis of an epithelial sheet [GO:0002011]; morphogenesis of an epithelium [GO:0002009]; muscle attachment [GO:0016203]; myelination in peripheral nervous system [GO:0022011]; negative regulation of cell migration [GO:0030336]; negative regulation of MAPK cascade [GO:0043409]; negative regulation of protein kinase B signaling [GO:0051898]; nerve development [GO:0021675]; nerve maturation [GO:0021682]; positive regulation of basement membrane assembly involved in embryonic body morphogenesis [GO:1904261]; positive regulation of cell-matrix adhesion [GO:0001954]; positive regulation of myelination [GO:0031643]; positive regulation of oligodendrocyte differentiation [GO:0048714]; positive regulation of protein kinase activity [GO:0045860]; regulation of embryonic cell shape [GO:0016476]; regulation of epithelial to mesenchymal transition [GO:0010717]; regulation of gastrulation [GO:0010470]; regulation of neurotransmitter receptor localization to postsynaptic specialization membrane [GO:0098696]; regulation of synapse organization [GO:0050807]; response to denervation involved in regulation of muscle adaptation [GO:0014894]; response to peptide hormone [GO:0043434]; retrograde trans-synaptic signaling by trans-synaptic protein complex [GO:0098942]; skeletal muscle tissue regeneration [GO:0043403]	adherens junction [GO:0005912]; basement membrane [GO:0005604]; basolateral plasma membrane [GO:0016323]; collagen-containing extracellular matrix [GO:0062023]; contractile ring [GO:0070938]; costamere [GO:0043034]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; dystroglycan complex [GO:0016011]; dystrophin-associated glycoprotein complex [GO:0016010]; endoplasmic reticulum lumen [GO:0005788]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; filopodium [GO:0030175]; focal adhesion [GO:0005925]; GABA-ergic synapse [GO:0098982]; glutamatergic synapse [GO:0098978]; Golgi lumen [GO:0005796]; integral component of membrane [GO:0016021]; intracellular membrane-bounded organelle [GO:0043231]; lamellipodium [GO:0030027]; node of Ranvier [GO:0033268]; nuclear periphery [GO:0034399]; nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; plasma membrane raft [GO:0044853]; postsynaptic cytosol [GO:0099524]; postsynaptic membrane [GO:0045211]; sarcolemma [GO:0042383]	actin binding [GO:0003779]; alpha-actinin binding [GO:0051393]; calcium ion binding [GO:0005509]; dystroglycan binding [GO:0002162]; laminin-1 binding [GO:0043237]; laminin binding [GO:0043236]; SH2 domain binding [GO:0042169]; structural constituent of muscle [GO:0008307]; tubulin binding [GO:0015631]; vinculin binding [GO:0017166]; virus receptor activity [GO:0001618]
152	Interferon regulatory factor 9 (IRF-9) (IFN-alpha-responsive transcription factor subunit) (ISGF3 p48 subunit) (Interferon-stimulated gene factor 3 gamma) (ISGF-3 gamma) (Transcriptional regulator ISGF3 subunit gamma)	IRF9 ISGF3G	393	cell surface receptor signaling pathway [GO:0007166]; defense response to virus [GO:0051607]; immune system process [GO:0002376]; regulation of transcription by RNA polymerase II [GO:0006357]; transcription by RNA polymerase II [GO:0006366]	chromatin [GO:0000785]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; DNA-binding transcription factor activity, RNA polymerase II-specific [GO:0000981]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]; sequence-specific double-stranded DNA binding [GO:1990837]
153	Integrin alpha-6 (CD49 antigen-like family member F) (VLA-6) (CD antigen CD49f) [Cleaved into: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain; Processed integrin alpha-6 (Alpha6p)]	ITGA6	1130	cell-cell adhesion [GO:0098609]; cell-substrate adhesion [GO:0031589]; cell-substrate junction assembly [GO:0007044]; cellular response to organic cyclic compound [GO:0071407]; ectodermal cell differentiation [GO:0010668]; integrin-mediated signaling pathway [GO:0007229]; nail development [GO:0035878]; negative regulation of extrinsic apoptotic signaling pathway [GO:2001237]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cell migration [GO:0030335]; positive regulation of cell-substrate adhesion [GO:0010811]; positive regulation of GTPase activity [GO:0043547]; positive regulation of neuron projection development [GO:0010976]; positive regulation of phosphorylation [GO:0042327]; positive regulation of transcription by RNA polymerase II [GO:0045944]; skin morphogenesis [GO:0043589]	adherens junction [GO:0005912]; cell surface [GO:0009986]; filopodium [GO:0030175]; focal adhesion [GO:0005925]; integrin alpha6-beta4 complex [GO:0034676]; plasma membrane [GO:0005886]	cadherin binding [GO:0045296]; insulin-like growth factor I binding [GO:0031994]; laminin binding [GO:0043236]; metal ion binding [GO:0046872]; neuregulin binding [GO:0038132]; protein-containing complex binding [GO:0044877]
154	Importin subunit alpha-5 (Karyopherin subunit alpha-1) (Nucleoprotein interactor 1) (NPI-1) (RAG cohort protein 2) (SRP1-beta) [Cleaved into: Importin subunit alpha-5, N-terminally processed]	KPNA1 RCH2	538	NLS-bearing protein import into nucleus [GO:0006607]; postsynapse to nucleus signaling pathway [GO:0099527]; regulation of apoptotic process [GO:0042981]; regulation of canonical Wnt signaling pathway [GO:0060828]; regulation of DNA recombination [GO:0000018]; satellite cell activation involved in skeletal muscle regeneration [GO:0014901]; skeletal muscle satellite cell proliferation [GO:0014841]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; dendrite [GO:0030425]; glutamatergic synapse [GO:0098978]; nuclear pore [GO:0005643]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; postsynaptic density [GO:0014069]	nuclear import signal receptor activity [GO:0061608]; nuclear localization sequence binding [GO:0008139]

155	Arylsulfatase A (ASA) (EC 3.1.6.8) (Cerebroside-sulfatase) [Cleaved into: Arylsulfatase A component B; Arylsulfatase A component C]	ARSA	507		azurophil granule lumen [GO:0035578]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; lysosomal lumen [GO:0043202]; lysosome [GO:0005764]	arylsulfatase activity [GO:0004065]; calcium ion binding [GO:0005509]; cerebroside-sulfatase activity [GO:0004098]; sulfuric ester hydrolase activity [GO:0008484]
156	C-type lectin domain family 4 member A (C-type lectin DDB27) (C-type lectin superfamily member 6) (Dendritic cell immunoreceptor) (Lectin-like immunoreceptor) (CD antigen CD367)	CLEC4A CLECSF6 DCIRLLIR HDCGC13P	237	adaptive immune response [GO:0002250]; antigen processing and presentation of exogenous peptide antigen via MHC class I [GO:0042590]; CD8-positive, alpha-beta T cell activation [GO:0036037]; cell adhesion [GO:0007155]; cell surface receptor signaling pathway [GO:0007166]; innate immune response [GO:0045087]; negative regulation of cytokine production [GO:0001818]; negative regulation of tumor necrosis factor production [GO:0032720]; plasmacytoid dendritic cell antigen processing and presentation [GO:0002470]	integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	calcium ion binding [GO:0005509]; carbohydrate binding [GO:0030246]; mannose binding [GO:0005537]; transmembrane signaling receptor activity [GO:0004888]
157	SH2 domain-containing protein 1A (Duncan disease SH2-protein) (Signaling lymphocytic activation molecule-associated protein) (SLAM-associated protein) (T-cell signal transduction molecule SAP)	SH2D1A DSHPSAP	128	adaptive immune response [GO:0002250]; cell-cell signaling [GO:0007267]; cellular defense response [GO:0006968]; humoral immune response [GO:0006959]; innate immune response [GO:0045087]; negative regulation of T cell receptor signaling pathway [GO:0050860]; positive regulation of natural killer cell mediated cytotoxicity [GO:0045954]; regulation of immune response [GO:0050776]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	
158	Protein HEXIM1 (Cardiac lineage protein 1) (Estrogen down-regulated gene 1 protein) (Hexamethylene bis-acetamide-inducible protein 1) (Menage a quatre protein 1)	HEXIM1 CLP1EDG1 HIS1MAQ1	359	activation of innate immune response [GO:0002218]; heart development [GO:0007507]; innate immune response [GO:0045087]; negative regulation of cyclin-dependent protein serine/threonine kinase activity [GO:0045736]; negative regulation of transcription, DNA-templated [GO:0045892]; negative regulation of transcription by RNA polymerase II [GO:0000122]; negative regulation of transcription elongation from RNA polymerase II promoter [GO:0034244]; negative regulation of viral transcription [GO:0032897]; positive regulation of signal transduction by p53 class mediator [GO:1901798]	7SK snRNP [GO:0120259]; cytoplasm [GO:0005737]; intracellular membrane-bounded organelle [GO:0043231]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	7SK snRNA binding [GO:0097322]; cyclin-dependent protein serine/threonine kinase inhibitor activity [GO:0004861]; identical protein binding [GO:0042802]; protein kinase inhibitor activity [GO:0004860]; P-TEFb complex binding [GO:0106140]; snRNA binding [GO:0017069]
159	Protein kinase C theta type (EC 2.7.11.13) (nPKC-theta)	PRKCQ PRKCT	706	axon guidance [GO:0007411]; cell chemotaxis [GO:0060326]; Fc-epsilon receptor signaling pathway [GO:0038095]; immune system process [GO:0002376]; inflammatory response [GO:0006954]; intracellular signal transduction [GO:0035556]; membrane protein ectodomain proteolysis [GO:0006509]; negative regulation of insulin receptor signaling pathway [GO:0046627]; negative regulation of T cell apoptotic process [GO:0070233]; peptidyl-serine phosphorylation [GO:0018105]; positive regulation of interleukin-17 production [GO:0032740]; positive regulation of interleukin-2 production [GO:0032743]; positive regulation of interleukin-4 production [GO:0032753]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of T cell activation [GO:0050870]; positive regulation of T cell proliferation [GO:0042102]; positive regulation of telomerase activity [GO:0051973]; positive regulation of telomere capping [GO:1904355]; positive regulation of telomere maintenance via telomerase [GO:0032212]; positive regulation of T-helper 17 type immune response [GO:2000318]; positive regulation of T-helper 2 cell activation [GO:2000570]; regulation of cell growth [GO:0001558]; regulation of platelet aggregation [GO:0090330]; regulation of transcription, DNA-templated [GO:0006355]	aggresome [GO:0016235]; centriolar satellite [GO:0034451]; cytosol [GO:0005829]; immunological synapse [GO:0001772]; plasma membrane [GO:0005886]	ATP binding [GO:0005524]; calcium-dependent protein kinase C activity [GO:0004698]; metal ion binding [GO:0046872]; protein kinase C activity [GO:0004697]; protein serine/threonine kinase activity [GO:0004674]; protein serine kinase activity [GO:0106310]; protein threonine kinase activity [GO:0106311]
160	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.24) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog) (Thioredoxin-dependent peroxiredoxin 3)	PRDX3 AOP1	256	cell redox homeostasis [GO:0045454]; cellular response to oxidative stress [GO:0034599]; cellular response to reactive oxygen species [GO:0034614]; hydrogen peroxide catabolic process [GO:0042744]; maternal placenta development [GO:0001893]; mitochondrion organization [GO:0007005]; myeloid cell differentiation [GO:0030099]; negative regulation of apoptotic process [GO:0043066]; negative regulation of kinase activity [GO:0033673]; peptidyl-cysteine oxidation [GO:0018171]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; regulation of mitochondrial membrane potential [GO:0051881]; response to hydrogen peroxide [GO:0042542]; response to lipopolysaccharide [GO:0032496]; response to oxidative stress [GO:0006979]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; early endosome [GO:0005769]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; protein-containing complex [GO:0032991]	alkyl hydroperoxide reductase activity [GO:0008785]; cysteine-type endopeptidase inhibitor activity involved in apoptotic process [GO:0043027]; identical protein binding [GO:0042802]; kinase binding [GO:0019900]; protein C-terminus binding [GO:0008022]; protein kinase binding [GO:0019901]; thioredoxin peroxidase activity [GO:0008379]
161	Dynactin subunit 1 (150 kDa dynein-associated polypeptide) (DAP-150) (DP-150) (p135) (p150-glued)	DCTN1	1278	cell division [GO:0051301]; centriole-centriole cohesion [GO:0010457]; cytoplasmic microtubule organization [GO:0031122]; establishment of mitotic spindle orientation [GO:0000132]; maintenance of synapse structure [GO:0099558]; microtubule anchoring at centrosome [GO:0034454]; mitotic cell cycle [GO:0000278]; motor behavior [GO:0061744]; nervous system development [GO:0007399]; neuromuscular junction development [GO:0007528]; neuromuscular process [GO:0050905]; neuron cellular homeostasis [GO:0070050]; neuron projection maintenance [GO:1990535]; non-motile cilium assembly [GO:1905515]; nuclear membrane disassembly [GO:0051081]; nuclear migration [GO:0007097]; positive regulation of microtubule nucleation [GO:0090063]; positive regulation of microtubule polymerization [GO:0031116]; positive regulation of neuromuscular junction development [GO:1904398]; regulation of mitotic spindle organization [GO:0060236]; retrograde transport, endosome to Golgi [GO:0042147]; ventral spinal cord development [GO:0021517]	axon [GO:0030424]; cell cortex [GO:0005938]; cell cortex region [GO:0099738]; centriolar subdistal appendage [GO:0120103]; centriole [GO:0005814]; centrosome [GO:0005813]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; dynein complex [GO:0030286]; intercellular bridge [GO:0045171]; kinetochore [GO:0000776]; membrane [GO:0016020]; microtubule [GO:0005874]; microtubule associated complex [GO:0005875]; microtubule cytoskeleton [GO:0015630]; microtubule plus-end [GO:0035371]; mitotic spindle [GO:0072686]; neuronal cell body [GO:0043025]; neuron projection [GO:0043005]; nuclear envelope [GO:0005635]; nucleus [GO:0005634]; spindle [GO:0005819]; spindle pole [GO:0000922]	microtubule binding [GO:0008017]; microtubule plus-end binding [GO:0051010]; protein kinase binding [GO:0019901]; tau protein binding [GO:0048156]; tubulin binding [GO:0015631]
162	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G 1) (eIF-4G1) (p220)	EIF4G1 EIF4FEIF4GEIF4GI	1599	behavioral fear response [GO:0001662]; cap-dependent translational initiation [GO:0002191]; cellular macromolecule biosynthetic process [GO:0034645]; cellular response to nutrient levels [GO:0031669]; developmental process [GO:0032502]; energy homeostasis [GO:0097009]; negative regulation of autophagy [GO:0010507]; negative regulation of neuron death [GO:1901215]; negative regulation of peptidyl-threonine phosphorylation [GO:0010801]; positive regulation of cell death [GO:0010942]; positive regulation of cell growth [GO:0030307]; positive regulation of cellular protein metabolic process [GO:0032270]; positive regulation of eukaryotic translation initiation factor 4F complex assembly [GO:1905537]; positive regulation of	cytoplasm [GO:0005737]; cytoplasmic stress granule [GO:0010494]; cytosol [GO:0005829]; eukaryotic translation initiation factor 4F complex [GO:0016281]; membrane [GO:0016020]; nucleus [GO:0005634]; polysome [GO:0005844]	ATP binding [GO:0005524]; eukaryotic initiation factor 4E binding [GO:0008190]; identical protein binding [GO:0042802]; molecular adaptor activity [GO:0060090]; mRNA binding [GO:0003729]; RNA binding [GO:0003723]; translation factor activity, RNA binding [GO:0008135]; translation initiation factor activity

				G1/S transition of mitotic cell cycle [GO:1900087]; positive regulation of miRNA mediated inhibition of translation [GO:1905618]; positive regulation of mRNA cap binding [GO:1905612]; positive regulation of neuron differentiation [GO:0045666]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; positive regulation of translation in response to endoplasmic reticulum stress [GO:0036493]; regulation of cellular response to stress [GO:0080135]; regulation of gene silencing by miRNA [GO:0060964]; regulation of polysome binding [GO:1905696]; regulation of presynapse assembly [GO:1905606]; regulation of translational initiation [GO:0006446]; translation [GO:0006412]; translational initiation [GO:0006413]		[GO:0003743]; translation initiation factor binding [GO:0031369]
163	Phosphoinositide 3-kinase adapter protein 1 (B-cell adapter for phosphoinositide 3-kinase) (B-cell phosphoinositide 3-kinase adapter protein 1)	PIK3AP1 BCAP	805	positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; regulation of inflammatory response [GO:0050727]; toll-like receptor 2 signaling pathway [GO:0034134]; toll-like receptor 4 signaling pathway [GO:0034142]; toll-like receptor 7 signaling pathway [GO:0034154]; toll-like receptor 9 signaling pathway [GO:0034162]	cytosol [GO:0005829]; membrane [GO:0016020]; plasma membrane [GO:0005886]	identical protein binding [GO:0042802]; phosphatidylinositol 3-kinase regulatory subunit binding [GO:0036312]; signaling receptor binding [GO:0005102]
164	Neurotrophin-4 (NT-4) (Neurotrophin-5) (NT-5) (Neutrophic factor 4)	NTF4 NTF5	210	adult locomotory behavior [GO:0008344]; epidermis development [GO:0008544]; ganglion mother cell fate determination [GO:0007402]; innervation [GO:0060384]; long-term memory [GO:0007616]; mechanoreceptor differentiation [GO:0042490]; memory [GO:0007613]; modulation of chemical synaptic transmission [GO:0050804]; negative regulation of neuron apoptotic process [GO:0043524]; nerve development [GO:0021675]; nerve growth factor signaling pathway [GO:0038180]; neuron projection morphogenesis [GO:0048812]; peripheral nervous system development [GO:0007422]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; regulation of neuron differentiation [GO:0045664]; sensory organ boundary specification [GO:0008052]; taste bud development [GO:0061193]; transmembrane receptor protein tyrosine kinase signaling pathway [GO:0007169]	axon [GO:0030424]; dendrite [GO:0030425]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; synaptic vesicle [GO:0008021]	growth factor activity [GO:0008083]; nerve growth factor receptor binding [GO:0005163]
165	Amphiregulin (AR) (Colorectum cell-derived growth factor) (CRDGF)	AREG AREGB SDGF	252	cell-cell signaling [GO:0007267]; dichotomous subdivision of terminal units involved in mammary gland duct morphogenesis [GO:0060598]; epidermal growth factor receptor signaling pathway [GO:0007173]; epithelial cell proliferation involved in mammary gland duct elongation [GO:0060750]; glial cell proliferation [GO:0014009]; G protein-coupled receptor signaling pathway [GO:0007186]; mammary gland alveolus development [GO:0060749]; mammary gland branching involved in thelarche [GO:0060744]; negative regulation of osteoblast differentiation [GO:0045668]; neuron projection development [GO:0031175]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of epidermal growth factor-activated receptor activity [GO:0045741]; positive regulation of keratinocyte proliferation [GO:0010838]; response to cAMP [GO:0051591]; response to estradiol [GO:0032355]; response to glucocorticoid [GO:0051384]; response to hydrogen peroxide [GO:0042542]; response to peptide hormone [GO:0043434]	cell surface [GO:0009986]; clathrin-coated endocytic vesicle membrane [GO:0030669]; endoplasmic reticulum-Golgi intermediate compartment membrane [GO:0033116]; endoplasmic reticulum membrane [GO:0005789]; ER to Golgi transport vesicle membrane [GO:0012507]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; integral component of membrane [GO:0016021]; nucleus [GO:0005634]	cytokine activity [GO:0005125]; epidermal growth factor receptor binding [GO:0005154]; growth factor activity [GO:0008083]
166	SRSF protein kinase 2 (EC 2.7.11.1) (SFRS protein kinase 2) (Serine/arginine-rich protein-specific kinase 2) (SR-protein-specific kinase 2) [Cleaved into: SRSF protein kinase 2 N-terminal; SRSF protein kinase 2 C-terminal]	SRPK2	688	angiogenesis [GO:0001525]; cell differentiation [GO:0030154]; innate immune response [GO:0045087]; intracellular signal transduction [GO:0035556]; negative regulation of viral genome replication [GO:0045071]; nuclear speck organization [GO:0035063]; peptidyl-serine phosphorylation [GO:0018105]; positive regulation of cell cycle [GO:0045787]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of gene expression [GO:0010628]; positive regulation of neuron apoptotic process [GO:0043525]; positive regulation of viral genome replication [GO:0045070]; protein phosphorylation [GO:0006468]; regulation of mRNA processing [GO:0050684]; regulation of mRNA splicing, via spliceosome [GO:0048024]; R-loop disassembly [GO:0062176]; RNA splicing [GO:0008380]; spliceosomal complex assembly [GO:0000245]	chromatin [GO:0000785]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; nuclear speck [GO:0016607]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	14-3-3 protein binding [GO:0071889]; ATP binding [GO:0005524]; magnesium ion binding [GO:0000287]; protein serine/threonine kinase activity [GO:0004674]; protein serine kinase activity [GO:0106310]; protein threonine kinase activity [GO:0106311]; RNA binding [GO:0003723]
167	Contactin-associated protein-like 2 (Cell recognition molecule Caspr2)	CNTNAP2 CASPR2 KIAA0868	1331	adult behavior [GO:0030534]; brain development [GO:0007420]; cell adhesion [GO:0007155]; cerebral cortex development [GO:0021987]; clustering of voltage-gated potassium channels [GO:0045163]; learning [GO:0007612]; limbic system development [GO:0021761]; neuron projection development [GO:0031175]; neuron projection morphogenesis [GO:0048812]; neuron recognition [GO:0008038]; positive regulation of gap junction assembly [GO:1903598]; protein localization to juxtaparanode region of axon [GO:0071205]; social behavior [GO:0035176]; striatum development [GO:0021756]; superior temporal gyrus development [GO:0071109]; thalamus development [GO:0021794]; transmission of nerve impulse [GO:0019226]; vocalization behavior [GO:0071625]; vocal learning [GO:0042297]	axolemma [GO:0030673]; axon [GO:0030424]; cell surface [GO:0009986]; dendrite [GO:0030425]; early endosome [GO:0005769]; Golgi apparatus [GO:0005794]; integral component of membrane [GO:0016021]; juxtaparanode region of axon [GO:0044224]; membrane [GO:0016020]; neuronal cell body [GO:0043025]; paranodal junction [GO:0033010]; perikaryon [GO:0043204]; voltage-gated potassium channel complex [GO:0008076]	enzyme binding [GO:0019899]
168	FXYD domain-containing ion transport regulator 5 (Dysadherin)	FXYD5 DYSAD IWU1 HSPC113 UNQ2561/PRO6241	178	ion transport [GO:0006811]; microvillus assembly [GO:0030033]; negative regulation of calcium-dependent cell-cell adhesion [GO:0046588]; regulation of sodium ion transmembrane transporter activity [GO:2000649]	integral component of membrane [GO:0016021]	actin binding [GO:0003779]; cadherin binding [GO:0045296]; sodium channel regulator activity [GO:0017080]
169	Merlin (Moesin-ezrin-radixin-like protein) (Neurofibromin-2) (Schwannomerlin) (Schwannomin)	NF2 SCH	595	actin cytoskeleton organization [GO:0030036]; cell-cell junction organization [GO:0045216]; ectoderm development [GO:0007398]; hippocampus development [GO:0021766]; lens fiber cell differentiation [GO:0070306]; mesoderm formation [GO:0001707]; negative regulation of cell-cell adhesion [GO:0022408]; negative regulation of cell-matrix adhesion [GO:0001953]; negative regulation of cell migration [GO:0030336]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of MAPK cascade [GO:0043409]; negative regulation of protein kinase activity [GO:0006469]; negative regulation of receptor signaling pathway via JAK-STAT [GO:0046426]; negative regulation of tyrosine phosphorylation of STAT protein [GO:0042532]; odontogenesis of dentin-containing tooth [GO:0042475]; positive regulation of cell differentiation [GO:0045597]; positive regulation of stress fiber assembly [GO:0051496]; regulation of apoptotic process [GO:0042981]; regulation of cell cycle [GO:0051726]; regulation of gliogenesis [GO:0014013]; regulation of hippo signaling [GO:0035330]; regulation of neural precursor cell proliferation [GO:2000177]; regulation of protein localization to nucleus [GO:1900180]; regulation of protein stability [GO:0031647]; regulation of stem cell proliferation [GO:0072091]; Schwann cell proliferation [GO:0014010]	adherens junction [GO:0005912]; apical part of cell [GO:0045177]; cell body [GO:0044297]; cleavage furrow [GO:0032154]; cortical actin cytoskeleton [GO:0030864]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; early endosome [GO:0005769]; filopodium membrane [GO:0031527]; lamellipodium [GO:0030027]; membrane [GO:0016020]; neuron projection [GO:0043005]; nucleolus [GO:0005730]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; ruffle membrane [GO:0032587]	actin binding [GO:0003779]
170	Aggrecan core protein (Cartilage-specific proteoglycan core protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1)	ACAN AGC1 CSPG1 MSK16	2530	cell adhesion [GO:0007155]; central nervous system development [GO:0007417]; proteolysis [GO:0006508]; skeletal system development [GO:0001501]	collagen-containing extracellular matrix [GO:0062023]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]	carbohydrate binding [GO:0030246]; extracellular matrix structural constituent [GO:0005201]; hyaluronic acid binding [GO:0005540]; metal ion binding [GO:0046872]

