Supplementary Table S1

GeneName	Database
PLA2G2A	OMIM
EPHB2	OMIM
MUTYH	OMIM
RAD54L	OMIM
BCAR3	OMIM
AMY2B	OMIM
AMY2A	OMIM
NRAS	OMIM
FALEC	OMIM
FASLG	OMIM
RNASEL	OMIM
BLACAT1	OMIM
PCAP	OMIM
FH	OMIM
SDCCAG8	OMIM
GACAT3	OMIM
EPCAM	OMIM
MSH2	OMIM
MSH6	OMIM
EHBP1	OMIM
REGL	OMIM
REG1A	OMIM
C2orf40	OMIM
BUB1	OMIM
LCO	OMIM
IL1B	OMIM
IL1RN	OMIM
SCHLAP1	OMIM
DIRC1	OMIM
CASP10	OMIM
CASP8	OMIM
BARD1	OMIM
HPC5	OMIM
OVCAS1	OMIM
ST11	OMIM
TGFBR2	OMIM
SCLC1	OMIM
MLH1	OMIM
DLEC1	OMIM
CTNNB1	OMIM
RASSF1	OMIM
NPHP3	OMIM

ATR	OMIM
PIK3CA	OMIM
EIF4G1	OMIM
LNCR5	OMIM
FGFR3	OMIM
PCAT4	OMIM
ADH1B	OMIM
TLR2	OMIM
PALLD	OMIM
KMHN1	OMIM
LNCR3	OMIM
DAB2	OMIM
APC	OMIM
MCC	OMIM
IRF1	OMIM
SPINK1	OMIM
HMMR	OMIM
FGFR4	OMIM
NQO2	OMIM
CTAG3	OMIM
HULC	OMIM
CASC15	OMIM
LNCR4	OMIM
PBCA	OMIM
CLPS	OMIM
LNCR1	OMIM
PBOV1	OMIM
ESR1	OMIM
MAD1L1	OMIM
PMS2	OMIM
MACC1	OMIM
HPC4	OMIM
EGFR	OMIM
VOPP1	OMIM
HIP1	OMIM
PTPN12	OMIM
GAEC1	OMIM
CPA2	OMIM
BRAF	OMIM
MNX1	OMIM
DLC1	OMIM
MSR1	OMIM
PDGFRL	OMIM
DBC1	OMIM

C8orf4	OMIM
RB1CC1	OMIM
RAD54B	OMIM
CRCS6	OMIM
CRCS2	OMIM
HPC10	OMIM
PCAT1	OMIM
PRNCR1	OMIM
CDKN2A	OMIM
PCA3	OMIM
FOXE1	OMIM
GALNT12	OMIM
1-Dec	OMIM
KLF6	OMIM
CRCS5	OMIM
PTF1A	OMIM
GAD2	OMIM
MAP3K8	OMIM
MSMB	OMIM
PPYR1	OMIM
ERCC6	OMIM
SNCG	OMIM
PTEN	OMIM
MXI1	OMIM
HABP2	OMIM
PNLIP	OMIM
PNLIPRP1	OMIM
PNLIPRP2	OMIM
CASC2	OMIM
FGFR2	OMIM
HRAS	OMIM
SLC22A1L	OMIM
TSG101	OMIM
CD82	OMIM
PTPRJ	OMIM
HPC14	OMIM
BRMS1	OMIM
CCND1	OMIM
ORAOV1	OMIM
CTTN	OMIM
GCRG224	OMIM
ATM	OMIM
BRCATA	OMIM
CRCS7	OMIM

TSG11	OMIM
COLCA1	OMIM
COLCA2	OMIM
PPP2R1B	OMIM
HEPN1	OMIM
OPCML	OMIM
CASC1	OMIM
KRAS	OMIM
ACVR1B	OMIM
SRGAP1	OMIM
ALDH2	OMIM
PLA2G1B	OMIM
CDK2AP1	OMIM
POLE1	OMIM
PDX1	OMIM
BRCA2	OMIM
RB1	OMIM
BRCA3	OMIM
RNASE1	OMIM
NKX2-1	OMIM
CRCS8	OMIM
MLH3	OMIM
XRCC3	OMIM
AKT1	OMIM
HPC7	OMIM
BUB1B	OMIM
RAD51A	OMIM
HMPS1	OMIM
PCAT29	OMIM
CHRNA5	OMIM
CHRNA3	OMIM
IQGAP1	OMIM
BCAR4	OMIM
PALB2	OMIM
CRCS9	OMIM
CDH1	OMIM
NQO1	OMIM
ZFHX3	OMIM
BCAR1	OMIM
BCPR	OMIM
DPH1	OMIM
OVCA2	OMIM
HIC1	OMIM
TP53	OMIM

ELAC2	OMIM
FLCN	OMIM
PPY2	OMIM
NEK8	OMIM
HPC11	OMIM
RAD51D	OMIM
ERBB2	OMIM
HPC9	OMIM
BRCA1	OMIM
PPY	OMIM
PHB	OMIM
MPO	OMIM
RNF43	OMIM
RAD51C	OMIM
PTRH2	OMIM
PPM1D	OMIM
BRIP1	OMIM
AXIN2	OMIM
C17orf28	OMIM
RHBDF2	OMIM
GACAT2	OMIM
GATA6	OMIM
RBBP8	OMIM
SMAD7	OMIM
SMAD4	OMIM
DCC	OMIM
MIR1290	DisGeNET
KLF10	DisGeNET
ANXA8	DisGeNET
MAPK1	DisGeNET
PIK3CG	DisGeNET
PIK3CD	DisGeNET
PIK3CB	DisGeNET
GPC1	DisGeNET
ANXA8L1	DisGeNET

Supplementary Table S2

Order	Term	Name
1	GO:0042476	odontogenesis
2	GO:0009368	endopeptidase Clp complex
3	GO:0071786	endoplasmic reticulum tubular network organization
4	GO:0014043	negative regulation of neuron maturation
5	GO:0000439	core TFIIH complex
6	GO:0034101	erythrocyte homeostasis
7	GO:0048668	collateral sprouting
8	GO:0048149	behavioral response to ethanol
9	GO:0060670	branching involved in labyrinthine layer morphogenesis
10	GO:0070436	Grb2-EGFR complex
11	KEGG:Type_II_diabetes_mellitus	
12	GO:0005765	lysosomal membrane
13	KEGG:Regulation_of_autophagy	
14	GO:0031902	late endosome membrane
15	GO:0060136	embryonic process involved in female pregnancy
16	GO:0008373	sialyltransferase activity
17	GO:0001547	antral ovarian follicle growth
18	GO:1902336	positive regulation of retinal ganglion cell axon guidance
19	GO:0042022	interleukin-12 receptor complex
20	GO:0005849	mRNA cleavage factor complex
21	GO:0060100	positive regulation of phagocytosis, engulfment
22	GO:0035881	amacrine cell differentiation
23	GO:0031665	negative regulation of lipopolysaccharide-mediated signaling pathway
24	GO:0048485	sympathetic nervous system development
25	GO:0001931	uropod
26	GO:0008046	axon guidance receptor activity
27	GO:0005497	androgen binding
28	GO:0032729	positive regulation of interferon-gamma production
29	GO:2000377	regulation of reactive oxygen species metabolic process
30	GO:0005977	glycogen metabolic process
31	GO:0033630	positive regulation of cell adhesion mediated by integrin
32	GO:0007292	female gamete generation
33	GO:0050658	RNA transport
34	GO:0048609	multicellular organismal reproductive process

35	GO:0070742	C2H2 zinc finger domain binding
36	GO:0000012	single strand break repair
37	GO:0035605	peptidyl-cysteine S-nitrosylase activity
38	GO:0042613	MHC class II protein complex
39	GO:0001849	complement component C1q binding
40	GO:0001556	oocyte maturation
41	GO:0031668	cellular response to extracellular stimulus
42	GO:0031223	auditory behavior
43	GO:0032302	MutSbeta complex
44	GO:0034113	heterotypic cell-cell adhesion
45	GO:0005112	Notch binding
46	GO:0051276	chromosome organization
47	GO:0034063	stress granule assembly
48	GO:0061198	fungiform papilla formation
49	GO:0060736	prostate gland growth
50	GO:0048703	embryonic viscerocranium morphogenesis
51	GO:0048843	negative regulation of axon extension involved in axon guidance
52	GO:0000075	cell cycle checkpoint
53	GO:0032481	positive regulation of type I interferon production
54	GO:0016331	morphogenesis of embryonic epithelium
55	GO:0048408	epidermal growth factor binding
56	KEGG:Circadian_rhythm	
57	GO:1902204	positive regulation of hepatocyte growth factor receptor signaling pathway
58	KEGG:Neuroactive_ligand_receptor_interaction	
59	GO:0031214	biomineral tissue development
60	GO:0033993	response to lipid
61	GO:0002686	negative regulation of leukocyte migration
62	GO:0010181	FMN binding
63	GO:0071000	response to magnetism
64	GO:0070087	chromo shadow domain binding
65	GO:0060206	estrous cycle phase
66	GO:0030666	endocytic vesicle membrane
67	GO:0006311	meiotic gene conversion
68	GO:0090259	regulation of retinal ganglion cell axon guidance
69	GO:0002031	G-protein coupled receptor internalization
70	GO:0030276	clathrin binding
71	GO:0048733	sebaceous gland development
72	GO:0003995	acyl-CoA dehydrogenase activity
73	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity

74	GO:0052856	NADHX epimerase activity
75	GO:0001786	phosphatidylserine binding
76	GO:0072588	box H/ACA RNP complex
77	GO:0000266	mitochondrial fission
78	GO:1901165	positive regulation of trophoblast cell migration
79	GO:0060005	vestibular reflex
80	GO:0045955	negative regulation of calcium ion-dependent exocytosis
81	GO:0045124	regulation of bone resorption
82	GO:0097025	MPP7-DLG1-LIN7 complex
83	GO:0007004	telomere maintenance via telomerase
84	GO:0044780	bacterial-type flagellum assembly
85	GO:0035441	cell migration involved in vasculogenesis
86	GO:0060292	long term synaptic depression
87	GO:0048671	negative regulation of collateral sprouting
88	GO:0032395	MHC class II receptor activity
89	GO:0002064	epithelial cell development
90	GO:0016829	lyase activity
91	GO:0007289	spermatid nucleus differentiation
92	GO:0021535	cell migration in hindbrain
93	GO:0051344	negative regulation of cyclic-nucleotide phosphodiesterase activity
94	GO:0004864	protein phosphatase inhibitor activity
95	GO:0031669	cellular response to nutrient levels
96	GO:0031077	post-embryonic camera-type eye development
97	GO:0051017	actin filament bundle assembly
98	GO:0010159	specification of organ position
99	GO:0016740	transferase activity
100	GO:0016922	ligand-dependent nuclear receptor binding
101	GO:0005635	nuclear envelope
102	GO:0046983	protein dimerization activity
103	GO:0031208	POZ domain binding
104	GO:0009566	fertilization
105	GO:0050663	cytokine secretion
106	GO:0048608	reproductive structure development
107	GO:0005847	mRNA cleavage and polyadenylation specificity factor complex
108	GO:0031595	nuclear proteasome complex
109	GO:0030258	lipid modification
110	GO:0030122	AP-2 adaptor complex
111	GO:0002218	activation of innate immune response
112	GO:0032584	growth cone membrane
113	GO:0008366	axon ensheathment
114	GO:0002384	hepatic immune response

115	GO:2000179	positive regulation of neural precursor cell proliferation
116	GO:0045161	neuronal ion channel clustering
117	GO:0005308	creatine transmembrane transporter activity
118	GO:0005522	profilin binding
119	GO:2000310	regulation of N-methyl-D-aspartate selective glutamate receptor activity
120	GO:0006970	response to osmotic stress
121	GO:0030201	heparan sulfate proteoglycan metabolic process
122	GO:0031225	anchored component of membrane
123	GO:0051014	actin filament severing
124	GO:0000045	autophagic vacuole assembly
125	GO:0006796	phosphate-containing compound metabolic process
126	GO:0043279	response to alkaloid
127	GO:0035900	response to isolation stress
128	GO:0034021	response to silicon dioxide
129	GO:0051209	release of sequestered calcium ion into cytosol
130	GO:0006069	ethanol oxidation
131	GO:0006449	regulation of translational termination
132	GO:0060235	lens induction in camera-type eye
133	GO:0004479	methionyl-tRNA formyltransferase activity
134	GO:0048730	epidermis morphogenesis
135	GO:0050729	positive regulation of inflammatory response
136	GO:0032211	negative regulation of telomere maintenance via telomerase
137	GO:0097362	MCM8-MCM9 complex
138	GO:0008047	enzyme activator activity
139	GO:0060745	mammary gland branching involved in pregnancy
140	GO:0043085	positive regulation of catalytic activity
141	GO:0001912	positive regulation of leukocyte mediated cytotoxicity
142	GO:0008340	determination of adult lifespan
143	GO:0030991	intraciliary transport particle A
144	GO:0001835	blastocyst hatching
145	GO:0016831	carboxy-lyase activity
146	GO:0051974	negative regulation of telomerase activity
147	GO:0001825	blastocyst formation
148	GO:0010940	positive regulation of necrotic cell death
149	GO:0014842	regulation of satellite cell proliferation
150	GO:0005415	nucleoside:sodium symporter activity
151	KEGG:Steroid_biosynthesis	
152	GO:0051591	response to cAMP

153	GO:0048007	antigen processing and presentation, exogenous lipid antigen via MHC class Ib
154	GO:0033791	3alpha,7alpha,12alpha-trihydroxy-5beta-cholestanoyl-CoA 24-hydroxylase activity
155	GO:0006906	vesicle fusion
156	GO:0009620	response to fungus
157	GO:0090265	positive regulation of immune complex clearance by monocytes and macrophages
158	GO:0090082	positive regulation of heart induction by negative regulation of canonical Wnt signaling pathway
159	GO:0072044	collecting duct development
160	GO:0000783	nuclear telomere cap complex
161	GO:0008504	monoamine transmembrane transporter activity
162	GO:0030718	germ-line stem cell maintenance
163	GO:0032757	positive regulation of interleukin-8 production
164	GO:0002906	negative regulation of mature B cell apoptotic process
165	GO:2000872	positive regulation of progesterone secretion
166	GO:0031461	cullin-RING ubiquitin ligase complex
167	GO:0022028	tangential migration from the subventricular zone to the olfactory bulb
168	GO:0032794	GTPase activating protein binding
169	GO:0044292	dendrite terminus
170	GO:0005658	alpha DNA polymerase:primase complex
171	GO:0021979	hypothalamus cell differentiation
172	GO:0032479	regulation of type I interferon production
173	GO:0008483	transaminase activity
174	GO:0006820	anion transport
175	GO:0035640	exploration behavior
176	KEGG:Notch_signaling_pathway	
177	GO:0008066	glutamate receptor activity
178	GO:0045947	negative regulation of translational initiation
179	GO:0030502	negative regulation of bone mineralization
180	GO:0030540	female genitalia development
181	GO:0060152	microtubule-based peroxisome localization
182	GO:0071226	cellular response to molecule of fungal origin
183	GO:0035239	tube morphogenesis
184	GO:0043398	HLH domain binding
185	GO:0043587	tongue morphogenesis
186	GO:0042645	mitochondrial nucleoid
187	GO:0070300	phosphatidic acid binding
188	GO:1902560	GMP reductase complex
189	GO:0043030	regulation of macrophage activation

190	GO:0030234	enzyme regulator activity
191	GO:0065010	extracellular membrane-bounded organelle
192	GO:0080132	fatty acid alpha-hydroxylase activity
193	GO:0051353	positive regulation of oxidoreductase activity
194	GO:0005964	phosphorylase kinase complex
195	GO:0071837	HMG box domain binding
196	GO:0050434	positive regulation of viral transcription
197	GO:0001306	age-dependent response to oxidative stress
198	GO:0031519	PcG protein complex
199	GO:0000308	cytoplasmic cyclin-dependent protein kinase holoenzyme complex
200	GO:0051097	negative regulation of helicase activity
201	GO:0032202	telomere assembly
202	GO:0048660	regulation of smooth muscle cell proliferation
203	GO:0051963	regulation of synapse assembly
204	GO:0060033	anatomical structure regression
205	GO:0006003	fructose 2,6-bisphosphate metabolic process
206	GO:0051901	positive regulation of mitochondrial depolarization
207	GO:0032588	trans-Golgi network membrane
208	GO:0043626	PCNA complex
209	GO:0072277	metanephric glomerular capillary formation
210	GO:0031262	Ndc80 complex
211	GO:0051279	regulation of release of sequestered calcium ion into cytosol
212	GO:0015844	monoamine transport
213	GO:0003245	cardiac muscle tissue growth involved in heart morphogenesis
214	GO:0032714	negative regulation of interleukin-5 production
215	GO:0035851	Krueppel-associated box domain binding
216	GO:0090051	negative regulation of cell migration involved in sprouting angiogenesis
217	GO:0042135	neurotransmitter catabolic process
218	GO:0019534	toxin transporter activity
219	GO:0021895	cerebral cortex neuron differentiation
220	GO:0071674	mononuclear cell migration
221	GO:0060004	reflex
222	GO:0034273	Atg1p signaling complex
223	GO:0000775	chromosome, centromeric region
224	GO:0002682	regulation of immune system process
225	GO:0007141	male meiosis I
226	GO:0042169	SH2 domain binding
227	GO:0032722	positive regulation of chemokine production
228	GO:0021984	adenohypophysis development

229	GO:0035726	common myeloid progenitor cell proliferation
230	GO:0045059	positive thymic T cell selection
231	GO:0015238	drug transmembrane transporter activity
232	GO:0072284	metanephric S-shaped body morphogenesis
233	GO:0019900	kinase binding
234	GO:0006700	C21-steroid hormone biosynthetic process
235	GO:0016857	racemase and epimerase activity, acting on carbohydrates and derivatives
236	GO:0051525	NFAT protein binding
237	GO:0005753	mitochondrial proton-transporting ATP synthase complex
238	GO:0050878	regulation of body fluid levels
239	GO:0003006	developmental process involved in reproduction
240	GO:0060252	positive regulation of glial cell proliferation
241	GO:0040012	regulation of locomotion
242	GO:0008276	protein methyltransferase activity
243	GO:0055093	response to hyperoxia
244	GO:2001022	positive regulation of response to DNA damage stimulus
245	GO:0030278	regulation of ossification
246	GO:0002237	response to molecule of bacterial origin
247	GO:0090261	positive regulation of inclusion body assembly
248	GO:0001961	positive regulation of cytokine-mediated signaling pathway
249	GO:1900181	negative regulation of protein localization to nucleus
250	GO:2000036	regulation of stem cell maintenance
251	GO:0042610	CD8 receptor binding
252	GO:0030500	regulation of bone mineralization
253	GO:0031497	chromatin assembly
254	GO:0031965	nuclear membrane
255	GO:0006066	alcohol metabolic process
256	GO:0034260	negative regulation of GTPase activity
257	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
258	GO:0042628	mating plug formation
259	GO:0030658	transport vesicle membrane
260	GO:0007422	peripheral nervous system development
261	GO:0002095	caveolar macromolecular signaling complex
262	GO:0043277	apoptotic cell clearance
263	GO:0061029	eyelid development in camera-type eye
264	GO:0034452	dynactin binding
265	GO:0038085	vascular endothelial growth factor binding
266	GO:0003016	respiratory system process

267	GO:0021522	spinal cord motor neuron differentiation
268	GO:0050709	negative regulation of protein secretion
269	GO:0003181	atrioventricular valve morphogenesis
270	GO:0007040	lysosome organization
271	GO:0006812	cation transport
272	GO:0032270	positive regulation of cellular protein metabolic process
273	GO:0043203	axon hillock
274	GO:0030864	cortical actin cytoskeleton
275	GO:0008194	UDP-glycosyltransferase activity
276	GO:0060242	contact inhibition
277	GO:0043931	ossification involved in bone maturation
278	GO:0030321	transepithelial chloride transport
279	GO:0007098	centrosome cycle
280	GO:1901998	toxin transport
281	GO:0051788	response to misfolded protein
282	GO:0060017	parathyroid gland development
283	GO:0001726	ruffle
284	GO:0022612	gland morphogenesis
285	GO:0019003	GDP binding
286	GO:0060385	axonogenesis involved in innervation
287	GO:0010891	negative regulation of sequestering of triglyceride
288	GO:0023026	MHC class II protein complex binding
289	GO:0071502	cellular response to temperature stimulus
290	GO:0001964	startle response
291	KEGG:Folate_biosynthesis	
292	GO:0032839	dendrite cytoplasm
293	GO:2001190	positive regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell
294	GO:0071529	cementum mineralization
295	GO:0010269	response to selenium ion
296	KEGG:Tryptophan_metabolism	
297	GO:0033599	regulation of mammary gland epithelial cell proliferation
298	GO:0090399	replicative senescence
299	GO:0030970	retrograde protein transport, ER to cytosol
300	GO:0008023	transcription elongation factor complex
301	GO:0072179	nephric duct formation
302	GO:0033603	positive regulation of dopamine secretion
303	GO:0048515	spermatid differentiation
304	GO:0019985	translesion synthesis
305	GO:0030177	positive regulation of Wnt signaling pathway