	(Chondroitin sulfate proteoglycan 1) [Cleaved into: Aggrecan core protein 2]					
171	Discoidin, CUB and LCCL domain-containing protein 2 (CUB, LCCL and coagulation factor V/VIII-homology domains protein 1) (Endothelial and smooth muscle cell-derived neuropilin-like protein)	DCBLD2 CLCP1 ESDN	775	intracellular receptor signaling pathway [GO:0030522]; negative regulation of cell growth [GO:0030308]; wound healing [GO:0042060]	cell surface [GO:0009986]; integral component of plasma membrane [GO:0005887]	
172	Fc receptor-like protein 3 (FcR-like protein 3) (FcRL3) (Fc receptor homolog 3) (FcRH3) (IFGP family protein 3) (hIFGP3) (Immune receptor translocation-associated protein 3) (SH2 domain-containing phosphatase anchor protein 2) (CD antigen CD307c)	FCRL3 FCRH3 IFGP3 IRTA3 SPAP2	734	cell surface receptor signaling pathway [GO:0007166]; negative regulation of B cell receptor signaling pathway [GO:0050859]; negative regulation of immunoglobulin production [GO:0002638]; positive regulation of B cell proliferation [GO:0030890]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of protein serine/threonine phosphatase activity [GO:1905184]; regulation of B cell activation [GO:0050864]; regulation of B cell differentiation [GO:0045577]; regulation of calcium ion import [GO:0090279]; regulation of toll-like receptor 9 signaling pathway [GO:0034163]	cell surface [GO:0009986]; integral component of plasma membrane [GO:0005887]	kinase binding [GO:0019900]; phosphatase binding [GO:0019902]; protein phosphatase binding [GO:0019903]; protein tyrosine kinase binding [GO:1990782]; transmembrane signaling receptor activity [GO:0004888]
173	Fc receptor-like protein 6 (FcR-like protein 6) (FcRL6) (Fc receptor homolog 6) (FcRH6) (IFGP6)	FCRL6 FCRH6	434	cell surface receptor signaling pathway [GO:0007166]	external side of plasma membrane [GO:0009897]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	MHC class II protein binding [GO:0042289]; phosphatase binding [GO:0019902]; protein phosphatase binding [GO:0019903]; transmembrane signaling receptor activity [GO:0004888]
174	Transcription regulator protein BACH1 (BTB and CNC homolog 1) (HA2303)	BACH1	736	DNA repair [GO:0006281]; negative regulation of transcription by RNA polymerase II [GO:0000122]; regulation of transcription, DNA-templated [GO:0006355]; regulation of transcription by RNA polymerase II [GO:0006357]; regulation of transcription from RNA polymerase II promoter in response to hypoxia [GO:0061418]; regulation of transcription involved in G1/S transition of mitotic cell cycle [GO:0000083]; regulation of transcription involved in G2/M transition of mitotic cell cycle [GO:0000117]	chromatin [GO:0000785]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	DNA-binding transcription activator activity, RNA polymerase II-specific [GO:0001228]; DNA-binding transcription factor activity [GO:0003700]; DNA-binding transcription factor activity, RNA polymerase II-specific [GO:0000981]; DNA-binding transcription repressor activity, RNA polymerase II-specific [GO:0001227]; heme binding [GO:0020037]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]
175	Semaphorin-7A (CDw108) (JMH blood group antigen) (John-Milton-Hargen human blood group Ag) (Semaphorin-K1) (Sema K1) (Semaphorin-L) (Sema L) (CD antigen CD108)	SEMA7A CD108 SEMAL	666	axon extension [GO:0048675]; axon guidance [GO:0007411]; immune response [GO:0006955]; inflammatory response [GO:0006954]; integrin-mediated signaling pathway [GO:0007229]; negative chemotaxis [GO:0050919]; negative regulation of axon extension involved in axon guidance [GO:0048843]; neural crest cell migration [GO:0001755]; olfactory lobe development [GO:0021988]; osteoblast differentiation [GO:0001649]; positive regulation of axon extension [GO:0045773]; positive regulation of cell migration [GO:0030335]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of macrophage cytokine production [GO:0060907]; positive regulation of protein phosphorylation [GO:0001934]; regulation of inflammatory response [GO:0050727]; semaphorin-plexin signaling pathway [GO:0071526]	anchored component of membrane [GO:0031225]; external side of plasma membrane [GO:0009897]; extracellular space [GO:0005615]; integral component of plasma membrane [GO:0005887]; membrane [GO:0016020]; plasma membrane [GO:0005886]	chemorepellent activity [GO:0045499]; integrin binding [GO:0005178]; semaphorin receptor binding [GO:0030215]
176	Nuclear factor of activated T-cells, cytoplasmic 3 (NF-ATc3) (NFATc3) (NFATx) (T-cell transcription factor NFAT4) (NF-AT4) (NF-AT4c)	NFATC3 NFAT4	1075	calcineurin-NFAT signaling cascade [GO:0033173]; inflammatory response [GO:0006954]; negative regulation of pri-miRNA transcription by RNA polymerase II [GO:1902894]; negative regulation of vascular associated smooth muscle cell differentiation [GO:1905064]; positive regulation of transcription by RNA polymerase II [GO:0045944]; regulation of transcription by RNA polymerase II [GO:0006357]	chromatin [GO:0000785]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; transcription regulator complex [GO:0005667]	DNA-binding transcription activator activity, RNA polymerase II-specific [GO:0001228]; DNA-binding transcription factor activity, RNA polymerase II-specific [GO:0000981]; DNA-binding transcription repressor activity, RNA polymerase II-specific [GO:0001227]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]; sequence-specific double-stranded DNA binding [GO:1990837]
177	CD83 antigen (hCD83) (B-cell activation protein) (Cell surface protein HB15) (CD antigen CD83)	CD83	205	defense response [GO:0006952]; humoral immune response [GO:0006959]; negative regulation of interleukin-4 production [GO:0032713]; positive regulation of CD4-positive, alpha-beta T cell differentiation [GO:0043372]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-2 production [GO:0032743]; response to organic cyclic compound [GO:0014070]; signal transduction [GO:0007165]	external side of plasma membrane [GO:0009897]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]	
178	Mannan-binding lectin serine protease 1 (EC 3.4.21.-) (Complement factor MASP-3) (Complement-activating component of Ra-reactive factor) (Mannose-binding lectin-associated serine protease 1) (MASP-1) (Mannose-binding protein-associated serine protease) (Ra-reactive factor serine protease p100) (RaRF) (Serine protease 5) [Cleaved into: Mannan-binding lectin serine protease 1 heavy chain; Mannan-binding	MASP1 CRARF CRARF1 PRSS5	699	complement activation, lectin pathway [GO:0001867]; negative regulation of complement activation [GO:0045916]	cytosol [GO:0005829]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; nucleoplasm [GO:0005654]	calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; peptidase activity [GO:0008233]; protein homodimerization activity [GO:0042803]; serine-type endopeptidase activity [GO:0004252]

	lectin serine protease 1 light chain]					
179	C-type lectin domain family 4 member D (C-type lectin superfamily member 8) (C-type lectin-like receptor 6) (CLEC-6) (Dendritic cell-associated C-type lectin 3) (DC-associated C-type lectin 3) (Dectin-3) (CD antigen CD368)	CLEC4D CLECSF8 MCL	215	adaptive immune response [GO:0002250]; antifungal innate immune response [GO:0061760]; positive regulation of myeloid dendritic cell activation [GO:0030887]	ficolin-1-rich granule membrane [GO:0101003]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]; specific granule membrane [GO:0035579]; tertiary granule membrane [GO:0070821]	mannose binding [GO:0005537]; metal ion binding [GO:0046872]; pattern recognition receptor activity [GO:0038187]
180	Serine protease inhibitor Kazal-type 5 (Lympho-epithelial Kazal-type-related inhibitor) (LEKTI) [Cleaved into: Hemofiltrate peptide HF6478; Hemofiltrate peptide HF7665]	SPINK5	1064	cell differentiation [GO:0030154]; central nervous system development [GO:0007417]; epidermal cell differentiation [GO:0009913]; epithelial cell differentiation [GO:0030855]; extracellular matrix organization [GO:0030198]; hair cell differentiation [GO:0035315]; negative regulation of angiogenesis [GO:0016525]; negative regulation of antibacterial peptide production [GO:0002787]; negative regulation of immune response [GO:0050777]; negative regulation of serine-type endopeptidase activity [GO:1900004]; negative regulation of serine-type peptidase activity [GO:1902572]; regulation of cell adhesion [GO:0030155]; regulation of T cell differentiation [GO:0045580]; regulation of timing of anagen [GO:0051884]	cell cortex [GO:0005938]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]; epidermal lamellar body [GO:0097209]; extracellular region [GO:0005576]; intracellular membrane-bounded organelle [GO:0043231]; perinuclear region of cytoplasm [GO:0048471]	serine-type endopeptidase inhibitor activity [GO:0004867]
181	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB CYPB	216	bone development [GO:0060348]; chaperone-mediated protein folding [GO:0061077]; neutrophil chemotaxis [GO:0030593]; positive regulation by host of viral genome replication [GO:0044829]; positive regulation by host of viral process [GO:0044794]; positive regulation of multicellular organism growth [GO:0040018]; protein folding [GO:0006457]; protein peptidyl-prolyl isomerization [GO:0000413]; protein stabilization [GO:0050821]	cytoplasm [GO:0005737]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum chaperone complex [GO:0034663]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; intracellular membrane-bounded organelle [GO:0043231]; melanosome [GO:0042470]; membrane [GO:0016020]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; protein-containing complex [GO:0032991]; smooth endoplasmic reticulum [GO:0005790]	cyclosporin A binding [GO:0016018]; peptidyl-prolyl cis-trans isomerase activity [GO:0003755]; RNA binding [GO:0003723]; RNA polymerase binding [GO:0070063]; unfolded protein binding [GO:0051082]
182	Amyloid-beta precursor protein (APP) (ABPP) (APPI) (Alzheimer disease amyloid A4 protein homolog) (Alzheimer disease amyloid protein) (Amyloid precursor protein) (Amyloid-beta (A4) precursor protein) (Amyloid-beta A4 protein) (Cerebral vascular amyloid peptide) (CVAP) (PreA4) (Protease nexin-II) (PN-II) [Cleaved into: N-APP; Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99 (Beta-secretase C-terminal fragment) (Beta-CTF); Amyloid-beta protein 42 (Abeta42) (Beta-APP42); Amyloid-beta protein 40 (Abeta40) (Beta-APP40); C83 (Alpha-secretase C-terminal fragment) (Alpha-CTF); P3(42); P3(40); C80; Gamma-secretase C-terminal fragment 59 (Amyloid intracellular domain 59) (AICD-59) (AID(59)) (Gamma-CTF(59)); Gamma-secretase C-terminal fragment 57 (Amyloid intracellular domain 57) (AICD-57) (AID(57)) (Gamma-CTF(57)); Gamma-secretase C-terminal fragment 50 (Amyloid intracellular domain 50) (AICD-50) (AID(50)) (Gamma-CTF(50)); C31]	APP A4 AD1	770	adenylate cyclase-activating G protein-coupled receptor signaling pathway [GO:0007189]; adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway [GO:0007193]; adult locomotory behavior [GO:0008344]; amyloid fibril formation [GO:1990000]; antibacterial humoral response [GO:0019731]; antifungal humoral response [GO:0019732]; antimicrobial humoral immune response mediated by antimicrobial peptide [GO:0061844]; associative learning [GO:0008306]; astrocyte activation [GO:0048143]; astrocyte activation involved in immune response [GO:0002265]; axo-dendritic transport [GO:0008088]; axon midline choice point recognition [GO:0016199]; axonogenesis [GO:0007409]; calcium-mediated signaling [GO:0019722]; cell adhesion [GO:0007155]; cellular copper ion homeostasis [GO:0006878]; cellular process [GO:0009987]; cellular response to amyloid-beta [GO:1904646]; cellular response to cAMP [GO:0071320]; cellular response to copper ion [GO:0071280]; cellular response to manganese ion [GO:0071287]; cellular response to nerve growth factor stimulus [GO:1990090]; cellular response to norepinephrine stimulus [GO:0071874]; cholesterol metabolic process [GO:0008203]; cognition [GO:0050890]; collateral sprouting in absence of injury [GO:0048669]; defense response to Gram-negative bacterium [GO:0050829]; defense response to Gram-positive bacterium [GO:0050830]; dendrite development [GO:0016358]; endocytosis [GO:0006897]; extracellular matrix organization [GO:0030198]; forebrain development [GO:0030900]; G protein-coupled receptor signaling pathway [GO:0007186]; innate immune response [GO:0045087]; ionotropic glutamate receptor signaling pathway [GO:0035235]; learning [GO:0007612]; learning or memory [GO:0007611]; lipoprotein metabolic process [GO:0042157]; locomotory behavior [GO:0007626]; mating behavior [GO:0007617]; memory [GO:0007613]; microglia development [GO:0014005]; microglial cell activation [GO:0001774]; modulation of age-related behavioral decline [GO:0090647]; modulation of excitatory postsynaptic potential [GO:0098815]; mRNA polyadenylation [GO:0006378]; negative regulation of blood circulation [GO:1903523]; negative regulation of canonical Wnt signaling pathway [GO:0090090]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of gene expression [GO:0010629]; negative regulation of long-term synaptic potentiation [GO:1900272]; negative regulation of mitochondrion organization [GO:0010823]; negative regulation of neuron death [GO:1901215]; negative regulation of neuron differentiation [GO:0045665]; negative regulation of pri-miRNA transcription by RNA polymerase II [GO:1902894]; negative regulation of protein localization to nucleus [GO:1900181]; negative regulation of transcription by RNA polymerase II [GO:0000122]; neuromuscular process controlling balance [GO:0050885]; neuron apoptotic process [GO:0051402]; neuron projection development [GO:0031175]; neuron projection maintenance [GO:1990535]; neuron remodeling [GO:0016322]; Notch signaling pathway [GO:0007219]; positive regulation of 1-phosphatidylinositol-3-kinase activity [GO:0061903]; positive regulation of amyloid fibril formation [GO:1905908]; positive regulation of apoptotic process [GO:0043065]; positive regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process [GO:1902961]; positive regulation of cell activation [GO:0050867]; positive regulation of cellular response to thapsigargin [GO:1905893]; positive regulation of cellular response to tunicamycin [GO:1905896]; positive regulation of chemokine production [GO:0032722]; positive regulation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0043280]; positive regulation of cytosolic calcium ion concentration [GO:0007204]; positive regulation of DNA-binding transcription factor activity [GO:0051091]; positive regulation of endothelin production [GO:1904472]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of excitatory postsynaptic potential [GO:2000463]; positive regulation of G2/M transition of mitotic cell cycle [GO:0010971]; positive regulation of gene expression [GO:0010628]; positive regulation of glycolytic process [GO:0045821]; positive regulation of G protein-coupled receptor internalization [GO:1904022]; positive regulation of G protein-coupled receptor signaling pathway [GO:0045745]; positive regulation of histone acetylation [GO:0035066]; positive regulation of inflammatory response [GO:0050729]; positive regulation of interferon-gamma production [GO:0032729]; positive regulation of interleukin-1 beta production [GO:0032731]; positive regulation of interleukin-6 production [GO:0032755]; positive regulation of JNK cascade [GO:0046330]; positive regulation of long-term synaptic potentiation [GO:1900273]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of MAP kinase activity [GO:0043406]; positive regulation of membrane protein ectodomain	amyloid-beta complex [GO:0106003]; apical part of cell [GO:0045177]; astrocyte projection [GO:0097449]; axon [GO:0030424]; cell-cell junction [GO:0005911]; cell surface [GO:0009986]; ciliary rootlet [GO:0035253]; clathrin-coated pit [GO:0005905]; COPII-coated ER to Golgi transport vesicle [GO:0030134]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; dendritic shaft [GO:0043198]; dendritic spine [GO:0043197]; early endosome [GO:0005769]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]; endosome [GO:0005768]; endosome lumen [GO:0031904]; endosome to plasma membrane transport vesicle [GO:0070381]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]; Golgi-associated vesicle [GO:0005798]; Golgi lumen [GO:0005796]; growth cone filopodium [GO:1990812]; growth cone lamellipodium [GO:1990761]; high-density lipoprotein particle [GO:0034364]; integral component of membrane [GO:0016021]; integral component of plasma membrane [GO:0005887]; intermediate-density lipoprotein particle [GO:0034363]; lipoprotein particle [GO:1990777]; main axon [GO:0044304]; membrane [GO:0016020]; membrane raft [GO:0045121]; mitochondrion [GO:0005739]; neuromuscular junction [GO:0031594]; nuclear envelope lumen [GO:0005641]; nucleus [GO:0005634]; perikaryon [GO:0043204]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; platelet alpha granule lumen [GO:0031093]; presynaptic active zone [GO:0048786]; protein-containing complex [GO:0032991]; receptor complex [GO:0043235]; recycling endosome [GO:0055037]; rough endoplasmic reticulum [GO:0005791]; smooth endoplasmic reticulum [GO:0005790]; spindle midzone [GO:0051233]; synapse [GO:0045202]; synaptic vesicle [GO:0008021]; trans-Golgi network membrane [GO:0032588]	acetylcholine receptor activator activity [GO:0030549]; acetylcholine receptor binding [GO:0033130]; amylin binding [GO:0097645]; apolipoprotein binding [GO:0034185]; chaperone binding [GO:0051087]; chemoattractant activity [GO:0042056]; chromatin binding [GO:0003682]; DNA binding [GO:0003677]; enzyme binding [GO:0019899]; ephrin receptor binding [GO:0046875]; frizzled binding [GO:0005109]; G protein-coupled receptor binding [GO:0001664]; growth factor receptor binding [GO:0070851]; heparan sulfate binding [GO:1904399]; heparan sulfate proteoglycan binding [GO:0043395]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; insulin receptor binding [GO:0005158]; integrin binding [GO:0005178]; low-density lipoprotein particle receptor binding [GO:0050750]; peptidase activator activity [GO:0016504]; protein dimerization activity [GO:0046983]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; PTB domain binding [GO:0051425]; RAGE receptor binding [GO:0050786]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]; serine-type endopeptidase inhibitor activity [GO:0004867]; signaling receptor activator activity [GO:0030546]; signaling receptor binding [GO:0005102]; transition metal ion binding [GO:0046914]

				proteolysis [GO:0051044]; positive regulation of mitotic cell cycle [GO:0045931]; positive regulation of monocyte chemotaxis [GO:0090026]; positive regulation of neuron apoptotic process [GO:0043525]; positive regulation of neuron death [GO:1901216]; positive regulation of neuron differentiation [GO:0045666]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of NIK/NF-kappaB signaling [GO:1901224]; positive regulation of nitric oxide biosynthetic process [GO:0045429]; positive regulation of oxidative stress-induced neuron death [GO:1903223]; positive regulation of peptidyl-serine phosphorylation [GO:0033138]; positive regulation of peptidyl-threonine phosphorylation [GO:0010800]; positive regulation of phosphorylation [GO:0042327]; positive regulation of protein binding [GO:0032092]; positive regulation of protein import [GO:1904591]; positive regulation of protein kinase A signaling [GO:0010739]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of protein metabolic process [GO:0051247]; positive regulation of protein phosphorylation [GO:0001934]; positive regulation of protein tyrosine kinase activity [GO:0061098]; positive regulation of receptor binding [GO:1900122]; positive regulation of response to endoplasmic reticulum stress [GO:1905898]; positive regulation of superoxide anion generation [GO:0032930]; positive regulation of tau-protein kinase activity [GO:1902949]; positive regulation of T cell migration [GO:2000406]; positive regulation of transcription by RNA polymerase II [GO:0045944]; positive regulation of tumor necrosis factor production [GO:0032760]; protein homooligomerization [GO:0051260]; protein phosphorylation [GO:0006468]; protein tetramerization [GO:0051262]; protein trimerization [GO:0070206]; regulation of acetylcholine-gated cation channel activity [GO:1903048]; regulation of amyloid-beta clearance [GO:1900221]; regulation of amyloid fibril formation [GO:1905906]; regulation of dendritic spine maintenance [GO:1902950]; regulation of epidermal growth factor-activated receptor activity [GO:0007176]; regulation of gene expression [GO:0010468]; regulation of long-term neuronal synaptic plasticity [GO:0048169]; regulation of multicellular organism growth [GO:0040014]; regulation of NMDA receptor activity [GO:2000310]; regulation of peptidyl-tyrosine phosphorylation [GO:0050730]; regulation of presynapse assembly [GO:1905606]; regulation of response to calcium ion [GO:1905945]; regulation of spontaneous synaptic transmission [GO:0150003]; regulation of synapse structure or activity [GO:0050803]; regulation of toll-like receptor signaling pathway [GO:0034121]; regulation of transcription by RNA polymerase II [GO:0006357]; regulation of translation [GO:0006417]; regulation of Wnt signaling pathway [GO:0030111]; response to interleukin-1 [GO:0070555]; response to lead ion [GO:0010288]; response to oxidative stress [GO:0006979]; response to yeast [GO:0001878]; smooth endoplasmic reticulum calcium ion homeostasis [GO:0051563]; suckling behavior [GO:0001967]; synapse organization [GO:0050808]; synaptic assembly at neuromuscular junction [GO:0051124]; visual learning [GO:0008542]		
183	Beta-galactosidase (EC 3.2.1.23) (Acid beta-galactosidase) (Lactase) (Elastin receptor 1)	GLB1 ELNR 1	677	cellular carbohydrate metabolic process [GO:0044262]; galactose catabolic process [GO:0019388]; glycosaminoglycan catabolic process [GO:0006027]; glycosphingolipid metabolic process [GO:0006687]; keratan sulfate catabolic process [GO:0042340]; response to cortisone [GO:0051413]; response to Thyroglobulin triiodothyronine [GO:1904016]	azurophil granule lumen [GO:0035578]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; ficolin-1-rich granule lumen [GO:1904813]; Golgi apparatus [GO:0005794]; intracellular membrane-bounded organelle [GO:0043231]; lysosomal lumen [GO:0043202]; perinuclear region of cytoplasm [GO:0048471]; vacuole [GO:0005773]	beta-galactosidase activity [GO:0004565]; galactoside binding [GO:0016936]; protein homodimerization activity [GO:0042803]
184	Beta-glucuronidase (EC 3.2.1.31) (Beta-G1)	GUSB	651	carbohydrate metabolic process [GO:0005975]; glucuronoside catabolic process [GO:0019391]; glycosaminoglycan catabolic process [GO:0006027]	azurophil granule lumen [GO:0035578]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; ficolin-1-rich granule lumen [GO:1904813]; intracellular membrane-bounded organelle [GO:0043231]; lysosomal lumen [GO:0043202]; membrane [GO:0016020]	beta-glucuronidase activity [GO:0004566]; carbohydrate binding [GO:0030246]; protein domain specific binding [GO:0019904]; signaling receptor binding [GO:0005102]