306	GO:2001028	positive regulation of endothelial cell chemotaxis
307	GO:0043117	positive regulation of vascular permeability
308	GO:0016504	peptidase activator activity
309	GO:0046010	positive regulation of circadian sleep/wake cycle, non-REM sleep
310	GO:0002227	innate immune response in mucosa
311	GO:0002021	response to dietary excess
312	GO:0016757	transferase activity, transferring glycosyl groups
313	GO:0046928	regulation of neurotransmitter secretion
314	GO:0090325	regulation of locomotion involved in locomotory behavior
315	GO:0006337	nucleosome disassembly
316	GO:0051648	vesicle localization
317	GO:0046855	inositol phosphate dephosphorylation
318	GO:0032393	MHC class I receptor activity
319	KEGG:NOD_like_receptor_signaling_pathway	
320	GO:0033257	Bcl3/NF-kappaB2 complex
321	GO:0015797	mannitol transport
322	GO:0001833	inner cell mass cell proliferation
323	GO:0010842	retina layer formation
324	GO:0010008	endosome membrane
325	GO:0031346	positive regulation of cell projection organization
326	GO:0008053	mitochondrial fusion
327	GO:2000020	positive regulation of male gonad development
328	GO:0031915	positive regulation of synaptic plasticity
329	GO:0032675	regulation of interleukin-6 production
330	GO:0021747	cochlear nucleus development
331	GO:0060428	lung epithelium development
332	GO:0006900	membrane budding
333	GO:0002455	humoral immune response mediated by circulating immunoglobulin
334	GO:0007144	female meiosis I
335	GO:0048588	developmental cell growth
336	GO:0042113	B cell activation
337	GO:0097452	GAIT complex
338	GO:0071922	regulation of cohesin localization to chromatin
339	GO:0003136	negative regulation of heart induction by canonical Wnt signaling pathway
340	GO:0030229	very-low-density lipoprotein particle receptor activity
341	GO:0032490	detection of molecule of bacterial origin

342	GO:0005544	calcium-dependent phospholipid binding
343	GO:0030337	DNA polymerase processivity factor activity
344	GO:0000275	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)
345	GO:0009893	positive regulation of metabolic process
346	GO:0090344	negative regulation of cell aging
347	GO:0070491	repressing transcription factor binding
348	GO:0050772	positive regulation of axonogenesis
349	GO:0006605	protein targeting
350	GO:0005721	centromeric heterochromatin
351	GO:0030322	stabilization of membrane potential
352	GO:0003360	brainstem development
353	KEGG:Pantothenate_and_CoA_biosynthesis	
354	GO:0042809	vitamin D receptor binding
355	GO:0001965	G-protein alpha-subunit binding
356	GO:0070557	PCNA-p21 complex
357	GO:0061303	cornea development in camera-type eye
358	GO:0014878	response to electrical stimulus involved in regulation of muscle adaptation
359	GO:0022857	transmembrane transporter activity
360	GO:0035240	dopamine binding
361	GO:0016742	hydroxymethyl-, formyl- and related transferase activity
362	GO:2000687	negative regulation of rubidium ion transmembrane transporter activity
363	GO:0007618	mating
364	GO:0019048	modulation by virus of host morphology or physiology
365	GO:0032549	ribonucleoside binding
366	GO:2000681	negative regulation of rubidium ion transport
367	GO:0010871	negative regulation of receptor biosynthetic process
368	GO:0042118	endothelial cell activation
369	GO:0010259	multicellular organismal aging
370	GO:0060730	regulation of intestinal epithelial structure maintenance
371	GO:0043254	regulation of protein complex assembly
372	GO:0060058	positive regulation of apoptotic process involved in mammary gland involution
373	GO:0048332	mesoderm morphogenesis
374	GO:0032754	positive regulation of interleukin-5 production
375	GO:0051656	establishment of organelle localization
376	GO:0007268	synaptic transmission

377	GO:0090191	negative regulation of branching involved in ureteric bud morphogenesis
378	GO:0019905	syntaxin binding
379	GO:0006390	transcription from mitochondrial promoter
380	GO:0016234	inclusion body
381	GO:0048562	embryonic organ morphogenesis
382	GO:0050673	epithelial cell proliferation
383	GO:0007548	sex differentiation
384	GO:0030014	CCR4-NOT complex
385	GO:0044183	protein binding involved in protein folding
386	GO:0016578	histone deubiquitination
387	GO:0010977	negative regulation of neuron projection development
388	GO:0043148	mitotic spindle stabilization
389	GO:0071257	cellular response to electrical stimulus
390	GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway
391	GO:0032304	negative regulation of icosanoid secretion
392	GO:0034188	apolipoprotein A-I receptor activity
393	GO:0070507	regulation of microtubule cytoskeleton organization
394	GO:0070194	synaptonemal complex disassembly
395	GO:0043647	inositol phosphate metabolic process
396	GO:0048599	oocyte development
397	GO:0048755	branching morphogenesis of a nerve
398	KEGG:Valine_leucine_and_isoleucine_biosynthesis	
399	GO:0019135	deoxyhypusine monooxygenase activity
400	GO:0061108	seminal vesicle epithelium development
401	GO:0031937	positive regulation of chromatin silencing
402	GO:0008503	benzodiazepine receptor activity
403	GO:0032715	negative regulation of interleukin-6 production
404	GO:2000505	regulation of energy homeostasis
405	GO:0002819	regulation of adaptive immune response
406	GO:0060037	pharyngeal system development
407	GO:2000301	negative regulation of synaptic vesicle exocytosis
408	GO:0051900	regulation of mitochondrial depolarization
409	GO:0055123	digestive system development
410	GO:0048550	negative regulation of pinocytosis
411	GO:0042393	histone binding
412	GO:0000731	DNA synthesis involved in DNA repair
413	GO:0051787	misfolded protein binding
414	GO:0042592	homeostatic process

415	GO:0072358	cardiovascular system development
416	GO:0035014	phosphatidylinositol 3-kinase regulator activity
417	GO:2001193	positive regulation of gamma-delta T cell activation involved in immune response
418	GO:0007059	chromosome segregation
419	GO:0015660	formate efflux transmembrane transporter activity
420	GO:0002080	acrosomal membrane
421	GO:0007398	ectoderm development
422	GO:0005750	mitochondrial respiratory chain complex III
423	GO:0042723	thiamine-containing compound metabolic process
424	GO:0060324	face development
425	GO:0006342	chromatin silencing
426	GO:0009838	abscission
427	GO:0019915	lipid storage
428	GO:0010941	regulation of cell death
429	GO:0048311	mitochondrion distribution
430	KEGG:Phagosome	
431	GO:0010266	response to vitamin B1
432	GO:0030534	adult behavior
433	KEGG:Selenoamino_acid_metabolism	
434	GO:0032480	negative regulation of type I interferon production
435	GO:0002860	positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target
436	GO:0050427	3'-phosphoadenosine 5'-phosphosulfate metabolic process
437	GO:0008593	regulation of Notch signaling pathway
438	GO:0007405	neuroblast proliferation
439	GO:0034189	very-low-density lipoprotein particle binding
440	GO:0015659	formate uptake transmembrane transporter activity
441	GO:0030975	thiamine binding
442	GO:0008622	epsilon DNA polymerase complex
443	GO:0060769	positive regulation of epithelial cell proliferation involved in prostate gland development
444	GO:0050733	RS domain binding
445	GO:0042473	outer ear morphogenesis
446	GO:0097016	L27 domain binding
447	GO:0030119	AP-type membrane coat adaptor complex
448	GO:1990111	spermatoproteasome complex
449	GO:0032466	negative regulation of cytokinesis

450	GO:0003192	mitral valve formation
451	GO:0030516	regulation of axon extension
452	GO:0002821	positive regulation of adaptive immune response
453	GO:0000139	Golgi membrane
454	GO:0030323	respiratory tube development
455	GO:0072089	stem cell proliferation
456	GO:0008093	cytoskeletal adaptor activity
457	GO:0044530	supraspliceosomal complex
458	GO:0036120	cellular response to platelet-derived growth factor stimulus
459	GO:0010172	embryonic body morphogenesis
460	GO:0030896	checkpoint clamp complex
461	GO:0002764	immune response-regulating signaling pathway
462	GO:0010369	chromocenter
463	GO:0015211	purine nucleoside transmembrane transporter activity
464	GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process
465	GO:0046907	intracellular transport
466	GO:0006983	ER overload response
467	GO:0038091	positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor signaling pathway
468	GO:0032801	receptor catabolic process
469	GO:0019209	kinase activator activity
470	GO:0019871	sodium channel inhibitor activity
471	GO:0045023	G0 to G1 transition
472	GO:0032878	regulation of establishment or maintenance of cell polarity
473	GO:0050710	negative regulation of cytokine secretion
474	GO:0010952	positive regulation of peptidase activity
475	GO:0031528	microvillus membrane
476	GO:0006959	humoral immune response
477	GO:0030100	regulation of endocytosis
478	GO:0048539	bone marrow development
479	GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis
480	KEGG:Cysteine_and_methionine_metabolism	
481	GO:0048854	brain morphogenesis
482	GO:0010826	negative regulation of centrosome duplication
483	GO:0055098	response to low-density lipoprotein particle
484	GO:0043393	regulation of protein binding
485	GO:0051798	positive regulation of hair follicle development

486	GO:0042734	presynaptic membrane
487	GO:0060716	labyrinthine layer blood vessel development
488	GO:0097227	sperm annulus
489	GO:0006282	regulation of DNA repair
490	GO:0043296	apical junction complex
491	GO:0000151	ubiquitin ligase complex
492	GO:0006520	cellular amino acid metabolic process
493	GO:0010997	anaphase-promoting complex binding
494	GO:0051438	regulation of ubiquitin-protein ligase activity
495	GO:0043237	laminin-1 binding
496	GO:0030870	Mre11 complex
497	GO:0042019	interleukin-23 binding
498	GO:0035358	regulation of peroxisome proliferator activated receptor signaling pathway
499	GO:0060523	prostate epithelial cord elongation
500	GO:0001546	preantral ovarian follicle growth
501	GO:0006450	regulation of translational fidelity
502	GO:0060253	negative regulation of glial cell proliferation
503	GO:0012501	programmed cell death
504	GO:0005758	mitochondrial intermembrane space
505	KEGG:Peroxisome	
506	GO:0070603	SWI/SNF superfamily-type complex
507	GO:0050682	AF-2 domain binding
508	GO:0022405	hair cycle process
509	GO:0042168	heme metabolic process
510	GO:0030131	clathrin adaptor complex
511	GO:0019043	establishment of viral latency
512	GO:0016574	histone ubiquitination
513	GO:0031072	heat shock protein binding
514	GO:0045747	positive regulation of Notch signaling pathway
515	GO:0005096	GTPase activator activity
516	GO:0042589	zymogen granule membrane
517	GO:0048144	fibroblast proliferation
518	GO:0035176	social behavior
519	GO:0010718	positive regulation of epithelial to mesenchymal transition
520	GO:1990138	neuron projection extension
521	GO:0032066	nucleolus to nucleoplasm transport
522	GO:0046500	S-adenosylmethionine metabolic process
523	GO:0002639	positive regulation of immunoglobulin production
524	GO:0030031	cell projection assembly
525	GO:0035148	tube formation
526	GO:0005602	complement component C1 complex

527	GO:0060042	retina morphogenesis in camera-type eye
528	GO:0004509	steroid 21-monooxygenase activity
529	GO:0045070	positive regulation of viral genome replication
530	GO:0035276	ethanol binding
531	GO:0014740	negative regulation of muscle hyperplasia
532	GO:0005761	mitochondrial ribosome
533	GO:0030431	sleep
534	GO:0003180	aortic valve morphogenesis
535	GO:0007126	meiosis
536	GO:0048306	calcium-dependent protein binding
537	GO:0005344	oxygen transporter activity
538	GO:0003143	embryonic heart tube morphogenesis
539	GO:0031428	box C/D snoRNP complex
540	GO:0008277	regulation of G-protein coupled receptor protein signaling pathway
541	GO:0043412	macromolecule modification
542	GO:0048853	forebrain morphogenesis
543	GO:0030332	cyclin binding
544	GO:0003906	DNA-(apurinic or apyrimidinic site) lyase activity
545	GO:0016998	cell wall macromolecule catabolic process
546	GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
547	GO:0007420	brain development
548	GO:0006071	glycerol metabolic process
549	GO:1902233	negative regulation of positive thymic T cell selection
550	GO:0043586	tongue development
551	GO:0016942	insulin-like growth factor binding protein complex
552	GO:0043204	perikaryon
553	GO:0072536	interleukin-23 receptor complex
554	GO:0005759	mitochondrial matrix
555	GO:0032606	type I interferon production
556	GO:0043312	neutrophil degranulation
557	GO:0043125	ErbB-3 class receptor binding
558	GO:0031295	T cell costimulation
559	GO:2000679	positive regulation of transcription regulatory region DNA binding
560	GO:0051096	positive regulation of helicase activity
561	GO:0019731	antibacterial humoral response
562	GO:0030307	positive regulation of cell growth
563	GO:0046651	lymphocyte proliferation
564	GO:0060219	camera-type eye photoreceptor cell

		differentiation
565	GO:0034124	regulation of MyD88-dependent toll-like receptor signaling pathway
566	GO:0019207	kinase regulator activity
567	GO:0097060	synaptic membrane
568	GO:0017126	nucleologenesis
569	GO:0070403	NAD+ binding
570	GO:0007494	midgut development
571	GO:0045298	tubulin complex
572	GO:0070997	neuron death
573	GO:0048019	receptor antagonist activity
574	GO:0048265	response to pain
575	GO:0031023	microtubule organizing center organization
576	GO:0007084	mitotic nuclear envelope reassembly
577	GO:0016788	hydrolase activity, acting on ester bonds
578	GO:0060694	regulation of cholesterol transporter activity
579	GO:0071565	nBAF complex
580	GO:0007143	female meiosis
581	GO:0043415	positive regulation of skeletal muscle tissue regeneration
582	GO:0070365	hepatocyte differentiation
583	GO:0022602	ovulation cycle process
584	GO:0005328	neurotransmitter:sodium symporter activity
585	GO:0061025	membrane fusion
586	GO:0017183	peptidyl-diphthamide biosynthetic process from peptidyl-histidine
587	GO:0003032	detection of oxygen
588	KEGG:Primary_immunodeficiency	
589	GO:0050687	negative regulation of defense response to virus
590	GO:0005794	Golgi apparatus
591	GO:0045921	positive regulation of exocytosis
592	GO:0045948	positive regulation of translational initiation
593	GO:0033962	cytoplasmic mRNA processing body assembly
594	GO:0070064	proline-rich region binding
595	GO:0007399	nervous system development
596	GO:0003209	cardiac atrium morphogenesis
597	GO:0009235	cobalamin metabolic process
598	GO:0006518	peptide metabolic process
599	GO:0009279	cell outer membrane
600	GO:0015671	oxygen transport
601	GO:0016050	vesicle organization
602	GO:0002092	positive regulation of receptor internalization
603	GO:0034127	regulation of MyD88-independent toll-like receptor signaling pathway

604	GO:0006839	mitochondrial transport
605	GO:0015949	nucleobase-containing small molecule interconversion
606	GO:0036336	dendritic cell migration
607	GO:1900116	extracellular negative regulation of signal transduction
608	KEGG:Base_excision_repair	
609	GO:0030010	establishment of cell polarity
610	GO:1901898	negative regulation of relaxation of cardiac muscle
611	GO:0030548	acetylcholine receptor regulator activity
612	GO:0004859	phospholipase inhibitor activity
613	GO:0045056	transcytosis
614	GO:0060429	epithelium development
615	GO:2000311	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity
616	GO:0008347	glial cell migration
617	GO:0002381	immunoglobulin production involved in immunoglobulin mediated immune response
618	GO:0070848	response to growth factor
619	GO:0060742	epithelial cell differentiation involved in prostate gland development
620	GO:0007062	sister chromatid cohesion
621	GO:0043588	skin development
622	GO:0050795	regulation of behavior
623	GO:0070221	sulfide oxidation, using sulfide:quinone oxidoreductase
624	GO:0002520	immune system development
625	GO:0045743	positive regulation of fibroblast growth factor receptor signaling pathway
626	GO:0043514	interleukin-12 complex
627	GO:0007290	spermatid nucleus elongation
628	GO:0002161	aminoacyl-tRNA editing activity
629	GO:0043023	ribosomal large subunit binding
630	GO:0051013	microtubule severing
631	GO:0031253	cell projection membrane
632	GO:0045726	positive regulation of integrin biosynthetic process
633	GO:0030981	cortical microtubule cytoskeleton
634	GO:0005739	mitochondrion
635	GO:0031683	G-protein beta/gamma-subunit complex binding
636	GO:0031720	haptoglobin binding
637	GO:0043517	positive regulation of DNA damage response,

		signal transduction by p53 class mediator
638	GO:0005833	hemoglobin complex
639	GO:0034465	response to carbon monoxide
640	GO:0034122	negative regulation of toll-like receptor signaling pathway
641	GO:0031047	gene silencing by RNA
642	GO:0021591	ventricular system development
643	GO:0046541	saliva secretion
644	GO:0000900	translation repressor activity, nucleic acid binding
645	GO:0035035	histone acetyltransferase binding
646	GO:0032876	negative regulation of DNA endoreduplication
647	GO:0016080	synaptic vesicle targeting
648	GO:0016339	calcium-dependent cell-cell adhesion
649	GO:0042692	muscle cell differentiation
650	GO:0045744	negative regulation of G-protein coupled receptor protein signaling pathway
651	GO:0032620	interleukin-17 production
652	GO:0006302	double-strand break repair
653	GO:0001655	urogenital system development
654	GO:0051983	regulation of chromosome segregation
655	GO:0001671	ATPase activator activity
656	GO:0032580	Golgi cisterna membrane
657	GO:0051973	positive regulation of telomerase activity
658	GO:0033688	regulation of osteoblast proliferation
659	GO:0060022	hard palate development
660	KEGG:Sulfur_relay_system	
661	GO:0051100	negative regulation of binding
662	GO:0035861	site of double-strand break
663	GO:0040020	regulation of meiosis
664	GO:0019898	extrinsic component of membrane
665	GO:0050765	negative regulation of phagocytosis
666	GO:0031664	regulation of lipopolysaccharide-mediated signaling pathway
667	GO:0032793	positive regulation of CREB transcription factor activity
668	GO:0032421	stereocilium bundle
669	GO:2000773	negative regulation of cellular senescence
670	GO:0002250	adaptive immune response
671	GO:0042101	T cell receptor complex
672	GO:0060529	squamous basal epithelial stem cell differentiation involved in prostate gland acinus development
673	GO:0017119	Golgi transport complex

674	GO:0045823	positive regulation of heart contraction
675	GO:2000543	positive regulation of gastrulation
676	GO:0042743	hydrogen peroxide metabolic process
677	GO:0010574	regulation of vascular endothelial growth factor production
678	GO:0030282	bone mineralization
679	GO:0046620	regulation of organ growth
680	GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway
681	GO:0016242	negative regulation of macroautophagy
682	GO:0030522	intracellular receptor signaling pathway
683	GO:0007030	Golgi organization
684	GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway
685	GO:0016874	ligase activity
686	GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity
687	GO:0061351	neural precursor cell proliferation
688	GO:0050819	negative regulation of coagulation
689	GO:0060135	maternal process involved in female pregnancy
690	GO:0061304	retinal blood vessel morphogenesis
691	GO:0071110	histone biotinylation
692	GO:0000002	mitochondrial genome maintenance
693	GO:0042805	actinin binding
694	GO:0005041	low-density lipoprotein receptor activity
695	GO:0048633	positive regulation of skeletal muscle tissue growth
696	GO:0007638	mechanosensory behavior
697	GO:0008494	translation activator activity
698	GO:0042447	hormone catabolic process
699	GO:0021680	cerebellar Purkinje cell layer development
700	GO:2000402	negative regulation of lymphocyte migration
701	GO:0002369	T cell cytokine production
702	GO:0071229	cellular response to acid
703	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
704	GO:0016780	phosphotransferase activity, for other substituted phosphate groups
705	GO:0072520	seminiferous tubule development
706	GO:0007617	mating behavior
707	GO:0090045	positive regulation of deacetylase activity
708	GO:0005845	mRNA cap binding complex
709	KEGG:Glycosaminoglycan_biosynthesis	
710	GO:0045606	positive regulation of epidermal cell

		differentiation
711	GO:2000548	negative regulation of dendritic cell dendrite assembly
712	GO:0031526	brush border membrane
713	GO:0048278	vesicle docking
714	GO:0070840	dynein complex binding
715	GO:0017145	stem cell division
716	GO:0006690	icosanoid metabolic process
717	GO:0051443	positive regulation of ubiquitin-protein ligase activity
718	GO:0001915	negative regulation of T cell mediated cytotoxicity
719	GO:0048645	organ formation
720	GO:0001302	replicative cell aging
721	GO:0033613	activating transcription factor binding
722	KEGG:Pyruvate_metabolism	
723	GO:0007530	sex determination
724	GO:0005542	folic acid binding
725	GO:0071438	invadopodium membrane
726	GO:2000549	positive regulation of dendritic cell dendrite assembly
727	GO:0031017	exocrine pancreas development
728	GO:0070435	Shc-EGFR complex
729	GO:0001846	opsonin binding
730	GO:0060433	bronchus development
731	GO:0004738	pyruvate dehydrogenase activity
732	GO:0043268	positive regulation of potassium ion transport
733	GO:0022409	positive regulation of cell-cell adhesion
734	GO:0031404	chloride ion binding
735	GO:0060768	regulation of epithelial cell proliferation involved in prostate gland development
736	GO:0019054	modulation by virus of host process
737	GO:0021631	optic nerve morphogenesis
738	GO:0061003	positive regulation of dendritic spine morphogenesis
739	GO:0050811	GABA receptor binding
740	GO:0071575	integral component of external side of plasma membrane
741	GO:0010834	telomere maintenance via telomere shortening
742	GO:0051298	centrosome duplication
743	GO:0071460	cellular response to cell-matrix adhesion
744	GO:0051382	kinetochore assembly
745	GO:0015036	disulfide oxidoreductase activity
746	GO:1901888	regulation of cell junction assembly

747	GO:0006281	DNA repair
748	GO:0001780	neutrophil homeostasis
749	GO:0060687	regulation of branching involved in prostate gland morphogenesis
750	GO:0017157	regulation of exocytosis
751	GO:0043084	penile erection
752	GO:0006344	maintenance of chromatin silencing
753	GO:0015886	heme transport
754	GO:0006705	mineralocorticoid biosynthetic process
755	GO:0060406	positive regulation of penile erection
756	GO:0033177	proton-transporting two-sector ATPase complex, proton-transporting domain
757	GO:0043008	ATP-dependent protein binding
758	GO:0030414	peptidase inhibitor activity
759	GO:0032456	endocytic recycling
760	GO:0072054	renal outer medulla development
761	GO:0006086	acetyl-CoA biosynthetic process from pyruvate
762	GO:0007346	regulation of mitotic cell cycle
763	GO:0002830	positive regulation of type 2 immune response
764	GO:0032420	stereocilium
765	GO:0045820	negative regulation of glycolysis
766	GO:0005793	endoplasmic reticulum-Golgi intermediate compartment
767	GO:0006471	protein ADP-ribosylation
768	GO:0035641	locomotory exploration behavior
769	GO:0000785	chromatin
770	GO:0002429	immune response-activating cell surface receptor signaling pathway
771	GO:0021527	spinal cord association neuron differentiation
772	GO:0007080	mitotic metaphase plate congression
773	GO:0010592	positive regulation of lamellipodium assembly
774	GO:0060066	oviduct development
775	GO:0031666	positive regulation of lipopolysaccharide-mediated signaling pathway
776	GO:0045835	negative regulation of meiosis
777	KEGG:Phenylalanine_metabolism	
778	GO:0006887	exocytosis
779	GO:0070849	response to epidermal growth factor
780	GO:0048038	quinone binding
781	GO:0030492	hemoglobin binding
782	GO:0061299	retina vasculature morphogenesis in camera-type eye
783	GO:0070584	mitochondrion morphogenesis
784	GO:0006408	snRNA export from nucleus

785	GO:0010469	regulation of receptor activity
786	GO:0004518	nuclease activity
787	GO:0007010	cytoskeleton organization
788	GO:0044088	regulation of vacuole organization
789	GO:0097194	execution phase of apoptosis
790	GO:0045254	pyruvate dehydrogenase complex
791	GO:0030238	male sex determination
792	GO:0051537	2 iron, 2 sulfur cluster binding
793	GO:0004129	cytochrome-c oxidase activity
794	GO:0072053	renal inner medulla development
795	GO:0005639	integral component of nuclear inner membrane
796	GO:0034750	Scrib-APC-beta-catenin complex
797	GO:0006801	superoxide metabolic process
798	GO:0030279	negative regulation of ossification
799	GO:0019213	deacetylase activity
800	GO:1900006	positive regulation of dendrite development
801	GO:0002443	leukocyte mediated immunity
802	GO:0036270	response to diuretic
803	GO:0051928	positive regulation of calcium ion transport
804	GO:0042826	histone deacetylase binding
805	GO:1901558	response to metformin
806	GO:0002523	leukocyte migration involved in inflammatory response
807	GO:0000938	GARP complex
808	GO:0032990	cell part morphogenesis
809	GO:0005540	hyaluronic acid binding
810	GO:0005159	insulin-like growth factor receptor binding
811	GO:0097062	dendritic spine maintenance
812	GO:2000146	negative regulation of cell motility
813	GO:0031340	positive regulation of vesicle fusion
814	GO:0001820	serotonin secretion
815	GO:0045732	positive regulation of protein catabolic process
816	GO:0032288	myelin assembly
817	GO:0032039	integrator complex
818	GO:0031932	TORC2 complex
819	GO:0033005	positive regulation of mast cell activation
820	GO:0045095	keratin filament
821	GO:0050699	WW domain binding
822	GO:0019725	cellular homeostasis
823	GO:0032052	bile acid binding
824	GO:0002385	mucosal immune response
825	GO:1902177	positive regulation of intrinsic apoptotic signaling pathway in response to oxidative stress

826	GO:0060978	angiogenesis involved in coronary vascular morphogenesis
827	GO:0072218	metanephric ascending thin limb development
828	GO:0022891	substrate-specific transmembrane transporter activity
829	GO:0006974	cellular response to DNA damage stimulus
830	KEGG:Sulfur_metabolism	
831	GO:0071402	cellular response to lipoprotein particle stimulus
832	GO:0008190	eukaryotic initiation factor 4E binding
833	GO:0017151	DEAD/H-box RNA helicase binding
834	GO:0097038	perinuclear endoplasmic reticulum
835	GO:0070306	lens fiber cell differentiation
836	GO:0030295	protein kinase activator activity
837	GO:0001848	complement binding
838	GO:0043313	regulation of neutrophil degranulation
839	GO:0006405	RNA export from nucleus
840	GO:0001829	trophectodermal cell differentiation
841	GO:0035932	aldosterone secretion
842	GO:2000008	regulation of protein localization to cell surface
843	GO:0051539	4 iron, 4 sulfur cluster binding
844	GO:0060627	regulation of vesicle-mediated transport
845	GO:0030674	protein binding, bridging
846	GO:0042719	mitochondrial intermembrane space protein transporter complex
847	GO:0007097	nuclear migration
848	GO:0045622	regulation of T-helper cell differentiation
849	GO:0003344	pericardium morphogenesis
850	GO:0000050	urea cycle
851	GO:0005795	Golgi stack
852	GO:0016035	zeta DNA polymerase complex
853	GO:0030185	nitric oxide transport
854	GO:0033269	internode region of axon
855	KEGG:Arginine_and_proline_metabolism	
856	GO:0015884	folic acid transport
857	GO:0051018	protein kinase A binding
858	GO:0033179	proton-transporting V-type ATPase, V0 domain
859	GO:0070182	DNA polymerase binding
860	GO:2000655	negative regulation of cellular response to testosterone stimulus
861	GO:0060789	hair follicle placode formation
862	GO:0030382	sperm mitochondrion organization
863	GO:0005319	lipid transporter activity
864	GO:0035374	chondroitin sulfate binding

865	GO:0002366	leukocyte activation involved in immune response
866	KEGG:Fatty_acid_metabolism	
867	GO:0005742	mitochondrial outer membrane translocase complex
868	GO:0005826	actomyosin contractile ring
869	GO:0006880	intracellular sequestering of iron ion
870	GO:0060384	innervation
871	GO:0043178	alcohol binding
872	GO:0015226	carnitine transmembrane transporter activity
873	GO:0010524	positive regulation of calcium ion transport into cytosol
874	GO:0060296	regulation of cilium beat frequency involved in ciliary motility
875	GO:0045026	plasma membrane fusion
876	GO:0043231	intracellular membrane-bounded organelle
877	GO:1901661	quinone metabolic process
878	GO:0090129	positive regulation of synapse maturation
879	GO:0045780	positive regulation of bone resorption
880	GO:0042255	ribosome assembly
881	GO:0060197	cloacal septation
882	GO:0017076	purine nucleotide binding
883	GO:0016192	vesicle-mediated transport
884	GO:0051604	protein maturation
885	GO:0070971	endoplasmic reticulum exit site
886	GO:0060369	positive regulation of Fc receptor mediated stimulatory signaling pathway
887	GO:0046415	urate metabolic process
888	KEGG:Glycolysis___Gluconeogenesis	
889	GO:0008278	cohesin complex
890	GO:0051654	establishment of mitochondrion localization
891	GO:0060997	dendritic spine morphogenesis
892	GO:0007176	regulation of epidermal growth factor-activated receptor activity
893	GO:0005087	Ran guanyl-nucleotide exchange factor activity
894	GO:0034663	endoplasmic reticulum chaperone complex
895	GO:0042713	sperm ejaculation
896	GO:0070938	contractile ring
897	GO:0060741	prostate gland stromal morphogenesis
898	GO:0042277	peptide binding
899	GO:0071933	Arp2/3 complex binding
900	GO:0051280	negative regulation of release of sequestered calcium ion into cytosol
901	GO:0008298	intracellular mRNA localization

902	GO:0018271	biotin-protein ligase activity
903	GO:0007625	grooming behavior
904	GO:0005614	interstitial matrix
905	GO:0005851	eukaryotic translation initiation factor 2B complex
906	GO:0050855	regulation of B cell receptor signaling pathway
907	GO:0072205	metanephric collecting duct development
908	GO:0048806	genitalia development
909	GO:0051051	negative regulation of transport
910	GO:0001773	myeloid dendritic cell activation
911	GO:0004667	prostaglandin-D synthase activity
912	GO:0045665	negative regulation of neuron differentiation
913	GO:0051347	positive regulation of transferase activity
914	GO:0048598	embryonic morphogenesis
915	GO:0005883	neurofilament
916	GO:0019969	interleukin-10 binding
917	GO:0060664	epithelial cell proliferation involved in salivary gland morphogenesis
918	GO:0000421	autophagic vacuole membrane
919	GO:0004887	thyroid hormone receptor activity
920	GO:0034399	nuclear periphery
921	GO:0031616	spindle pole centrosome
922	GO:0019884	antigen processing and presentation of exogenous antigen
923	GO:0072657	protein localization to membrane
924	GO:0007049	cell cycle
925	GO:0008146	sulfotransferase activity
926	GO:0042788	polysomal ribosome
927	GO:0097320	membrane tubulation
928	GO:0016572	histone phosphorylation
929	GO:0006703	estrogen biosynthetic process
930	GO:0033558	protein deacetylase activity
931	GO:0003162	atrioventricular node development
932	GO:0003161	cardiac conduction system development
933	GO:0019216	regulation of lipid metabolic process
934	GO:0035794	positive regulation of mitochondrial membrane permeability
935	GO:0030120	vesicle coat
936	GO:0016023	cytoplasmic membrane-bounded vesicle
937	GO:0032091	negative regulation of protein binding
938	GO:0014047	glutamate secretion
939	GO:0009792	embryo development ending in birth or egg hatching
940	GO:0043219	lateral loop

941	GO:0060438	trachea development
942	GO:0044615	nuclear pore nuclear basket
943	GO:0042272	nuclear RNA export factor complex
944	GO:0005762	mitochondrial large ribosomal subunit
945	GO:0034447	very-low-density lipoprotein particle clearance
946	GO:0046980	tapasin binding
947	KEGG:Citrate_cycle__TCA_cycle_	
948	GO:0008537	proteasome activator complex
949	GO:0030048	actin filament-based movement
950	GO:0007288	sperm axoneme assembly
951	GO:0009880	embryonic pattern specification
952	GO:0021854	hypothalamus development
953	GO:0008200	ion channel inhibitor activity
954	GO:0060157	urinary bladder development
955	GO:0031016	pancreas development
956	KEGG:Biotin_metabolism	
957	GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
958	GO:0046814	coreceptor-mediated virion attachment to host cell
959	GO:0047485	protein N-terminus binding
960	GO:0042997	negative regulation of Golgi to plasma membrane protein transport
961	KEGG:Riboflavin_metabolism	
962	GO:0002693	positive regulation of cellular extravasation
963	GO:0019694	alkanesulfonate metabolic process
964	GO:0071756	pentameric IgM immunoglobulin complex
965	GO:0006730	one-carbon metabolic process
966	GO:0071817	MMXD complex
967	GO:0060056	mammary gland involution
968	GO:1900029	positive regulation of ruffle assembly
969	GO:0005746	mitochondrial respiratory chain
970	KEGG:p53_signaling_pathway	
971	GO:0009236	cobalamin biosynthetic process
972	GO:0008354	germ cell migration
973	GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis
974	GO:0030992	intraciliary transport particle B
975	GO:0045762	positive regulation of adenylate cyclase activity
976	GO:0008517	folic acid transporter activity
977	GO:0060968	regulation of gene silencing
978	GO:0051205	protein insertion into membrane
979	GO:0016239	positive regulation of macroautophagy

980	GO:0002193	MAML1-RBP-Jkappa- ICN1 complex
981	GO:0048535	lymph node development
982	GO:0050806	positive regulation of synaptic transmission
983	GO:0042405	nuclear inclusion body
984	GO:0031838	haptoglobin-hemoglobin complex
985	GO:0043305	negative regulation of mast cell degranulation
986	GO:0003160	endocardium morphogenesis
987	GO:0014010	Schwann cell proliferation
988	GO:2000808	negative regulation of synaptic vesicle clustering
989	GO:2000678	negative regulation of transcription regulatory region DNA binding
990	GO:0005903	brush border
991	GO:0046661	male sex differentiation
992	GO:0050777	negative regulation of immune response
993	GO:0045927	positive regulation of growth
994	GO:0021794	thalamus development
995	GO:0019955	cytokine binding
996	GO:0060548	negative regulation of cell death
997	GO:0033025	regulation of mast cell apoptotic process
998	GO:2000121	regulation of removal of superoxide radicals
999	GO:1901303	negative regulation of cargo loading into COPII-coated vesicle
1000	GO:0043495	protein anchor
1001	GO:0035095	behavioral response to nicotine
1002	GO:0008170	N-methyltransferase activity
1003	GO:0021915	neural tube development
1004	GO:0046878	positive regulation of saliva secretion
1005	GO:0060916	mesenchymal cell proliferation involved in lung development
1006	GO:0031298	replication fork protection complex
1007	GO:0000777	condensed chromosome kinetochore
1008	GO:0033197	response to vitamin E
1009	GO:0008428	ribonuclease inhibitor activity
1010	GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
1011	GO:0022624	proteasome accessory complex
1012	GO:0046625	sphingolipid binding
1013	GO:0030218	erythrocyte differentiation
1014	GO:0050832	defense response to fungus
1015	GO:0008328	ionotropic glutamate receptor complex
1016	GO:0006099	tricarboxylic acid cycle
1017	GO:0021702	cerebellar Purkinje cell differentiation
1018	GO:0051595	response to methylglyoxal

1019	GO:0006110	regulation of glycolysis
1020	GO:2000641	regulation of early endosome to late endosome transport
1021	GO:0048286	lung alveolus development
1022	GO:0000904	cell morphogenesis involved in differentiation
1023	GO:0019222	regulation of metabolic process
1024	GO:0030878	thyroid gland development
1025	GO:0005083	small GTPase regulator activity
1026	GO:0046697	decidualization
1027	GO:0048840	otolith development
1028	GO:0060710	chorio-allantoic fusion
1029	GO:0045778	positive regulation of ossification
1030	GO:0043488	regulation of mRNA stability
1031	KEGG:Glycine_serine_and_threonine_metabolism	
1032	GO:0034341	response to interferon-gamma
1033	GO:0039689	negative stranded viral RNA replication
1034	KEGG:Oxidative_phosphorylation	
1035	GO:0016876	ligase activity, forming aminoacyl-tRNA and related compounds
1036	GO:0019208	phosphatase regulator activity
1037	GO:0007156	homophilic cell adhesion
1038	GO:1900025	negative regulation of substrate adhesion-dependent cell spreading
1039	GO:0090170	regulation of Golgi inheritance
1040	GO:0005586	collagen type III
1041	GO:0001771	immunological synapse formation
1042	GO:0005089	Rho guanyl-nucleotide exchange factor activity
1043	GO:0071748	monomeric IgA immunoglobulin complex
1044	GO:0048644	muscle organ morphogenesis
1045	GO:0001893	maternal placenta development
1046	GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle
1047	GO:0034103	regulation of tissue remodeling
1048	GO:0008043	intracellular ferritin complex
1049	GO:0033674	positive regulation of kinase activity
1050	KEGG:Aminoacyl_tRNA_biosynthesis	
1051	GO:0021517	ventral spinal cord development
1052	GO:0005520	insulin-like growth factor binding
1053	GO:0048069	eye pigmentation
1054	GO:0042596	fear response
1055	GO:1901203	positive regulation of extracellular matrix assembly
1056	GO:0002513	tolerance induction to self antigen

1057	GO:0019907	cyclin-dependent protein kinase activating kinase holoenzyme complex
1058	GO:0046677	response to antibiotic
1059	GO:0032836	glomerular basement membrane development
1060	GO:0043589	skin morphogenesis
1061	GO:0031503	protein complex localization
1062	GO:0060425	lung morphogenesis
1063	GO:0031090	organelle membrane
1064	GO:0080111	DNA demethylation
1065	GO:0006914	autophagy
1066	GO:0050804	regulation of synaptic transmission
1067	GO:0001540	beta-amyloid binding
1068	GO:0048496	maintenance of organ identity
1069	GO:0001778	plasma membrane repair
1070	GO:0035625	epidermal growth factor-activated receptor transactivation by G-protein coupled receptor signaling pathway
1071	GO:0090073	positive regulation of protein homodimerization activity
1072	GO:0051683	establishment of Golgi localization
1073	GO:2000774	positive regulation of cellular senescence
1074	GO:0060440	trachea formation
1075	GO:0060023	soft palate development
1076	GO:0060323	head morphogenesis
1077	GO:0010466	negative regulation of peptidase activity
1078	GO:0022029	telencephalon cell migration
1079	GO:0010884	positive regulation of lipid storage
1080	GO:0060113	inner ear receptor cell differentiation
1081	GO:0050808	synapse organization
1082	GO:0061298	retina vasculature development in camera-type eye
1083	GO:0016208	AMP binding
1084	GO:0050877	neurological system process
1085	GO:0090003	regulation of establishment of protein localization to plasma membrane
1086	GO:0032119	sequestering of zinc ion
1087	GO:0060008	Sertoli cell differentiation
1088	GO:0010447	response to acidity
1089	GO:0048168	regulation of neuronal synaptic plasticity
1090	GO:0030030	cell projection organization
1091	GO:0005740	mitochondrial envelope
1092	KEGG:Endocytosis	
1093	GO:1901214	regulation of neuron death
1094	GO:0060915	mesenchymal cell differentiation involved in

		lung development
1095	GO:0021756	striatum development
1096	GO:0090071	negative regulation of ribosome biogenesis
1097	GO:0006139	nucleobase-containing compound metabolic process
1098	GO:0043032	positive regulation of macrophage activation
1099	GO:2001014	regulation of skeletal muscle cell differentiation
1100	KEGG:Antigen_processing_and_presentation	
1101	GO:0008582	regulation of synaptic growth at neuromuscular junction
1102	GO:0070937	CRD-mediated mRNA stability complex
1103	GO:0005844	polysome
1104	GO:0033151	V(D)J recombination
1105	GO:0060055	angiogenesis involved in wound healing
1106	GO:0051149	positive regulation of muscle cell differentiation
1107	GO:0042908	xenobiotic transport
1108	GO:1900180	regulation of protein localization to nucleus
1109	GO:0060053	neurofilament cytoskeleton
1110	GO:0005006	epidermal growth factor-activated receptor activity
1111	GO:0071773	cellular response to BMP stimulus
1112	KEGG:SNARE_interactions_in_vesicular_transport	
1113	GO:0010887	negative regulation of cholesterol storage
1114	GO:0001568	blood vessel development
1115	GO:0002418	immune response to tumor cell
1116	GO:0050544	arachidonic acid binding
1117	GO:0035268	protein mannosylation
1118	GO:0015889	cobalamin transport
1119	GO:0042641	actomyosin
1120	GO:0060044	negative regulation of cardiac muscle cell proliferation
1121	GO:0048246	macrophage chemotaxis
1122	GO:0001818	negative regulation of cytokine production
1123	GO:0046889	positive regulation of lipid biosynthetic process
1124	GO:0043171	peptide catabolic process
1125	GO:0060615	mammary gland bud formation
1126	GO:0046621	negative regulation of organ growth
1127	GO:0051444	negative regulation of ubiquitin-protein ligase activity
1128	GO:0045786	negative regulation of cell cycle
1129	GO:0017025	TBP-class protein binding
1130	GO:0022604	regulation of cell morphogenesis