Number	Pathway	Keywords	Involvement in disease	Biotechnological use	PubMed ID
1		3D-structure;Acetylation;Cytokine;Cytoplasm;Direct protein sequencing;Immunity;Inflammatory response;Innate immunity;Isomerase;Reference proteome;Secreted	DISEASE: Rheumatoid arthritis systemic juvenile (RASJ) [MIM:604302]: An inflammatory articular disorder with systemic onset beginning before the age of 16. It represents a subgroup of juvenile arthritis associated with severe extraarticular features and occasionally fatal complications. During active phases of the disorder, patients display a typical daily spiking fever, an evanescent macular rash, lymphadenopathy, hepatosplenomegaly, serositis, myalgia and arthritis. {ECO:0000269|PubMed:11508429}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		2552447; 8234256; 7947826; 8188240; 15461802; 14702039; 15489334; 12665801; 1286669; 7683862; 7679497; 11089976; 11508429; 11439086; 12681488; 12782713; 15908412; 17443469; 19454686; 19608861; 21269460; 22223895; 22814378; 24275569; 25944712; 8766818; 8610159; 8643551; 10353846; 11170644; 17526494; 19090677; 23776208
2		Coiled coil;Developmental protein;Direct protein sequencing;Disulfide bond;Glycoprotein;Reference proteome;Secreted;Signal;Wnt signaling pathway			10570958; 10652205; 11814687; 12975309; 14702039; 16554811; 15489334; 15340161; 17143291; 19838169; 23234360
3		Cell junction;Cytoplasm;Direct protein sequencing;Disulfide bond;Gap junction;Glycoprotein;Growth factor;Lipoprotein;Palmitate;Reference proteome;Secreted;Signal			7520150; 8622864; 14702039; 15489334; 1756408; 15340161; 9927660; 12050162; 12695522; 12665631; 15181016; 15213231; 15611078; 17463287; 20139355; 21063504; 21871891; 21344378; 24722330
4		3D-structure;Disease variant;Disulfide bond;Ectodermal dysplasia;Glycoprotein;Protease inhibitor;Reference proteome;Secreted;Signal;Thiol protease inhibitor	DISEASE: Ectodermal dysplasia 15, hypohidrotic/hair type (ECTD15) [MIM:618535]: A form of ectodermal dysplasia, a disorder due to abnormal development of two or more ectodermal structures. ECTD15 is an autosomal recessive form characterized by hypotrichosis and absence of sweating except with extreme exercise. Skin is dry from birth and eczematous lesions may develop in adulthood. Other features include blepharitis and photophobia. {ECO:0000269|PubMed:30425301}. Note=The disease may be caused by variants affecting the gene represented in this entry.		8995380; 9099741; 12839564; 15489334; 11348457; 30425301
5		Amelogenesis imperfecta;Apoptosis;Cell membrane;Cytoplasm;Direct protein sequencing;Disease variant;Disulfide bond;Glycoprotein;Membrane;Phosphoprotein;Receptor;Reference proteome;Signal;Transmembrane;Transmembrane helix	DISEASE: Amelogenesis imperfecta 3C (AI3C) [MIM:618386]: An autosomal recessive form of amelogenesis imperfecta, a defect of enamel formation. AI3C is characterized by generalized enamel hypocalcification affecting primary and secondary dentition. The surface of the enamel is rough and often stained. After eruption, the occlusal enamel on the molars disappears due to attrition, leaving a ring of intact enamel remaining on the sides. {ECO:0000269|PubMed:30506946}. Note=The disease is caused by variants affecting the gene represented in this entry.		11313261; 14702039; 15489334; 15340161; 16530727; 16389068; 19969290; 22052202; 23186163; 28688764; 30506946
6		Alternative splicing;Cell adhesion;Direct protein sequencing;Reference proteome;Secreted;Signal			10358067; 9843955; 12975309; 14702039; 11780052; 15489334; 15340161
7		3D-structure;Adaptive immunity;Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunity;Immunoglobulin domain;Membrane;Phosphoprotein;Receptor;Reference proteome;Signal;Transmembrane;Transmembrane helix			9285412; 10229813; 10764762; 15489334; 9692876; 10540327; 11069054; 11160222; 12072189; 14565933; 12757266; 14604962; 15939744; 15950745; 16380958; 19349973; 19690332; 25944712; 20007810
8		Acetylation;Actin-binding;Cytoplasm;Cytoskeleton;Phosphoprotein;Reference proteome			3365256; 2169566; 8425765; 14702039; 15815621; 15489334; 18669648; 19413330; 19608861; 21269460; 22814378; 23186163
9		Alternative splicing;Cell membrane;Direct protein sequencing;Disulfide bond;Endosome;Glycoprotein;Immunity;Immunoglobulin domain;Membrane;Receptor;Reference proteome;Signal;Transmembrane;Transmembrane helix			12975309; 14702039; 16625196; 15489334; 15340161; 16876123
10		3D-structure;Alternative splicing;Direct protein sequencing;Disulfide bond;Glycoprotein;Hydrolase;Protease;Reference proteome;Secreted;Serine protease;Signal;Zymogen	DISEASE: Note=Hereditary alpha tryptasemia is caused by an increase in the copy number (usually between two and three copies) of the alpha allele. Affected individuals have elevated basal serum tryptase levels that are associated with cutaneous flushing and pruritus, dysautonomia, functional gastrointestinal symptoms, chronic pain, and connective tissue abnormalities. It is not clear if the associated multisystem complaints might be due to the coinheritance of a second functional genetic variant. {ECO:0000269|PubMed:27749843}.		2677049; 2187193; 9920877; 18854315; 19748655; 15616553; 15489334; 3543004; 14670919; 18039527; 19159218; 25944712; 27749843; 12162961; 10898108
11		3D-structure;Autophagy;Cell membrane;Cell projection;Cilium;Cilium biogenesis/degradation;Coiled coil;Cytoplasm;Cytoplasmic vesicle;Golgi apparatus;Ichthyosis;Membrane;Neuropathy;Palmoplantar keratoderma;Phosphoprotein;Protein transport;Reference proteome;Transport	DISEASE: Cerebral dysgenesis, neuropathy, ichthyosis, and palmoplantar keratoderma syndrome (CEDNIK) [MIM:609528]: A neurocutaneous syndrome characterized by cerebral dysgenesis, neuropathy, ichthyosis and palmoplantar keratoderma. {ECO:0000269|PubMed:15968592}. Note=The disease is caused by variants affecting the gene represented in this entry.		9852078; 15461802; 15489334; 15968592; 21269460; 23217709; 23186163; 24275569; 25686250; 25944712; 31806350; 25686604; 27440922; 33422265
12		3D-structure;Alternative splicing;Deafness;Disease variant;Disulfide bond;Extracellular matrix;Glycoprotein;Hearing;Non-syndromic deafness;Reference proteome;Repeat;Secreted;Signal	DISEASE: Deafness, autosomal dominant, 9 (DFNA9) [MIM:601369]: A form of non-syndromic hearing loss characterized by onset in the fourth or fifth decade of life and initially involves the high frequencies. Hearing loss is progressive and usually complete by the sixth decade. In addition to cochlear involvement, DFNA9 patients also exhibit a spectrum of vestibular dysfunctions. Penetrance of the vestibular symptoms is often incomplete, and some patients are minimally affected, whereas others suffer from severe balance disturbances and episodes of vertigo. Affected individuals have mucopolysaccharide depositions in the channels of the cochlear and vestibular nerves. These depositions apparently cause strangulation and degeneration of dendritic fibers. {ECO:0000269|PubMed:10400989, ECO:0000269|PubMed:11295836, ECO:0000269|PubMed:12928864, ECO:0000269|PubMed:14512963, ECO:0000269|PubMed:16835921, ECO:0000269|PubMed:17561763, ECO:0000269|PubMed:18312449, ECO:0000269|PubMed:22610276, ECO:0000269|PubMed:22931125, ECO:0000269|PubMed:23993205, ECO:0000269|PubMed:25388789, ECO:0000269|PubMed:9806553, ECO:0000269|PubMed:9931344}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Deafness, autosomal recessive, 110 (DFNB110) [MIM:618094]: A form of non-syndromic, sensorineural deafness		9441737; 12975309; 14702039; 12508121; 15489334; 12843317; 17926100; 21886777; 11574466; 9806553; 9931344; 10400989; 11295836; 14512963; 12928864; 16835921; 17561763; 18312449; 22610276; 22931125; 23993205; 25388789; 29449721

			characterized by prelingual hearing loss. Sensorineural deafness results from damage to the neural receptors of the inner ear, the nerve pathways to the brain, or the area of the brain that receives sound information. DFNB110 affected individuals additionally exhibit mild, age-dependent vestibular dysfunction. {ECO:0000269|PubMed:29449721}. Note=The disease is caused by variants affecting the gene represented in this entry.		
13		3D-structure;Calcium;Coiled coil;Collagen;Disulfide bond;Glycoprotein;Lectin;Membrane;Metal-binding;Receptor;Reference proteome;Repeat;Signal-anchor;Transmembrane;Transmembrane helix			11162630; 11564734; 12761161; 16177791; 15489334; 17974005; 12601552; 15845541; 16868960; 17420244
14		3D-structure;Calcium;Cell membrane;Direct protein sequencing;Disulfide bond;Glycoprotein;IgE-binding protein;Lectin;Lipoprotein;Membrane;Metal-binding;Palmitate;Receptor;Reference proteome;Repeat;Secreted;Signal-anchor;Transmembrane;Transmembrane helix			2949326; 2877743; 3034567; 15057824; 15489334; 2972386; 1417742; 17389606; 22615937; 8142907; 8745401; 16172256; 16765898; 23424103
15		3D-structure;Alternative splicing;Cytoplasm;Disease variant;Mental retardation;Methyltransferase;Reference proteome;S-adenosyl-L-methionine;Transferase	DISEASE: Mental retardation, autosomal recessive 51 (MRT51) [MIM:616739]: A form of mental retardation, a disorder characterized by significantly below average general intellectual functioning associated with impairments in adaptive behavior and manifested during the developmental period. {ECO:0000269|PubMed:26206890}. Note=The disease is caused by variants affecting distinct genetic loci, including the gene represented in this entry.		7943261; 8145732; 8605025; 14667820; 14702039; 15815621; 15489334; 21269460; 24275569; 11566133; 9547362; 10803682; 26206890
16		3D-structure;Alternative splicing;Complement alternate pathway;Direct protein sequencing;Disulfide bond;Immunity;Immunoglobulin domain;Innate immunity;Membrane;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			11004523; 12975309; 15772651; 15489334; 15340161; 17016562; 17051150
17		Alternative splicing;Blood group antigen;Cell membrane;Glycoprotein;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix			8054981; 15772651; 15489334; 7533029; 10688843
18		3D-structure;Direct protein sequencing;Disease variant;Disulfide bond;Protease inhibitor;Reference proteome;Secreted;Serine protease inhibitor;Signal	DISEASE: Pancreatitis, hereditary (PCTT) [MIM:167800]: A disease characterized by pancreas inflammation, permanent destruction of the pancreatic parenchyma, maldigestion, and severe abdominal pain attacks. {ECO:0000269|PubMed:10691414, ECO:0000269|PubMed:10835640, ECO:0000269|PubMed:12974284, ECO:0000269|PubMed:18617776, ECO:0000269|PubMed:19888199}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.; DISEASE: Tropical calcific pancreatitis (TCP) [MIM:608189]: Idiopathic, juvenile, nonalcoholic form of chronic pancreatitis widely prevalent in several tropical countries. It can be associated with fibrocalculous pancreatic diabetes (FCPD) depending on both environmental and genetic factors. TCP differs from alcoholic pancreatitis by a much younger age of onset, pancreatic calcification, a high incidence of insulin dependent but ketosis resistant diabetes mellitus, and an exceptionally high incidence of pancreatic cancer. {ECO:0000269|PubMed:12011155, ECO:0000269|PubMed:12187509}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		3501289; 3877508; 2961612; 10835640; 15489334; 843082; 7142173; 1613792; 8433367; 10691414; 12187509; 12011155; 12974284; 18617776; 19888199
19		3D-structure;ATP-binding;Alternative splicing;Cell membrane;Chemotaxis;Chromosomal rearrangement;Cytoplasmic vesicle;Developmental protein;Direct protein sequencing;Disease variant;Disulfide bond;Glycoprotein;Immunoglobulin domain;Kinase;Lysosome;Membrane;Nucleotide-binding;Phosphoprotein;Proto-oncogene;Receptor;Reference proteome;Repeat;Signal;Transferase;Transmembrane;Transmembrane helix;Tyrosine-protein kinase;Ubl conjugation	DISEASE: Note=A chromosomal aberration involving PDGFRB is found in a form of chronic myelomonocytic leukemia (CMML). Translocation t(5;12)(q33;p13) with EVT6/TEL. It is characterized by abnormal clonal myeloid proliferation and by progression to acute myelogenous leukemia (AML).; DISEASE: Myeloproliferative disorder chronic with eosinophilia (MPE) [MIM:131440]: A hematologic disorder characterized by malignant eosinophils proliferation. Note=The gene represented in this entry may be involved in disease pathogenesis. Chromosomal aberrations involving PDGFRB have been found in many instances of chronic myeloproliferative disorder with eosinophilia. Translocation t(5;12) with ETV6 on chromosome 12 creating an PDGFRB-ETV6 fusion protein (PubMed:12181402). Translocation t(5;15)(q33;q22) with TP53BP1 creating a PDGFRB-TP53BP1 fusion protein (PubMed:15492236). Translocation t(1;5)(q23;q33) that forms a PDE4DIP-PDGFRB fusion protein (PubMed:12907457). Translocation t(5;6)(q33-34;q23) with CEP85L that fuses the 5'-end of CEP85L (isoform 4) to the 3'-end of PDGFRB (PubMed:21938754). {ECO:0000269|PubMed:12181402, ECO:0000269|PubMed:12907457, ECO:0000269|PubMed:15492236, ECO:0000269|PubMed:21938754}.; DISEASE: Leukemia, acute myelogenous (AML) [MIM:601626]: A subtype of acute leukemia, a cancer of the white blood cells. AML is a malignant disease of bone marrow characterized by maturational arrest of hematopoietic precursors at an early stage of development. Clonal expansion of myeloid blasts occurs in bone marrow, blood, and other tissue. Myelogenous leukemias develop from changes in cells that normally produce neutrophils, basophils, eosinophils and monocytes. Note=The gene represented in this entry may be involved in disease pathogenesis. A chromosomal aberration involving PDGFRB has been found in a patient with AML. Translocation t(5;14)(q33;q32) with TRIP11 (PubMed:9373237). {ECO:0000269|PubMed:9373237}.; DISEASE: Leukemia, juvenile myelomonocytic (JMML) [MIM:607785]: An aggressive pediatric myelodysplastic syndrome/myeloproliferative disorder characterized by malignant transformation in the hematopoietic stem cell compartment with proliferation of differentiated progeny. Patients have splenomegaly, enlarged lymph nodes, rashes, and hemorrhages. Note=The gene represented in this entry may be involved in disease pathogenesis. A chromosomal aberration involving PDGFRB has been found in a patient with JMML. Translocation t(5;17)(q33;p11.2) with SPECC1 (PubMed:15087372). {ECO:0000269|PubMed:15087372}.; DISEASE: Basal ganglia calcification, idiopathic, 4 (IBGC4) [MIM:615007]: A form of basal ganglia calcification, an autosomal dominant condition characterized by symmetric calcification in the basal ganglia and other brain regions. Affected individuals can either be asymptomatic or show a wide spectrum of neuropsychiatric symptoms, including parkinsonism, dystonia, tremor, ataxia, dementia, psychosis, seizures, and chronic headache. Serum levels of		2835772; 2850496; 18593464; 15372022; 15489334; 9285559; 21938754; 2846185; 15340161; 2550144; 2554309; 1653029; 1709159; 1846866; 1314164; 1396585; 1313434; 1375321; 7685273; 7679113; 7691811; 7692233; 8302579; 8940081; 9373237; 10454568; 9989826; 10821867; 10805725; 11297552; 11331881; 12181402; 12907457; 15087372; 15492236; 14966296; 15902258; 17620338; 21098708; 20494825; 20529858; 21733313; 8195171; 21679854; 26279204; 25454926; 26599395; 9739761; 15207817; 17419949; 18483217; 11567151; 11882663; 20534510; 17344846; 23731542; 23731537; 24065723; 23255827

			calcium, phosphate, alkaline phosphatase and parathyroid hormone are normal. The neuropathological hallmark of the disease is vascular and pericapillary calcification, mainly of calcium phosphate, in the affected brain areas. {ECO:0000269|PubMed:23255827, ECO:0000269|PubMed:24065723, ECO:0000269|PubMed:26599395}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Myofibromatosis, infantile 1 (IMF1) [MIM:228550]: A rare mesenchymal disorder characterized by the development of benign tumors in the skin, striated muscles, bones, and, more rarely, visceral organs. Subcutaneous or soft tissue nodules commonly involve the skin of the head, neck, and trunk. Skeletal and muscular lesions occur in about half of the patients. Lesions may be solitary or multicentric, and they may be present at birth or become apparent in early infancy or occasionally in adult life. Visceral lesions are associated with high morbidity and mortality. {ECO:0000269|PubMed:23731537, ECO:0000269|PubMed:23731542}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Kosaki overgrowth syndrome (KOGS) [MIM:616592]: A syndrome characterized by somatic overgrowth, distinctive facial features, hyperelastic and fragile skin, and progressive neurologic deterioration with white matter lesions on brain imaging. {ECO:0000269|PubMed:25454926}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Premature aging syndrome, Penttinen type (PENTT) [MIM:601812]: A syndrome characterized by a prematurely aged appearance with lipoatrophy, epidermal and dermal atrophy along with hypertrophic lesions that resemble scars, thin hair, proptosis, underdeveloped cheekbones, and marked acro-osteolysis. {ECO:0000269|PubMed:26279204}. Note=The disease is caused by variants affecting the gene represented in this entry.		
20		3D-structure;Alternative splicing;Calcium;Cell adhesion;Cell membrane;Disulfide bond;EGF-like domain;G-protein coupled receptor;Glycoprotein;Membrane;Phosphoprotein;Receptor;Reference proteome;Repeat;Secreted;Signal;Transducer;Transmembrane;Transmembrane helix			7636245; 8786105; 8955192; 14702039; 15057824; 15489334; 11297558; 12829604; 14647991; 18691976; 18669648; 19159218; 19349973; 20068231; 23186163; 24275569; 25944712
21		3D-structure;Direct protein sequencing;Disulfide bond;Glycoprotein;Hormone;Reference proteome;Secreted;Signal			481597; 8196184; 15489334; 6286817; 7462224; 890569; 5065401; 1158880; 4835135; 1150658; 4745444; 6774759; 7410374; 1991473; 2494176; 8202136; 8898911; 15662415; 24692546
22		Alternative splicing;Cell adhesion;Disulfide bond;EGF-like domain;Glycoprotein;Membrane;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			9395444; 11978792; 8590280; 16625196; 15489334; 18088087; 24275569
23		3D-structure;Alternative initiation;Chromosomal rearrangement;Direct protein sequencing;Disulfide bond;Glycoprotein;Nucleus;Osteogenesis;Phosphoprotein;Proto-oncogene;Reference proteome;Repeat;Secreted;Signal;Transcription;Transcription regulation	DISEASE: Note=A chromosomal aberration involving FSTL3 is found in a case of B-cell chronic lymphocytic leukemia. Translocation t(11;19)(q13;p13) with CCDN1. {ECO:0000269|PubMed:9671416}.		9671416; 12975309; 14702039; 15489334; 15340161; 11459787; 11948405; 12697670; 12970321; 15451575; 15574124; 16150905; 16336961; 17868029; 17878677; 26091039; 18768470; 22052913
24		3D-structure;Acetylation;Autophagy;Cell membrane;Chaperone;Copper;Cytoplasm;DNA damage;DNA repair;Direct protein sequencing;Disease variant;Endoplasmic reticulum;Fertilization;Hydrolase;Inflammatory response;Isopeptide bond;Lipoprotein;Membrane;Mitochondrion;Neurodegeneration;Nucleus;Oxidation;Palmitate;Parkinson disease;Parkinsonism;Phosphoprotein;Protease;RNA-binding;Reference proteome;Stress response;Tumor suppressor;Ubl conjugation;Zymogen	DISEASE: Parkinson disease 7 (PARK7) [MIM:606324]: A neurodegenerative disorder characterized by resting tremor, postural tremor, bradykinesia, muscular rigidity, anxiety and psychotic episodes. PARK7 has onset before 40 years, slow progression and initial good response to levodopa. Some patients may show traits reminiscent of amyotrophic lateral sclerosis-parkinsonism/dementia complex (Guam disease). {ECO:0000269|PubMed:12446870, ECO:0000269|PubMed:12851414, ECO:0000269|PubMed:12953260, ECO:0000269|PubMed:14607841, ECO:0000269|PubMed:14713311, ECO:0000269|PubMed:15254937, ECO:0000269|PubMed:15365989, ECO:0000269|PubMed:17846173, ECO:0000269|PubMed:18785233, ECO:0000269|PubMed:19229105, ECO:0000269|PubMed:22523093, ECO:0000269|PubMed:23792957, ECO:0000269|PubMed:23847046, ECO:0000269|PubMed:26972524, ECO:0000269|PubMed:28993701, ECO:0000269|PubMed:30928208}. Note=The disease is caused by variants affecting the gene represented in this entry.		9070310; 14702039; 16710414; 15489334; 11223268; 11477070; 12851414; 14713311; 12612053; 14579415; 14705119; 14662519; 14749723; 15502874; 15592455; 15976810; 16390825; 17015834; 18626009; 19229105; 18711745; 20304780; 21269460; 21097510; 22523093; 22611253; 23847046; 23792957; 24275569; 25416785; 25944712; 27903648; 28013050; 26995087; 28596309; 28993701; 30150385; 31536960; 31653696; 30894531; 12914946; 12761214; 12796482; 12939276; 12855764; 15181200; 12953260; 12446870; 14705128; 15365989; 14607841; 15254937; 14872018; 16240358; 16632486; 17846173; 18785233; 20186336; 26972524; 30928208
25		3D-structure;ATP-binding;Cytoplasm;Direct protein sequencing;Disulfide bond;Lipid-binding;Nucleotide-binding;Phosphoprotein;Protease inhibitor;Reference proteome;Serine protease inhibitor			8144042; 7637590; 14702039; 15489334; 1286669; 7807553; 10622376; 10490027; 17081983; 18294816; 18669648; 19690332; 20068231; 21269460; 21831839; 21406692; 22905912; 23186163; 24275569; 25944712; 9782050
26		Direct protein sequencing;Disulfide bond;EGF-like domain;Glycoprotein;Lectin;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix			15636369; 12975309; 12508121; 15489334; 15340161; 24275569
27		3D-structure;Acetylation;Antioxidant;Cytoplasm;Direct protein sequencing;Disulfide bond;Isopeptide bond;Oxidoreductase;Peroxidase;Phosphoprotein;Redox-active center;Reference proteome;Ubl			8496166; 8026862; 19054851; 16710414; 15489334; 9497357; 12059788; 11986303; 12161445; 12853451; 14654843; 12714748; 15105503; 17081065; 19608861; 21269460; 21969592; 22905912; 23186163; 24275569; 25114211; 25944712; 28112733; 18172504; 19812042;