1131	GO:0031083	BLOC-1 complex
1132	GO:0042953	lipoprotein transport
1133	GO:0031536	positive regulation of exit from mitosis
1134	GO:0032602	chemokine production
1135	GO:0051489	regulation of filopodium assembly
1136	GO:0001654	eye development
1137	GO:0048807	female genitalia morphogenesis
1138	GO:0046005	positive regulation of circadian sleep/wake cycle, REM sleep
1139	GO:0005539	glycosaminoglycan binding
1140	GO:0046703	natural killer cell lectin-like receptor binding
1141	GO:0002368	B cell cytokine production
1142	GO:0033391	chromatoid body
1143	GO:0060685	regulation of prostatic bud formation
1144	GO:0010812	negative regulation of cell-substrate adhesion
1145	GO:2000521	negative regulation of immunological synapse formation
1146	GO:0042448	progesterone metabolic process
1147	GO:0016684	oxidoreductase activity, acting on peroxide as acceptor
1148	GO:0007275	multicellular organismal development
1149	GO:0006903	vesicle targeting
1150	GO:0035166	post-embryonic hemopoiesis
1151	GO:0042923	neuropeptide binding
1152	GO:0071158	positive regulation of cell cycle arrest
1153	GO:2001214	positive regulation of vasculogenesis
1154	GO:0030672	synaptic vesicle membrane
1155	GO:0048193	Golgi vesicle transport
1156	GO:0005677	chromatin silencing complex
1157	GO:0032133	chromosome passenger complex
1158	GO:0007417	central nervous system development
1159	GO:2000172	regulation of branching morphogenesis of a nerve
1160	GO:0007194	negative regulation of adenylate cyclase activity
1161	GO:0004839	ubiquitin activating enzyme activity
1162	GO:0032526	response to retinoic acid
1163	GO:0048145	regulation of fibroblast proliferation
1164	GO:0039534	negative regulation of MDA-5 signaling pathway
1165	GO:0043199	sulfate binding
1166	GO:0045737	positive regulation of cyclin-dependent protein kinase activity
1167	GO:0034988	Fc-gamma receptor I complex binding
1168	GO:0001675	acrosome assembly

1169	GO:0043392	negative regulation of DNA binding
1170	GO:0060492	lung induction
1171	GO:0030984	kininogen binding
1172	GO:0071664	catenin-TCF7L2 complex
1173	GO:0045926	negative regulation of growth
1174	GO:0061047	positive regulation of branching involved in lung morphogenesis
1175	GO:0031529	ruffle organization
1176	GO:0021533	cell differentiation in hindbrain
1177	GO:0042633	hair cycle
1178	GO:0001542	ovulation from ovarian follicle
1179	GO:0002079	inner acrosomal membrane
1180	GO:0015130	mevalonate transmembrane transporter activity
1181	GO:0046626	regulation of insulin receptor signaling pathway
1182	GO:0005057	receptor signaling protein activity
1183	KEGG:Histidine_metabolism	
1184	GO:0016461	unconventional myosin complex
1185	GO:0048557	embryonic digestive tract morphogenesis
1186	GO:0034185	apolipoprotein binding
1187	GO:0039536	negative regulation of RIG-I signaling pathway
1188	GO:0070442	alphaIIb-beta3 integrin complex
1189	GO:0046951	ketone body biosynthetic process
1190	GO:0070369	beta-catenin-TCF7L2 complex
1191	GO:0005783	endoplasmic reticulum
1192	GO:0008228	opsonization
1193	GO:0032467	positive regulation of cytokinesis
1194	GO:0097433	dense body
1195	GO:0036053	glomerular endothelium fenestra
1196	GO:0007031	peroxisome organization
1197	GO:0009081	branched-chain amino acid metabolic process
1198	GO:0007621	negative regulation of female receptivity
1199	GO:0051294	establishment of spindle orientation
1200	GO:0043086	negative regulation of catalytic activity
1201	GO:0090343	positive regulation of cell aging
1202	GO:0072572	poly-ADP-D-ribose binding
1203	GO:0060479	lung cell differentiation
1204	GO:0048738	cardiac muscle tissue development
1205	GO:0046833	positive regulation of RNA export from nucleus
1206	GO:0097177	mitochondrial ribosome binding
1207	GO:0030595	leukocyte chemotaxis
1208	GO:0050920	regulation of chemotaxis
1209	GO:0031667	response to nutrient levels
1210	KEGG:Huntington_s_disease	
1211	GO:0070984	SET domain binding

1212	GO:0045475	locomotor rhythm
1213	GO:0048808	male genitalia morphogenesis
1214	GO:0035112	genitalia morphogenesis
1215	GO:1900035	negative regulation of cellular response to heat
1216	GO:0030261	chromosome condensation
1217	GO:0031259	uropod membrane
1218	GO:0043433	negative regulation of sequence-specific DNA binding transcription factor activity
1219	GO:0007136	meiotic prophase II
1220	GO:0008060	ARF GTPase activator activity
1221	GO:0017077	oxidative phosphorylation uncoupler activity
1222	GO:0032880	regulation of protein localization
1223	GO:0030517	negative regulation of axon extension
1224	KEGG:PPAR_signaling_pathway	
1225	GO:0032781	positive regulation of ATPase activity
1226	GO:0046658	anchored component of plasma membrane
1227	GO:0000165	MAPK cascade
1228	GO:0031985	Golgi cisterna
1229	GO:0008265	Mo-molybdopterin cofactor sulfurase activity
1230	GO:0030902	hindbrain development
1231	GO:0036396	MIS complex
1232	GO:0031527	filopodium membrane
1233	GO:0007158	neuron cell-cell adhesion
1234	GO:0097169	AIM2 inflammasome complex
1235	GO:0009966	regulation of signal transduction
1236	GO:0061384	heart trabecula morphogenesis
1237	GO:0016779	nucleotidyltransferase activity
1238	GO:0048592	eye morphogenesis
1239	GO:0051495	positive regulation of cytoskeleton organization
1240	GO:0010614	negative regulation of cardiac muscle hypertrophy
1241	GO:0016811	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
1242	GO:0046835	carbohydrate phosphorylation
1243	GO:0048646	anatomical structure formation involved in morphogenesis
1244	GO:0051208	sequestering of calcium ion
1245	GO:0010243	response to organonitrogen compound
1246	GO:0031406	carboxylic acid binding
1247	GO:0046903	secretion
1248	GO:0005846	nuclear cap binding complex
1249	GO:0007369	gastrulation
1250	GO:0043545	molybdopterin cofactor metabolic process
1251	GO:0071971	extracellular vesicular exosome assembly

1252	GO:0008287	protein serine/threonine phosphatase complex
1253	GO:0035265	organ growth
1254	GO:0043221	SMC family protein binding
1255	GO:0051602	response to electrical stimulus
1256	GO:0015695	organic cation transport
1257	GO:0043132	NAD transport
1258	KEGG:Linoleic_acid_metabolism	
1259	GO:0070086	ubiquitin-dependent endocytosis
1260	GO:0097371	MDM2/MDM4 family protein binding
1261	GO:0021795	cerebral cortex cell migration
1262	GO:0036117	hyaluranon cable
1263	GO:0010575	positive regulation vascular endothelial growth factor production
1264	GO:0009629	response to gravity
1265	GO:0019060	intracellular transport of viral protein in host cell
1266	GO:0031640	killing of cells of other organism
1267	GO:0032090	Pyrin domain binding
1268	GO:0000781	chromosome, telomeric region
1269	GO:0002076	osteoblast development
1270	GO:0015645	fatty acid ligase activity
1271	GO:0002090	regulation of receptor internalization
1272	GO:0003211	cardiac ventricle formation
1273	GO:0045597	positive regulation of cell differentiation
1274	GO:0032996	Bcl3-Bcl10 complex
1275	GO:0021986	habenula development
1276	GO:0016624	oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
1277	GO:1900038	negative regulation of cellular response to hypoxia
1278	GO:0010841	positive regulation of circadian sleep/wake cycle, wakefulness
1279	GO:0061133	endopeptidase activator activity
1280	KEGG:Systemic_lupus_erythematosus	
1281	GO:0008601	protein phosphatase type 2A regulator activity
1282	GO:0023051	regulation of signaling
1283	KEGG:Lysine_biosynthesis	
1284	GO:0005749	mitochondrial respiratory chain complex II
1285	GO:0051709	regulation of killing of cells of other organism
1286	GO:0006662	glycerol ether metabolic process
1287	GO:0070988	demethylation
1288	GO:0021575	hindbrain morphogenesis
1289	GO:0001657	ureteric bud development
1290	GO:2001027	negative regulation of endothelial cell chemotaxis

1291	GO:0000178	exosome (RNase complex)
1292	GO:0051866	general adaptation syndrome
1293	KEGG:Thyroid_cancer	
1294	GO:0001959	regulation of cytokine-mediated signaling pathway
1295	GO:0006259	DNA metabolic process
1296	GO:0051984	positive regulation of chromosome segregation
1297	GO:0030362	protein phosphatase type 4 regulator activity
1298	GO:0060463	lung lobe morphogenesis
1299	GO:0016812	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides
1300	GO:0016226	iron-sulfur cluster assembly
1301	GO:0033026	negative regulation of mast cell apoptotic process
1302	GO:0032900	negative regulation of neurotrophin production
1303	GO:0097386	glial cell projection
1304	GO:0001944	vasculature development
1305	GO:0045682	regulation of epidermis development
1306	GO:0032449	CBM complex
1307	GO:0090219	negative regulation of lipid kinase activity
1308	GO:0045916	negative regulation of complement activation
1309	GO:0019730	antimicrobial humoral response
1310	GO:0000303	response to superoxide
1311	KEGG:Lipoic_acid_metabolism	
1312	GO:0003007	heart morphogenesis
1313	GO:0000104	succinate dehydrogenase activity
1314	GO:0031010	ISWI-type complex
1315	GO:0042982	amyloid precursor protein metabolic process
1316	GO:0019897	extrinsic component of plasma membrane
1317	GO:0090249	regulation of cell motility involved in somitogenic axis elongation
1318	GO:0032797	SMN complex
1319	GO:0002177	manchette
1320	GO:0031102	neuron projection regeneration
1321	GO:0005685	U1 snRNP
1322	GO:1900119	positive regulation of execution phase of apoptosis
1323	GO:0005955	calcineurin complex
1324	GO:0044254	multicellular organismal protein catabolic process
1325	GO:1901216	positive regulation of neuron death
1326	GO:0072141	renal interstitial cell development
1327	GO:0044344	cellular response to fibroblast growth factor stimulus

1328	KEGG:beta_Alanine_metabolism	
1329	GO:0000176	nuclear exosome (RNase complex)
1330	GO:0097350	neutrophil clearance
1331	GO:0003157	endocardium development
1332	GO:0090288	negative regulation of cellular response to growth factor stimulus
1333	GO:0001763	morphogenesis of a branching structure
1334	GO:0006611	protein export from nucleus
1335	GO:0015728	mevalonate transport
1336	GO:0032093	SAM domain binding
1337	GO:0051987	positive regulation of attachment of spindle microtubules to kinetochore
1338	GO:0071338	positive regulation of hair follicle cell proliferation
1339	GO:0032244	positive regulation of nucleoside transport
1340	GO:0051128	regulation of cellular component organization
1341	GO:0000964	mitochondrial RNA 5'-end processing
1342	GO:0048266	behavioral response to pain
1343	GO:0030289	protein phosphatase 4 complex
1344	GO:0060748	tertiary branching involved in mammary gland duct morphogenesis
1345	GO:0003148	outflow tract septum morphogenesis
1346	GO:0008074	guanylate cyclase complex, soluble
1347	GO:0005868	cytoplasmic dynein complex
1348	GO:0006740	NADPH regeneration
1349	GO:0090398	cellular senescence
1350	GO:0060674	placenta blood vessel development
1351	GO:1902268	negative regulation of polyamine transmembrane transport
1352	KEGG:Spliceosome	
1353	GO:0032204	regulation of telomere maintenance
1354	GO:0033031	positive regulation of neutrophil apoptotic process
1355	GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
1356	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
1357	GO:0006975	DNA damage induced protein phosphorylation
1358	GO:0035749	myelin sheath adaxonal region
1359	GO:0042472	inner ear morphogenesis
1360	GO:0061441	renal artery morphogenesis
1361	GO:0004896	cytokine receptor activity
1362	GO:0043518	negative regulation of DNA damage response,

		signal transduction by p53 class mediator
1363	GO:0006284	base-excision repair
1364	GO:0007162	negative regulation of cell adhesion
1365	GO:0060661	submandibular salivary gland formation
1366	GO:0002091	negative regulation of receptor internalization
1367	GO:0051780	behavioral response to nutrient
1368	GO:0006865	amino acid transport
1369	GO:0001709	cell fate determination
1370	GO:0003093	regulation of glomerular filtration
1371	GO:0009306	protein secretion
1372	GO:0001221	transcription cofactor binding
1373	GO:0030948	negative regulation of vascular endothelial growth factor receptor signaling pathway
1374	GO:0048247	lymphocyte chemotaxis
1375	GO:0014802	terminal cisterna
1376	GO:0000159	protein phosphatase type 2A complex
1377	GO:0045263	proton-transporting ATP synthase complex, coupling factor F(o)
1378	GO:0036023	embryonic skeletal limb joint morphogenesis
1379	GO:0051536	iron-sulfur cluster binding
1380	GO:0042542	response to hydrogen peroxide
1381	GO:0009582	detection of abiotic stimulus
1382	GO:0071864	positive regulation of cell proliferation in bone marrow
1383	GO:0072049	comma-shaped body morphogenesis
1384	GO:1901666	positive regulation of NAD+ ADP-ribosyltransferase activity
1385	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I
1386	GO:0021589	cerebellum structural organization
1387	GO:0008219	cell death
1388	GO:0007166	cell surface receptor signaling pathway
1389	GO:0008073	ornithine decarboxylase inhibitor activity
1390	GO:0016272	prefoldin complex
1391	GO:0006637	acyl-CoA metabolic process
1392	GO:2000252	negative regulation of feeding behavior
1393	GO:0060513	prostatic bud formation
1394	GO:0051493	regulation of cytoskeleton organization
1395	GO:0072033	renal vesicle formation
1396	GO:0047496	vesicle transport along microtubule
1397	GO:0060201	clathrin-sculpted acetylcholine transport vesicle membrane
1398	GO:1902176	negative regulation of intrinsic apoptotic signaling pathway in response to oxidative

		stress
1399	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system
1400	GO:0032613	interleukin-10 production
1401	GO:0003273	cell migration involved in endocardial cushion formation
1402	GO:0008608	attachment of spindle microtubules to kinetochore
1403	GO:0072278	metanephric comma-shaped body morphogenesis
1404	GO:0022601	menstrual cycle phase
1405	GO:0005072	transforming growth factor beta receptor, cytoplasmic mediator activity
1406	GO:0048880	sensory system development
1407	KEGG:Cardiac_muscle_contraction	
1408	KEGG:Viral_myocarditis	
1409	GO:0010807	regulation of synaptic vesicle priming
1410	GO:0007435	salivary gland morphogenesis
1411	GO:0007567	parturition
1412	GO:0030057	desmosome
1413	GO:0035999	tetrahydrofolate interconversion
1414	GO:0016992	lipoate synthase activity
1415	GO:0045103	intermediate filament-based process
1416	GO:0072275	metanephric glomerulus morphogenesis
1417	GO:0070412	R-SMAD binding
1418	GO:0071204	histone pre-mRNA 3'end processing complex
1419	GO:0043331	response to dsRNA
1420	GO:0097332	response to antipsychotic drug
1421	GO:0021549	cerebellum development
1422	GO:0072669	tRNA-splicing ligase complex
1423	GO:0048662	negative regulation of smooth muscle cell proliferation
1424	GO:0008528	G-protein coupled peptide receptor activity
1425	GO:0060762	regulation of branching involved in mammary gland duct morphogenesis
1426	GO:0090316	positive regulation of intracellular protein transport
1427	GO:0010724	regulation of definitive erythrocyte differentiation
1428	GO:0005689	U12-type spliceosomal complex
1429	GO:0045596	negative regulation of cell differentiation
1430	GO:0048680	positive regulation of axon regeneration
1431	GO:0032098	regulation of appetite
1432	GO:0070172	positive regulation of tooth mineralization

1433	GO:0034613	cellular protein localization
1434	GO:0034361	very-low-density lipoprotein particle
1435	GO:0021682	nerve maturation
1436	GO:0045638	negative regulation of myeloid cell differentiation
1437	GO:0097449	astrocyte projection
1438	GO:0045089	positive regulation of innate immune response
1439	KEGG:Basal_transcription_factors	
1440	GO:0002548	monocyte chemotaxis
1441	GO:0090235	regulation of metaphase plate congression
1442	GO:0032970	regulation of actin filament-based process
1443	GO:0070062	extracellular vesicular exosome
1444	GO:0030130	clathrin coat of trans-Golgi network vesicle
1445	GO:0031579	membrane raft organization
1446	GO:0015934	large ribosomal subunit
1447	GO:0005643	nuclear pore
1448	GO:0051425	PTB domain binding
1449	GO:0007631	feeding behavior
1450	GO:2001189	negative regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell
1451	GO:0070411	I-SMAD binding
1452	GO:0009986	cell surface
1453	GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
1454	GO:0006096	glycolysis
1455	GO:0060711	labyrinthine layer development
1456	GO:0048291	isotype switching to IgG isotypes
1457	GO:0043932	ossification involved in bone remodeling
1458	GO:0031370	eukaryotic initiation factor 4G binding
1459	GO:2000017	positive regulation of determination of dorsal identity
1460	GO:0007440	foregut morphogenesis
1461	GO:0043382	positive regulation of memory T cell differentiation
1462	GO:0010989	negative regulation of low-density lipoprotein particle clearance
1463	GO:0005773	vacuole
1464	GO:0016668	oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor
1465	GO:0007159	leukocyte cell-cell adhesion
1466	GO:0000096	sulfur amino acid metabolic process
1467	GO:0071985	multivesicular body sorting pathway
1468	GO:0000145	exocyst

1469	GO:0003207	cardiac chamber formation
1470	GO:0030097	hemopoiesis
1471	GO:0005829	cytosol
1472	GO:0016032	viral process
1473	GO:0043206	extracellular fibril organization
1474	GO:0045598	regulation of fat cell differentiation
1475	GO:0007389	pattern specification process
1476	GO:0038001	paracrine signaling
1477	GO:0000940	condensed chromosome outer kinetochore
1478	GO:0071942	XPC complex
1479	GO:0051081	nuclear envelope disassembly
1480	GO:0050764	regulation of phagocytosis
1481	GO:0008188	neuropeptide receptor activity
1482	GO:0042605	peptide antigen binding
1483	GO:0030377	urokinase plasminogen activator receptor activity
1484	GO:0035418	protein localization to synapse
1485	GO:0008540	proteasome regulatory particle, base subcomplex
1486	GO:0009725	response to hormone
1487	GO:0004882	androgen receptor activity
1488	GO:0051726	regulation of cell cycle
1489	GO:0071417	cellular response to organonitrogen compound
1490	GO:0097150	neuronal stem cell maintenance
1491	GO:0071556	integral component of lumenal side of endoplasmic reticulum membrane
1492	GO:0097421	liver regeneration
1493	GO:0005484	SNAP receptor activity
1494	GO:0005501	retinoid binding
1495	GO:0038025	reelin receptor activity
1496	GO:0050790	regulation of catalytic activity
1497	GO:0051054	positive regulation of DNA metabolic process
1498	GO:0044267	cellular protein metabolic process
1499	GO:0001878	response to yeast
1500	GO:1901299	negative regulation of hydrogen peroxide-mediated programmed cell death
1501	GO:0010833	telomere maintenance via telomere lengthening
1502	GO:0006853	carnitine shuttle
1503	GO:0031333	negative regulation of protein complex assembly
1504	GO:0035093	spermatogenesis, exchange of chromosomal proteins
1505	GO:0003241	growth involved in heart morphogenesis
1506	GO:0010745	negative regulation of macrophage derived foam cell differentiation