		conjugation			
28		3D-structure;Adaptive immunity;Alternative splicing;Cell junction;Cell membrane;Disease variant;Disulfide bond;Glycoprotein;Immunity;Immunoglobulin domain;Inflammatory response;Innate immunity;Membrane;Metal-binding;Phosphoprotein;Reference proteome;Signal;Transmembrane;Transmembrane helix	DISEASE: Note=May be involved in T-cell exhaustion associated with chronic viral infections such as with human immunodeficiency virus (HIV) and hepatitic C virus (HCV). {ECO:0000269|PubMed:19001139, ECO:0000269|PubMed:19587053}.; DISEASE: T-cell lymphoma, subcutaneous panniculitis-like (SPTCL) [MIM:618398]: An uncommon form of T-cell non-Hodgkin lymphoma, in which cytotoxic CD8+ T-cells infiltrate subcutaneous adipose tissue, and rimming adipocytes in a lace-like pattern. Affected individuals typically present with multiple subcutaneous nodules, systemic B-cell symptoms, and, in a subset of cases, autoimmune disorders, most commonly systemic lupus erythematosus. A subset of patients develop hemophagocytic lymphohistiocytosis. SPTCL transmission pattern is consistent with autosomal recessive inheritance with incomplete penetrance. {ECO:0000269|PubMed:30374066, ECO:0000269|PubMed:30792187, ECO:0000269|Ref.2}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		11823861; 14702039; 15372022; 15489334; 14556005; 16286920; 17069754; 18006747; 19001139; 19587053; 20083673; 22171320; 22323453; 22383801; 23555261; 24838857; 24825777; 24337741; 26492563; 30374066; 30429576; 30792187
29		3D-structure;Alternative splicing;Direct protein sequencing;Disease variant;Disulfide bond;Glycoprotein;Membrane;Protease inhibitor;Reference proteome;Repeat;Serine protease inhibitor;Signal;Transmembrane;Transmembrane helix	DISEASE: Diarrhea 3, secretory sodium, congenital, with or without other congenital anomalies (DIAR3) [MIM:270420]: A disease characterized by life-threatening secretory diarrhea, severe metabolic acidosis and hyponatremia. Hyponatremia is secondary to extraordinarily high fecal sodium loss, with low or normal excretion of urinary sodium, in the absence of infectious, autoimmune and endocrine causes. {ECO:0000269|PubMed:19185281}. Note=The disease is caused by variants affecting the gene represented in this entry.		9346890; 9115294; 9434156; 14702039; 15057824; 15489334; 15340161; 19185281
30		3D-structure;Adaptive immunity;Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunity;Immunoglobulin domain;Innate immunity;Membrane;Receptor;Reference proteome;Secreted;Signal;Transmembrane;Transmembrane helix			10799849; 11922939; 14702039; 14574404; 15489334; 11323674; 17568691; 17098818; 21659545; 21393102; 25595774; 26561551; 29568119; 14656437; 15351648; 16959974
31	PATHWAY: Protein modification; protein glycosylation.	Alternative splicing;Disease variant;Disulfide bond;Glycoprotein;Glycosyltransferase;Golgi apparatus;Lectin;Manganese;Membrane;Metal-binding;Reference proteome;Signal-anchor;Transferase;Transmembrane;Transmembrane helix	DISEASE: Tumoral calcinosis, hyperphosphatemic, familial, 1 (HFTC1) [MIM:211900]: A form of hyperphosphatemic tumoral calcinosis, a rare autosomal recessive metabolic disorder that manifests with hyperphosphatemia and massive calcium deposits in the skin and subcutaneous tissues. Some patients have recurrent, transient, painful swellings of the long bones associated with the radiographic findings of periosteal reaction and cortical hyperostosis and absence of skin involvement. {ECO:0000269|PubMed:15133511, ECO:0000269|PubMed:15599692}. Note=The disease is caused by variants affecting the gene represented in this entry.		8663203; 15815621; 15489334; 9295285; 9394011; 12708471; 15133511; 15599692; 16638743; 21269460
32		3D-structure;Cytoplasm;Direct protein sequencing;NADP;Oxidoreductase;Phosphoprotein;Reference proteome			8117274; 8799475; 14702039; 15057824; 15489334; 8280170; 7929092; 1286669; 8313871; 8687377; 10620517; 18241201; 21269460; 23186163; 24275569; 25944712; 11224564
33		Direct protein sequencing;Glycoprotein;Hypotrichosis;Reference proteome;Secreted;Signal	DISEASE: Hypotrichosis 2 (HYPT2) [MIM:146520]: A condition characterized by the presence of less than the normal amount of hair. Affected individuals have normal hair in early childhood but experience progressive hair loss limited to the scalp beginning in the middle of the first decade and almost complete baldness by the third decade. Body hair, beard, eyebrows, axillary hair, teeth, and nails develop normally. HYPT2 inheritance is autosomal dominant. {ECO:0000269|PubMed:12754508}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Peeling skin syndrome 1 (PSS1) [MIM:270300]: A genodermatosis characterized by generalized, continuous shedding of the outer layers of the epidermis. Two main PSS subtypes have been suggested. Patients with non-inflammatory PSS (type A) manifest white scaling, with painless and easy removal of the skin, irritation when in contact with water, dust and sand, and no history of erythema, pruritis or atopy. Inflammatory PSS (type B) is associated with generalized erythema, pruritus and atopy. It is an ichthyosiform erythroderma characterized by lifelong patchy peeling of the entire skin with onset at birth or shortly after. Several patients have been reported with high IgE levels. {ECO:0000269|PubMed:20691404}. Note=The disease is caused by variants affecting the gene represented in this entry. CDNS mutations are responsible for generalized, inflammatory peeling skin syndrome type B (PubMed:20691404). {ECO:0000269|PubMed:20691404}.		8415725; 9712893; 12366786; 14574404; 15489334; 11169256; 10599883; 9395522; 12754508; 20691404; 10844560; 12472658
34		Alternative splicing;Cell adhesion;Cell junction;Cell membrane;Glycoprotein;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix			12706889; 11230166; 12975309; 14702039; 15772651; 15489334; 20068231; 25944712
35		3D-structure;Alternative splicing;Autocatalytic cleavage;Calcium;Direct protein sequencing;Disease variant;Disulfide bond;Epilepsy;Glycoprotein;Hydrolase;Lysosome;Metal-binding;Neurodegeneration;Neuronal ceroid lipofuscinosis;Protease;Reference proteome;Serine protease;Signal;Spinocerebellar ataxia;Zymogen	DISEASE: Ceroid lipofuscinosis, neuronal, 2 (CLN2) [MIM:204500]: A form of neuronal ceroid lipofuscinosis. Neuronal ceroid lipofuscinoses are progressive neurodegenerative, lysosomal storage diseases characterized by intracellular accumulation of autofluorescent liposomal material, and clinically by seizures, dementia, visual loss, and/or cerebral atrophy. The lipopigment pattern seen most often in CLN2 consists of curvilinear profiles. {ECO:0000269|PubMed:10330339, ECO:0000269|PubMed:10665500, ECO:0000269|PubMed:11241479, ECO:0000269|PubMed:11339651, ECO:0000269|PubMed:11589012, ECO:0000269|PubMed:12376936, ECO:0000269|PubMed:12414822, ECO:0000269|PubMed:12698559, ECO:0000269|PubMed:14736728, ECO:0000269|PubMed:19201763, ECO:0000269|PubMed:20340139, ECO:0000269|PubMed:21990111, ECO:0000269|PubMed:22612257, ECO:0000269|PubMed:9295267}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Spinocerebellar ataxia, autosomal recessive, 7 (SCAR7) [MIM:609270]: A form of spinocerebellar ataxia, a clinically and genetically heterogeneous group of cerebellar disorders. Patients show progressive incoordination of gait and often poor coordination of hands, speech and eye movements, due to degeneration of the cerebellum with variable involvement of the brainstem and spinal cord. SCAR7 patients show difficulty walking and writing, dysarthria, limb ataxia, and cerebellar atrophy. {ECO:0000269|PubMed:23418007}. Note=The disease is caused by variants affecting the gene represented in this entry.		9295267; 9653647; 12975309; 15489334; 11054422; 12643545; 12754519; 10477428; 17081065; 17237713; 19941651; 19159218; 21269460; 24275569; 25944712; 19038966; 19038967; 10330339; 10665500; 11339651; 11241479; 11589012; 11462245; 12376936; 12414822; 12698559; 14736728; 19201763; 20340139; 22612257; 21990111; 23418007
36		Cell membrane;Direct protein sequencing;Glycoprotein;Membrane;Phosphoprotein;Reference proteome;Repeat;Secreted;Signal;Transmembrane;Transmembrane helix			10642437; 12975309; 15489334; 12805376; 15340161; 12464430; 18669648; 23186163
37		3D-structure;ATP-binding;Acetylation;Alternative	DISEASE: Immunodeficiency 67 (IMD67) [MIM:607676]: An autosomal recessive primary immunodeficiency characterized by recurrent, life-threatening systemic and		11960013; 10508479; 14702039; 16541075; 15489334; 12496252; 12538665; 12925671;

		splicing;Cytoplasm;Disease variant;Immunity;Innate immunity;Kinase;Magnesium;Nucleotide-binding;Phosphoprotein;Reference proteome;Serine/threonine-protein kinase;Transferase	invasive bacterial infections beginning in infancy or early childhood. {ECO:0000269|PubMed:12637671, ECO:0000269|PubMed:12925671, ECO:0000269|PubMed:16950813, ECO:0000269|PubMed:17878374, ECO:0000269|PubMed:19663824, ECO:0000269|PubMed:21057262, ECO:0000269|PubMed:24316379}. Note=The disease is caused by variants affecting the gene represented in this entry.		15084582; 12637671; 16286016; 16951688; 17217339; 17337443; 16950813; 17997719; 18691976; 18669648; 19690332; 19608861; 20400509; 20068231; 21269460; 21325272; 21269878; 22814378; 23186163; 33238146; 17161373; 17312103; 20485341; 17878374; 17344846; 19663824; 21057262; 24316379
38		3D-structure;Alternative splicing;Cell membrane;Glycoprotein;Host-virus interaction;Immunoglobulin domain;Membrane;Phosphoprotein;Receptor;Reference proteome;Secreted;Signal;Transmembrane;Transmembrane helix			10660620; 10903717; 12853948; 15489334; 18358807; 19159218; 21241660
39		Acetylation;Cell membrane;Coiled coil;Cytoplasm;Cytoskeleton;Direct protein sequencing;Endoplasmic reticulum;Lipoprotein;Membrane;Palmitate;Phosphoprotein;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			8314870; 16541075; 15489334; 15703217; 17081983; 17030514; 17567679; 18296695; 18669648; 19144824; 20068231; 21269460; 24275569; 26091039; 25944712
40		3D-structure;Adaptive immunity;Alternative splicing;Calcium;Cell adhesion;Cell membrane;Disulfide bond;Endocytosis;Glycoprotein;Host cell receptor for virus entry;Host-virus interaction;Immunity;Innate immunity;Lectin;Mannose-binding;Membrane;Metal-binding;Receptor;Reference proteome;Repeat;Secreted;Signal-anchor;Transmembrane;Transmembrane helix			1518869; 10975799; 11257134; 11337487; 14702039; 15057824; 15489334; 10721995; 11017109; 11384997; 12433371; 11799126; 11859097; 11825572; 12502850; 12682107; 12692233; 12574325; 12949494; 12960229; 12504546; 15371595; 15140961; 15479853; 16246332; 15838506; 16092920; 16379498; 16537615; 16415006; 16816373; 21203928; 22700724; 18796707; 21191006; 21767814; 11739956; 22496863; 22090124; 24623090; 23966408; 22440960
41		3D-structure;Alternative splicing;Direct protein sequencing;Disulfide bond;Reference proteome;Secreted;Signal	DISEASE: Prostate cancer, hereditary, 13 (HPC13) [MIM:611928]: A condition associated with familial predisposition to cancer of the prostate. Most prostate cancers are adenocarcinomas that develop in the acini of the prostatic ducts. Other rare histopathologic types of prostate cancer that occur in approximately 5% of patients include small cell carcinoma, mucinous carcinoma, prostatic ductal carcinoma, transitional cell carcinoma, squamous cell carcinoma, basal cell carcinoma, adenoid cystic carcinoma (basaloid), signet-ring cell carcinoma and neuroendocrine carcinoma. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		3829888; 2590204; 2322265; 2054385; 7506990; 7566962; 15164054; 15489334; 10491085; 3995056; 6434350; 1930232; 7671139; 11788998; 15344909; 18264096; 22887727; 16930619; 20184897
42	PATHWAY: Membrane lipid metabolism; glycerophospholipid metabolism. {ECO:00002 50|UniProtKB:P47 713}.; PATHWAY: Lipid metabolism; arachidonate metabolism. {ECO:00002 69|PubMed:1 84519 93}.; PATHWAY: Lipid metabolism; prostaglandin biosynthesis. {ECO:00002 69|PubMed:1 84519 93}.; PATHWAY: Lipid	3D-structure;Calcium;Cytoplasm;Direct protein sequencing;Disease variant;Fatty acid biosynthesis;Fatty acid metabolism;Glycerol metabolism;Golgi apparatus;Hydrolase;Isopeptide bond;Leukotriene biosynthesis;Lipid biosynthesis;Lipid degradation;Lipid metabolism;Lipid-binding;Membrane;Metal-binding;Nucleus;Phospholipid degradation;Phospholipid metabolism;Phosphoprotein;Prostaglandin biosynthesis;Prostaglandin metabolism;Reference proteome;Ubl conjugation	DISEASE: Gastrointestinal ulceration, recurrent, with dysfunctional platelets (GURDP) [MIM:618372]: An autosomal recessive disorder characterized by recurrent gastrointestinal mucosal ulcers, gastrointestinal bleeding, chronic anemia, iron deficiency, and abdominal pain. Disease features also include platelet dysfunction, and globally decreased eicosanoid synthesis. {ECO:0000269|PubMed:18451993, ECO:0000269|PubMed:23268370, ECO:0000269|PubMed:25102815}. Note=The disease is caused by variants affecting the gene represented in this entry.		1904318; 1869522; 16710414; 15489334; 8381049; 8083230; 7794891; 8619991; 8702602; 9425121; 9468497; 10358058; 11375391; 11416127; 12672805; 14709560; 17081983; 16617059; 16964243; 17472963; 18088087; 18669648; 20068231; 21269460; 21406692; 23186163; 27642067; 28112733; 9430701; 9665851; 10319815; 16959974; 18451993; 23268370; 25102815

	metabolism; leukotriene B4 biosynthesis. {ECO:00002 69|PubMed:18451993}.				
43		Alternative splicing;Cell adhesion;Cell junction;Cell membrane;Direct protein sequencing;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Phosphoprotein;Reference proteome;Repeat;Signal;Tight junction;Transmembrane;Transmembrane helix			11279107; 12975309; 14702039; 16554811; 15489334; 15340161; 19159218
44		3D-structure;Alternative splicing;Angiogenesis;Coiled coil;Direct protein sequencing;Disulfide bond;Extracellular matrix;Glycoprotein;Lipid metabolism;Reference proteome;Secreted;Signal			10698685; 10866690; 11953136; 14583458; 12975309; 14702039; 15057824; 15489334; 12015030; 17068295; 19270337; 21398697; 27929370; 29899144; 29713054; 17322881; 29899519
45		3D-structure;Alternative splicing;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Phosphoprotein;Reference proteome;Signal;Transmembrane;Transmembrane helix			2825196; 2162892; 11916166; 11877290; 14702039; 15815621; 15489334; 11735222; 8617933; 15144186; 15067037; 19349973; 19690332; 15696168; 24098653
46		Cytoplasm;Direct protein sequencing;Disulfide bond;Glycoprotein;Growth factor;Lectin;Osteogenesis;Reference proteome;Secreted;Signal			9442024; 9705843; 10198175; 14702039; 15489334; 11920266; 11803813; 25944712; 27976999
47		3D-structure;Alternative splicing;Cell membrane;Disease variant;Disulfide bond;Glycoprotein;Holoprosencephaly;Immunoglobulin domain;Membrane;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Holoprosencephaly 11 (HPE11) [MIM:614226]: A structural anomaly of the brain, in which the developing forebrain fails to correctly separate into right and left hemispheres. Holoprosencephaly is genetically heterogeneous and associated with several distinct facies and phenotypic variability. {ECO:0000269|PubMed:21802063}. Note=The disease is caused by variants affecting the gene represented in this entry.		9214393; 16554811; 15489334; 18794898; 20519495; 21802063
48		Alternative splicing;Chaperone;Disease variant;Endoplasmic reticulum;Glycoprotein;Osteogenesis imperfecta;Reference proteome;Signal;Wnt signaling pathway	DISEASE: Osteogenesis imperfecta 20 (OI20) [MIM:618644]: An autosomal recessive form of osteogenesis imperfecta, a connective tissue disorder characterized by low bone mass, bone fragility and susceptibility to fractures after minimal trauma. Disease severity ranges from very mild forms without fractures to intrauterine fractures and perinatal lethality. Extraskeletal manifestations, which affect a variable number of patients, are dentinogenesis imperfecta, hearing loss, and blue sclerae. OI20 is a progressive deforming form characterized by osteopenia, skeletal deformity, healed fractures, and newly-acquired fractures. Death due to respiratory failure can occur in some patients. {ECO:0000269|PubMed:31564437}. Note=The disease is caused by variants affecting the gene represented in this entry.		7788527; 12168954; 12975309; 14702039; 16572171; 15489334; 10508479; 15014448; 17488095; 21269460; 24275569; 25944712; 31564437
49		3D-structure;Acetylation;Alternative initiation;Alternative splicing;Antioxidant;Cytoplasm;Direct protein sequencing;Disulfide bond;Lipoprotein;Mitochondrion;Oxidoreductase;Palmitate;Peroxidase;Peroxisome;Phosphoprotein;Redox-active center;Reference proteome;Transit peptide			10095767; 10514471; 10521424; 10679306; 10751410; 10931946; 16554811; 15489334; 1286669; 19608861; 21269460; 24275569; 25944712; 11518528; 18489898; 20643143; 31740833; 16959974
50		Alternative splicing;Cell adhesion;Cell membrane;Cell projection;Direct protein sequencing;GPI-anchor;Glycoprotein;Immunity;Innate immunity;Lipoprotein;Membrane;Reference proteome;Repeat;Secreted;Signal			10753836; 11465086; 12010833; 12975309; 15489334; 15340161; 12239154; 12377969; 12675722; 17244676; 17580308; 18462208; 21193407; 23202369; 23461681; 24926686; 28807980; 28240246; 12623849; 14692971; 27227454
51		3D-structure;Acetylation;Hydrolase;Isopeptide bond;Magnesium;Metal-binding;Nucleus;Phosphoprotein;RNA-binding;Reference proteome;Transferase;Ubl conjugation			10567213; 10722730; 11042152; 14702039; 15489334; 15592455; 19413330; 19699693; 19608861; 20068231; 21269460; 21389046; 21406692; 22905912; 22223895; 23186163; 27257257; 28112733; 17052728; 18462755; 21768126
52		3D-structure;Direct protein sequencing;Disulfide bond;Glycoprotein;Lectin;Membrane;Phosphoprotein;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			8496594; 8340758; 8100776; 8026529; 15489334; 23186163; 11101293; 11036086; 18959746
53		3D-structure;Cell adhesion;Disulfide bond;Extracellular			12975309; 15164053; 15489334; 14551184

		matrix;Glycoprotein;Leucine-rich repeat;Proteoglycan;Reference proteome;Repeat;Secreted;Signal;Sulfation			
54		3D-structure;Alternative splicing;Direct protein sequencing;Disulfide bond;Glycoprotein;Protease inhibitor;Reference proteome;Repeat;Secreted;Serine protease inhibitor;Signal			9045658; 12975309; 15489334; 10373425; 15340161; 18669648; 15713485
55		Alternative splicing;Cell junction;Cytoplasm;Cytoplasmic vesicle;Golgi apparatus;Membrane;Neurotransmitter transport;Reference proteome;Synapse;Transport			8326004; 7918678; 8975715; 14702039; 12853948; 15489334; 12682071
56		Alternative splicing;Calcium;Direct protein sequencing;Disulfide bond;EGF-like domain;Endoplasmic reticulum;Glycoprotein;Isomerase;Redox-active center;Reference proteome;Repeat;Signal			16238698; 16919896; 12975309; 10591208; 15489334; 15340161; 21269460
57		Actin-binding;Cell junction;Cell membrane;Cell projection;Coiled coil;Cytoplasm;Cytoskeleton;Developmental protein;Differentiation;Membrane;Neurogenesis;Nucleus;Phosphoprotein;Reference proteome;Synapse			11278317; 16625196; 17974005; 18669648; 19413330; 19151759; 19690332; 20068231; 21406692; 23186163; 24114805; 24275569
58		3D-structure;Alternative splicing;Calcium;Cardiomyopathy;Cell adhesion;Cell junction;Cell membrane;Cleavage on pair of basic residues;Disease variant;Glycoprotein;Membrane;Metal-binding;Phosphoprotein;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Arrhythmogenic right ventricular dysplasia, familial, 11 (ARVD11) [MIM:610476]: A congenital heart disease characterized by infiltration of adipose and fibrous tissue into the right ventricle and loss of myocardial cells, resulting in ventricular and supraventricular arrhythmias. {ECO:0000269|PubMed:17033975, ECO:0000269|PubMed:19863551, ECO:0000269|PubMed:21062920, ECO:0000269|PubMed:28256248}. Note=The disease is caused by variants affecting the gene represented in this entry.		2037591; 15489334; 16335952; 16740002; 17033975; 19139490; 21062920; 24275569; 18678517; 20031617; 19863551; 28256248
59		3D-structure;Acetylation;Alternative splicing;Calcium;Cell adhesion;Cell junction;Cell membrane;Cell projection;Direct protein sequencing;Disulfide bond;Endosome;Glycoprotein;Host cell receptor for virus entry;Host-virus interaction;Integrin;Isopeptide bond;Magnesium;Membrane;Metal-binding;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix;Ubl conjugation		BIOTECHNOLOGY: Antibodies against integrin beta-1 ITGB1 protects epithelial cells from invasion by the fungus R.delemar, a causative agent of mucormycosis, and could thus potentially be used to treat mucormycosis disease (PubMed:32487760). Antibodies against the protein also protect a neutropenic mouse model against mucormycosis (PubMed:32487760). {ECO:00002 69|PubMed: 32487760}.	2958481; 14702039; 17974005; 15164054; 15489334; 7681433; 7523423; 2249781; 1551917; 7545396; 7544298; 9494094; 15276642; 8411387; 8567725; 9501082; 10397733; 10455171; 10613898; 11741838; 11919189; 11807098; 11807099; 12907437; 12473654; 12695522; 12807887; 12941907; 14722085; 15466886; 15181153; 15156152; 16256741; 16076904; 16335952; 16754960; 17081065; 16501085; 17956333; 17925226; 17158881; 18804435; 18635536; 19064666; 17945327; 19159218; 19349973; 19690332; 19608861; 20660204; 21269460; 22027826; 21768292; 21325030; 23125415; 23186163; 24275569; 25114211; 25398877; 24789099; 25944712; 29030430; 31331973; 32487760; 33102950; 22645133; 22451694; 23317506
60		3D-structure;Cell membrane;Disease variant;Disulfide bond;Dwarfism;G-protein coupled receptor;Glycoprotein;Membrane;Phosphoprotein;Receptor;Reference proteome;Signal;Transducer;Transmembrane;Transmembrane helix	DISEASE: Metaphyseal chondrodysplasia, Jansen type (MCDJ) [MIM:156400]: A rare autosomal dominant disorder characterized by a short-limbed dwarfism associated with hypercalcemia and normal or low serum concentrations of the two parathyroid hormones. {ECO:0000269|PubMed:10487664, ECO:0000269|PubMed:15240651, ECO:0000269|PubMed:27160269, ECO:0000269|PubMed:7701349, ECO:0000269|PubMed:8703170, ECO:0000269|PubMed:9178745}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Chondrodysplasia Blomstrand type (BOCD) [MIM:215045]: Severe skeletal dysplasia. {ECO:0000269|PubMed:9745456}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Eiken skeletal dysplasia (EISD) [MIM:600002]: A rare skeletal dysplasia characterized by severely retarded ossification, principally of the epiphyses, pelvis, hands and feet, as well as by abnormal modeling of the bones in hands and feet, abnormal persistence of cartilage in the pelvis and mild growth retardation. {ECO:0000269|PubMed:15525660}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Primary failure of tooth eruption (PFE) [MIM:125350]: Rare condition that has high penetrance and variable expressivity and in which tooth retention occurs without evidence of any		8386612; 8397094; 7745008; 15489334; 10913300; 24275569; 9737850; 18375760; 18611381; 21827955; 19674967; 20172855; 7701349; 8703170; 9178745; 9745456; 10487664; 11850620; 15523647; 15240651; 15525660; 19061984; 27160269