1507	GO:0021615	glossopharyngeal nerve morphogenesis
1508	GO:0005886	plasma membrane
1509	KEGG:RNA_polymerase	
1510	GO:0016282	eukaryotic 43S preinitiation complex
1511	GO:0019855	calcium channel inhibitor activity
1512	GO:0071455	cellular response to hyperoxia
1513	GO:0060628	regulation of ER to Golgi vesicle-mediated transport
1514	GO:0045738	negative regulation of DNA repair
1515	GO:0001508	regulation of action potential
1516	GO:0021515	cell differentiation in spinal cord
1517	GO:0002024	diet induced thermogenesis
1518	GO:0031588	AMP-activated protein kinase complex
1519	GO:0021545	cranial nerve development
1520	GO:0010715	regulation of extracellular matrix disassembly
1521	GO:0016459	myosin complex
1522	GO:0031100	organ regeneration
1523	GO:0035581	sequestering of extracellular ligand from receptor
1524	GO:0005899	insulin receptor complex
1525	GO:0022037	metencephalon development
1526	GO:1902546	positive regulation of DNA N-glycosylase activity
1527	GO:0004716	receptor signaling protein tyrosine kinase activity
1528	GO:0031419	cobalamin binding
1529	GO:0009982	pseudouridine synthase activity
1530	GO:0032455	nerve growth factor processing
1531	GO:1901201	regulation of extracellular matrix assembly
1532	GO:0060402	calcium ion transport into cytosol
1533	GO:0007028	cytoplasm organization
1534	GO:0012507	ER to Golgi transport vesicle membrane
1535	GO:0019013	viral nucleocapsid
1536	GO:0044242	cellular lipid catabolic process
1537	GO:0005788	endoplasmic reticulum lumen
1538	GO:0007423	sensory organ development
1539	GO:0042594	response to starvation
1540	GO:0010467	gene expression
1541	GO:0001921	positive regulation of receptor recycling
1542	GO:0021569	rhombomere 3 development
1543	GO:0043497	regulation of protein heterodimerization activity
1544	GO:0071159	NF-kappaB complex
1545	GO:0008191	metalloendopeptidase inhibitor activity
1546	GO:0016627	oxidoreductase activity, acting on the CH-CH

		group of donors
1547	GO:0003254	regulation of membrane depolarization
1548	GO:0021568	rhombomere 2 development
1549	GO:0001503	ossification
1550	GO:0043190	ATP-binding cassette (ABC) transporter complex
1551	GO:0032964	collagen biosynthetic process
1552	GO:0046683	response to organophosphorus
1553	GO:0045668	negative regulation of osteoblast differentiation
1554	GO:0033629	negative regulation of cell adhesion mediated by integrin
1555	KEGG:Vasopressin_regulated_water_reabsorption	
1556	GO:2000643	positive regulation of early endosome to late endosome transport
1557	GO:0021796	cerebral cortex regionalization
1558	GO:0009437	carnitine metabolic process
1559	GO:0007175	negative regulation of epidermal growth factor-activated receptor activity
1560	GO:0010032	meiotic chromosome condensation
1561	GO:0032473	cytoplasmic side of mitochondrial outer membrane
1562	GO:0048638	regulation of developmental growth
1563	GO:2001275	positive regulation of glucose import in response to insulin stimulus
1564	GO:0043512	inhibin A complex
1565	GO:0010481	epidermal cell division
1566	GO:0035650	AP-1 adaptor complex binding
1567	GO:0071558	histone demethylase activity (H3-K27 specific)
1568	GO:0001501	skeletal system development
1569	GO:0000776	kinetochore
1570	GO:1901164	negative regulation of trophoblast cell migration
1571	GO:0032792	negative regulation of CREB transcription factor activity
1572	GO:0045836	positive regulation of meiosis
1573	GO:0043394	proteoglycan binding
1574	GO:0046950	cellular ketone body metabolic process
1575	GO:0002142	stereocilia ankle link complex
1576	GO:0005965	protein farnesyltransferase complex
1577	GO:0001935	endothelial cell proliferation
1578	GO:0007499	ectoderm and mesoderm interaction
1579	GO:0060484	lung-associated mesenchyme development
1580	GO:0060279	positive regulation of ovulation
1581	GO:0016667	oxidoreductase activity, acting on a sulfur group

		of donors
1582	GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen
1583	GO:0002507	tolerance induction
1584	GO:1901383	negative regulation of chorionic trophoblast cell proliferation
1585	GO:0097009	energy homeostasis
1586	GO:0031670	cellular response to nutrient
1587	KEGG:Glyoxylate_and_dicarboxylate_metabolism	
1588	GO:0035564	regulation of kidney size
1589	GO:0030027	lamellipodium
1590	KEGG:Glycerolipid_metabolism	
1591	KEGG:Cell_adhesion_molecules__CAMs_	
1592	GO:0005953	CAAX-protein geranylgeranyltransferase complex
1593	GO:1990023	mitotic spindle midzone
1594	GO:1901194	negative regulation of formation of translation preinitiation complex
1595	GO:0047484	regulation of response to osmotic stress
1596	GO:0030539	male genitalia development
1597	KEGG:Nitrogen_metabolism	
1598	GO:0002637	regulation of immunoglobulin production
1599	GO:0019908	nuclear cyclin-dependent protein kinase holoenzyme complex
1600	GO:0002551	mast cell chemotaxis
1601	GO:0009360	DNA polymerase III complex
1602	GO:0018342	protein prenylation
1603	GO:2000381	negative regulation of mesoderm development
1604	GO:0019809	spermidine binding
1605	GO:2000969	positive regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity
1606	KEGG:Synthesis_and_degradation_of_ketone_bodies	
1607	GO:0030178	negative regulation of Wnt signaling pathway
1608	GO:0042574	retinal metabolic process
1609	GO:0060312	regulation of blood vessel remodeling
1610	GO:0010923	negative regulation of phosphatase activity
1611	GO:0033503	HULC complex
1612	GO:0009404	toxin metabolic process

1613	GO:0042138	meiotic DNA double-strand break formation
1614	GO:0046836	glycolipid transport
1615	GO:0003183	mitral valve morphogenesis
1616	GO:0005751	mitochondrial respiratory chain complex IV
1617	GO:0033327	Leydig cell differentiation
1618	GO:0060998	regulation of dendritic spine development
1619	GO:0003676	nucleic acid binding
1620	GO:0043547	positive regulation of GTPase activity
1621	GO:0048147	negative regulation of fibroblast proliferation
1622	GO:0071467	cellular response to pH
1623	GO:0001881	receptor recycling
1624	GO:0005744	mitochondrial inner membrane presequence translocase complex
1625	GO:0060259	regulation of feeding behavior
1626	GO:0050679	positive regulation of epithelial cell proliferation
1627	GO:0071453	cellular response to oxygen levels
1628	GO:0005662	DNA replication factor A complex
1629	GO:0030496	midbody
1630	GO:0005743	mitochondrial inner membrane
1631	GO:0006766	vitamin metabolic process
1632	GO:0004888	transmembrane signaling receptor activity
1633	GO:2000189	positive regulation of cholesterol homeostasis
1634	GO:0030011	maintenance of cell polarity
1635	GO:0030325	adrenal gland development
1636	GO:0033186	CAF-1 complex
1637	GO:0045667	regulation of osteoblast differentiation
1638	GO:0030070	insulin processing
1639	GO:0045879	negative regulation of smoothened signaling pathway
1640	GO:0005902	microvillus
1641	GO:0071676	negative regulation of mononuclear cell migration
1642	GO:0006886	intracellular protein transport
1643	GO:0043546	molybdopterin cofactor binding
1644	GO:0031233	intrinsic component of external side of plasma membrane
1645	GO:0045271	respiratory chain complex I
1646	GO:0031641	regulation of myelination
1647	GO:0060413	atrial septum morphogenesis
1648	GO:0015833	peptide transport
1649	GO:0014806	smooth muscle hyperplasia
1650	GO:0035253	ciliary rootlet
1651	GO:0001756	somitogenesis
1652	GO:0010988	regulation of low-density lipoprotein particle

		clearance
1653	GO:0050839	cell adhesion molecule binding
1654	GO:0014063	negative regulation of serotonin secretion
1655	GO:0031681	G-protein beta-subunit binding
1656	GO:0006788	heme oxidation
1657	GO:1901301	regulation of cargo loading into COPII-coated vesicle
1658	GO:0002040	sprouting angiogenesis
1659	GO:0016281	eukaryotic translation initiation factor 4F complex
1660	GO:0034709	methylosome
1661	GO:0003309	type B pancreatic cell differentiation
1662	GO:0090074	negative regulation of protein homodimerization activity
1663	GO:0005811	lipid particle
1664	GO:0021675	nerve development
1665	GO:0010470	regulation of gastrulation
1666	GO:0022626	cytosolic ribosome
1667	GO:0009409	response to cold
1668	GO:0005534	galactose binding
1669	GO:1900063	regulation of peroxisome organization
1670	GO:2000002	negative regulation of DNA damage checkpoint
1671	GO:0043256	laminin complex
1672	GO:0060735	regulation of eIF2 alpha phosphorylation by dsRNA
1673	GO:0050680	negative regulation of epithelial cell proliferation
1674	GO:0019838	growth factor binding
1675	GO:0010886	positive regulation of cholesterol storage
1676	GO:0005760	gamma DNA polymerase complex
1677	GO:0000296	spermine transport
1678	GO:0034362	low-density lipoprotein particle
1679	GO:0071800	podosome assembly
1680	GO:0004392	heme oxygenase (decyclizing) activity
1681	GO:0090096	positive regulation of metanephric cap mesenchymal cell proliferation
1682	GO:0050665	hydrogen peroxide biosynthetic process
1683	GO:0048313	Golgi inheritance
1684	GO:0060575	intestinal epithelial cell differentiation
1685	GO:0021543	pallium development
1686	GO:0050859	negative regulation of B cell receptor signaling pathway
1687	GO:0001750	photoreceptor outer segment
1688	GO:0016298	lipase activity

1689	GO:0034616	response to laminar fluid shear stress
1690	GO:0070083	clathrin-sculpted monoamine transport vesicle membrane
1691	GO:0015908	fatty acid transport
1692	GO:0032095	regulation of response to food
1693	GO:0032623	interleukin-2 production
1694	GO:2000609	regulation of thyroid hormone generation
1695	GO:0004766	spermidine synthase activity
1696	GO:0004728	receptor signaling protein tyrosine phosphatase activity
1697	GO:0030917	midbrain-hindbrain boundary development
1698	GO:0045502	dynein binding
1699	GO:0001889	liver development
1700	GO:0002176	male germ cell proliferation
1701	GO:0009890	negative regulation of biosynthetic process
1702	GO:0072592	oxygen metabolic process
1703	GO:0001823	mesonephros development
1704	GO:0005125	cytokine activity
1705	GO:0005887	integral component of plasma membrane
1706	GO:0016559	peroxisome fission
1707	GO:0032808	lacrimal gland development
1708	GO:0042166	acetylcholine binding
1709	GO:0031175	neuron projection development
1710	KEGG:Proximal_tubule_bicarbonate_reclamation	
1711	GO:0070664	negative regulation of leukocyte proliferation
1712	GO:0051287	NAD binding
1713	GO:0033063	Rad51B-Rad51C-Rad51D-XRCC2 complex
1714	GO:0032092	positive regulation of protein binding
1715	GO:0046824	positive regulation of nucleocytoplasmic transport
1716	GO:0051835	positive regulation of synapse structural plasticity
1717	GO:0072210	metanephric nephron development
1718	GO:0001955	blood vessel maturation
1719	GO:0005892	acetylcholine-gated channel complex
1720	GO:0022617	extracellular matrix disassembly
1721	GO:0046540	U4/U6 x U5 tri-snRNP complex
1722	KEGG:Vibrio_cholerae_infection	
1723	GO:0030552	cAMP binding
1724	GO:0097057	TRAF2-GSTP1 complex
1725	GO:0031510	SUMO activating enzyme complex
1726	GO:0097114	N-methyl-D-aspartate receptor clustering
1727	GO:0032902	nerve growth factor production

1728	KEGG:Asthma	
1729	GO:0045294	alpha-catenin binding
1730	GO:0010256	endomembrane system organization
1731	GO:0043270	positive regulation of ion transport
1732	GO:0060623	regulation of chromosome condensation
1733	GO:0043462	regulation of ATPase activity
1734	GO:0005686	U2 snRNP
1735	GO:0002407	dendritic cell chemotaxis
1736	GO:0003404	optic vesicle morphogenesis
1737	GO:0015464	acetylcholine receptor activity
1738	GO:0050678	regulation of epithelial cell proliferation
1739	GO:0004601	peroxidase activity
1740	GO:0010766	negative regulation of sodium ion transport
1741	KEGG:Bacterial_invasion_of_epithelial_cells	
1742	GO:0070324	thyroid hormone binding
1743	GO:0031514	motile cilium
1744	GO:0086004	regulation of cardiac muscle cell contraction
1745	GO:0044770	cell cycle phase transition
1746	GO:0005095	GTPase inhibitor activity
1747	GO:0032543	mitochondrial translation
1748	GO:0002945	cyclin K-CDK13 complex
1749	KEGG:Pancreatic_secretion	
1750	GO:0005916	fascia adherens
1751	GO:0071364	cellular response to epidermal growth factor stimulus
1752	GO:0003105	negative regulation of glomerular filtration
1753	GO:0042989	sequestering of actin monomers
1754	GO:0050867	positive regulation of cell activation
1755	GO:0044111	development involved in symbiotic interaction
1756	GO:0042978	ornithine decarboxylase activator activity
1757	GO:0051388	positive regulation of neurotrophin TRK receptor signaling pathway
1758	GO:0048495	Roundabout binding
1759	GO:0003409	optic cup structural organization
1760	GO:0032299	ribonuclease H2 complex
1761	KEGG:Nucleotide_excision_repair	
1762	GO:0061034	olfactory bulb mitral cell layer development
1763	GO:0007320	insemination
1764	GO:0002162	dystroglycan binding
1765	GO:0007154	cell communication
1766	GO:0035845	photoreceptor cell outer segment organization
1767	GO:2000738	positive regulation of stem cell differentiation
1768	GO:0080164	regulation of nitric oxide metabolic process

1769	GO:0090136	epithelial cell-cell adhesion
1770	GO:0001667	ameboidal cell migration
1771	GO:0019089	transmission of virus
1772	GO:0021623	oculomotor nerve formation
1773	GO:0061078	positive regulation of prostaglandin secretion involved in immune response
1774	GO:0043116	negative regulation of vascular permeability
1775	GO:0006289	nucleotide-excision repair
1776	GO:0042262	DNA protection
1777	GO:2000785	regulation of autophagic vacuole assembly
1778	GO:0005971	ribonucleoside-diphosphate reductase complex
1779	GO:0042640	anagen
1780	GO:0000302	response to reactive oxygen species
1781	GO:0006307	DNA dealkylation involved in DNA repair
1782	GO:0060346	bone trabecula formation
1783	GO:0050807	regulation of synapse organization
1784	GO:0001553	luteinization
1785	GO:0051156	glucose 6-phosphate metabolic process
1786	GO:0043560	insulin receptor substrate binding
1787	GO:0035902	response to immobilization stress
1788	GO:0030667	secretory granule membrane
1789	GO:0072554	blood vessel lumenization
1790	GO:0060561	apoptotic process involved in morphogenesis
1791	GO:0071782	endoplasmic reticulum tubular network
1792	GO:0031314	extrinsic component of mitochondrial inner membrane
1793	GO:0048407	platelet-derived growth factor binding
1794	KEGG:Cell_cycle	
1795	GO:0007492	endoderm development
1796	GO:0036035	osteoclast development
1797	GO:0055105	ubiquitin-protein ligase inhibitor activity
1798	GO:1900195	positive regulation of oocyte maturation
1799	GO:0035612	AP-2 adaptor complex binding
1800	GO:0005838	proteasome regulatory particle
1801	GO:0009408	response to heat
1802	GO:0010468	regulation of gene expression
1803	GO:0048260	positive regulation of receptor-mediated endocytosis
1804	GO:0030154	cell differentiation
1805	GO:0033605	positive regulation of catecholamine secretion
1806	GO:0044393	microspike
1807	GO:0034098	Cdc48p-Npl4p-Ufd1p AAA ATPase complex
1808	GO:0001504	neurotransmitter uptake
1809	GO:0051021	GDP-dissociation inhibitor binding

1810	GO:2000648	positive regulation of stem cell proliferation
1811	GO:0097454	Schwann cell microvillus
1812	GO:0015026	coreceptor activity
1813	GO:0042089	cytokine biosynthetic process
1814	GO:0021819	layer formation in cerebral cortex
1815	GO:0005523	tropomyosin binding
1816	GO:1900182	positive regulation of protein localization to nucleus
1817	GO:0018171	peptidyl-cysteine oxidation
1818	GO:0016446	somatic hypermutation of immunoglobulin genes
1819	GO:0009968	negative regulation of signal transduction
1820	GO:0007379	segment specification
1821	GO:0032301	MutSalpha complex
1822	GO:0002792	negative regulation of peptide secretion
1823	GO:0046326	positive regulation of glucose import
1824	GO:0005608	laminin-3 complex
1825	GO:0033505	floor plate morphogenesis
1826	GO:0007051	spindle organization
1827	GO:0051047	positive regulation of secretion
1828	GO:0008210	estrogen metabolic process
1829	GO:0035718	macrophage migration inhibitory factor binding
1830	GO:0070969	ULK1-ATG13-FIP200 complex
1831	GO:0060138	fetal process involved in parturition
1832	GO:0044262	cellular carbohydrate metabolic process
1833	GO:0048039	ubiquinone binding
1834	GO:0090010	transforming growth factor beta receptor signaling pathway involved in primitive streak formation
1835	GO:0009649	entrainment of circadian clock
1836	GO:0000710	meiotic mismatch repair
1837	GO:0008484	sulfuric ester hydrolase activity
1838	GO:0035693	NOS2-CD74 complex
1839	GO:0035867	alphav-beta3 integrin-IGF-1-IGF1R complex
1840	GO:0005176	ErbB-2 class receptor binding
1841	GO:2000021	regulation of ion homeostasis
1842	GO:0060802	epiblast cell-extraembryonic ectoderm cell signaling involved in anterior/posterior axis specification
1843	GO:0009410	response to xenobiotic stimulus
1844	GO:0008038	neuron recognition
1845	GO:0000046	autophagic vacuole fusion
1846	GO:0040036	regulation of fibroblast growth factor receptor signaling pathway

1847	GO:0048538	thymus development
1848	GO:0071944	cell periphery
1849	GO:0010811	positive regulation of cell-substrate adhesion
1850	GO:0050918	positive chemotaxis
1851	GO:0035692	macrophage migration inhibitory factor receptor complex
1852	GO:0021540	corpus callosum morphogenesis
1853	GO:0002085	inhibition of neuroepithelial cell differentiation
1854	GO:0046649	lymphocyte activation
1855	GO:2000645	negative regulation of receptor catabolic process
1856	GO:0004784	superoxide dismutase activity
1857	GO:0060045	positive regulation of cardiac muscle cell proliferation
1858	GO:0031936	negative regulation of chromatin silencing
1859	GO:2000536	negative regulation of entry of bacterium into host cell
1860	GO:0001831	trophectodermal cellular morphogenesis
1861	GO:0070053	thrombospondin receptor activity
1862	GO:0010324	membrane invagination
1863	GO:1900747	negative regulation of vascular endothelial growth factor signaling pathway
1864	GO:0019883	antigen processing and presentation of endogenous antigen
1865	GO:0005768	endosome
1866	GO:0002199	zona pellucida receptor complex
1867	GO:0042167	heme catabolic process
1868	GO:0051799	negative regulation of hair follicle development
1869	GO:0001520	outer dense fiber
1870	GO:0033342	negative regulation of collagen binding
1871	GO:0016342	catenin complex
1872	GO:0048382	mesendoderm development
1873	GO:0048678	response to axon injury
1874	GO:0070410	co-SMAD binding
1875	GO:0050748	negative regulation of lipoprotein metabolic process
1876	GO:0005832	chaperonin-containing T-complex
1877	GO:0001010	sequence-specific DNA binding transcription factor recruiting transcription factor activity
1878	GO:0042733	embryonic digit morphogenesis
1879	GO:0031369	translation initiation factor binding
1880	GO:0030426	growth cone
1881	GO:0006629	lipid metabolic process
1882	GO:0019682	glyceraldehyde-3-phosphate metabolic process
1883	GO:0010957	negative regulation of vitamin D biosynthetic

		process
1884	GO:0005604	basement membrane
1885	GO:0051028	mRNA transport
1886	GO:0006809	nitric oxide biosynthetic process
1887	GO:0006644	phospholipid metabolic process
1888	GO:0042176	regulation of protein catabolic process
1889	GO:0070765	gamma-secretase complex
1890	GO:0045751	negative regulation of Toll signaling pathway
1891	GO:0031362	anchored component of external side of plasma membrane
1892	GO:0000117	regulation of transcription involved in G2/M transition of mitotic cell cycle
1893	GO:0032809	neuronal cell body membrane
1894	KEGG:RNA_degradation	
1895	GO:0001917	photoreceptor inner segment
1896	GO:0001135	RNA polymerase II transcription factor recruiting transcription factor activity
1897	GO:0071013	catalytic step 2 spliceosome
1898	GO:0016615	malate dehydrogenase activity
1899	GO:0002060	purine nucleobase binding
1900	GO:0016202	regulation of striated muscle tissue development
1901	GO:0071157	negative regulation of cell cycle arrest
1902	GO:0042035	regulation of cytokine biosynthetic process
1903	GO:0031491	nucleosome binding
1904	GO:0000932	cytoplasmic mRNA processing body
1905	GO:0032389	MutLalpha complex
1906	KEGG:Nicotinate_and_nicotinamide_metabolism	
1907	GO:0030501	positive regulation of bone mineralization
1908	GO:0030884	exogenous lipid antigen binding
1909	GO:0033290	eukaryotic 48S preinitiation complex
1910	GO:0002116	semaphorin receptor complex
1911	GO:0060166	olfactory pit development
1912	GO:0006869	lipid transport
1913	GO:0034719	SMN-Sm protein complex
1914	GO:0009432	SOS response
1915	GO:0010494	cytoplasmic stress granule
1916	KEGG:TGF_beta_signaling_pathway	
1917	GO:0021636	trigeminal nerve morphogenesis
1918	GO:0001731	formation of translation preinitiation complex
1919	GO:0045728	respiratory burst after phagocytosis
1920	GO:0050922	negative regulation of chemotaxis
1921	GO:0005687	U4 snRNP
1922	GO:0071243	cellular response to arsenic-containing

		substance
1923	GO:0071425	hematopoietic stem cell proliferation
1924	GO:0051255	spindle midzone assembly
1925	GO:0043616	keratinocyte proliferation
1926	GO:0060021	palate development
1927	GO:0034505	tooth mineralization
1928	GO:0003743	translation initiation factor activity
1929	GO:0010460	positive regulation of heart rate
1930	GO:0051645	Golgi localization
1931	GO:0045333	cellular respiration
1932	GO:0034641	cellular nitrogen compound metabolic process
1933	GO:0017154	semaphorin receptor activity
1934	GO:0032680	regulation of tumor necrosis factor production
1935	GO:0071541	eukaryotic translation initiation factor 3 complex, eIF3m
1936	GO:0016469	proton-transporting two-sector ATPase complex
1937	GO:0051642	centrosome localization
1938	GO:0003416	endochondral bone growth
1939	GO:0030532	small nuclear ribonucleoprotein complex
1940	GO:0046449	creatinine metabolic process
1941	GO:0031201	SNARE complex
1942	GO:0060244	negative regulation of cell proliferation involved in contact inhibition
1943	GO:0016079	synaptic vesicle exocytosis
1944	GO:0042274	ribosomal small subunit biogenesis
1945	GO:0035869	ciliary transition zone
1946	GO:0009266	response to temperature stimulus
1947	GO:0016941	natriuretic peptide receptor activity
1948	GO:0005683	U7 snRNP
1949	GO:0010942	positive regulation of cell death
1950	KEGG:Autoimmune_thyroid_disease	
1951	GO:0051087	chaperone binding
1952	GO:0036297	interstrand cross-link repair
1953	GO:0016841	ammonia-lyase activity
1954	GO:0042273	ribosomal large subunit biogenesis
1955	GO:0014070	response to organic cyclic compound
1956	GO:2000824	negative regulation of androgen receptor activity
1957	GO:0003310	pancreatic A cell differentiation
1958	GO:0030214	hyaluronan catabolic process
1959	GO:0042116	macrophage activation
1960	GO:0032099	negative regulation of appetite
1961	GO:0001562	response to protozoan
1962	GO:0005852	eukaryotic translation initiation factor 3 complex

1963	GO:0016447	somatic recombination of immunoglobulin gene segments
1964	GO:0048813	dendrite morphogenesis
1965	GO:0061379	inferior colliculus development
1966	GO:0045113	regulation of integrin biosynthetic process
1967	GO:0016222	procollagen-proline 4-dioxygenase complex
1968	GO:0016525	negative regulation of angiogenesis
1969	KEGG:Parkinson_s_disease	
1970	GO:0045639	positive regulation of myeloid cell differentiation
1971	GO:0035092	sperm chromatin condensation
1972	GO:0072197	ureter morphogenesis
1973	GO:2001020	regulation of response to DNA damage stimulus
1974	GO:0014737	positive regulation of muscle atrophy
1975	GO:0005840	ribosome
1976	GO:0045191	regulation of isotype switching
1977	GO:0003171	atrioventricular valve development
1978	GO:1901605	alpha-amino acid metabolic process
1979	GO:0072686	mitotic spindle
1980	GO:0030742	GTP-dependent protein binding
1981	GO:2000195	negative regulation of female gonad development
1982	GO:0050786	RAGE receptor binding
1983	GO:0022904	respiratory electron transport chain
1984	GO:0009611	response to wounding
1985	GO:0006771	riboflavin metabolic process
1986	GO:0008398	sterol 14-demethylase activity
1987	GO:0061325	cell proliferation involved in outflow tract morphogenesis
1988	GO:0072563	endothelial microparticle
1989	GO:0015935	small ribosomal subunit
1990	GO:0030663	COPI-coated vesicle membrane
1991	GO:0006710	androgen catabolic process
1992	GO:0001824	blastocyst development
1993	GO:0032637	interleukin-8 production
1994	GO:0005923	tight junction
1995	GO:0016505	peptidase activator activity involved in apoptotic process
1996	GO:0070033	synaptobrevin 2-SNAP-25-syntaxin-1a-complexin II complex
1997	GO:0006446	regulation of translational initiation
1998	GO:0043031	negative regulation of macrophage activation
1999	GO:0046685	response to arsenic-containing substance
2000	GO:0050921	positive regulation of chemotaxis

2001	KEGG:Primary_bile_acid_biosynthesis	
2002	GO:0050891	multicellular organismal water homeostasis
2003	GO:0007128	meiotic prophase I
2004	GO:0071310	cellular response to organic substance
2005	GO:0072040	negative regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis
2006	GO:0045906	negative regulation of vasoconstriction
2007	GO:0017101	aminoacyl-tRNA synthetase multienzyme complex
2008	GO:0006413	translational initiation
2009	GO:0008272	sulfate transport
2010	GO:0060760	positive regulation of response to cytokine stimulus
2011	GO:0047066	phospholipid-hydroperoxide glutathione peroxidase activity
2012	GO:0007507	heart development
2013	KEGG:Endometrial_cancer	
2014	GO:0071731	response to nitric oxide
2015	KEGG:Terpenoid_backbone_biosynthesis	
2016	GO:1990089	response to nerve growth factor
2017	GO:0019083	viral transcription
2018	GO:0015116	sulfate transmembrane transporter activity
2019	GO:0031228	intrinsic component of Golgi membrane
2020	GO:0035988	chondrocyte proliferation
2021	GO:0032849	positive regulation of cellular pH reduction
2022	GO:0016358	dendrite development
2023	GO:0000407	pre-autophagosomal structure
2024	GO:0048752	semicircular canal morphogenesis
2025	GO:0022900	electron transport chain
2026	GO:0004998	transferrin receptor activity
2027	GO:0035360	positive regulation of peroxisome proliferator activated receptor signaling pathway
2028	GO:0031427	response to methotrexate
2029	GO:0000166	nucleotide binding
2030	GO:0019058	viral life cycle
2031	GO:0021570	rhombomere 4 development
2032	GO:0001076	RNA polymerase II transcription factor binding transcription factor activity
2033	GO:0016021	integral component of membrane
2034	GO:1901031	regulation of response to reactive oxygen species
2035	GO:0045920	negative regulation of exocytosis

2036	GO:0048705	skeletal system morphogenesis
2037	GO:0031247	actin rod assembly
2038	GO:0030529	ribonucleoprotein complex
2039	GO:0061193	taste bud development
2040	GO:0071621	granulocyte chemotaxis
2041	GO:0021571	rhombomere 5 development
2042	GO:0034437	glycoprotein transporter activity
2043	KEGG:Long_term_depression	
2044	GO:0005055	laminin receptor activity
2045	GO:0048468	cell development
2046	GO:0060203	clathrin-sculpted glutamate transport vesicle membrane
2047	GO:0030207	chondroitin sulfate catabolic process
2048	GO:0060025	regulation of synaptic activity
2049	GO:0014009	glial cell proliferation
2050	GO:0006999	nuclear pore organization
2051	GO:0016070	RNA metabolic process
2052	GO:0044252	negative regulation of multicellular organismal metabolic process
2053	GO:0030235	nitric-oxide synthase regulator activity
2054	GO:0014895	smooth muscle hypertrophy
2055	GO:0021754	facial nucleus development
2056	KEGG:Vascular_smooth_muscle_contraction	
2057	GO:0021771	lateral geniculate nucleus development
2058	GO:0005589	collagen type VI
2059	GO:0030424	axon
2060	GO:0050656	3'-phosphoadenosine 5'-phosphosulfate binding
2061	GO:0003723	RNA binding
2062	GO:0021871	forebrain regionalization
2063	GO:0060297	regulation of sarcomere organization
2064	GO:0051668	localization within membrane
2065	GO:0003106	negative regulation of glomerular filtration by angiotensin
2066	GO:0046832	negative regulation of RNA export from nucleus
2067	GO:0090327	negative regulation of locomotion involved in locomotory behavior
2068	GO:0033007	negative regulation of mast cell activation involved in immune response
2069	GO:0042622	photoreceptor outer segment membrane
2070	KEGG:Vitamin_B6_metabolism	
2071	GO:0045652	regulation of megakaryocyte differentiation
2072	GO:0003166	bundle of His development
2073	GO:0061138	morphogenesis of a branching epithelium

2074	GO:0031651	negative regulation of heat generation
2075	GO:0005578	proteinaceous extracellular matrix
2076	GO:0000445	THO complex part of transcription export complex
2077	GO:0035928	rRNA import into mitochondrion
2078	GO:0031380	nuclear RNA-directed RNA polymerase complex
2079	GO:0072347	response to anesthetic
2080	GO:0050688	regulation of defense response to virus
2081	GO:0070075	tear secretion
2082	GO:0016524	latrotoxin receptor activity
2083	KEGG:Bladder_cancer	
2084	GO:2001016	positive regulation of skeletal muscle cell differentiation
2085	KEGG:Graft_versus_host_disease	
2086	GO:0030910	olfactory placode formation
2087	GO:0033065	Rad51C-XRCC3 complex
2088	GO:0016765	transferase activity, transferring alkyl or aryl (other than methyl) groups
2089	GO:0040030	regulation of molecular function, epigenetic
2090	GO:0006935	chemotaxis
2091	GO:0016486	peptide hormone processing
2092	GO:0060049	regulation of protein glycosylation
2093	GO:0071910	determination of liver left/right asymmetry
2094	GO:0072233	metanephric thick ascending limb development
2095	GO:0043515	kinetochore binding
2096	GO:0031589	cell-substrate adhesion
2097	KEGG:Type_I_diabetes_mellitus	
2098	GO:0019516	lactate oxidation
2099	GO:0014894	response to denervation involved in regulation of muscle adaptation
2100	GO:2000253	positive regulation of feeding behavior
2101	GO:0000347	THO complex
2102	GO:0009636	response to toxic substance
2103	GO:0006996	organelle organization
2104	GO:2000313	regulation of fibroblast growth factor receptor signaling pathway involved in neural plate anterior/posterior pattern formation
2105	GO:0031105	septin complex
2106	GO:0016570	histone modification
2107	GO:0031901	early endosome membrane
2108	GO:0005641	nuclear envelope lumen
2109	GO:0051702	interaction with symbiont
2110	GO:0021889	olfactory bulb interneuron differentiation

2111	GO:0005850	eukaryotic translation initiation factor 2 complex
2112	GO:0019948	SUMO activating enzyme activity
2113	GO:0019888	protein phosphatase regulator activity
2114	GO:0022408	negative regulation of cell-cell adhesion
2115	GO:0016445	somatic diversification of immunoglobulins
2116	GO:0090193	positive regulation of glomerulus development
2117	GO:0003185	sinoatrial valve morphogenesis
2118	GO:0019865	immunoglobulin binding
2119	GO:0009609	response to symbiotic bacterium
2120	GO:0005527	macrolide binding
2121	GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway
2122	GO:0060280	negative regulation of ovulation
2123	GO:0000722	telomere maintenance via recombination
2124	GO:0021510	spinal cord development
2125	GO:0040037	negative regulation of fibroblast growth factor receptor signaling pathway
2126	GO:0035562	negative regulation of chromatin binding
2127	GO:0017059	serine C-palmitoyltransferase complex
2128	KEGG:Allograft_rejection	
2129	GO:0016176	superoxide-generating NADPH oxidase activator activity
2130	GO:0003954	NADH dehydrogenase activity
2131	GO:0032947	protein complex scaffold
2132	GO:0045143	homologous chromosome segregation
2133	GO:0045040	protein import into mitochondrial outer membrane
2134	GO:0043083	synaptic cleft
2135	GO:0010591	regulation of lamellipodium assembly
2136	GO:0042765	GPI-anchor transamidase complex
2137	GO:1900276	regulation of proteinase activated receptor activity
2138	GO:0051781	positive regulation of cell division
2139	GO:0001867	complement activation, lectin pathway
2140	GO:0045179	apical cortex
2141	GO:0071598	neuronal ribonucleoprotein granule
2142	GO:0097167	circadian regulation of translation
2143	GO:0003923	GPI-anchor transamidase activity
2144	GO:0044065	regulation of respiratory system process
2145	GO:0048565	digestive tract development
2146	GO:0042612	MHC class I protein complex
2147	GO:0010035	response to inorganic substance
2148	GO:0043022	ribosome binding

2149	GO:0043620	regulation of DNA-templated transcription in response to stress
2150	GO:0005664	nuclear origin of replication recognition complex
2151	GO:0061053	somite development
2152	GO:0002944	cyclin K-CDK12 complex
2153	GO:0048566	embryonic digestive tract development
2154	GO:0050902	leukocyte adhesive activation
2155	GO:0001832	blastocyst growth
2156	GO:0030915	Smc5-Smc6 complex
2157	GO:0045840	positive regulation of mitosis
2158	GO:0045261	proton-transporting ATP synthase complex, catalytic core F(1)
2159	GO:0001916	positive regulation of T cell mediated cytotoxicity
2160	GO:0070438	mTOR-FKBP12-rapamycin complex
2161	KEGG:Purine_metabolism	
2162	GO:0060126	somatotropin secreting cell differentiation
2163	GO:0043062	extracellular structure organization
2164	GO:0002046	opsin binding
2165	GO:0042731	PH domain binding
2166	GO:0042834	peptidoglycan binding
2167	GO:0031523	Myb complex
2168	GO:0005697	telomerase holoenzyme complex
2169	GO:0045112	integrin biosynthetic process
2170	GO:0055087	Ski complex
2171	GO:0009892	negative regulation of metabolic process
2172	GO:0014889	muscle atrophy
2173	KEGG:Pyrimidine_metabolism	
2174	GO:0032958	inositol phosphate biosynthetic process
2175	GO:0061072	iris morphogenesis
2176	GO:0021516	dorsal spinal cord development
2177	GO:0043610	regulation of carbohydrate utilization
2178	GO:0021514	ventral spinal cord interneuron differentiation
2179	GO:0044308	axonal spine
2180	GO:0003420	regulation of growth plate cartilage chondrocyte proliferation
2181	GO:2000491	positive regulation of hepatic stellate cell activation
2182	GO:0030695	GTPase regulator activity
2183	GO:0030574	collagen catabolic process
2184	GO:0016817	hydrolase activity, acting on acid anhydrides
2185	GO:0060421	positive regulation of heart growth
2186	GO:0021855	hypothalamus cell migration

2187	GO:0000808	origin recognition complex
2188	GO:0016768	spermine synthase activity
2189	GO:0006109	regulation of carbohydrate metabolic process
2190	GO:0060872	semicircular canal development
2191	GO:0007632	visual behavior
2192	GO:0001179	RNA polymerase I transcription factor binding
2193	GO:0016442	RISC complex
2194	GO:0021707	cerebellar granule cell differentiation
2195	GO:0005584	collagen type I
2196	GO:0044297	cell body
2197	GO:0005898	interleukin-13 receptor complex
2198	GO:0001505	regulation of neurotransmitter levels
2199	GO:0070345	negative regulation of fat cell proliferation
2200	GO:0031585	regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity
2201	GO:0021869	forebrain ventricular zone progenitor cell division
2202	GO:0034121	regulation of toll-like receptor signaling pathway
2203	GO:0005588	collagen type V
2204	GO:1990075	periciliary membrane compartment
2205	GO:0002118	aggressive behavior
2206	GO:0006097	glyoxylate cycle
2207	GO:0003195	tricuspid valve formation
2208	GO:0032330	regulation of chondrocyte differentiation
2209	GO:0008559	xenobiotic-transporting ATPase activity
2210	GO:0007155	cell adhesion
2211	GO:0050942	positive regulation of pigment cell differentiation
2212	GO:0051970	negative regulation of transmission of nerve impulse
2213	GO:0097165	nuclear stress granule
2214	GO:0044691	tooth eruption
2215	GO:1902231	positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage
2216	GO:0071062	alphav-beta3 integrin-vitronectin complex
2217	GO:0051409	response to nitrosative stress
2218	GO:0005905	coated pit
2219	GO:0030317	sperm motility
2220	GO:0007611	learning or memory
2221	GO:0005779	integral component of peroxisomal membrane
2222	GO:0033631	cell-cell adhesion mediated by integrin
2223	GO:0030904	retromer complex

2224	GO:0035686	sperm fibrous sheath
2225	GO:0046982	protein heterodimerization activity
2226	GO:0035229	positive regulation of glutamate-cysteine ligase activity
2227	GO:0031205	endoplasmic reticulum Sec complex
2228	GO:0017162	aryl hydrocarbon receptor binding
2229	GO:0008541	proteasome regulatory particle, lid subcomplex
2230	GO:0030061	mitochondrial crista
2231	GO:0035226	glutamate-cysteine ligase catalytic subunit binding
2232	GO:0038061	NIK/NF-kappaB signaling
2233	GO:0002922	positive regulation of humoral immune response
2234	GO:0045730	respiratory burst
2235	GO:0008609	alkylglycerone-phosphate synthase activity
2236	GO:0030239	myofibril assembly
2237	GO:0090166	Golgi disassembly
2238	GO:0070051	fibrinogen binding
2239	GO:0097542	ciliary tip
2240	GO:0019430	removal of superoxide radicals
2241	GO:0048870	cell motility
2242	GO:0015837	amine transport
2243	GO:0070628	proteasome binding
2244	GO:0007620	copulation
2245	GO:0050746	regulation of lipoprotein metabolic process
2246	GO:0007431	salivary gland development
2247	GO:0010822	positive regulation of mitochondrion organization
2248	GO:0046784	viral mRNA export from host cell nucleus
2249	GO:0043020	NADPH oxidase complex
2250	GO:0061038	uterus morphogenesis
2251	GO:0017109	glutamate-cysteine ligase complex
2252	GO:0070576	vitamin D 24-hydroxylase activity
2253	GO:0032388	positive regulation of intracellular transport
2254	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)

Supplementary Table S3

GeneID	Name	Description
ENSG00000000938	FGR	FGR proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:3697]
ENSG00000001626	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7) [Source:HGNC Symbol;Acc:HGNC:1884]
ENSG00000004468	CD38	CD38 molecule [Source:HGNC Symbol;Acc:HGNC:1667]
ENSG00000004848	ARX	aristaless related homeobox [Source:HGNC Symbol;Acc:HGNC:18060]
ENSG00000005381	MPO	myeloperoxidase [Source:HGNC Symbol;Acc:HGNC:7218]
ENSG00000007908	SELE	selectin E [Source:HGNC Symbol;Acc:HGNC:10718]
ENSG00000008018	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1 [Source:HGNC Symbol;Acc:HGNC:9537]
ENSG00000010278	CD9	CD9 molecule [Source:HGNC Symbol;Acc:HGNC:1709]
ENSG00000010610	CD4	CD4 molecule [Source:HGNC Symbol;Acc:HGNC:1678]
ENSG00000011422	PLAUR	plasminogen activator, urokinase receptor [Source:HGNC Symbol;Acc:HGNC:9053]
ENSG00000011465	DCN	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
ENSG00000012048	BRCA1	breast cancer 1, early onset [Source:HGNC Symbol;Acc:HGNC:1100]
ENSG00000012124	CD22	CD22 molecule [Source:HGNC Symbol;Acc:HGNC:1643]
ENSG00000017427	IGF1	insulin-like growth factor 1 (somatomedin C) [Source:HGNC Symbol;Acc:HGNC:5464]
ENSG00000019549	SNAI2	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:11094]
ENSG00000020633	RUNX3	runt-related transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:10473]
ENSG00000020922	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:7230]
ENSG00000021461	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43 [Source:HGNC Symbol;Acc:HGNC:17450]
ENSG00000025423	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 [Source:HGNC Symbol;Acc:HGNC:23316]
ENSG00000026508	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:HGNC:1681]
ENSG00000028137	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B [Source:HGNC Symbol;Acc:HGNC:11917]
ENSG00000029534	ANK1	ankyrin 1, erythrocytic [Source:HGNC Symbol;Acc:HGNC:492]
ENSG00000036549	ZZZ3	zinc finger, ZZ-type containing 3 [Source:HGNC Symbol;Acc:HGNC:24523]
ENSG00000037280	FLT4	fms-related tyrosine kinase 4 [Source:HGNC Symbol;Acc:HGNC:3767]

ENSG00000037965	HOXC8	homeobox C8 [Source:HGNC Symbol;Acc:HGNC:5129]
ENSG00000039068	CDH1	cadherin 1, type 1, E-cadherin (epithelial) [Source:HGNC Symbol;Acc:HGNC:1748]
ENSG00000041357	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4 [Source:HGNC Symbol;Acc:HGNC:9533]
ENSG00000043462	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) [Source:HGNC Symbol;Acc:HGNC:6529]
ENSG00000047315	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa [Source:HGNC Symbol;Acc:HGNC:9188]
ENSG00000047457	CP	ceruloplasmin (ferroxidase) [Source:HGNC Symbol;Acc:HGNC:2295]
ENSG00000047849	MAP4	microtubule-associated protein 4 [Source:HGNC Symbol;Acc:HGNC:6862]
ENSG00000054598	FOXC1	forkhead box C1 [Source:HGNC Symbol;Acc:HGNC:3800]
ENSG00000055118	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2 [Source:HGNC Symbol;Acc:HGNC:6251]
ENSG00000063660	GPC1	glypican 1 [Source:HGNC Symbol;Acc:HGNC:4449]
ENSG00000064300	NGFR	nerve growth factor receptor [Source:HGNC Symbol;Acc:HGNC:7809]
ENSG00000066336	SPI1	Spi-1 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:11241]
ENSG00000067646	ZFY	zinc finger protein, Y-linked [Source:HGNC Symbol;Acc:HGNC:12870]
ENSG00000068024	HDAC4	histone deacetylase 4 [Source:HGNC Symbol;Acc:HGNC:14063]
ENSG00000069956	MAPK6	mitogen-activated protein kinase 6 [Source:HGNC Symbol;Acc:HGNC:6879]
ENSG00000070018	LRP6	low density lipoprotein receptor-related protein 6 [Source:HGNC Symbol;Acc:HGNC:6698]
ENSG00000070193	FGF10	fibroblast growth factor 10 [Source:HGNC Symbol;Acc:HGNC:3666]
ENSG00000070831	CDC42	cell division cycle 42 [Source:HGNC Symbol;Acc:HGNC:1736]
ENSG00000073756	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) [Source:HGNC Symbol;Acc:HGNC:9605]
ENSG00000075618	FSCN1	fascin actin-bundling protein 1 [Source:HGNC Symbol;Acc:HGNC:11148]
ENSG00000076242	MLH1	mutL homolog 1 [Source:HGNC Symbol;Acc:HGNC:7127]
ENSG00000076248	UNG	uracil-DNA glycosylase [Source:HGNC Symbol;Acc:HGNC:12572]
ENSG00000078401	EDN1	endothelin 1 [Source:HGNC Symbol;Acc:HGNC:3176]
ENSG00000080166	DCT	dopachrome tautomerase [Source:HGNC