			obvious mechanical interference. Instead, malfunction of the eruptive mechanism itself appears to cause nonankylosed permanent teeth to fail to erupt, although the eruption pathway has been cleared by bone resorption. {ECO:0000269|PubMed:19061984}. Note=The disease is caused by variants affecting the gene represented in this entry.		
61		Alternative splicing;Basement membrane;Cardiomyopathy;Cell adhesion;Coiled coil;Disease variant;Disulfide bond;Extracellular matrix;Glycoprotein;Laminin EGF-like domain;Reference proteome;Repeat;Secreted;Signal	DISEASE: Cardiomyopathy, dilated 1JJ (CMD1JJ) [MIM:615235]: A disorder characterized by ventricular dilation and impaired systolic function, resulting in congestive heart failure and arrhythmia. Patients are at risk of premature death. {ECO:0000269|PubMed:17646580}. Note=The disease is caused by variants affecting the gene represented in this entry.		7781776; 8706685; 14574404; 15489334; 9310354; 7959779; 19159218; 17646580
62		3D-structure;Cytokine;Direct protein sequencing;Disease variant;Disulfide bond;Glycoprotein;Reference proteome;Secreted;Signal			1847510; 9405662; 15340161; 1940799; 8364028; 7512027; 8144879; 11564774; 14657427; 16982608; 18025162; 7547951; 8590020; 8897595; 11485736; 12121653; 15837194; 12825869
63		3D-structure;Alternative splicing;Cell membrane;Direct protein sequencing;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix			3309127; 3313052; 9510189; 14702039; 16710414; 14759258; 17566972; 28813417; 10380930; 10200255
64		3D-structure;Acetylation;Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Membrane;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			14702039; 12853948; 12690205; 15489334; 12975309; 17974005; 10997877; 12168954; 19608861
65	PATHWAY: Protein modification; protein glycosylation. {ECO:00002 69|PubMed:7 72177 6}.	Glycoprotein;Glycosyltransferase;Golgi apparatus;Lipid metabolism;Membrane;Reference proteome;Signal-anchor;Transferase;Transmembrane;Transmembrane helix			1740457; 7650030; 14702039; 15057824; 15489334; 7721776; 9737988; 9737989; 14718375; 17604274
66		3D-structure;Alternative splicing;Disease variant;Disulfide bond;Glycoprotein;Membrane;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Immunodeficiency 30 (IMD30) [MIM:614891]: A form of Mendelian susceptibility to mycobacterial disease, a rare condition caused by impairment of interferon-gamma mediated immunity. It is characterized by predisposition to illness caused by moderately virulent mycobacterial species, such as Bacillus Calmette-Guerin (BCG) vaccine, environmental non-tuberculous mycobacteria, and by the more virulent Mycobacterium tuberculosis. Other microorganisms rarely cause severe clinical disease in individuals with susceptibility to mycobacterial infections, with the exception of Salmonella which infects less than 50% of these individuals. Clinical outcome severity depends on the degree of impairment of interferon-gamma mediated immunity. Some patients die of overwhelming mycobacterial disease with lepromatous-like lesions in early childhood, whereas others develop, later in life, disseminated but curable infections with tuberculoid granulomas. IMD30 has low penetrance, and affected individuals have relatively mild disease and good prognosis. BCG disease and salmonellosis are the most frequent infections in IMD30 patients. {ECO:0000269|PubMed:11424023}. Note=The disease is caused by variants affecting the gene represented in this entry.		7911493; 14702039; 15057824; 15489334; 8943050; 12023369; 11424023
67		Alternative splicing;Bait region;Cell membrane;Direct protein sequencing;Disulfide bond;GPI-anchor;Glycoprotein;Lipoprotein;Membrane;Protease inhibitor;Reference proteome;Serine protease inhibitor;Signal;Thioester bond			11861284; 14980714; 16754747; 14702039; 17974005; 14574404; 11861285; 1984805; 16335952; 16263699; 19159218; 19349973; 21269460; 16959974; 25787250
68		3D-structure;Calcium;Cell adhesion;Cell junction;Cleavage on pair of basic residues;Direct protein sequencing;Disulfide bond;Glycoprotein;Host cell receptor for virus entry;Host-virus interaction;Integrin;Membrane;Metal-binding;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			2958481; 15489334; 1834647; 2450560; 2944883; 3033641; 10397733; 11912194; 14596610; 12907437; 12695522; 12807887; 16051604; 16754960; 17158881; 18635536; 19159218; 19349973; 21269460; 22740495; 24011356; 23186163; 24275569; 24478423; 25398877; 25944712; 29030430; 31331973; 33102950; 22451694
69		Acetylation;Alternative splicing;Cytoplasm;Direct protein sequencing;Membrane;Mitochondrion;Phosphoprotein;Reference proteome;Repeat;SH3 domain			2587259; 14702039; 16641997; 15489334; 7682714; 8713105; 8611520; 9058808; 10066823; 12522270; 15144186; 19690332; 19608861; 21269460; 23186163; 24275569
70		3D-structure;Acute phase;Cytokine;Direct protein sequencing;Disulfide bond;Glycoprotein;Growth factor;Phosphoprotein;Reference proteome;Secreted;Signal	DISEASE: Rheumatoid arthritis systemic juvenile (RASJ) [MIM:604302]: An inflammatory articular disorder with systemic onset beginning before the age of 16. It represents a subgroup of juvenile arthritis associated with severe extraarticular features and occasionally fatal complications. During active phases of the disorder, patients display a typical daily spiking fever, an evanescent macular rash, lymphadenopathy, hepatosplenomegaly, serositis, myalgia and arthritis. {ECO:0000269|PubMed:9769329}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.; DISEASE: Note=A IL6 promoter polymorphism is associated with a lifetime risk of development of Kaposi sarcoma in HIV-infected men. {ECO:0000269|PubMed:11001912}.		3491322; 3500852; 3538015; 3023045; 3320204; 2789513; 3758081; 3266463; 1291290; 15489334; 3279116; 2610854; 1883960; 7851440; 2472117; 2037043; 11080265; 12794819; 15124018; 17075861; 20823453; 22037645; 26091039; 25731159; 28265003; 30995492; 8555185; 9159484; 9118960; 12829785; 9769329; 11001912; 11355017; 12768442
71		3D-structure;Blood group			7777537; 15057824; 15489334; 7954395;

		antigen;Cell adhesion;Direct protein sequencing;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			9166867; 9192786; 9616226; 12754519; 15975931; 16335952; 17319831; 21269460; 24275569; 17638854
72		Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Phosphoprotein;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			20526344; 14702039; 15489334
73		3D-structure;Alternative splicing;Disulfide bond;Glycoprotein;Lyase;Metal-binding;Reference proteome;Secreted;Signal;Zinc			1899030; 16710414; 17705204; 17314045; 19186056; 19206230; 4628675
74	PATHWAY: Protein modification; protein glycosylation. {ECO:00002 69|PubMed:16157350}.	3D-structure;Alternative initiation;Cell membrane;Cell projection;Congenital disorder of glycosylation;Direct protein sequencing;Disulfide bond;Glycoprotein;Glycosyltransferase;Golgi apparatus;Lipid metabolism;Manganese;Membrane;Metal-binding;Reference proteome;Secreted;Signal-anchor;Transferase;Transmembrane;Transmembrane helix	DISEASE: Congenital disorder of glycosylation 2D (CDG2D) [MIM:607091]: A multisystem disorder caused by a defect in glycoprotein biosynthesis and characterized by under-glycosylated serum glycoproteins. Congenital disorders of glycosylation result in a wide variety of clinical features, such as defects in the nervous system development, psychomotor retardation, dysmorphic features, hypotonia, coagulation disorders, and immunodeficiency. The broad spectrum of features reflects the critical role of N-glycoproteins during embryonic development, differentiation, and maintenance of cell functions. {ECO:0000269|PubMed:11901181}. Note=The disease is caused by variants affecting the gene represented in this entry.		3144273; 2124683; 1903938; 1384956; 7579794; 7540104; 14702039; 15164053; 3094506; 3091013; 2120039; 1714903; 7744867; 10580128; 11901181; 20378551; 20068231; 24275569; 16157350; 16497331; 19106107
75		Disulfide bond;Glycoprotein;Immunoglobulin domain;Metalloenzyme inhibitor;Metalloprotease inhibitor;Protease inhibitor;Reference proteome;Repeat;Secreted;Serine protease inhibitor;Signal			11928817; 12975309; 12595574
76		3D-structure;Alternative splicing;Cytoplasm;Hydrolase;Nucleus;Phosphoprotein;Protein phosphatase;Reference proteome;Repeat;SH2 domain			1732748; 1652101; 1736296; 7665165; 9074930; 10497187; 14702039; 16541075; 15489334; 7781604; 9285411; 9842885; 9712903; 10574931; 11162587; 11414741; 11266449; 14654843; 14597715; 15184070; 15526160; 16129412; 18604210; 19591923; 19843936; 19690332; 21269460; 21262353; 20933011; 21258366; 23112346; 23186163; 25944712; 9774441; 12482860; 21465528
77		3D-structure;Acetylation;Alternative splicing;Apoptosis;Cytoplasm;Direct protein sequencing;Phosphoprotein;Reference proteome			9108473; 10409614; 10497265; 14702039; 16710414; 15489334; 16964243; 17525332; 18669648; 19413330; 20068231; 21269460; 21406692; 22223895; 22814378; 23186163; 24275569; 11371636
78		3D-structure;Acetylation;Activator;Alternative splicing;DNA-binding;Direct protein sequencing;Isopeptide bond;Nucleus;Phosphoprotein;Reference proteome;Repeat;Transcription;Transcription regulation;Ubl conjugation			1852076; 14702039; 11230166; 16710414; 7539918; 1317062; 8621524; 10395741; 18669648; 20699359; 22814378; 23186163; 24275569; 28904176; 28112733; 16181639; 19196990; 28396409
79		3D-structure;Alternative splicing;Cell membrane;Cell projection;Chemotaxis;Developmental protein;Differentiation;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Neurogenesis;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix;Ubl conjugation			9458045; 16641997; 15489334; 17974005; 10102268; 9608531; 9796701; 10892742; 11404413; 12082532; 17081983; 18669648; 20068231; 21269460; 23186163; 24673457; 24560577; 26529257; 17848514;
80		3D-structure;Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			9730896; 15057824; 15489334; 14754506; 12951052; 12960161; 16959974
81		3D-structure;Disease variant;Disulfide bond;Glycoprotein;Hydrolase;Lysosome;Neurodegeneration;Neuronal ceroid lipofuscinosis;Protease;Reference proteome;Signal;Thiol protease;Zymogen	DISEASE: Ceroid lipofuscinosis, neuronal, 13 (CLN13) [MIM:615362]: A form of neuronal ceroid lipofuscinosis characterized by adult onset of progressive cognitive decline and motor dysfunction leading to dementia and often early death. Some patients develop seizures. Neuronal ceroid lipofuscinoses are progressive neurodegenerative, lysosomal storage diseases characterized by intracellular accumulation of autofluorescent liposomal material. {ECO:0000269|PubMed:23297359}. Note=The disease is caused by variants affecting the gene represented in this entry.		10318784; 10198209; 10661872; 10362521; 14702039; 15489334; 9822672; 17974005; 19159218; 12225749; 23297359
82	PATHWAY: Protein	3D-structure;Alternative splicing;Cell cycle;Coiled coil;Cytoplasm;Cytoplasmic			1985094; 1985112; 7713506; 8625517; 9933563; 16554811; 15489334; 7561701; 8666824; 12699405; 16297862; 16316627; 16472766;

	modification; protein ubiquitination.	vesicle;DNA-binding;Metal-binding;Nucleus;Phosphoprotein;RNA-binding;Reference proteome;Ribonucleoprotein;Transferase;Ubl conjugation;Ubl conjugation pathway;Zinc;Zinc-finger			16880511; 17156811; 18361920; 18845142; 18641315; 18022694; 18669648; 19675099; 20407604; 20013343; 20068231; 21406692; 23186163; 26347139; 26342464
83		3D-structure;Cell membrane;Cell projection;Cytoplasm;Cytoskeleton;Developmental protein;Disease variant;Membrane;Microtubule;Reference proteome	DISEASE: IgA nephropathy 3 (IGAN3) [MIM:616818]: A form of IgA nephropathy, a common primary glomerulonephritis characterized by glomerular sclerosis, interstitial fibrosis, and mesangial glomerular deposits of immunoglobulin A and immunoglobulin G visible on renal biopsies. IgA nephropathy is associated with renal insufficiency that can progress to end-stage renal disease. Proteinuria and hematuria are characteristic clinical presentations. {ECO:0000269|PubMed:25782674}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		9458049; 14702039; 17974005; 15057823; 15489334; 10887178; 16877379; 12717443; 17974561; 19690332; 21288888; 23186163; 29408807; 25782674
84		3D-structure;Alternative splicing;Disulfide bond;Glycoprotein;Membrane;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			9013879; 8910586; 14702039; 15772651; 15489334; 10791955; 18243101
85		3D-structure;Cytokine;Direct protein sequencing;Disulfide bond;Glycoprotein;Growth factor;Reference proteome;Secreted;Signal			3024129; 2824500; 3498940; 2823259; 15489334; 2361960; 2037074; 8483502; 22153509
86		Diabetes mellitus;Phosphoprotein;Reference proteome;SH2 domain	DISEASE: Celiac disease 13 (CELIAC13) [MIM:612011]: A multifactorial, chronic disorder of the small intestine caused by intolerance to gluten. It is characterized by immune-mediated enteropathy associated with failed intestinal absorption, and malnutrition. In predisposed individuals, the ingestion of gluten-containing food such as wheat and rye induces a flat jejunal mucosa with infiltration of lymphocytes. {ECO:0000269|PubMed:18311140}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.; DISEASE: Diabetes mellitus, insulin-dependent (IDDM) [MIM:222100]: A multifactorial disorder of glucose homeostasis that is characterized by susceptibility to ketoacidosis in the absence of insulin therapy. Clinical features are polydipsia, polyphagia and polyuria which result from hyperglycemia-induced osmotic diuresis and secondary thirst. These derangements result in long-term complications that affect the eyes, kidneys, nerves, and blood vessels. {ECO:0000269|PubMed:17554260}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		10799879; 15489334; 17554260; 18311140; 21406692; 23186163; 20843259
87		3D-structure;Alternative splicing;Chromosomal rearrangement;Citrullination;Coiled coil;DNA-binding;Direct protein sequencing;Host-virus interaction;Isopeptide bond;Nucleus;Phosphoprotein;Reference proteome;Transcription;Transcription regulation;Ubl conjugation	DISEASE: Note=A chromosomal aberration involving PSIP1 is associated with pediatric acute myeloid leukemia (AML) with intermediate characteristics between M2-M3 French-American-British (FAB) subtypes. Translocation t(9;11)(p22;p15) with NUP98. The chimeric transcript is an in-frame fusion of NUP98 exon 8 to PSIP1 exon 4. {ECO:0000269|PubMed:15725483}.		9822615; 10623627; 10721720; 12200376; 15164053; 15489334; 10856157; 15642333; 15475359; 15749713; 15797927; 9885563; 15725483; 17081983; 17525332; 19367720; 18669648; 18318008; 19413330; 19244240; 19690332; 20068231; 21269460; 21406692; 23186163; 24275569; 28112733; 15895093; 16260736; 22327296; 25305204; 25082813; 29997176
88		3D-structure;Adaptive immunity;Cytoplasmic vesicle;Disulfide bond;Endosome;Glycoprotein;Host-virus interaction;Immunity;Lysosome;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix			9721848; 9768752; 15489334; 21930964; 21810281; 24434718; 25681212; 27329040; 29056532; 32295904; 22809326
89		Alternative splicing;Amyloid;Angiogenesis;Cell adhesion;Cytoplasmic vesicle;Direct protein sequencing;Disulfide bond;EGF-like domain;Fertilization;Glycoprotein;Membrane;Phosphoprotein;Reference proteome;Repeat;Secreted;Signal			8639264; 14702039; 17974005; 16572171; 15489334; 1909932; 9535276; 10411933; 9260929; 18780401; 19204935; 26091039
90	PATHWAY: Protein modification; protein glycosylation. {ECO:00002669|PubMed:25279697, ECO:00002699|PubMed:25279699, ECO:00002699|PubMed:9405606}.	Congenital muscular dystrophy;Disease variant;Dystroglycanopathy;Glycoprotein;Glycosyltransferase;Golgi apparatus;Lissencephaly;Manganese;Membrane;Metal-binding;Reference proteome;Signal-anchor;Transferase;Transmembrane;Transmembrane helix	DISEASE: Muscular dystrophy-dystroglycanopathy congenital with brain and eye anomalies A13 (MDDGA13) [MIM:615287]: An autosomal recessive disorder characterized by congenital muscular dystrophy associated with cobblestone lissencephaly and other brain anomalies, eye malformations, profound mental retardation, and death usually in the first years of life. Included diseases are the more severe Walker-Warburg syndrome and the slightly less severe muscle-eye-brain disease. {ECO:0000269|PubMed:23359570, ECO:0000269|PubMed:23877401}. Note=The disease is caused by variants affecting the gene represented in this entry.		9405606; 15489334; 19587235; 23359570; 23877401; 25279699; 25279697
91		3D-structure;Acetylation;Cell membrane;Cytoplasm;Direct protein sequencing;Disease variant;Lyase;Membrane;Metal-binding;Osteopetrosis;Phosphoprotein;Reference proteome;Zinc	DISEASE: Osteopetrosis, autosomal recessive 3 (OPTB3) [MIM:259730]: A rare genetic disease characterized by abnormally dense bone, due to defective resorption of immature bone. Osteopetrosis occurs in two forms: a severe autosomal recessive form occurring in utero, infancy, or childhood, and a benign autosomal dominant form occurring in adolescence or adulthood. Recessive osteopetrosis commonly manifests in early infancy with macrocephaly, feeding difficulties, evolving blindness and deafness,		3108857; 3121496; 14702039; 15489334; 4207120; 823150; 3000449; 14567693; 14736710; 15218065; 15990874; 17314045; 18618712; 21269460; 24275569; 4621826; 3151019; 3151020; 1909891; 1932029; 1910042; 1336460; 1433293; 1474587; 8431430; 8485129; 8399159;

			bone marrow failure, severe anemia, and hepatosplenomegaly. Deafness and blindness are generally thought to represent effects of pressure on nerves. OPTB3 is associated with renal tubular acidosis, cerebral calcification (marble brain disease) and in some cases with mental retardation. {ECO:0000269|PubMed:15300855, ECO:0000269|PubMed:1542674, ECO:0000269|PubMed:1928091, ECO:0000269|PubMed:8834238, ECO:0000269|PubMed:9143915}. Note=The disease is caused by variants affecting the gene represented in this entry.		8218160; 8482389; 8262987; 8331673; 8451242; 7901850; 15299481; 15299482; 7803386; 8070585; 8142888; 7696263; 7608893; 7761440; 8639494; 8987974; 8557623; 9265618; 9398308; 9541386; 9865942; 10550681; 11015219; 11076507; 11327835; 11572683; 11802772; 12056894; 12171926; 11831900; 12166932; 11818565; 12499545; 14736236; 15453828; 15667203; 15865431; 16214338; 16134940; 16106378; 16511248; 16820676; 16290146; 16759856; 17000110; 16807956; 16506782; 16787097; 16686544; 16942027; 17125255; 17181151; 17705204; 17319692; 17330962; 17127057; 17251017; 17346964; 17540563; 17588751; 17071654; 17407288; 18266323; 18942852; 18024029; 18162396; 18374572; 18359629; 18640037; 18161740; 18461940; 18768466; 18260615; 18481843; 18723489; 19170619; 19583303; 19186056; 19206230; 19115843; 19731956; 19827837; 19778001; 19520834; 6817747; 6407977; 1928091; 1542674; 8834238; 9143915; 15300855
92		3D-structure;Alternative splicing;Cell membrane;Disulfide bond;GPI-anchor;Glycoprotein;Hydrolase;Lipoprotein;Membrane;NAD;NADP;Reference proteome;Signal;Transferase			8202488; 14702039; 15815621; 15489334; 16335952; 19159218; 25944712; 11866528
93		Alternative splicing;Apoptosis;Developmental protein;Differentiation;Direct protein sequencing;Disease variant;Disulfide bond;Ectodermal dysplasia;Glycoprotein;Membrane;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Ectodermal dysplasia 10A, hypohidrotic/hair/nail type, autosomal dominant (ECTD10A) [MIM:129490]: A form of ectodermal dysplasia, a heterogeneous group of disorders due to abnormal development of two or more ectodermal structures. It is an autosomal dominant condition characterized by hypotrichosis, abnormal or missing teeth, and hypohidrosis due to the absence of sweat glands. {ECO:0000269|PubMed:10431241, ECO:0000269|PubMed:18231121}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Ectodermal dysplasia 10B, hypohidrotic/hair/tooth type, autosomal recessive (ECTD10B) [MIM:224900]: A disorder due to abnormal development of two or more ectodermal structures, and characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands. {ECO:0000269|PubMed:10431241, ECO:0000269|PubMed:15373768, ECO:0000269|PubMed:16029325, ECO:0000269|PubMed:16435307, ECO:0000269|PubMed:18231121, ECO:0000269|PubMed:19438931, ECO:0000269|PubMed:20979233, ECO:0000269|PubMed:27657131}. Note=The disease is caused by variants affecting the gene represented in this entry.		10431241; 14702039; 15815621; 15489334; 15340161; 11039935; 11035039; 15373768; 16029325; 16435307; 18231121; 18065779; 18561327; 19438931; 20979233; 27657131
94		3D-structure;Acetylation;Alternative splicing;Coiled coil;Cytoplasm;DNA damage;Host-virus interaction;Metal-binding;Phosphoprotein;Reference proteome;Zinc;Zinc-finger			8710854; 8855313; 15815621; 15489334; 10581243; 10759890; 12133833; 17568778; 18691976; 18669648; 19369195; 20068231; 21931631; 21931555; 22814378; 23186163; 24275569; 25861989; 26363073; 28487378; 28566380; 29251827; 12005438
95		3D-structure;Alternative splicing;Antiviral defense;Disulfide bond;Glycoprotein;Membrane;Receptor;Reference proteome;Signal;Transmembrane;Transmembrane helix			12521379; 12469119; 12483210; 14702039; 16710414; 15489334; 20934432
96		Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Note=A chromosomal aberration involving FCRL5 has been found in cell lines with 1q21 abnormalities derived from Burkitt lymphoma. Duplication dup(1)(q21q32). {ECO:0000269|PubMed:11290337}.		11453668; 11290337; 11493702; 12975309; 17974005; 16710414; 15489334; 11929751; 16849395; 16959974
97		Alternative splicing;Coiled coil;Disulfide bond;EGF-like domain;Glycoprotein;Reference proteome;Repeat;Secreted;Signal			11124542; 12975309; 14702039; 17974005; 16421571; 15489334; 9083061
98		3D-structure;Calcium;Cell projection;Cilium;Coiled coil;Cytoplasmic vesicle;Direct protein sequencing;Disease variant;Disulfide bond;Endoplasmic reticulum;Extracellular matrix;Glaucoma;Glycoprotein;Golgi apparatus;Lipoprotein;Membrane;Metal-binding;Mitochondrion;Mitochondrion inner membrane;Mitochondrion outer membrane;Palmitate;Reference proteome;Secreted;Signal	DISEASE: Glaucoma 1, open angle, A (GLC1A) [MIM:137750]: A form of primary open angle glaucoma (POAG). POAG is characterized by a specific pattern of optic nerve and visual field defects. The angle of the anterior chamber of the eye is open, and usually the intraocular pressure is increased. However, glaucoma can occur at any intraocular pressure. The disease is generally asymptomatic until the late stages, by which time significant and irreversible optic nerve damage has already taken place. {ECO:0000269|PubMed:10196380, ECO:0000269|PubMed:10330365, ECO:0000269|PubMed:10340788, ECO:0000269|PubMed:10644174, ECO:0000269|PubMed:10798654, ECO:0000269|PubMed:10819638, ECO:0000269|PubMed:10873982, ECO:0000269|PubMed:10916185, ECO:0000269|PubMed:10980537, ECO:0000269|PubMed:11004290, ECO:0000269|PubMed:11774072, ECO:0000269|PubMed:12189160, ECO:0000269|PubMed:12356829, ECO:0000269|PubMed:12362081, ECO:0000269|PubMed:12442283, ECO:0000269|PubMed:12860809, ECO:0000269|PubMed:12872267, ECO:0000269|PubMed:15025728, ECO:0000269|PubMed:15255110, ECO:0000269|PubMed:15534471, ECO:0000269|PubMed:15795224, ECO:0000269|PubMed:16401791, ECO:0000269|PubMed:17210859, ECO:0000269|PubMed:17499207, ECO:0000269|PubMed:25524706, ECO:0000269|PubMed:9005853, ECO:0000269|PubMed:9328473, ECO:0000269|PubMed:9345106, ECO:0000269|PubMed:9361308, ECO:0000269|PubMed:9490287, ECO:0000269|PubMed:9510647, ECO:0000269|PubMed:9521427, ECO:0000269|PubMed:9535666, ECO:0000269|PubMed:9697688, ECO:0000269|PubMed:9792882, ECO:0000269|PubMed:9863594}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Glaucoma 3, primary congenital, A (GLC3A) [MIM:231300]: An autosomal recessive form of primary congenital glaucoma (PCG). PCG is characterized by marked increase of intraocular pressure at birth or early childhood, large ocular globes (buphthalmos) and corneal edema. It results from developmental defects of the trabecular meshwork and		9280311; 9169133; 9328473; 9005853; 9446806; 9548973; 14702039; 16710414; 15489334; 9497363; 19287508; 15795224; 11053284; 11431441; 12019210; 11773026; 11773029; 11923248; 12615070; 12697062; 15944158; 17650508; 17516541; 17984096; 18855004; 19188438; 19959812; 21656515; 23629661; 23897819; 25524706; 9345106; 9510647; 9361308; 9792882; 9490287; 9521427; 9863594; 9697688; 9535666; 10330365; 10196380; 10340788; 11004290; 10873982; 10644174; 10980537; 10798654; 10819638; 10916185; 11774072; 12189160; 12442283; 12356829; 12362081; 12860809; 12872267; 15025728; 15534471; 15255110; 15733270; 16401791; 17499207; 17210859

			anterior chamber angle of the eye that prevent adequate drainage of aqueous humor. {ECO:0000269|PubMed:15733270}. Note=The disease is caused by variants affecting distinct genetic loci, including the gene represented in this entry. MYOC mutations may contribute to GLC3A via digenic inheritance with CYP1B1 and/or another locus associated with the disease (PubMed:15733270). {ECO:0000269|PubMed:15733270}.		
99		3D-structure;Chemotaxis;Cytokine;Direct protein sequencing;Disulfide bond;Glycoprotein;Inflammatory response;Reference proteome;Secreted;Signal			8597956; 8609214; 8631813; 8780731; 9169149; 9299399; 15489334; 9578468; 9712872
100		Disease variant;Glycoprotein;Glycosidase;Hydrolase;Lipid metabolism;Lysosome;Phosphoprotein;Reference proteome;Signal	DISEASE: Fucosidosis (FUCA1D) [MIM:230000]: An autosomal recessive lysosomal storage disease characterized by accumulation of fucose-containing glycolipids and glycoproteins in various tissues. Clinical signs include facial dysmorphism, dysostosis multiplex, moderate hepatomegaly, severe intellectual deficit, deafness, and according to age, angiokeratomas. {ECO:0000269|PubMed:7874128, ECO:0000269|PubMed:8504303, ECO:0000269|PubMed:9762612}. Note=The disease is caused by variants affecting the gene represented in this entry.		8504303; 12880961; 14702039; 16710414; 15489334; 2803312; 2174090; 2983333; 6096099; 2894306; 9741689; 19159218; 21269460; 21406692; 24275569; 25944712; 8399358; 7874128; 7815431; 9762612; 10094192; 12408193
101		Alternative splicing;Calcium;Cell adhesion;Disulfide bond;Glycoprotein;Integrin;Magnesium;Membrane;Metal-binding;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			10486209; 10464311; 16572171; 16754960; 19159218
102		Direct protein sequencing;Disulfide bond;Glycoprotein;Reference proteome;Secreted;Signal			1846945; 8307998; 15489334; 8198617
103		Cell membrane;Direct protein sequencing;Disulfide bond;EGF-like domain;Glycoprotein;Membrane;Phosphoprotein;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			15851471; 16710414;
104		3D-structure;Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			9062191; 14702039; 11780052; 15489334; 10940905; 10604985; 16081415; 16335952; 18657508;
105		Alternative splicing;Basement membrane;Calcium;Cell adhesion;Direct protein sequencing;Disulfide bond;EGF-like domain;Extracellular matrix;Glycoprotein;Methylation;Reference proteome;Repeat;Secreted;Signal			9733643; 14702039; 12508121; 11956183; 19159218; 22905912; 16959974; 24275569
106		3D-structure;Acetylation;Alternative splicing;Congenital erythrocytosis;Cytoplasm;Dioxygenase;Disease variant;Iron;Metal-binding;Nucleus;Oxidoreductase;Phosphoprotein;Reference proteome;S-nitrosylation;Vitamin C;Zinc;Zinc-finger	DISEASE: Erythrocytosis, familial, 3 (ECYT3) [MIM:609820]: An autosomal dominant disorder characterized by elevated serum hemoglobin and hematocrit, and normal serum erythropoietin levels. {ECO:0000269|PubMed:16407130, ECO:0000269|PubMed:17579185}. Note=The disease is caused by variants affecting the gene represented in this entry.		11056053; 11574160; 12788921; 17974005; 16710414; 11595178; 11595184; 12181324; 12351678; 12163023; 12670503; 12615973; 15247232; 15897452; 18063574; 19413330; 19631610; 19339211; 19208626; 20840591; 20838600; 20068231; 20466884; 21269460; 21792862; 22286099; 22814378; 23186163; 24681946; 25974097; 16782814; 19604478; 21601578; 28594552; 16407130; 17579185; 24711448; 25129147
107		Alternative splicing;Cell membrane;Cytoplasm;Disulfide bond;Glycoprotein;Immunity;Inflammatory response;Innate immunity;Lectin;Membrane;Metal-binding;Phosphoprotein;Receptor;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix	DISEASE: Candidiasis, familial, 4 (CANDF4) [MIM:613108]: A primary immunodeficiency disorder with altered immune responses and impaired clearance of fungal infections, selective against Candida. It is characterized by persistent and/or recurrent infections of the skin, nails and mucous membranes caused by organisms of the genus Candida, mainly Candida albicans. {ECO:0000269|PubMed:19864674}. Note=The disease may be caused by variants affecting the gene represented in this entry.		11745369; 11470510; 11491532; 11567029; 12423684; 12975309; 14702039; 16541075; 15489334; 16870151; 17230442; 19864674; 20807886
108		3D-structure;Adaptive immunity;Alternative splicing;Calcium;Cell membrane;Disulfide bond;Glycoprotein;Immunity;Innate immunity;Lectin;Membrane;Metal-binding;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			11536172; 11748283; 12975309; 15489334; 11031109; 21880719; 24425442; 25995448
109		3D-structure;Adaptive immunity;Alternative splicing;Cell membrane;Coiled coil;Disulfide bond;Glycoprotein;Immunity;Immunoglobulin domain;Membrane;Phosphoprotein;Reference proteome;Signal;Transmembrane;Transmembrane helix			9149941; 9382921; 11170752; 14702039; 14574404; 15489334; 19690332; 20610803; 21918970; 22767497; 22846996
110	PATHWAY: Protein modification; protein ubiquitination.	3D-structure;Acetylation;Alternative splicing;Antiviral defense;Autophagy;Coiled coil;Cytoplasm;Host-virus interaction;Immunity;Innate immunity;Metal-binding;Nucleus;Phosphoprotein;Reference			11331580; 15249690; 16401428; 18312418; 21632761; 14702039; 16554811; 15489334; 12878161; 16474118; 16809279; 16643975; 16956947; 17156811; 20053985; 20357094; 21247355; 21575904; 21680743; 21512569; 21512573; 21572451; 22078707; 21035162; 21866272; 22482711; 22291694; 22223895; 23186163; 25127057; 24275569; 21734049;

		proteome;Transferase;Ubl conjugation;Ubl conjugation pathway;Zinc;Zinc-finger			
111		3D-structure;Acetylation;Direct protein sequencing;Disulfide bond;Endosome;Glycoprotein;Golgi apparatus;Lipoprotein;Membrane;Methylation;Palmitate;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix;Transport			2957598; 2963003; 9892739; 14574404; 10900005; 11387475; 12754519; 17081983; 17487921; 18220336; 19367720; 18691976; 18669648; 18318008; 18817523; 19413330; 19159218; 19369195; 19690332; 19608861; 20068231; 21269460; 21406692; 23186163; 24275569; 25944712; 18046459
112		3D-structure;Adaptive immunity;Alternative splicing;Cell membrane;Disulfide bond;Immunity;Immunoglobulin domain;Membrane;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			9278324; 9548455; 10941837; 15057824; 15489334; 9151699; 11875462; 24275569; 21454581
113		3D-structure;ATP-binding;Acetylation;Alternative splicing;Antiviral defense;Cell junction;Cell membrane;Cell projection;Cytoplasm;Cytoskeleton;Disease variant;Helicase;Host-virus interaction;Hydrolase;Immunity;Innate immunity;Isopeptide bond;Membrane;Metal-binding;Nucleotide-binding;Phosphoprotein;RNA-binding;Reference proteome;Repeat;Tight junction;Ubl conjugation;Zinc	DISEASE: Singleton-Merten syndrome 2 (SGMRT2) [MIM:616298]: A form of Singleton-Merten syndrome, an autosomal dominant disorder characterized by marked aortic calcification, dental anomalies, osteopenia, acro-osteolysis, and to a lesser extent glaucoma, psoriasis, muscle weakness, and joint laxity. Additional clinical manifestations include particular facial characteristics and abnormal joint and muscle ligaments. SGMRT2 is an atypical form characterized by variable expression of glaucoma, aortic calcification, and skeletal abnormalities, without dental anomalies. {ECO:0000269|PubMed:25620203}. Note=The disease is caused by variants affecting the gene represented in this entry.		11890704; 15164053; 15489334; 17974005; 15181474; 15219805; 15208624; 16125763; 16281057; 15708988; 16153868; 16127453; 16009940; 17392790; 17190814; 17460044; 18636086; 18057259; 18724357; 19631370; 19576794; 19017631; 19122199; 19211564; 19419966; 19193793; 19609254; 19484123; 19608861; 20434986; 20368735; 21175414; 20127681; 20007272; 21269460; 21616437; 21884169; 21742966; 21813773; 20950133; 21068236; 21791617; 21102435; 22152002; 22301138; 23399697; 23843640; 23950712; 24755855; 24390337; 26471729; 27824081; 27866900; 25620203; 27312109; 28469175; 29117565; 29288164; 30193849; 31006531; 18243112; 18242112; 25018021
114		Coiled coil;Direct protein sequencing;Host-virus interaction;Intermediate filament;Keratin;Methylation;Phosphoprotein;Reference proteome			2447559; 2468493; 2448790; 2469734; 10623642; 14702039; 16625196; 15489334; 11682035; 1286667; 10212274; 10809736; 15846844; 16000376; 21049038; 22814378; 23186163; 24129315; 21269460
115		Cleavage on pair of basic residues;Disulfide bond;Glycoprotein;Growth factor;Hormone;Reference proteome;Secreted;Signal			7826378; 15489334; 9428386
116		3D-structure;DNA damage;DNA repair;DNA-binding;Direct protein sequencing;Metal-binding;Methyltransferase;Nucleus;Phosphoprotein;Reference proteome;Transferase;Zinc			2405387; 2188979; 2394694; 2359121; 15164054; 15489334; 1985934; 8202360; 7954470; 7766621; 7614699; 23186163; 24275569; 10747039; 10606635; 15964013
117		3D-structure;Alternative splicing;Calcium;Chemotaxis;Cleavage on pair of basic residues;Direct protein sequencing;Disulfide bond;Glycoprotein;Hydrolase;Lipid degradation;Lipid metabolism;Metal-binding;Obesity;Reference proteome;Repeat;Secreted;Signal;Zinc			7982964; 8586446; 8579579; 15769751; 18175805; 16421571; 15489334; 12176993; 1733949; 11559573; 12354767; 14500380; 15700135; 21393252; 21240271; 26371182; 28414242; 27754931
118		3D-structure;Alternative splicing;Apoptosis;Autocatalytic cleavage;Direct protein sequencing;Disease variant;Epilepsy;Hydrolase;Membrane;Mitochondrion;Neurodegeneration;Parkinson disease;Parkinsonism;Protease;Reference proteome;Serine protease;Transit peptide;Transmembrane;Transmembrane helix;Zymogen	DISEASE: 3-methylglutaconic aciduria 8 (MGCA8) [MIM:617248]: An autosomal recessive inborn error of metabolism resulting in early death. Clinical features include extreme hypertonia observed at birth, alternating with hypotonia, subsequent appearance of extrapyramidal symptoms, lack of psychomotor development, microcephaly, and intractable seizures. Patients show lactic acidemia, 3-methylglutaconic aciduria, intermittent neutropenia, and progressive brain atrophy. {ECO:0000269|PubMed:27208207, ECO:0000269|PubMed:27696117}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Parkinson disease 13 (PARK13) [MIM:610297]: A complex neurodegenerative disorder characterized by bradykinesia, resting tremor, muscular rigidity and postural instability, as well as by a clinically significant response to treatment with levodopa. The pathology involves the loss of dopaminergic neurons in the substantia nigra and the presence of Lewy bodies (intraneuronal accumulations of aggregated proteins), in surviving neurons in various areas of the brain. {ECO:0000269|PubMed:15961413, ECO:0000269|PubMed:18401856}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		10644717; 10971580; 10995577; 15815621; 15489334; 11583623; 10873535; 15200957; 19502560; 21269460; 24275569; 25944712; 11967569; 15961413; 18401856; 18364387; 25422467; 27208207; 27535533; 27696117
119		3D-structure;Alternative splicing;Direct protein sequencing;Disulfide bond;Endocytosis;Glycoprotein;Lectin;Membrane;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			9862343; 9553150; 12824192; 15815621; 18669648
120		3D-structure;Adaptive immunity;Alternative initiation;Alternative splicing;Cell membrane;Chaperone;Direct protein sequencing;Disulfide bond;Endoplasmic reticulum;Endosome;Glycoprotein;Golgi apparatus;Immunity;Lysosome;Membrane;Phosphoprotein;Proteoglycan;Reference proteome;Signal-	DISEASE: Note=A chromosomal aberration involving CD74 is found in a non-small cell lung tumor. Results in the formation of a CD74-ROS1 chimeric protein. {ECO:0000269|PubMed:12661006}.		6324166; 6586420; 3001652; 3459184; 14702039; 15372022; 15489334; 1448172; 3104027; 12661006; 12782713; 19092054; 19159218; 21269460; 22171320; 23234360; 25944712; 32855215; 7477400; 9843486; 10022822

		anchor;Transmembrane;Transmembrane helix			
121		3D-structure;Alternative splicing;Chemotaxis;Cytokine;Disulfide bond;Growth factor;Host-virus interaction;Reference proteome;Secreted;Signal			7490086; 16626895; 14702039; 16344560; 15164054; 15489334; 8752281; 9427609; 10446158; 11069075; 11859124; 14525775; 16107333; 15741341; 16725153; 18802065; 19255243; 21802105; 22457824; 29301984; 9384579; 9618518; 10954912; 15588815; 17264079; 17357154; 18799424; 19551879; 20077567
122		3D-structure;Alternative splicing;Cytoplasm;Membrane;Phosphoprotein;Reference proteome;SH2 domain			10432293; 10770799; 11042152; 15489334; 17974005; 10983984
123		Alternative splicing;Cell adhesion;Cell membrane;Chromosomal rearrangement;Disulfide bond;GPI-anchor;Glycoprotein;Immunoglobulin domain;Lipoprotein;Membrane;Reference proteome;Repeat;Secreted;Signal	DISEASE: Note=A chromosomal aberration involving CNTN4 has been found in a boy with characteristic physical features of 3p deletion syndrome (3PDS). Translocation t(3;10)(p26;q26). 3PDS is a rare contiguous gene disorder involving the loss of the telomeric portion of the short arm of chromosome 3 and characterized by developmental delay, growth retardation, and dysmorphic features. {ECO:0000269|PubMed:15106122}.		12202991; 14571131; 14702039; 16641997; 15489334; 11013081; 15106122; 16335952; 20133774; 16959974
124		Alternative splicing;Apoptosis;Cytokine;Direct protein sequencing;Disulfide bond;Glycoprotein;Reference proteome;Secreted;Signal			11707072; 12160727; 12975309; 15489334; 16114871
125		3D-structure;Adaptive immunity;Alternative splicing;Calcium;Cell membrane;Disulfide bond;Glycoprotein;Immunity;Innate immunity;Lectin;Membrane;Metal-binding;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			15368084; 15175046; 16541075; 15489334; 15810886; 23911656; 28652405
126		3D-structure;Alternative splicing;Calcium;Cytoplasm;Hydrolase;Metal-binding;Reference proteome			12392711; 15087120; 10231032; 16710414; 15489334; 30044909; 25621824
127		3D-structure;Alternative splicing;Direct protein sequencing;Disulfide bond;Glycoprotein;Hydrolase;Lysosome;Protease;Reference proteome;Signal;Thiol protease;Zymogen			9065484; 8893817; 12508121; 15489334; 11085925; 9821970; 19159218; 21269460; 24275569; 30425301; 23776206
128	PATHWAY: Protein modification; protein ubiquitination.	3D-structure;Alternative splicing;Chromosomal rearrangement;DNA-binding;Disease variant;Mental retardation;Metal-binding;Nucleus;Phosphoprotein;Proto-oncogene;Reference proteome;Repeat;Repressor;Transcription;Transcription regulation;Ubl conjugation pathway;Zinc;Zinc-finger	DISEASE: Skeletal defects, genital hypoplasia, and mental retardation (SGYMR) [MIM:612447]: A disorder characterized by mental retardation, craniofacial dysmorphism, microcephaly and short stature. Additional features include absence of the thumbs, hypoplasia of the radii and ulnae, additional vertebrae and ribs, retarded bone age and genital hypoplasia. {ECO:0000269|PubMed:18611983}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Note=A chromosomal aberration involving ZBTB16 may be a cause of acute promyelocytic leukemia (APL). Translocation t(11;17)(q32;q21) with RARA. {ECO:0000269|PubMed:8384553}.		8384553; 10500192; 15489334; 8387545; 10572087; 10688654; 11161217; 14528312; 16676348; 24359566; 9770450; 10537309; 18611983
129	PATHWAY: Lipid metabolism; glycerolipid metabolism. {ECO:00003 05|PubMed:8 626658 8}.	3D-structure;ANK repeat;ATP-binding;Alternative splicing;Cell membrane;Cell projection;Cytoplasm;Kinase;Lipid metabolism;Membrane;Metal-binding;Nucleotide-binding;Nucleus;Phosphoprotein;Reference proteome;Repeat;Transferase;Zinc;Zinc-finger			8626588; 9159104; 14702039; 16554811; 15489334; 9716136; 11352924; 11257115; 15544348; 15157668; 18004883; 17351151; 19744926; 22108654; 22627129; 23949095; 23186163; 24275569
130		3D-structure;Alternative splicing;Cell adhesion;Disulfide bond;Glycoprotein;Heparin-binding;Hydrolase;Immunoglobulin domain;Membrane;Phosphoprotein;Protein phosphatase;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Aplasia or hypoplasia of the breasts and/or nipples 2 (BNAH2) [MIM:616001]: A group of congenital deformities encompassing total absence of breasts and nipple (amastia), absence of the nipple (athelia), and absence of the mammary gland (amazia). {ECO:0000269|PubMed:24781087}. Note=The disease is caused by variants affecting the gene represented in this entry.		2972792; 15491607; 16710414; 15489334; 2554325; 1695146; 8995282; 9624153; 16335952; 19349973; 21269460; 23358419; 24275569; 10338209; 24781087
131		3D-structure;Alternative splicing;Amelogenesis imperfecta;Cell adhesion;Cell junction;Disease variant;Disulfide bond;Glycoprotein;Host cell receptor for virus entry;Host-virus interaction;Integrin;Membrane;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Amelogenesis imperfecta 1H (AI1H) [MIM:616221]: A disorder characterized by defective enamel formation, resulting in hypoplastic and hypomineralized tooth enamel that may be rough, pitted, and/or discolored. {ECO:0000269|PubMed:24305999, ECO:0000269|PubMed:24319098}. Note=The disease is caused by variants affecting the gene represented in this entry.		2365683; 14702039; 15815621; 15489334; 1382574; 9426447; 11807098; 15184403; 15194773; 17545607; 17158881; 22278742; 24367260; 24319098; 24305999; 28117447
132		3D-structure;Alternative splicing;Cell adhesion;Cell			9096397; 9036860; 10543405; 11573093; 14978041; 14702039; 10830953; 15489334;

		junction;Cell membrane;Disulfide bond;Glycoprotein;Host cell receptor for virus entry;Host-virus interaction;Immunoglobulin domain;Lipoprotein;Membrane;Palmitate;Phosphoprotein;Receptor;Reference proteome;Repeat;Secreted;Signal;Tight junction;Transmembrane;Transmembrane helix			10490761; 9733828; 10666333; 10814575; 11549277; 11457744; 11316797; 11734628; 12297051; 12021372; 12468544; 15533241; 15364909; 15304526; 15800062; 19064666; 18669648; 20068231; 21406692; 23186163; 24275569; 10567268; 11080637; 14967025
133		Cell membrane;Coiled coil;Disulfide bond;Glycoprotein;Host cell receptor for virus entry;Host-virus interaction;Lectin;Membrane;Phosphoprotein;Receptor;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			14711836; 12975309; 15489334; 16051304; 22156524; 22673088; 24623090; 24275569
134		3D-structure;Alternative initiation;Angiogenesis;Developmental protein;Differentiation;Direct protein sequencing;Growth factor;Heparin-binding;Isopeptide bond;Methylation;Mitogen;Nucleus;Phosphoprotein;Reference proteome;Secreted;Ubl conjugation			3472745; 3780670; 2538817; 19054851; 15815621; 1785797; 2435575; 1721615; 8564983; 3579930; 2435284; 3964259; 3732516; 1417798; 1885605; 8663044; 10358027; 11509569; 11964394; 16257968; 18669637; 20230531; 15863030; 20094046; 22321063; 23469107; 25114211; 28302677; 29501879; 1769963; 1707542; 1849658; 1702556; 7691311; 11390973; 8885834
135		Adaptive immunity;Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunity;Immunoglobulin domain;Membrane;Reference proteome;Repeat;Secreted;Signal;Transmembrane;Transmembrane helix			1692078; 14702039; 16541075; 15489334; 1380059; 7805750; 7589152; 8647185; 9159144; 9634475; 20421648; 30580966
136		3D-structure;ATP-binding;Alternative splicing;Cytoplasm;Direct protein sequencing;Host-virus interaction;Immunity;Innate immunity;Isopeptide bond;Kinase;Lipid droplet;Magnesium;Nucleotide-binding;Nucleus;Phosphoprotein;Reference proteome;Serine/threonine-protein kinase;Transferase;Ubl conjugation			8599092; 10723722; 11397809; 16024789; 15772651; 15489334; 9430229; 10854325; 11960013; 12496252; 12860405; 12538665; 12874243; 14684752; 14625308; 15084582; 15465816; 16286016; 15767370; 16951688; 16690127; 17997719; 18691976; 18347055; 18669648; 19675569; 20400509; 17890055; 18691762; 19022706; 21269460; 23186163; 28436939; 28659487; 29883609; 33673546; 17344846
137		3D-structure;Acetylation;Alternative splicing;Cytoplasm;Direct protein sequencing;Isopeptide bond;Nucleus;Phosphoprotein;Reference proteome;Repeat;TPR repeat;Ubl conjugation			1569099; 14702039; 16554811; 15489334; 1286667; 9195923; 10508479; 14532270; 15592455; 18669648; 19413330; 19608861; 20068231; 21269460; 21406692; 22223895; 23186163; 23349634; 24880080; 24275569; 25218447; 25114211; 25772364; 25944712; 27353360; 29127155; 28112733; 10786835
138		Adaptive immunity;Cell membrane;Direct protein sequencing;Disulfide bond;Glycoprotein;Immunity;Membrane;Phosphoprotein;Reference proteome;Signal;Transmembrane;Transmembrane helix			10209036; 11491537; 14702039; 15164053; 15489334; 11433379; 15144186; 16160011; 19690332
139		3D-structure;Chemotaxis;Cytokine;Direct protein sequencing;Disulfide bond;Inflammatory response;Reference proteome;Secreted;Signal			9235955; 9257816; 9300671; 9419363; 12975309; 14702039; 15489334; 9507024; 14978162; 23341447; 22221265
140	PATHWAY: Protein modification; protein ubiquitination.	3D-structure;Acetylation;Alternative splicing;Apoptosis;Coiled coil;Cytoplasm;Isopeptide bond;Lipid-binding;Metal-binding;Phosphoprotein;Reference proteome;Repeat;Transferase;Ubl conjugation;Ubl conjugation pathway;Zinc;Zinc-finger			7639698; 14702039; 17974005; 15164053; 15489334; 8069916; 8627180; 8710854; 9153189; 9104814; 9020361; 9718306; 9705938; 9692890; 9488716; 9774460; 9827693; 9607925; 9774977; 9418902; 10581243; 10463949; 21357251; 10346818; 10037686; 10514511; 10521462; 10809768; 10764746; 10880535; 11035039; 11278723; 12411493; 11784851; 11907583; 12917689; 12917691; 15310755; 15383523; 15121867; 16153868; 15870263; 15696169; 16214042; 17389591; 19413330; 19506082; 19150425; 18981220; 19969290; 19918265; 20447407; 20064526; 19937093; 20047764; 20577214; 20068231; 21269460; 21307340; 21302310; 21406692; 23453969; 23186163; 23332158; 25026888; 25609706; 29883609; 10206649; 10411888; 10892748; 19810754; 20385093
141		Alternative splicing;Disulfide bond;Glycoprotein;Membrane;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			9653160; 12975309; 14702039; 15772651; 15489334
142		3D-structure;Acetylation;Activator;DNA-binding;Direct protein			3194415; 2825349; 16710414; 15489334; 1846781; 8464713; 8855261; 8663478; 8837781; 9732876; 10196196; 10376527; 10995748;