		Symbol;Acc:HGNC:2709]
ENSG00000081051	AFP	alpha-fetoprotein [Source:HGNC Symbol;Acc:HGNC:317]
ENSG00000082153	BZW1	basic leucine zipper and W2 domains 1 [Source:HGNC Symbol;Acc:HGNC:18380]
ENSG00000082175	PGR	progesterone receptor [Source:HGNC Symbol;Acc:HGNC:8910]
ENSG00000083123	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide [Source:HGNC Symbol;Acc:HGNC:987]
ENSG00000084207	GSTP1	glutathione S-transferase pi 1 [Source:HGNC Symbol;Acc:HGNC:4638]
ENSG00000085276	MECOM	MDS1 and EVI1 complex locus [Source:HGNC Symbol;Acc:HGNC:3498]
ENSG00000085465	OVGP1	oviductal glycoprotein 1, 120kDa [Source:HGNC Symbol;Acc:HGNC:8524]
ENSG00000085563	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1 [Source:HGNC Symbol;Acc:HGNC:40]
ENSG00000085662	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase) [Source:HGNC Symbol;Acc:HGNC:381]
ENSG00000087088	BAX	BCL2-associated X protein [Source:HGNC Symbol;Acc:HGNC:959]
ENSG00000087111	PIGS	phosphatidylinositol glycan anchor biosynthesis, class S [Source:HGNC Symbol;Acc:HGNC:14937]
ENSG00000087191	PSMC5	proteasome (prosome, macropain) 26S subunit, ATPase, 5 [Source:HGNC Symbol;Acc:HGNC:9552]
ENSG00000087250	MT3	metallothionein 3 [Source:HGNC Symbol;Acc:HGNC:7408]
ENSG00000087586	AURKA	aurora kinase A [Source:HGNC Symbol;Acc:HGNC:11393]
ENSG00000088832	FKBP1A	FK506 binding protein 1A, 12kDa [Source:HGNC Symbol;Acc:HGNC:3711]
ENSG00000089902	RCOR1	REST corepressor 1 [Source:HGNC Symbol;Acc:HGNC:17441]
ENSG00000090104	RGS1	regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:HGNC:9991]
ENSG00000090339	ICAM1	intercellular adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:5344]
ENSG00000091831	ESR1	estrogen receptor 1 [Source:HGNC Symbol;Acc:HGNC:3467]
ENSG00000092847	AGO1	argonaute RISC catalytic component 1 [Source:HGNC Symbol;Acc:HGNC:3262]
ENSG00000092969	TGFB2	transforming growth factor, beta 2 [Source:HGNC Symbol;Acc:HGNC:11768]
ENSG00000094880	CDC23	cell division cycle 23 [Source:HGNC Symbol;Acc:HGNC:1724]
ENSG00000096717	SIRT1	sirtuin 1 [Source:HGNC Symbol;Acc:HGNC:14929]
ENSG00000096968	JAK2	Janus kinase 2 [Source:HGNC Symbol;Acc:HGNC:6192]
ENSG00000100030	MAPK1	mitogen-activated protein kinase 1 [Source:HGNC

		Symbol;Acc:HGNC:6871]
ENSG00000100031	GGT1	gamma-glutamyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:4250]
ENSG00000100234	TIMP3	TIMP metallopeptidase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:11822]
ENSG00000100292	HMOX1	heme oxygenase (decycling) 1 [Source:HGNC Symbol;Acc:HGNC:5013]
ENSG00000100300	TSPO	translocator protein (18kDa) [Source:HGNC Symbol;Acc:HGNC:1158]
ENSG00000100311	PDGFB	platelet-derived growth factor beta polypeptide [Source:HGNC Symbol;Acc:HGNC:8800]
ENSG00000100312	ACR	acrosin [Source:HGNC Symbol;Acc:HGNC:126]
ENSG00000100393	EP300	E1A binding protein p300 [Source:HGNC Symbol;Acc:HGNC:3373]
ENSG00000100453	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) [Source:HGNC Symbol;Acc:HGNC:4709]
ENSG00000100567	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3 [Source:HGNC Symbol;Acc:HGNC:9532]
ENSG00000100644	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) [Source:HGNC Symbol;Acc:HGNC:4910]
ENSG00000100811	YY1	YY1 transcription factor [Source:HGNC Symbol;Acc:HGNC:12856]
ENSG00000100842	EFS	embryonal Fyn-associated substrate [Source:HGNC Symbol;Acc:HGNC:16898]
ENSG00000101076	HNF4A	hepatocyte nuclear factor 4, alpha [Source:HGNC Symbol;Acc:HGNC:5024]
ENSG00000101384	JAG1	jagged 1 [Source:HGNC Symbol;Acc:HGNC:6188]
ENSG00000101981	F9	coagulation factor IX [Source:HGNC Symbol;Acc:HGNC:3551]
ENSG00000102081	FMR1	fragile X mental retardation 1 [Source:HGNC Symbol;Acc:HGNC:3775]
ENSG00000102225	CDK16	cyclin-dependent kinase 16 [Source:HGNC Symbol;Acc:HGNC:8749]
ENSG00000102265	TIMP1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:11820]
ENSG00000102524	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b [Source:HGNC Symbol;Acc:HGNC:11929]
ENSG00000102981	PARD6A	par-6 family cell polarity regulator alpha [Source:HGNC Symbol;Acc:HGNC:15943]
ENSG00000103197	TSC2	tuberous sclerosis 2 [Source:HGNC Symbol;Acc:HGNC:12363]
ENSG00000104067	TJP1	tight junction protein 1 [Source:HGNC Symbol;Acc:HGNC:11827]
ENSG00000104267	CA2	carbonic anhydrase II [Source:HGNC

		Symbol;Acc:HGNC:1373]
ENSG00000104290	FZD3	frizzled class receptor 3 [Source:HGNC Symbol;Acc:HGNC:4041]
ENSG00000104313	EYA1	EYA transcriptional coactivator and phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:3519]
ENSG00000104325	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial [Source:HGNC Symbol;Acc:HGNC:2753]
ENSG00000104368	PLAT	plasminogen activator, tissue [Source:HGNC Symbol;Acc:HGNC:9051]
ENSG00000104419	NDRG1	N-myc downstream regulated 1 [Source:HGNC Symbol;Acc:HGNC:7679]
ENSG00000104432	IL7	interleukin 7 [Source:HGNC Symbol;Acc:HGNC:6023]
ENSG00000104687	GSR	glutathione reductase [Source:HGNC Symbol;Acc:HGNC:4623]
ENSG00000104889	RNASEH2A	ribonuclease H2, subunit A [Source:HGNC Symbol;Acc:HGNC:18518]
ENSG00000105143	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 [Source:HGNC Symbol;Acc:HGNC:10944]
ENSG00000105173	CCNE1	cyclin E1 [Source:HGNC Symbol;Acc:HGNC:1589]
ENSG00000105329	TGFB1	transforming growth factor, beta 1 [Source:HGNC Symbol;Acc:HGNC:11766]
ENSG00000105369	CD79A	CD79a molecule, immunoglobulin-associated alpha [Source:HGNC Symbol;Acc:HGNC:1698]
ENSG00000105372	RPS19	ribosomal protein S19 [Source:HGNC Symbol;Acc:HGNC:10402]
ENSG00000105398	SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1 [Source:HGNC Symbol;Acc:HGNC:11458]
ENSG00000105697	HAMP	hepcidin antimicrobial peptide [Source:HGNC Symbol;Acc:HGNC:15598]
ENSG00000105698	USF2	upstream transcription factor 2, c-fos interacting [Source:HGNC Symbol;Acc:HGNC:12594]
ENSG00000105819	PMPCB	peptidase (mitochondrial processing) beta [Source:HGNC Symbol;Acc:HGNC:9119]
ENSG00000105894	PTN	pleiotrophin [Source:HGNC Symbol;Acc:HGNC:9630]
ENSG00000105968	H2AFV	H2A histone family, member V [Source:HGNC Symbol;Acc:HGNC:20664]
ENSG00000105989	WNT2	wingless-type MMTV integration site family member 2 [Source:HGNC Symbol;Acc:HGNC:12780]
ENSG00000106258	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5 [Source:HGNC Symbol;Acc:HGNC:2638]
ENSG00000106366	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 [Source:HGNC

		Symbol;Acc:HGNC:8583]
ENSG00000106546	AHR	aryl hydrocarbon receptor [Source:HGNC Symbol;Acc:HGNC:348]
ENSG00000106633	GCK	glucokinase (hexokinase 4) [Source:HGNC Symbol;Acc:HGNC:4195]
ENSG00000107317	PTGDS	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Symbol;Acc:HGNC:9592]
ENSG00000107338	SHB	Src homology 2 domain containing adaptor protein B [Source:HGNC Symbol;Acc:HGNC:10838]
ENSG00000107485	GATA3	GATA binding protein 3 [Source:HGNC Symbol;Acc:HGNC:4172]
ENSG00000107581	EIF3A	eukaryotic translation initiation factor 3, subunit A [Source:HGNC Symbol;Acc:HGNC:3271]
ENSG00000107882	SUFU	suppressor of fused homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:16466]
ENSG00000108312	UBTF	upstream binding transcription factor, RNA polymerase I [Source:HGNC Symbol;Acc:HGNC:12511]
ENSG00000108342	CSF3	colony stimulating factor 3 (granulocyte) [Source:HGNC Symbol;Acc:HGNC:2438]
ENSG00000108561	C1QBP	complement component 1, q subcomponent binding protein [Source:HGNC Symbol;Acc:HGNC:1243]
ENSG00000108654	DDX5	DEAD (Asp-Glu-Ala-Asp) box helicase 5 [Source:HGNC Symbol;Acc:HGNC:2746]
ENSG00000108773	KAT2A	K(lysine) acetyltransferase 2A [Source:HGNC Symbol;Acc:HGNC:4201]
ENSG00000108840	HDAC5	histone deacetylase 5 [Source:HGNC Symbol;Acc:HGNC:14068]
ENSG00000108946	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha [Source:HGNC Symbol;Acc:HGNC:9388]
ENSG00000109471	IL2	interleukin 2 [Source:HGNC Symbol;Acc:HGNC:6001]
ENSG00000109610	SOD3	superoxide dismutase 3, extracellular [Source:HGNC Symbol;Acc:HGNC:11181]
ENSG00000110092	CCND1	cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
ENSG00000110448	CD5	CD5 molecule [Source:HGNC Symbol;Acc:HGNC:1685]
ENSG00000110492	MDK	midkine (neurite growth-promoting factor 2) [Source:HGNC Symbol;Acc:HGNC:6972]
ENSG00000110799	VWF	von Willebrand factor [Source:HGNC Symbol;Acc:HGNC:12726]
ENSG00000110852	CLEC2B	C-type lectin domain family 2, member B [Source:HGNC Symbol;Acc:HGNC:2053]
ENSG00000111049	MYF5	myogenic factor 5 [Source:HGNC Symbol;Acc:HGNC:7565]
ENSG00000111057	KRT18	keratin 18 [Source:HGNC Symbol;Acc:HGNC:6430]
ENSG00000111144	LTA4H	leukotriene A4 hydrolase [Source:HGNC Symbol;Acc:HGNC:6710]

ENSG00000111206	FOXM1	forkhead box M1 [Source:HGNC Symbol;Acc:HGNC:3818]
ENSG00000111241	FGF6	fibroblast growth factor 6 [Source:HGNC Symbol;Acc:HGNC:3684]
ENSG00000111432	FZD10	frizzled class receptor 10 [Source:HGNC Symbol;Acc:HGNC:4039]
ENSG00000111537	IFNG	interferon, gamma [Source:HGNC Symbol;Acc:HGNC:5438]
ENSG00000111640	GAPDH	glyceraldehyde-3-phosphate dehydrogenase [Source:HGNC Symbol;Acc:HGNC:4141]
ENSG00000111642	CHD4	chromodomain helicase DNA binding protein 4 [Source:HGNC Symbol;Acc:HGNC:1919]
ENSG00000112062	MAPK14	mitogen-activated protein kinase 14 [Source:HGNC Symbol;Acc:HGNC:6876]
ENSG00000112096	SOD2	superoxide dismutase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:11180]
ENSG00000112175	BMP5	bone morphogenetic protein 5 [Source:HGNC Symbol;Acc:HGNC:1072]
ENSG00000112304	ACOT13	acyl-CoA thioesterase 13 [Source:HGNC Symbol;Acc:HGNC:20999]
ENSG00000112715	VEGFA	vascular endothelial growth factor A [Source:HGNC Symbol;Acc:HGNC:12680]
ENSG00000112761	WISP3	WNT1 inducible signaling pathway protein 3 [Source:HGNC Symbol;Acc:HGNC:12771]
ENSG00000113083	LOX	lysyl oxidase [Source:HGNC Symbol;Acc:HGNC:6664]
ENSG00000113282	CLINT1	clathrin interactor 1 [Source:HGNC Symbol;Acc:HGNC:23186]
ENSG00000113520	IL4	interleukin 4 [Source:HGNC Symbol;Acc:HGNC:6014]
ENSG00000113578	FGF1	fibroblast growth factor 1 (acidic) [Source:HGNC Symbol;Acc:HGNC:3665]
ENSG00000113580	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) [Source:HGNC Symbol;Acc:HGNC:7978]
ENSG00000114013	CD86	CD86 molecule [Source:HGNC Symbol;Acc:HGNC:1705]
ENSG00000114026	OGG1	8-oxoguanine DNA glycosylase [Source:HGNC Symbol;Acc:HGNC:8125]
ENSG00000114166	KAT2B	K(lysine) acetyltransferase 2B [Source:HGNC Symbol;Acc:HGNC:8638]
ENSG00000114315	HES1	hes family bHLH transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:5192]
ENSG00000114867	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1 [Source:HGNC Symbol;Acc:HGNC:3296]
ENSG00000115008	IL1A	interleukin 1, alpha [Source:HGNC Symbol;Acc:HGNC:5991]
ENSG00000115221	ITGB6	integrin, beta 6 [Source:HGNC Symbol;Acc:HGNC:6161]
ENSG00000115263	GCG	glucagon [Source:HGNC Symbol;Acc:HGNC:4191]
ENSG00000115266	APC2	adenomatosis polyposis coli 2 [Source:HGNC

		Symbol;Acc:HGNC:24036]
ENSG00000115414	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
ENSG00000115415	STAT1	signal transducer and activator of transcription 1, 91kDa [Source:HGNC Symbol;Acc:HGNC:11362]
ENSG00000115484	CCT4	chaperonin containing TCP1, subunit 4 (delta) [Source:HGNC Symbol;Acc:HGNC:1617]
ENSG00000115825	PRKD3	protein kinase D3 [Source:HGNC Symbol;Acc:HGNC:9408]
ENSG00000115956	PLEK	pleckstrin [Source:HGNC Symbol;Acc:HGNC:9070]
ENSG00000116030	SUMO1	small ubiquitin-like modifier 1 [Source:HGNC Symbol;Acc:HGNC:12502]
ENSG00000116106	EPHA4	EPH receptor A4 [Source:HGNC Symbol;Acc:HGNC:3388]
ENSG00000116128	BCL9	B-cell CLL/lymphoma 9 [Source:HGNC Symbol;Acc:HGNC:1008]
ENSG00000116251	RPL22	ribosomal protein L22 [Source:HGNC Symbol;Acc:HGNC:10315]
ENSG00000116544	DLGAP3	discs, large (Drosophila) homolog-associated protein 3 [Source:HGNC Symbol;Acc:HGNC:30368]
ENSG00000116791	CRYZ	crystallin, zeta (quinone reductase) [Source:HGNC Symbol;Acc:HGNC:2419]
ENSG00000116981	NT5C1A	5'-nucleotidase, cytosolic IA [Source:HGNC Symbol;Acc:HGNC:17819]
ENSG00000117118	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) [Source:HGNC Symbol;Acc:HGNC:10681]
ENSG00000117525	F3	coagulation factor III (thromboplastin, tissue factor) [Source:HGNC Symbol;Acc:HGNC:3541]
ENSG00000117560	FASLG	Fas ligand (TNF superfamily, member 6) [Source:HGNC Symbol;Acc:HGNC:11936]
ENSG00000117984	CTSD	cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]
ENSG00000118260	CREB1	cAMP responsive element binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2345]
ENSG00000118271	TTR	transthyretin [Source:HGNC Symbol;Acc:HGNC:12405]
ENSG00000118513	MYB	v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:7545]
ENSG00000118939	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) [Source:HGNC Symbol;Acc:HGNC:12515]
ENSG00000118972	FGF23	fibroblast growth factor 23 [Source:HGNC Symbol;Acc:HGNC:3680]
ENSG00000119042	SATB2	SATB homeobox 2 [Source:HGNC Symbol;Acc:HGNC:21637]
ENSG00000119138	KLF9	Kruppel-like factor 9 [Source:HGNC Symbol;Acc:HGNC:1123]
ENSG00000119953	SMNDC1	survival motor neuron domain containing 1 [Source:HGNC Symbol;Acc:HGNC:16900]
ENSG00000120057	SFRP5	secreted frizzled-related protein 5 [Source:HGNC Symbol;Acc:HGNC:10779]

ENSG00000120659	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11 [Source:HGNC Symbol;Acc:HGNC:11926]
ENSG00000120708	TGFBI	transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:HGNC:11771]
ENSG00000120738	EGR1	early growth response 1 [Source:HGNC Symbol;Acc:HGNC:3238]
ENSG00000120798	NR2C1	nuclear receptor subfamily 2, group C, member 1 [Source:HGNC Symbol;Acc:HGNC:7971]
ENSG00000120915	EPHX2	epoxide hydrolase 2, cytoplasmic [Source:HGNC Symbol;Acc:HGNC:3402]
ENSG00000121211	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:24839]
ENSG00000121594	CD80	CD80 molecule [Source:HGNC Symbol;Acc:HGNC:1700]
ENSG00000121691	CAT	catalase [Source:HGNC Symbol;Acc:HGNC:1516]
ENSG00000121966	CXCR4	chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;Acc:HGNC:2561]
ENSG00000122194	PLG	plasminogen [Source:HGNC Symbol;Acc:HGNC:9071]
ENSG00000122861	PLAU	plasminogen activator, urokinase [Source:HGNC Symbol;Acc:HGNC:9052]
ENSG00000122877	EGR2	early growth response 2 [Source:HGNC Symbol;Acc:HGNC:3239]
ENSG00000123342	MMP19	matrix metallopeptidase 19 [Source:HGNC Symbol;Acc:HGNC:7165]
ENSG00000123908	AGO2	argonaute RISC catalytic component 2 [Source:HGNC Symbol;Acc:HGNC:3263]
ENSG00000123999	INHA	inhibin, alpha [Source:HGNC Symbol;Acc:HGNC:6065]
ENSG00000124721	DNAH8	dynein, axonemal, heavy chain 8 [Source:HGNC Symbol;Acc:HGNC:2952]
ENSG00000124813	RUNX2	runt-related transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:10472]
ENSG00000125378	BMP4	bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:HGNC:1071]
ENSG00000125492	BARHL1	BarH-like homeobox 1 [Source:HGNC Symbol;Acc:HGNC:953]
ENSG00000125538	IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:HGNC:5992]
ENSG00000125618	PAX8	paired box 8 [Source:HGNC Symbol;Acc:HGNC:8622]
ENSG00000125845	BMP2	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:1069]
ENSG00000125952	MAX	MYC associated factor X [Source:HGNC Symbol;Acc:HGNC:6913]
ENSG00000126261	UBA2	ubiquitin-like modifier activating enzyme 2 [Source:HGNC Symbol;Acc:HGNC:30661]
ENSG00000126561	STAT5A	signal transducer and activator of transcription 5A [Source:HGNC Symbol;Acc:HGNC:11366]