		sequencing;Isopeptide bond;Nucleus;Phosphoprotein;Proto-oncogene;Reference proteome;Transcription;Transcription regulation;Ubl conjugation			11689449; 12087103; 15467742; 14739463; 17210646; 16478997; 17804415; 18650425; 18669648; 19413330; 19690332; 22083952; 20852630; 20068231; 21177766; 21406692; 22307329; 23624934; 23186163; 24559171; 24263171; 24623306; 26242913; 27458189; 28112733; 7816143; 8662824
143		3D-structure;Acetylation;Cell membrane;Chaperone;Craniosynostosis;Direct protein sequencing;Disease variant;Disulfide bond;Endoplasmic reticulum;Isomerase;Membrane;Osteogenesis imperfecta;Phosphoprotein;Redox-active center;Reference proteome;Repeat;Signal	DISEASE: Cole-Carpenter syndrome 1 (CLCRP1) [MIM:112240]: A form of Cole-Carpenter syndrome, a disorder characterized by features of osteogenesis imperfecta such as bone deformities and severe bone fragility with frequent fractures, in association with craniosynostosis, ocular proptosis, hydrocephalus, growth failure and distinctive facial features. Craniofacial findings include marked frontal bossing, midface hypoplasia, and micrognathia. Despite the craniosynostosis and hydrocephalus, intellectual development is normal. CLCRP1 inheritance is autosomal dominant. {ECO:0000269|PubMed:25683117}. Note=The disease is caused by variants affecting the gene represented in this entry.		3034602; 3611107; 2846539; 14702039; 15489334; 1597478; 9150948; 12665801; 2079031; 1286669; 9399589; 3342239; 1699755; 10636893; 11707400; 11181151; 12485997; 12095988; 12218051; 12218052; 12643545; 15158710; 14592831; 15644496; 16478722; 17081065; 21269460; 21670307; 23475612; 24275569; 26091039; 25683117; 26224785; 25944712; 8580850; 8672469; 10383197;
144		3D-structure;Alternative splicing;Asthma;Cell membrane;Glycoprotein;Membrane;Phosphoprotein;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix	DISEASE: Asthma (ASTHMA) [MIM:600807]: The most common chronic disease affecting children and young adults. It is a complex genetic disorder with a heterogeneous phenotype, largely attributed to the interactions among many genes and between these genes and the environment. It is characterized by recurrent attacks of paroxysmal dyspnea, with wheezing due to spasmodic contraction of the bronchi. {ECO:0000269|PubMed:14566338, ECO:0000269|PubMed:19237393}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.		12675227; 12662155; 14566338; 16899223; 10819331; 14702039; 15815621; 15489334; 15454437; 15671030; 18669648; 19237393; 22387313
145		3D-structure;Adaptive immunity;Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunity;Innate immunity;Lectin;Membrane;Receptor;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			7589107; 9472066; 9601951; 16541075; 15489334; 9430220; 9485206; 9754572; 9655483; 9486650; 10428963; 10669413; 12387742; 12165520; 15751767; 15940674; 18064301; 20952657; 21825173; 23335510; 30503213; 30134159; 30860984; 32859121; 10023772; 18083576; 18448674; 18332182
146		3D-structure;Activator;Alternative splicing;Apoptosis;Cytoplasm;Metal-binding;Nucleus;Reference proteome;Repeat;Transcription;Transcription regulation;Transferase;Ubl conjugation;Ubl conjugation pathway;Zinc;Zinc-finger			8548810; 8552191; 8643514; 14702039; 16554811; 15489334; 15665297; 18082613; 18414036; 18846110; 18669648; 19690332; 20888210; 21145488; 20651737; 21447281; 21653699; 21849505; 21931591; 22095281; 23453969; 25486457; 25681446; 10404221; 19153467; 21549626
147		3D-structure;Acetylation;Alternative splicing;Cytoplasm;Direct protein sequencing;Elongation factor;Endoplasmic reticulum;Hypusine;Membrane;Nuclear pore complex;Nucleus;Protein biosynthesis;Protein transport;RNA-binding;Reference proteome;Translocation;Transport;mRNA transport		BIOTECHNOLOGY: Mature eIF5A-1 may be used as an in situ diagnostic marker for aberrant proliferation in intraepithelial neoplasia of the vulva. {ECO:00002 69|PubMed: 15262146}.	2492279; 8253832; 7545941; 7622067; 14702039; 15489334; 10229683; 3095320; 1286667; 8660923; 10944119; 15303967; 15262146; 15371445; 15452064; 16519677; 16987817; 17187778; 17213197; 17360499; 18067580; 19379712; 21269460; 22771473; 24275569; 25944712; 11742107
148		Alternative splicing;Disulfide bond;EGF-like domain;Glycoprotein;Reference proteome;Repeat;Secreted;Serine protease homolog;Signal;Sushi			12975309; 14702039; 17974005; 16554811; 15489334; 15498874; 15111323; 16335952
149		3D-structure;Endoplasmic reticulum;Glycoprotein;Lipid metabolism;Membrane;NADP;Oxidoreductase;Reference proteome;Signal-anchor;Steroid metabolism;Transmembrane;Transmembrane helix	DISEASE: Cortisone reductase deficiency 2 (CORTRD2) [MIM:614662]: An autosomal dominant error of cortisone metabolism characterized by a failure to regenerate cortisol from cortisone, resulting in increased cortisol clearance, activation of the hypothalamic- pituitary axis and ACTH-mediated adrenal androgen excess. Clinical features include hyperandrogenism resulting in hirsutism, oligo- amenorrhea, and infertility in females and premature pseudopuberty in males. {ECO:0000269|PubMed:12858176}. Note=The disease is caused by variants affecting the gene represented in this entry.		1885595; 12414862; 14702039; 16710414; 15489334; 10497248; 12858176; 15152005; 19159218; 24275569; 15513927; 17070044; 17919905; 18485702; 18069989; 18553955; 19217779; 16959974
150		Alternative splicing;Direct protein sequencing;Disulfide bond;Glycoprotein;Hormone;Reference proteome;Secreted;Signal			7489828; 8700837; 14702039; 16421571; 15489334; 9794484; 15340161
151		3D-structure;Autocatalytic cleavage;Cell junction;Cell membrane;Congenital muscular dystrophy;Cytoplasm;Cytoskeleton;Disease variant;Disulfide bond;Dystroglycanopathy;Glycoprotein;Host cell receptor for virus entry;Host-virus interaction;Limb-girdle muscular dystrophy;Lissencephaly;Membrane;Nucleus;Phosphoprotein;Postsynaptic cell membrane;Receptor;Reference proteome;Secreted;Signal;Synapse;Transmembrane;Transmembrane helix	DISEASE: Muscular dystrophy-dystroglycanopathy limb-girdle C9 (MDDGC9) [MIM:613818]: An autosomal recessive muscular dystrophy showing onset in early childhood, and associated with mental retardation without structural brain anomalies. {ECO:0000269|PubMed:21388311, ECO:0000269|PubMed:25503980}. Note=The disease is caused by variants affecting the gene represented in this entry. MDDGC7 is caused by DAG1 mutations that interfere with normal post-translational processing, resulting in defective DAG1 glycosylation and impaired interactions with extracellular-matrix components. Other muscular dystrophy-dystroglycanopathies are caused by defects in enzymes involved in protein O-glycosylation.; DISEASE: Muscular dystrophy-dystroglycanopathy congenital with brain and eye anomalies A9 (MDDGA9) [MIM:616538]: An autosomal recessive disorder characterized by congenital muscular dystrophy associated with cobblestone lissencephaly and other brain anomalies, eye malformations, profound mental retardation, and death usually in the first years of life. Included diseases are the more severe Walker-Warburg syndrome and the slightly less severe muscle-eye-brain disease. {ECO:0000269|PubMed:24052401, ECO:0000269|PubMed:25934851}. Note=The disease is caused by variants affecting the gene represented in this entry.		8268918; 14702039; 16641997; 15489334; 7592992; 9851927; 10767429; 10988290; 10769203; 11724572; 11495720; 12140558; 12795607; 12592373; 15175026; 16254364; 17212656; 17360738; 17905726; 18764929; 19946898; 19838169; 19324387; 20507882; 20512930; 20044576; 21269460; 21388311; 21987822; 23186163; 23234360; 24052401; 24256719; 24275569; 25503980; 25934851; 10932245; 27493216; 28781947
152		Activator;Antiviral defense;Cytoplasm;DNA-binding;Direct protein sequencing;Nucleus;Phosphoprotein;Reference proteome;Transcription;Transcription regulation;Ubl conjugation	DISEASE: Immunodeficiency 65 (IMD65) [MIM:618648]: An autosomal recessive immunologic disorder characterized by recurrent viral infections from early infancy. Clinical consequences are pneumonia, bronchiectasis, and septic shock. Affected individuals have lymphopenia or hypogammaglobulinemia, particularly during infection, and impaired cellular type I interferon response. Patients may have adverse response to vaccination with live attenuated vaccines. {ECO:0000269|PubMed:30143481, ECO:0000269|PubMed:30826365}. Note=The		1630447; 15489334; 11846981; 10702714; 30143481; 30826365; 32699158

			disease is caused by variants affecting the gene represented in this entry.		
153		3D-structure;Alternative splicing;Calcium;Cell adhesion;Cell membrane;Cleavage on pair of basic residues;Direct protein sequencing;Disulfide bond;Epidermolysis bullosa;Glycoprotein;Integrin;Lipoprotein;Membrane;Metal-binding;Palmitate;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Epidermolysis bullosa letalis, with pyloric atresia (EB-PA) [MIM:226730]: An autosomal recessive, frequently lethal, epidermolysis bullosa with variable involvement of skin, nails, mucosa, and with variable effects on the digestive system. It is characterized by mucocutaneous fragility, aplasia cutis congenita, and gastrointestinal atresia, which most commonly affects the pylorus. Pyloric atresia is a primary manifestation rather than a scarring process secondary to epidermolysis bullosa. Note=The disease is caused by variants affecting the gene represented in this entry.		1976638; 14702039; 15815621; 15489334; 2070796; 1946438; 1476731; 8496190; 8253814; 7583007; 2649503; 2542022; 1953640; 8360143; 7681434; 11359780; 15023541; 15611341; 15466886; 16754960; 16263699; 19159218; 17303120; 20682778; 21269460; 22314500; 22351760; 25944712; 28873464
154		3D-structure;Acetylation;Cytoplasm;Direct protein sequencing;Host-virus interaction;Nucleus;Phosphoprotein;Protein transport;Reference proteome;Repeat;Transport;Ubl conjugation			7831767; 16641997; 15489334; 8052633; 7892216; 8692858; 7604027; 9463369; 12610148; 15942031; 16698996; 17652399; 17928350; 18691976; 19118899; 21269460; 21454664; 21385873; 22500989; 22814378; 23186163; 24275569; 29599122
155		3D-structure;Alternative splicing;Calcium;Direct protein sequencing;Disease variant;Disulfide bond;Endoplasmic reticulum;Glycoprotein;Hydrolase;Ichthyosis;Leukodystrophy;Lipid metabolism;Lysosome;Metachromatic leukodystrophy;Metal-binding;Reference proteome;Signal	DISEASE: Metachromatic leukodystrophy (MLD) [MIM:250100]: An autosomal recessive disease caused by abnormal intralysosomal accumulation of cerebroside-3-sulfate in central and peripheral nervous systems, as well as other organs. MLD is clinically characterized by leukodystrophy, progressive demyelination and a variety of neurological symptoms, including gait disturbances, ataxias, optical atrophy, dementia, seizures, and spastic tetraparesis. Decreased arylsulfatase A activity is detected in urine, leukocytes, and fibroblasts of affected individuals. Several forms of the disease can be distinguished according to the age at onset and disease severity: late infantile, juvenile and adult forms, partial cerebroside sulfate deficiency, and pseudoarylsulfatase A deficiency. Individuals with pseudoarylsulfatase A deficiency have low arylsulfatase A activity but lack neurological manifestations and are apparently healthy. {ECO:0000269|PubMed:10220151, ECO:0000269|PubMed:10381328, ECO:0000269|PubMed:10477432, ECO:0000269|PubMed:10533072, ECO:0000269|PubMed:10751093, ECO:0000269|PubMed:11020646, ECO:0000269|PubMed:11061266, ECO:0000269|PubMed:11456299, ECO:0000269|PubMed:11941485, ECO:0000269|PubMed:12503099, ECO:0000269|PubMed:12788103, ECO:0000269|PubMed:1353340, ECO:0000269|PubMed:14517960, ECO:0000269|PubMed:14680985, ECO:0000269|PubMed:15026521, ECO:0000269|PubMed:15326627, ECO:0000269|PubMed:15710861, ECO:0000269|PubMed:1670590, ECO:0000269|PubMed:1673291, ECO:0000269|PubMed:1678251, ECO:0000269|PubMed:18693274, ECO:0000269|PubMed:19606494, ECO:0000269|PubMed:20339381, ECO:0000269|PubMed:21265945, ECO:0000269|PubMed:2574462, ECO:0000269|PubMed:7581401, ECO:0000269|PubMed:7825603, ECO:0000269|PubMed:7860068, ECO:0000269|PubMed:7902317, ECO:0000269|PubMed:7906588, ECO:0000269|PubMed:7909527, ECO:0000269|PubMed:8095918, ECO:0000269|PubMed:8101038, ECO:0000269|PubMed:8101083, ECO:0000269|PubMed:8104633, ECO:0000269|PubMed:8891236, ECO:0000269|PubMed:9090526, ECO:0000269|PubMed:9272717, ECO:0000269|PubMed:9452102, ECO:0000269|PubMed:9490297, ECO:0000269|PubMed:9600244, ECO:0000269|PubMed:9819708}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Multiple sulfatase deficiency (MSD) [MIM:272200]: A clinically and biochemically heterogeneous disorder caused by the simultaneous impairment of all sulfatases, due to defective post-translational modification and activation. It combines features of individual sulfatase deficiencies such as metachromatic leukodystrophy, mucopolysaccharidosis, chondrodysplasia punctata, hydrocephalus, ichthyosis, neurologic deterioration and developmental delay. {ECO:0000269|PubMed:15146462}. Note=The protein represented in this entry is involved in disease pathogenesis. Arylsulfatase A activity is impaired in multiple sulfatase deficiency due to mutations in SUMF1 (PubMed:15146462). SUMF1 mutations result in defective post-translational modification of ARSA at residue Cys-69 that is not converted to 3-oxoalanine (PubMed:7628016). {ECO:0000269|PubMed:15146462, ECO:0000269|PubMed:7628016}.		2562955; 1975241; 19262745; 15461802; 14702039; 10591208; 15489334; 1352993; 7628016; 9342345; 15146462; 19159218; 24294900; 9521684; 11124905; 12888274; 16368756; 7866401; 2574462; 1673291; 1678251; 1670590; 1353340; 8101038; 8101083; 8095918; 7902317; 7906588; 8104633; 7909527; 7825603; 7860068; 7581401; 8891236; 8723680; 9272717; 9090526; 9490297; 9600244; 9744473; 9452102; 9819708; 9888390; 10220151; 10477432; 10533072; 10381328; 10751093; 11061266; 11020646; 11456299; 11941485; 12503099; 12788103; 14517960; 14680985; 15326627; 15026521; 15710861; 18693274; 19606494; 20339381; 21265945
156		3D-structure;Adaptive immunity;Alternative splicing;Calcium;Cell membrane;Disulfide bond;Glycoprotein;Host-virus interaction;Immunity;Innate immunity;Lectin;Membrane;Metal-binding;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			10438934; 11178971; 11994513; 16541075; 15489334; 18258799; 20530286; 21536857; 27015765
157		3D-structure;Acetylation;Adaptive immunity;Alternative splicing;Cytoplasm;Disease variant;Immunity;Innate immunity;Reference proteome;SH2 domain	DISEASE: Lymphoproliferative syndrome, X-linked, 1 (XLP1) [MIM:308240]: A rare immunodeficiency characterized by extreme susceptibility to infection with Epstein-Barr virus (EBV). Symptoms include severe or fatal mononucleosis, acquired hypogammaglobulinemia, pancytopenia and malignant lymphoma. {ECO:0000269|PubMed:10598819, ECO:0000269|PubMed:11034354, ECO:0000269|PubMed:11049992, ECO:0000269|PubMed:11477068, ECO:0000269|PubMed:11493483, ECO:0000269|PubMed:11823424, ECO:0000269|PubMed:12458214, ECO:0000269|PubMed:14674764, ECO:0000269|PubMed:15841490, ECO:0000269|PubMed:16720617, ECO:0000269|PubMed:9771704}. Note=The disease is caused by variants affecting the gene represented in this entry.		9771704; 9774102; 11282995; 14702039; 15772651; 15489334; 11389028; 11806999; 12115647; 12458214; 12545173; 19608861; 21219180; 10549287; 11823424; 12545174; 10598819; 11049992; 11034354; 11493483; 11477068; 14674764; 14583885; 15841490; 16720617
158		3D-structure;Coiled coil;Cytoplasm;Immunity;Innate immunity;Nucleus;Phosphoprotein;Reference proteome;Repressor;Transcription;Transcription regulation			14702039; 15489334; 12941847; 12581153; 14580347; 12832472; 15201869; 15169877; 16362050; 15713661; 15855166; 15965233; 16377779; 15940264; 15941832; 17088550; 17643375; 17452463; 17395637; 18669648; 19690332; 19883659; 20068231; 21269460; 21406692; 23186163; 28712728; 17724342
159		3D-structure;ATP-binding;Alternative splicing;Cell membrane;Cytoplasm;Immunity;Inflammatory response;Kinase;Magnesium;Me			7686153; 7983077; 8444877; 14702039; 15164054; 15489334; 8657160; 10636891; 10652356; 11342610; 11772397; 14988727; 15364919; 15254234; 16252004; 16356855; 16709830; 18691976; 19369195; 19549985;

		mbrane;Metal-binding;Nucleotide-binding;Phosphoprotein;Reference proteome;Repeat;Serine/threonine-protein kinase;Transferase;Zinc;Zinc-finger			11861617; 12473184; 15282562; 16978534; 17544292; 18328786; 19690332; 21269460; 21944869; 21406692; 23186163; 23509302; 24275569; 15364937; 17344846
160		3D-structure;Acetylation;Alternative splicing;Antioxidant;Cytoplasm;Direct protein sequencing;Disulfide bond;Endosome;Lipoprotein;Mitochondrion;Oxidoreductase;Palmitate;Peroxidase;Phosphoprotein;Redox-active center;Reference proteome;Transit peptide			7733872; 14702039; 15164054; 15489334; 1286669; 12059788; 12492477; 15750338; 17707404; 19462976; 19608861; 20873783; 21269460; 21850687; 24275569; 25944712; 27238969
161		3D-structure;Alternative splicing;Amyotrophic lateral sclerosis;Cell cycle;Cell division;Coiled coil;Cytoplasm;Cytoskeleton;Dynein;Microtubule;Mitosis;Neurodegeneration;Neuropathy;Nucleus;Parkinsonism;Phosphoprotein;Reference proteome;Transport;Ubl conjugation	DISEASE: Neuronopathy, distal hereditary motor, 7B (HMN7B) [MIM:607641]: A neuromuscular disorder. Distal hereditary motor neuronopathies constitute a heterogeneous group of neuromuscular disorders caused by selective degeneration of motor neurons in the anterior horn of the spinal cord, without sensory deficit in the posterior horn. The overall clinical picture consists of a classical distal muscular atrophy syndrome in the legs without clinical sensory loss. The disease starts with weakness and wasting of distal muscles of the anterior tibial and peroneal compartments of the legs. Later on, weakness and atrophy may expand to the proximal muscles of the lower limbs and/or to the distal upper limbs. {ECO:0000269|PubMed:12627231, ECO:0000269|PubMed:16505168, ECO:0000269|PubMed:19136952, ECO:0000269|PubMed:19279216, ECO:0000269|PubMed:22777741}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Amyotrophic lateral sclerosis (ALS) [MIM:105400]: A neurodegenerative disorder affecting upper motor neurons in the brain and lower motor neurons in the brain stem and spinal cord, resulting in fatal paralysis. Sensory abnormalities are absent. The pathologic hallmarks of the disease include pallor of the corticospinal tract due to loss of motor neurons, presence of ubiquitin-positive inclusions within surviving motor neurons, and deposition of pathologic aggregates. The etiology of amyotrophic lateral sclerosis is likely to be multifactorial, involving both genetic and environmental factors. The disease is inherited in 5-10% of the cases. {ECO:0000269|PubMed:15326253, ECO:0000269|PubMed:16240349}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.; DISEASE: Perry syndrome (PERRYS) [MIM:168605]: A neuropsychiatric disorder characterized by mental depression not responsive to antidepressant drugs or electroconvulsive therapy, sleep disturbances, exhaustion and marked weight loss. Parkinsonism develops later and respiratory failure occurred terminally. {ECO:0000269|PubMed:19136952, ECO:0000269|PubMed:23874158, ECO:0000269|PubMed:24676999, ECO:0000269|PubMed:24881494, ECO:0000269|PubMed:25185702, ECO:0000269|PubMed:26972003}. Note=The disease is caused by variants affecting the gene represented in this entry.		9799602; 14702039; 15815621; 15489334; 8838327; 8856662; 9805007; 14514668; 14654843; 16964243; 17532294; 18669648; 19935774; 19690332; 20682791; 20719959; 20978158; 20679239; 21269460; 22159412; 22261744; 22797915; 22327364; 23386061; 23509069; 23186163; 23985322; 24867236; 25189619; 24275569; 25774020; 26968983; 28394342; 16109370; 16949363; 17828277; 17828275; 12627231; 15326253; 16240349; 16505168; 17824900; 19136952; 19506225; 19279216; 22777741; 23874158; 24627108; 24676999; 25185702; 24881494; 26972003
162		3D-structure;Acetylation;Alternative initiation;Alternative splicing;Cytoplasm;Disease variant;Host-virus interaction;Initiation factor;Methylation;Neurodegeneration;Parkinson disease;Parkinsonism;Phosphoprotein;Protein biosynthesis;RNA-binding;Reference proteome;Translation regulation;Translational shunt	DISEASE: Parkinson disease 18 (PARK18) [MIM:614251]: An autosomal dominant, late-onset form of Parkinson disease. Parkinson disease is a complex neurodegenerative disorder characterized by bradykinesia, resting tremor, muscular rigidity and postural instability, as well as by a clinically significant response to treatment with levodopa. The pathology involves the loss of dopaminergic neurons in the substantia nigra and the presence of Lewy bodies (intraneuronal accumulations of aggregated proteins), in surviving neurons in various areas of the brain. {ECO:0000269|PubMed:21907011}. Note=The disease is caused by variants affecting the gene represented in this entry.		1429670; 9857202; 9418880; 12052860; 14702039; 17974005; 16641997; 9755181; 9372926; 7651417; 8396129; 7935836; 8521827; 8961935; 9755863; 10872469; 9878069; 10996799; 10970864; 11034318; 11154262; 15314025; 17081983; 16964243; 16513844; 17924679; 17284590; 18088087; 18799579; 18025107; 18669648; 19369195; 19690332; 19608861; 20068231; 21269460; 21576361; 21406692; 22872150; 22814378; 23186163; 24275569; 24129315; 24423872; 29062139; 19413330; 26740508; 12086624; 16698552; 16959974; 21907011
163		3D-structure;Alternative splicing;Cell membrane;Coiled coil;Cytoplasm;Membrane;Phosphoprotein;Reference proteome			14702039; 17974005; 15164054; 15489334; 15893754; 18337558; 23186163; 24275569
164		3D-structure;Cleavage on pair of basic residues;Disulfide bond;Glaucoma;Glycoprotein;Growth factor;Reference proteome;Secreted;Signal	DISEASE: Glaucoma 1, open angle, O (GLC1O) [MIM:613100]: A form of primary open angle glaucoma (POAG). POAG is characterized by a specific pattern of optic nerve and visual field defects. The angle of the anterior chamber of the eye is open, and usually the intraocular pressure is increased. However, glaucoma can occur at any intraocular pressure. The disease is generally asymptomatic until the late stages, by which time significant and irreversible optic nerve damage has already taken place. {ECO:0000269|PubMed:19765683, ECO:0000269|PubMed:20215012}. Note=Disease susceptibility may be associated with variants affecting the gene represented in this entry.		1742028; 1313578; 15489334; 10631974; 19765683; 20215012
165		3D-structure;Cytokine;Direct protein sequencing;Disulfide bond;EGF-like domain;Glycoprotein;Growth factor;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix			2325643; 15815621; 15489334; 2466334; 3413110; 2017164; 1333777; 22967896; 7679104; 17607000;
166		3D-structure;ATP-binding;Alternative splicing;Chromosome;Cytoplasm;Differentiation;Kinase;Nucleotide-binding;Nucleus;Phosphoprotein;Reference proteome;Serine/threonine-protein kinase;Transferase;mRNA processing;mRNA splicing			9472028; 12853948; 15489334; 12134018; 15144186; 16122776; 16964243; 18559500; 18691976; 18425142; 18669648; 19413330; 19592491; 19690332; 20068231; 21269460; 21157427; 21205200; 21056976; 21406692; 23186163; 24275569; 28076779; 17344846
167		3D-structure;Alternative splicing;Autism;Autism spectrum disorder;Cell adhesion;Cell junction;Cell projection;Chromosomal rearrangement;Disulfide bond;EGF-like domain;Epilepsy;Glycoprotein;Membrane;Mental	DISEASE: Autism 15 (AUTS15) [MIM:612100]: A complex multifactorial, pervasive developmental disorder characterized by impairments in reciprocal social interaction and communication, restricted and stereotyped patterns of interests and activities, and the presence of developmental abnormalities by 3 years of age. Most individuals with autism also manifest moderate mental retardation. {ECO:0000269|PubMed:18179895}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.; DISEASE: Note=A chromosomal aberration involving CNTNAP2 is found in a patient with autism spectrum disorder. Paracentric inversion 46,XY,inv(7)(q11.22;q35). The inversion breakpoints disrupt the genes AUTS2 and		10624965; 11352571; 10048485; 17974005; 15489334; 16571880; 19896112; 33238150; 18179895; 19690332

		retardation;Phosphoprotein;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	CNTNAP2.; DISEASE: Pitt-Hopkins-like syndrome 1 (PTHSL1) [MIM:610042]: A syndrome characterized by severe mental retardation and variable additional symptoms, such as impaired speech development, seizures, autistic behavior, breathing anomalies and a broad mouth, resembling Pitt-Hopkins syndrome. In contrast to patients with Pitt-Hopkins syndrome, PTHSL1 patients present with normal or only mildly to moderately delayed motor milestones. {ECO:0000269|PubMed:16571880, ECO:0000269|PubMed:19896112}. Note=The disease is caused by variants affecting the gene represented in this entry.		
168		Alternative splicing;Glycoprotein;Ion channel;Ion transport;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix;Transport			11342114; 11756660; 11042152; 12975309; 15057824; 15489334
169		3D-structure;Alternative splicing;Cell membrane;Cell projection;Cytoplasm;Cytoskeleton;Deafness;Disease variant;Membrane;Nucleus;Phosphoprotein;Reference proteome;Tumor suppressor;Ubl conjugation	DISEASE: Neurofibromatosis 2 (NF2) [MIM:101000]: Genetic disorder characterized by bilateral vestibular schwannomas (formerly called acoustic neuromas), schwannomas of other cranial and peripheral nerves, meningiomas, and ependymomas. It is inherited in an autosomal dominant fashion with full penetrance. Affected individuals generally develop symptoms of eighth-nerve dysfunction in early adulthood, including deafness and balance disorder. Although the tumors of NF2 are histologically benign, their anatomic location makes management difficult, and patients suffer great morbidity and mortality. {ECO:0000269|PubMed:10090912, ECO:0000269|PubMed:10669747, ECO:0000269|PubMed:10790209, ECO:0000269|PubMed:12709270, ECO:0000269|PubMed:20178741, ECO:0000269|PubMed:20445339, ECO:0000269|PubMed:7666400, ECO:0000269|PubMed:7759081, ECO:0000269|PubMed:7913580, ECO:0000269|PubMed:8081368, ECO:0000269|PubMed:8230593, ECO:0000269|PubMed:8566958, ECO:0000269|PubMed:8698340, ECO:0000269|PubMed:9643284}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Schwannomatosis 1 (SWNTS1) [MIM:162091]: A cancer syndrome in which patients develop multiple non-vestibular schwannomas, benign neoplasms that arise from Schwann cells of the cranial, peripheral, and autonomic nerves. {ECO:0000269|PubMed:18072270}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Mesothelioma, malignant (MESOM) [MIM:156240]: An aggressive neoplasm of the serosal lining of the chest. It appears as broad sheets of cells, with some regions containing spindle-shaped, sarcoma-like cells and other regions showing adenomatous patterns. Pleural mesotheliomas have been linked to exposure to asbestos. {ECO:0000269|PubMed:12136076}. Note=The disease may be caused by variants affecting the gene represented in this entry.		8453669; 8379998; 9817927; 10401006; 11827459; 15461802; 15489334; 9430655; 10861283; 10669747; 12136076; 15541357; 15598747; 17081983; 18332868; 18669648; 19144871; 20178741; 20159598; 20159599; 21269460; 21167305; 23186163; 11856822; 8230593; 7913580; 8004107; 8012353; 8081368; 7951231; 8162073; 7759081; 7666400; 8566958; 8655144; 8698340; 9643284; 10090912; 10790209; 12709270; 16959974; 18072270; 20445339
170		3D-structure;Alternative splicing;Calcium;Direct protein sequencing;Disease variant;Disulfide bond;Dwarfism;EGF-like domain;Extracellular matrix;Glycoprotein;Immunoglobulin domain;Lectin;Metal-binding;Proteoglycan;Reference proteome;Repeat;Secreted;Signal;Sushi	DISEASE: Spondyloepiphyseal dysplasia type Kimberley (SEDK) [MIM:608361]: Spondyloepiphyseal dysplasias are a heterogeneous group of congenital chondrodysplasias that specifically affect epiphyses and vertebrae. The autosomal dominant SEDK is associated with premature degenerative arthropathy. {ECO:0000269|PubMed:16080123}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Spondyloepimetaphyseal dysplasia, aggrecan type (SEMDAG) [MIM:612813]: A bone disease characterized by severe short stature, macrocephaly, severe midface hypoplasia, short neck, barrel chest and brachydactyly. The radiological findings comprise long bones with generalized irregular epiphyses with widened metaphyses, especially at the knees, platyspondyly, and multiple cervical-vertebral clefts. {ECO:0000269|PubMed:19110214}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Short stature and advanced bone age, with or without early-onset osteoarthritis and/or osteochondritis dissecans (SSOAOD) [MIM:165800]: An autosomal dominant disease characterized by short stature, advanced bone maturation, early-onset osteoarthritis, and mild dysmorphic features consisting of midface hypoplasia, brachydactyly, broad great toes, and lumbar lordosis. Other features include intervertebral disk disease and osteochondritis dissecans. Osteochondritis dissecans is defined as a separation of cartilage and subchondral bone from the surrounding tissue. {ECO:0000269|PubMed:20137779}. Note=The disease is caused by variants affecting the gene represented in this entry.		1985970; 16572171; 15489334; 7574678; 1569188; 7524681; 8216415; 7827755; 8611178; 2789216; 16080123; 16335952; 17588949; 19110214; 20137779
171		Alternative splicing;Disulfide bond;Glycoprotein;Membrane;Phosphoprotein;Reference proteome;Signal;Transmembrane;Transmembrane helix			11447234; 11973641; 16641997; 15489334; 18669648
172		Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix	DISEASE: Rheumatoid arthritis (RA) [MIM:180300]: An inflammatory disease with autoimmune features and a complex genetic component. It primarily affects the joints and is characterized by inflammatory changes in the synovial membranes and articular structures, widespread fibrinoid degeneration of the collagen fibers in mesenchymal tissues, and by atrophy and rarefaction of bony structures. {ECO:0000269|PubMed:15838509, ECO:0000269|PubMed:16176992, ECO:0000269|PubMed:16476711, ECO:0000269|PubMed:16859508, ECO:0000269|PubMed:17133579, ECO:0000269|PubMed:17179172, ECO:0000269|PubMed:17763442, ECO:0000269|PubMed:22392608, ECO:0000269|PubMed:26746625}. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.; DISEASE: Note=Genetic variation in FCRL3 may influence susceptibility to autoimmune disorders, including Graves disease or multiple sclerosis. Graves disease is an autoimmune disorder associated with overactivity of the thyroid gland and hyperthyroidism. Multiple sclerosis is an autoimmune/inflammatory neurodegenerative disease which mainly affects young adults and is characterized by destruction of myelin in the central nervous system. {ECO:0000269|PubMed:15838509, ECO:0000269|PubMed:16384851, ECO:0000269|PubMed:17952073, ECO:0000269|PubMed:25862376, ECO:0000269|PubMed:26629249}.		11493702; 12051764; 14702039; 16710414; 15489334; 11929751; 15838509; 16176992; 16476711; 16859508; 17133579; 16849395; 16384851; 17179172; 17763442; 17952073; 19843936; 19494275; 20190142; 22392608; 23857366; 26629249; 26746625; 25862376; 16959974
173		Alternative splicing;Cell membrane;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Phosphoprotein;Receptor;Reference proteome;Repeat;Signal;Transmembrane;Transmembrane helix			17213291; 14702039; 16710414; 18991291; 20519654; 20933011
174		3D-structure;Activator;DNA-binding;Nucleus;Phosphoprotein;Reference proteome;Repressor;Transcription;Transcription regulation;Ubl conjugation			9544839; 9479503; 14702039; 10830953; 15489334; 16964243; 18669648; 23186163; 24035498;
175		3D-structure;Alternative splicing;Cell			9721204; 10201933; 9712866; 17207242; 14702039; 16572171; 15489334; 10416131;

		membrane;Developmental protein;Differentiation;Disulfide bond;GPI-anchor;Glycoprotein;Immunoglobulin domain;Inflammatory response;Lipoprotein;Membrane;Methylation;Neurogenesis;Reference proteome;Signal			12879062; 17377534; 17671519; 20727575; 20854351
176		3D-structure;Acetylation;Activator;Alternative splicing;Cytoplasm;DNA-binding;Developmental protein;Direct protein sequencing;Nucleus;Phosphoprotein;Reference proteome;Repeat;Transcription;Transcription regulation			7749981; 7739550; 9759864; 10493829; 15489334; 9630228; 10089876; 18815128; 23186163
177		3D-structure;Direct protein sequencing;Disulfide bond;Glycoprotein;Immunoglobulin domain;Membrane;Reference proteome;Signal;Transmembrane;Transmembrane helix			1378080; 8422464; 14574404; 15489334; 15340161; 18669648; 19349973
178		3D-structure;Alternative splicing;Autocatalytic cleavage;Calcium;Complement activation lectin pathway;Direct protein sequencing;Disease variant;Disulfide bond;EGF-like domain;Glycoprotein;Hydrolase;Hydroxylation;Immunity;Innate immunity;Metal-binding;Protease;Reference proteome;Repeat;Secreted;Serine protease;Signal;Sushi	DISEASE: 3MC syndrome 1 (3MC1) [MIM:257920]: A form of 3MC syndrome, an autosomal recessive disorder characterized by facial dysmorphism, craniosynostosis, learning disability, and genital, limb and vesicorenal anomalies. Facial features include hypertelorism, blepharophimosis, blepharoptosis and highly arched eyebrows, cleft lip and/or palate. The term 3MC syndrome includes Carnevale, Mingarelli, Malpuech, and Michels syndromes. {ECO:0000269|PubMed:21258343, ECO:0000269|PubMed:26419238, ECO:0000269|PubMed:28301481}. Note=The disease is caused by variants affecting the gene represented in this entry.		8240317; 8018603; 8921412; 10475605; 11485744; 14702039; 17974005; 16641997; 15489334; 11290788; 9367419; 9087411; 10679061; 10878362; 10946292; 11527969; 11907111; 12421953; 12538697; 15034049; 16335952; 16554018; 17182967; 19139490; 20956340; 18596036; 21258343; 26419238; 28301481
179		3D-structure;Adaptive immunity;Calcium;Cell membrane;Disulfide bond;Glycoprotein;Immunity;Innate immunity;Lectin;Membrane;Metal-binding;Reference proteome;Signal-anchor;Transmembrane;Transmembrane helix			14971047; 15368084; 15489334; 23602766; 23911656; 24101491
180		3D-structure;Alternative splicing;Cleavage on pair of basic residues;Direct protein sequencing;Disulfide bond;Hypotrichosis;Ichthyosis;Protease inhibitor;Reference proteome;Repeat;Secreted;Serine protease inhibitor;Signal	DISEASE: Netherton syndrome (NETH) [MIM:256500]: An autosomal recessive congenital ichthyosis associated with hair shaft abnormalities and anomalies of the immune system. Typical features are ichthyosis linearis circumflexa, ichthyosiform erythroderma, trichorrhexis invaginata (bamboo hair), atopic dermatitis, and hayfever. High postnatal mortality is due to failure to thrive, infections and hypernatremic dehydration. {ECO:0000269|PubMed:10835624}. Note=The disease is caused by variants affecting the gene represented in this entry.		10419450; 10835624; 16374478; 15372022; 11511292; 11594460; 17596512; 20533828; 12684009; 15366933; 11544479
181		3D-structure;Acetylation;Direct protein sequencing;Disease variant;Dwarfism;Endoplasmic reticulum;Glycoprotein;Isomerase;Osteogenesis imperfecta;Reference proteome;Rotamase;S-nitrosylation;Signal;Virion	DISEASE: Osteogenesis imperfecta 9 (OI9) [MIM:259440]: A form of osteogenesis imperfecta, a connective tissue disorder characterized by low bone mass, bone fragility and susceptibility to fractures after minimal trauma. Disease severity ranges from very mild forms without fractures to intrauterine fractures and perinatal lethality. Extraskeletal manifestations, which affect a variable number of patients, are dentinogenesis imperfecta, hearing loss, and blue sclerae. OI9 is a severe autosomal recessive form of the disorder. {ECO:0000269|PubMed:19781681, ECO:0000269|PubMed:20089953}. Note=The disease is caused by variants affecting the gene represented in this entry.		2040592; 14702039; 16572171; 15489334; 2000394; 1710767; 12475965; 1286667; 1530944; 17081065; 19781681; 20147391; 20676357; 21269460; 21280149; 24275569; 25944712; 8197205; 20801878; 20089953
182		3D-structure;Alternative splicing;Alzheimer disease;Amyloid;Amyloidosis;Apoptosis;Cell adhesion;Cell membrane;Cell projection;Coated pit;Copper;Cytoplasm;Cytoplasmic vesicle;Direct protein sequencing;Disease variant;Disulfide bond;Endocytosis;Endoplasmic reticulum;Endosome;Glycoprotein;Golgi apparatus;Heparin-binding;Iron;Isopeptide bond;Membrane;Metal-binding;Neurodegeneration;Notch signaling pathway;Nucleus;Oxidation;Phosphoprotein;Protease inhibitor;Proteoglycan;Reference proteome;Secreted;Serine protease inhibitor;Signal;Sulfation;Transmembrane;Transmembrane helix;Ubl conjugation;Zinc	DISEASE: Alzheimer disease 1 (AD1) [MIM:104300]: A familial early-onset form of Alzheimer disease. It can be associated with cerebral amyloid angiopathy. Alzheimer disease is a neurodegenerative disorder characterized by progressive dementia, loss of cognitive abilities, and deposition of fibrillar amyloid proteins as intraneuronal neurofibrillary tangles, extracellular amyloid plaques and vascular amyloid deposits. The major constituents of these plaques are neurotoxic amyloid-beta protein 40 and amyloid-beta protein 42, that are produced by the proteolysis of the transmembrane APP protein. The cytotoxic C-terminal fragments (CTFs) and the caspase-cleaved products, such as C31, are also implicated in neuronal death. {ECO:0000269|PubMed:10097173, ECO:0000269|PubMed:10631141, ECO:0000269|PubMed:10656250, ECO:0000269|PubMed:10665499, ECO:0000269|PubMed:10677483, ECO:0000269|PubMed:10867787, ECO:0000269|PubMed:11063718, ECO:0000269|PubMed:11311152, ECO:0000269|PubMed:11528419, ECO:0000269|PubMed:12034808, ECO:0000269|PubMed:1302033, ECO:0000269|PubMed:1303239, ECO:0000269|PubMed:1303275, ECO:0000269|PubMed:1415269, ECO:0000269|PubMed:1465129, ECO:0000269|PubMed:15201367, ECO:0000269|PubMed:15365148, ECO:0000269|PubMed:15668448, ECO:0000269|PubMed:1671712, ECO:0000269|PubMed:1678058, ECO:0000269|PubMed:1908231, ECO:0000269|PubMed:1925564, ECO:0000269|PubMed:1944558, ECO:0000269|PubMed:8267572, ECO:0000269|PubMed:8290042, ECO:0000269|PubMed:8476439, ECO:0000269|PubMed:8577393, ECO:0000269|PubMed:8886002, ECO:0000269|PubMed:9328472, ECO:0000269|PubMed:9754958}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Cerebral amyloid angiopathy, APP-related (CAA-APP) [MIM:605714]: A hereditary localized amyloidosis due to amyloid-beta A4 peptide(s) deposition in the cerebral vessels. The principal clinical characteristics are recurrent cerebral and cerebellar hemorrhages, recurrent strokes, cerebral ischemia, cerebral infarction, and progressive mental deterioration. Patients develop cerebral hemorrhage because of the severe cerebral amyloid angiopathy. Parenchymal amyloid deposits are rare and largely in the form of pre-amyloid lesions or diffuse plaque-like structures. They are Congo red negative and lack the dense amyloid cores commonly present in Alzheimer disease. Some affected individuals manifest progressive aphasic dementia, leukoencephalopathy, and occipital calcifications. {ECO:0000269|PubMed:11409420, ECO:0000269|PubMed:12654973, ECO:0000269|PubMed:16178030, ECO:0000269|PubMed:20697050, ECO:0000269|PubMed:2111584}. Note=The disease is caused by variants affecting the gene represented in this entry.		2881207; 2893289; 2783775; 2110105; 1908403; 1587857; 9108164; 12859342; 14702039; 10830953; 15489334; 3140222; 2538123; 3597385; 12665801; 2893290; 2893291; 2893379; 8576160; 8476439; 2675837; 15201367; 3312495; 1406936; 8229004; 8248178; 8109908; 3810169; 2949367; 22576872; 16816112; 2569763; 3035574; 2900137; 2649245; 2506449; 1969731; 8344894; 8446172; 8131745; 7913895; 8158260; 7737970; 8626687; 8887653; 8855266; 9168929; 9357988; 9338779; 9585534; 9843960; 10413512; 10319819; 10535332; 10341243; 9890987; 10383380; 10461923; 10656250; 10081969; 10816430; 10681545; 12214090; 11775062; 11689470; 11278849; 11274207; 11438549; 11544248; 11238726; 11943163; 11724784; 11784781; 12032279; 8999878; 10806211; 10742146; 11517218; 11146006; 11851430; 11877420; 12142279; 14527950; 15084524; 15347684; 16335952; 16174740; 16407538; 17062754; 17855360; 18468999; 19366692; 19225519; 19901339; 20580937; 20811458; 21269460; 21712440; 23011729; 22457725; 24275569; 24336208; 25168729; 24523320; 26091039; 28720718; 2125487; 1718421; 7516706; 7588758; 8973180; 9300481; 9693002; 10201399; 10821838; 10940221; 10940222; 12611883; 15304215; 17051221; 17909280; 17239395; 17895381; 19923222; 20212142; 22584060; 22654059; 25122912; 26898943; 28570778; 28882996; 29282295; 30630874; 1363811; 2111584; 1671712; 1908231; 1678058; 1944558; 1925564; 1415269; 1303239; 1302033; 1465129; 1307241; 1303275; 8267572; 8154870; 8290042; 8577393; 8886002; 9328472; 9754958; 10097173; 10631141; 10665499; 10867787; 11063718; 10677483; 11409420; 11311152; 11528419; 12034808; 12654973; 15365148;

					16178030; 15668448; 20697050
183		3D-structure;Alternative splicing;Cytoplasm;Direct protein sequencing;Disease variant;Disulfide bond;Gangliosidosis;Glycoprotein;Glycosidase;Hydrolase;Lysosome;Mucopolysaccharidosis;Reference proteome;Signal;Zymogen	DISEASE: GM1-gangliosidosis 1 (GM1G1) [MIM:230500]: An autosomal recessive lysosomal storage disease marked by the accumulation of GM1 gangliosides, glycoproteins and keratan sulfate primarily in neurons of the central nervous system. GM1-gangliosidosis type 1 is characterized by onset within the first three months of life, central nervous system degeneration, coarse facial features, hepatosplenomegaly, skeletal dysmorphology reminiscent of Hurler syndrome, and rapidly progressive psychomotor deterioration. Urinary oligosaccharide levels are high. It leads to death usually between the first and second year of life. {ECO:0000269|PubMed:10338095, ECO:0000269|PubMed:10737981, ECO:0000269|PubMed:10839995, ECO:0000269|PubMed:1487238, ECO:0000269|PubMed:15365997, ECO:0000269|PubMed:15714521, ECO:0000269|PubMed:15791924, ECO:0000269|PubMed:16538002, ECO:0000269|PubMed:16941474, ECO:0000269|PubMed:17309651, ECO:0000269|PubMed:17664528, ECO:0000269|PubMed:1907800, ECO:0000269|PubMed:1909089, ECO:0000269|PubMed:1928092, ECO:0000269|PubMed:19472408, ECO:0000269|PubMed:24737316, ECO:0000269|PubMed:25936995, ECO:0000269|PubMed:8213816, ECO:0000269|Ref.28, ECO:0000269|Ref.31}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: GM1-gangliosidosis 2 (GM1G2) [MIM:230600]: A gangliosidosis characterized by onset between ages 1 and 5. The main symptom is locomotor ataxia, ultimately leading to a state of decerebration with epileptic seizures. Patients do not display the skeletal changes associated with the infantile form, but they nonetheless excrete elevated amounts of beta-linked galactose-terminal oligosaccharides. Inheritance is autosomal recessive. {ECO:0000269|PubMed:10737981, ECO:0000269|PubMed:12644936, ECO:0000269|PubMed:15714521, ECO:0000269|PubMed:16941474, ECO:0000269|PubMed:17309651, ECO:0000269|PubMed:1907800, ECO:0000269|PubMed:1909089, ECO:0000269|PubMed:19472408, ECO:0000269|PubMed:24737316, ECO:0000269|PubMed:25936995, ECO:0000269|PubMed:8213816}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: GM1-gangliosidosis 3 (GM1G3) [MIM:230650]: A gangliosidosis with a variable phenotype. Patients show mild skeletal abnormalities, dysarthria, gait disturbance, dystonia and visual impairment. Visceromegaly is absent. Intellectual deficit can initially be mild or absent but progresses over time. Inheritance is autosomal recessive. {ECO:0000269|PubMed:11511921, ECO:0000269|PubMed:15986423, ECO:0000269|PubMed:16941474, ECO:0000269|PubMed:17309651, ECO:0000269|PubMed:17664528, ECO:0000269|PubMed:1907800, ECO:0000269|PubMed:1909089, ECO:0000269|PubMed:19472408, ECO:0000269|PubMed:24737316, ECO:0000269|PubMed:25936995, ECO:0000269|PubMed:8198123, ECO:0000269|Ref.28, ECO:0000269|Ref.30}. Note=The disease is caused by variants affecting the gene represented in this entry.; DISEASE: Mucopolysaccharidosis 4B (MPS4B) [MIM:253010]: A form of mucopolysaccharidosis type 4, an autosomal recessive lysosomal storage disease characterized by intracellular accumulation of keratan sulfate and chondroitin-6-sulfate. Key clinical features include short stature, skeletal dysplasia, dental anomalies, and corneal clouding. Intelligence is normal and there is no direct central nervous system involvement, although the skeletal changes may result in neurologic complications. There is variable severity, but patients with the severe phenotype usually do not survive past the second or third decade of life. {ECO:0000269|PubMed:11511921, ECO:0000269|PubMed:12393180, ECO:0000269|PubMed:16538002, ECO:0000269|PubMed:16941474, ECO:0000269|PubMed:17664528, ECO:0000269|PubMed:1928092, ECO:0000269|PubMed:19472408, ECO:0000269|PubMed:7586649}. Note=The disease is caused by variants affecting the gene represented in this entry.		3143362; 2511208; 2111707; 14702039; 16641997; 15489334; 3084261; 8383699; 8200356; 8922281; 9497360; 10571006; 10841810; 16263699; 19159218; 21269460; 24275569; 25944712; 22128166; 24737316; 1928092; 1909089; 1907800; 1487238; 8213816; 8198123; 7586649; 9203065; 12393180; 10338095; 10839995; 10737981; 11511921; 12644936; 15365997; 15714521; 15791924; 15986423; 16941474; 16538002; 17309651; 17661814; 17664528; 19472408; 25936995
184		3D-structure;Alternative splicing;Direct protein sequencing;Disease variant;Glycoprotein;Glycosidase;Hydrolase;Lysosome;Mucopolysaccharidosis;Reference proteome;Signal	DISEASE: Mucopolysaccharidosis 7 (MPS7) [MIM:253220]: An autosomal recessive lysosomal storage disease characterized by inability to degrade glucuronic acid-containing glycosaminoglycans. The phenotype is highly variable, ranging from severe lethal hydrops fetalis to mild forms with survival into adulthood. Most patients with the intermediate phenotype show hepatomegaly, skeletal anomalies, coarse facies, and variable degrees of mental impairment. {ECO:0000269|PubMed:12522561, ECO:0000269|PubMed:12859417, ECO:0000269|PubMed:1702266, ECO:0000269|PubMed:7573038, ECO:0000269|PubMed:7633414, ECO:0000269|PubMed:7680524, ECO:0000269|PubMed:8089138, ECO:0000269|PubMed:8111412, ECO:0000269|PubMed:8111413, ECO:0000269|PubMed:8644704, ECO:0000269|PubMed:8707294, ECO:0000269|PubMed:9099834, ECO:0000269|PubMed:9490302}. Note=The disease is caused by variants affecting the gene represented in this entry.		3468507; 14702039; 12853948; 12690205; 15489334; 1916806; 1311180; 3924735; 11568288; 12754519; 16335952; 19159218; 24275569; 25944712; 8599764; 19224584; 8111412; 8111413; 1702266; 7680524; 8089138; 7573038; 7633414; 8644704; 8707294; 9099834; 9490302; 12859417; 12522561