ENSG00000127445	PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1 [Source:HGNC Symbol;Acc:HGNC:8988]
ENSG00000127554	GFER	growth factor, augmenter of liver regeneration [Source:HGNC Symbol;Acc:HGNC:4236]
ENSG00000128050	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase [Source:HGNC Symbol;Acc:HGNC:8587]
ENSG00000128052	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase) [Source:HGNC Symbol;Acc:HGNC:6307]
ENSG00000128268	MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Source:HGNC Symbol;Acc:HGNC:7046]
ENSG00000128272	ATF4	activating transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:786]
ENSG00000128602	SMO	smoothened, frizzled class receptor [Source:HGNC Symbol;Acc:HGNC:11119]
ENSG00000129226	CD68	CD68 molecule [Source:HGNC Symbol;Acc:HGNC:1693]
ENSG00000129460	NGDN	neuroguidin, EIF4E binding protein [Source:HGNC Symbol;Acc:HGNC:20271]
ENSG00000129965	INS-IGF2	INS-IGF2 readthrough [Source:HGNC Symbol;Acc:HGNC:33527]
ENSG00000129991	TNNI3	troponin I type 3 (cardiac) [Source:HGNC Symbol;Acc:HGNC:11947]
ENSG00000130164	LDLR	low density lipoprotein receptor [Source:HGNC Symbol;Acc:HGNC:6547]
ENSG00000130203	APOE	apolipoprotein E [Source:HGNC Symbol;Acc:HGNC:613]
ENSG00000130368	MAS1	MAS1 proto-oncogene, G protein-coupled receptor [Source:HGNC Symbol;Acc:HGNC:6899]
ENSG00000130675	MNX1	motor neuron and pancreas homeobox 1 [Source:HGNC Symbol;Acc:HGNC:4979]
ENSG00000131910	NR0B2	nuclear receptor subfamily 0, group B, member 2 [Source:HGNC Symbol;Acc:HGNC:7961]
ENSG00000132170	PPARG	peroxisome proliferator-activated receptor gamma [Source:HGNC Symbol;Acc:HGNC:9236]
ENSG00000132341	RAN	RAN, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9846]
ENSG00000132688	NES	nestin [Source:HGNC Symbol;Acc:HGNC:7756]
ENSG00000132693	CRP	C-reactive protein, pentraxin-related [Source:HGNC Symbol;Acc:HGNC:2367]
ENSG00000134001	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa [Source:HGNC Symbol;Acc:HGNC:3265]
ENSG00000134184	GSTM1	glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:HGNC:4632]
ENSG00000134259	NGF	nerve growth factor (beta polypeptide) [Source:HGNC

		Symbol;Acc:HGNC:7808]
ENSG00000134308	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta [Source:HGNC Symbol;Acc:HGNC:12854]
ENSG00000134363	FST	follistatin [Source:HGNC Symbol;Acc:HGNC:3971]
ENSG00000134460	IL2RA	interleukin 2 receptor, alpha [Source:HGNC Symbol;Acc:HGNC:6008]
ENSG00000134716	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2 [Source:HGNC Symbol;Acc:HGNC:2634]
ENSG00000134853	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide [Source:HGNC Symbol;Acc:HGNC:8803]
ENSG00000134909	ARHGAP32	Rho GTPase activating protein 32 [Source:HGNC Symbol;Acc:HGNC:17399]
ENSG00000134982	APC	adenomatous polyposis coli [Source:HGNC Symbol;Acc:HGNC:583]
ENSG00000135218	CD36	CD36 molecule (thrombospondin receptor) [Source:HGNC Symbol;Acc:HGNC:1663]
ENSG00000135624	CCT7	chaperonin containing TCP1, subunit 7 (eta) [Source:HGNC Symbol;Acc:HGNC:1622]
ENSG00000135821	GLUL	glutamate-ammonia ligase [Source:HGNC Symbol;Acc:HGNC:4341]
ENSG00000135999	EPC2	enhancer of polycomb homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:24543]
ENSG00000136146	MED4	mediator complex subunit 4 [Source:HGNC Symbol;Acc:HGNC:17903]
ENSG00000136238	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) [Source:HGNC Symbol;Acc:HGNC:9801]
ENSG00000136450	SRSF1	serine/arginine-rich splicing factor 1 [Source:HGNC Symbol;Acc:HGNC:10780]
ENSG00000136531	SCN2A	sodium channel, voltage-gated, type II, alpha subunit [Source:HGNC Symbol;Acc:HGNC:10588]
ENSG00000136574	GATA4	GATA binding protein 4 [Source:HGNC Symbol;Acc:HGNC:4173]
ENSG00000136634	IL10	interleukin 10 [Source:HGNC Symbol;Acc:HGNC:5962]
ENSG00000136869	TLR4	toll-like receptor 4 [Source:HGNC Symbol;Acc:HGNC:11850]
ENSG00000136929	HEMGN	hemogen [Source:HGNC Symbol;Acc:HGNC:17509]
ENSG00000136930	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7 [Source:HGNC Symbol;Acc:HGNC:9544]
ENSG00000136931	NR5A1	nuclear receptor subfamily 5, group A, member 1 [Source:HGNC Symbol;Acc:HGNC:7983]
ENSG00000136997	MYC	v-myc avian myelocytomatosis viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:7553]
ENSG00000137076	TLN1	talin 1 [Source:HGNC Symbol;Acc:HGNC:11845]

ENSG00000137154	RPS6	ribosomal protein S6 [Source:HGNC Symbol;Acc:HGNC:10429]
ENSG00000137267	TUBB2A	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:12412]
ENSG00000137312	FLOT1	flotillin 1 [Source:HGNC Symbol;Acc:HGNC:3757]
ENSG00000137413	TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa [Source:HGNC Symbol;Acc:HGNC:17300]
ENSG00000137710	RDX	radixin [Source:HGNC Symbol;Acc:HGNC:9944]
ENSG00000137752	CASP1	caspase 1, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:HGNC:1499]
ENSG00000137801	THBS1	thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
ENSG00000137868	STRA6	stimulated by retinoic acid 6 [Source:HGNC Symbol;Acc:HGNC:30650]
ENSG00000137955	RABGGTB	Rab geranylgeranyltransferase, beta subunit [Source:HGNC Symbol;Acc:HGNC:9796]
ENSG00000138039	LHCGR	luteinizing hormone/choriogonadotropin receptor [Source:HGNC Symbol;Acc:HGNC:6585]
ENSG00000138435	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle) [Source:HGNC Symbol;Acc:HGNC:1955]
ENSG00000138685	FGF2	fibroblast growth factor 2 (basic) [Source:HGNC Symbol;Acc:HGNC:3676]
ENSG00000138760	SCARB2	scavenger receptor class B, member 2 [Source:HGNC Symbol;Acc:HGNC:1665]
ENSG00000139318	DUSP6	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:HGNC:3072]
ENSG00000139668	WDFY2	WD repeat and FYVE domain containing 2 [Source:HGNC Symbol;Acc:HGNC:20482]
ENSG00000139687	RB1	retinoblastoma 1 [Source:HGNC Symbol;Acc:HGNC:9884]
ENSG00000140254	DUOXA1	dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:HGNC:26507]
ENSG00000140285	FGF7	fibroblast growth factor 7 [Source:HGNC Symbol;Acc:HGNC:3685]
ENSG00000140396	NCOA2	nuclear receptor coactivator 2 [Source:HGNC Symbol;Acc:HGNC:7669]
ENSG00000140443	IGF1R	insulin-like growth factor 1 receptor [Source:HGNC Symbol;Acc:HGNC:5465]
ENSG00000140465	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:2595]
ENSG00000140968	IRF8	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:HGNC:5358]
ENSG00000141646	SMAD4	SMAD family member 4 [Source:HGNC Symbol;Acc:HGNC:6770]
ENSG00000141968	VAV1	vav 1 guanine nucleotide exchange factor [Source:HGNC

		Symbol;Acc:HGNC:12657]
ENSG00000142168	SOD1	superoxide dismutase 1, soluble [Source:HGNC Symbol;Acc:HGNC:11179]
ENSG00000142192	APP	amyloid beta (A4) precursor protein [Source:HGNC Symbol;Acc:HGNC:620]
ENSG00000142208	AKT1	v-akt murine thymoma viral oncogene homolog 1 [Source:HGNC Symbol;Acc:HGNC:391]
ENSG00000142507	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6 [Source:HGNC Symbol;Acc:HGNC:9543]
ENSG00000142515	KLK3	kallikrein-related peptidase 3 [Source:HGNC Symbol;Acc:HGNC:6364]
ENSG00000142731	PLK4	polo-like kinase 4 [Source:HGNC Symbol;Acc:HGNC:11397]
ENSG00000143799	PARP1	poly (ADP-ribose) polymerase 1 [Source:HGNC Symbol;Acc:HGNC:270]
ENSG00000143933	CALM2	calmodulin 2 (phosphorylase kinase, delta) [Source:HGNC Symbol;Acc:HGNC:1445]
ENSG00000143947	RPS27A	ribosomal protein S27a [Source:HGNC Symbol;Acc:HGNC:10417]
ENSG00000144891	AGTR1	angiotensin II receptor, type 1 [Source:HGNC Symbol;Acc:HGNC:336]
ENSG00000145335	SNCA	synuclein, alpha (non A4 component of amyloid precursor) [Source:HGNC Symbol;Acc:HGNC:11138]
ENSG00000145839	IL9	interleukin 9 [Source:HGNC Symbol;Acc:HGNC:6029]
ENSG00000145907	G3BP1	GTPase activating protein (SH3 domain) binding protein 1 [Source:HGNC Symbol;Acc:HGNC:30292]
ENSG00000146085	MUT	methylmalonyl CoA mutase [Source:HGNC Symbol;Acc:HGNC:7526]
ENSG00000146674	IGFBP3	insulin-like growth factor binding protein 3 [Source:HGNC Symbol;Acc:HGNC:5472]
ENSG00000146678	IGFBP1	insulin-like growth factor binding protein 1 [Source:HGNC Symbol;Acc:HGNC:5469]
ENSG00000147162	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase [Source:HGNC Symbol;Acc:HGNC:8127]
ENSG00000147316	MCPH1	microcephalin 1 [Source:HGNC Symbol;Acc:HGNC:6954]
ENSG00000147437	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone) [Source:HGNC Symbol;Acc:HGNC:4419]
ENSG00000147869	CER1	cerberus 1, DAN family BMP antagonist [Source:HGNC Symbol;Acc:HGNC:1862]
ENSG00000147883	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) [Source:HGNC Symbol;Acc:HGNC:1788]
ENSG00000148082	SHC3	SHC (Src homology 2 domain containing) transforming protein 3 [Source:HGNC Symbol;Acc:HGNC:18181]
ENSG00000148400	NOTCH1	notch 1 [Source:HGNC Symbol;Acc:HGNC:7881]
ENSG00000148773	MKI67	marker of proliferation Ki-67 [Source:HGNC

		Symbol;Acc:HGNC:7107]
ENSG00000148835	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa [Source:HGNC Symbol;Acc:HGNC:11539]
ENSG00000149972	CNTN5	contactin 5 [Source:HGNC Symbol;Acc:HGNC:2175]
ENSG00000150782	IL18	interleukin 18 [Source:HGNC Symbol;Acc:HGNC:5986]
ENSG00000152256	PDK1	pyruvate dehydrogenase kinase, isozyme 1 [Source:HGNC Symbol;Acc:HGNC:8809]
ENSG00000152661	GJA1	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;Acc:HGNC:4274]
ENSG00000152785	BMP3	bone morphogenetic protein 3 [Source:HGNC Symbol;Acc:HGNC:1070]
ENSG00000154342	WNT3A	wingless-type MMTV integration site family, member 3A [Source:HGNC Symbol;Acc:HGNC:15983]
ENSG00000155011	DKK2	dickkopf WNT signaling pathway inhibitor 2 [Source:HGNC Symbol;Acc:HGNC:2892]
ENSG00000155090	KLF10	Kruppel-like factor 10 [Source:HGNC Symbol;Acc:HGNC:11810]
ENSG00000155093	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2 [Source:HGNC Symbol;Acc:HGNC:9677]
ENSG00000156313	RPGR	retinitis pigmentosa GTPase regulator [Source:HGNC Symbol;Acc:HGNC:10295]
ENSG00000156508	EEF1A1	eukaryotic translation elongation factor 1 alpha 1 [Source:HGNC Symbol;Acc:HGNC:3189]
ENSG00000156709	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1 [Source:HGNC Symbol;Acc:HGNC:8768]
ENSG00000157193	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor [Source:HGNC Symbol;Acc:HGNC:6700]
ENSG00000157933	SKI	SKI proto-oncogene [Source:HGNC Symbol;Acc:HGNC:10896]
ENSG00000158373	HIST1H2BD	histone cluster 1, H2bd [Source:HGNC Symbol;Acc:HGNC:4747]
ENSG00000158402	CDC25C	cell division cycle 25C [Source:HGNC Symbol;Acc:HGNC:1727]
ENSG00000158874	APOA2	apolipoprotein A-II [Source:HGNC Symbol;Acc:HGNC:601]
ENSG00000158941	CCAR2	cell cycle and apoptosis regulator 2 [Source:HGNC Symbol;Acc:HGNC:23360]
ENSG00000159352	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 [Source:HGNC Symbol;Acc:HGNC:9561]
ENSG00000159640	ACE	angiotensin I converting enzyme [Source:HGNC Symbol;Acc:HGNC:2707]
ENSG00000160014	CALM3	calmodulin 3 (phosphorylase kinase, delta) [Source:HGNC Symbol;Acc:HGNC:1449]

ENSG00000160211	G6PD	glucose-6-phosphate dehydrogenase [Source:HGNC Symbol;Acc:HGNC:4057]
ENSG00000160255	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Source:HGNC Symbol;Acc:HGNC:6155]
ENSG00000160867	FGFR4	fibroblast growth factor receptor 4 [Source:HGNC Symbol;Acc:HGNC:3691]
ENSG00000160868	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4 [Source:HGNC Symbol;Acc:HGNC:2637]
ENSG00000162551	ALPL	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symbol;Acc:HGNC:438]
ENSG00000162692	VCAM1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:12663]
ENSG00000162738	VANGL2	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;Acc:HGNC:15511]
ENSG00000162924	REL	v-rel avian reticuloendotheliosis viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:9954]
ENSG00000163041	H3F3A	H3 histone, family 3A [Source:HGNC Symbol;Acc:HGNC:4764]
ENSG00000163131	CTSS	cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
ENSG00000163217	BMP10	bone morphogenetic protein 10 [Source:HGNC Symbol;Acc:HGNC:20869]
ENSG00000163235	TGFA	transforming growth factor, alpha [Source:HGNC Symbol;Acc:HGNC:11765]
ENSG00000163273	NPPC	natriuretic peptide C [Source:HGNC Symbol;Acc:HGNC:7941]
ENSG00000163283	ALPP	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:HGNC:439]
ENSG00000163286	ALPPL2	alkaline phosphatase, placental-like 2 [Source:HGNC Symbol;Acc:HGNC:441]
ENSG00000163631	ALB	albumin [Source:HGNC Symbol;Acc:HGNC:399]
ENSG00000163666	HESX1	HESX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:4877]
ENSG00000163737	PF4	platelet factor 4 [Source:HGNC Symbol;Acc:HGNC:8861]
ENSG00000163781	TOPBP1	topoisomerase (DNA) II binding protein 1 [Source:HGNC Symbol;Acc:HGNC:17008]
ENSG00000163794	UCN	urocortin [Source:HGNC Symbol;Acc:HGNC:12516]
ENSG00000163810	TGM4	transglutaminase 4 [Source:HGNC Symbol;Acc:HGNC:11780]
ENSG00000164032	H2AFZ	H2A histone family, member Z [Source:HGNC Symbol;Acc:HGNC:4741]
ENSG00000164305	CASP3	caspase 3, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:HGNC:1504]
ENSG00000164326	CARTPT	CART prepropeptide [Source:HGNC Symbol;Acc:HGNC:24323]
ENSG00000164399	IL3	interleukin 3 [Source:HGNC Symbol;Acc:HGNC:6011]
ENSG00000164400	CSF2	colony stimulating factor 2 (granulocyte-macrophage) [Source:HGNC Symbol;Acc:HGNC:2434]

ENSG00000164532	TBX20	T-box 20 [Source:HGNC Symbol;Acc:HGNC:11598]
ENSG00000164611	PTTG1	pituitary tumor-transforming 1 [Source:HGNC Symbol;Acc:HGNC:9690]
ENSG00000164651	SP8	Sp8 transcription factor [Source:HGNC Symbol;Acc:HGNC:19196]
ENSG00000164692	COL1A2	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:HGNC:2198]
ENSG00000164733	CTSB	cathepsin B [Source:HGNC Symbol;Acc:HGNC:2527]
ENSG00000164867	NOS3	nitric oxide synthase 3 (endothelial cell) [Source:HGNC Symbol;Acc:HGNC:7876]
ENSG00000164902	PHAX	phosphorylated adaptor for RNA export [Source:HGNC Symbol;Acc:HGNC:10241]
ENSG00000165025	SYK	spleen tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:11491]
ENSG00000165097	KDM1B	lysine (K)-specific demethylase 1B [Source:HGNC Symbol;Acc:HGNC:21577]
ENSG00000165304	MELK	maternal embryonic leucine zipper kinase [Source:HGNC Symbol;Acc:HGNC:16870]
ENSG00000165392	WRN	Werner syndrome, RecQ helicase-like [Source:HGNC Symbol;Acc:HGNC:12791]
ENSG00000165841	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19 [Source:HGNC Symbol;Acc:HGNC:2621]
ENSG00000165983	PTER	phosphotriesterase related [Source:HGNC Symbol;Acc:HGNC:9590]
ENSG00000166508	MCM7	minichromosome maintenance complex component 7 [Source:HGNC Symbol;Acc:HGNC:6950]
ENSG00000166509	CLEC3A	C-type lectin domain family 3, member A [Source:HGNC Symbol;Acc:HGNC:2052]
ENSG00000166670	MMP10	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:HGNC:7156]
ENSG00000166803	KIAA0101	KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
ENSG00000166949	SMAD3	SMAD family member 3 [Source:HGNC Symbol;Acc:HGNC:6769]
ENSG00000167088	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa [Source:HGNC Symbol;Acc:HGNC:11158]
ENSG00000167468	GPX4	glutathione peroxidase 4 [Source:HGNC Symbol;Acc:HGNC:4556]
ENSG00000167548	KMT2D	lysine (K)-specific methyltransferase 2D [Source:HGNC Symbol;Acc:HGNC:7133]
ENSG00000167658	EEF2	eukaryotic translation elongation factor 2 [Source:HGNC Symbol;Acc:HGNC:3214]
ENSG00000168002	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G [Source:HGNC Symbol;Acc:HGNC:9194]
ENSG00000168214	RBPJ	recombination signal binding protein for immunoglobulin

		kappa J region [Source:HGNC Symbol;Acc:HGNC:5724]
ENSG00000168283	BMI1	BMI1 proto-oncogene, polycomb ring finger [Source:HGNC Symbol;Acc:HGNC:1066]
ENSG00000168505	GBX2	gastrulation brain homeobox 2 [Source:HGNC Symbol;Acc:HGNC:4186]
ENSG00000168610	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor) [Source:HGNC Symbol;Acc:HGNC:11364]
ENSG00000169083	AR	androgen receptor [Source:HGNC Symbol;Acc:HGNC:644]
ENSG00000169118	CSNK1G1	casein kinase 1, gamma 1 [Source:HGNC Symbol;Acc:HGNC:2454]
ENSG00000169218	RSPO1	R-spondin 1 [Source:HGNC Symbol;Acc:HGNC:21679]
ENSG00000169429	CXCL8	chemokine (C-X-C motif) ligand 8 [Source:HGNC Symbol;Acc:HGNC:6025]
ENSG00000169679	BUB1	BUB1 mitotic checkpoint serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:1148]
ENSG00000169710	FASN	fatty acid synthase [Source:HGNC Symbol;Acc:HGNC:3594]
ENSG00000169750	RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3) [Source:HGNC Symbol;Acc:HGNC:9803]
ENSG00000170017	ALCAM	activated leukocyte cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:400]
ENSG00000170262	MRAP	melanocortin 2 receptor accessory protein [Source:HGNC Symbol;Acc:HGNC:1304]
ENSG00000170315	UBB	ubiquitin B [Source:HGNC Symbol;Acc:HGNC:12463]
ENSG00000170345	FOS	FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:3796]
ENSG00000170421	KRT8	keratin 8 [Source:HGNC Symbol;Acc:HGNC:6446]
ENSG00000170430	MGMT	O-6-methylguanine-DNA methyltransferase [Source:HGNC Symbol;Acc:HGNC:7059]
ENSG00000170899	GSTA4	glutathione S-transferase alpha 4 [Source:HGNC Symbol;Acc:HGNC:4629]
ENSG00000171105	INSR	insulin receptor [Source:HGNC Symbol;Acc:HGNC:6091]
ENSG00000171243	SOSTDC1	sclerostin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:21748]
ENSG00000171431	KRT20	keratin 20 [Source:HGNC Symbol;Acc:HGNC:20412]
ENSG00000171552	BCL2L1	BCL2-like 1 [Source:HGNC Symbol;Acc:HGNC:992]
ENSG00000171747	LGALS4	lectin, galactoside-binding, soluble, 4 [Source:HGNC Symbol;Acc:HGNC:6565]
ENSG00000171791	BCL2	B-cell CLL/lymphoma 2 [Source:HGNC Symbol;Acc:HGNC:990]
ENSG00000171855	IFNB1	interferon, beta 1, fibroblast [Source:HGNC Symbol;Acc:HGNC:5434]
ENSG00000172115	CYCS	cytochrome c, somatic [Source:HGNC Symbol;Acc:HGNC:19986]

ENSG00000172179	PRL	prolactin [Source:HGNC Symbol;Acc:HGNC:9445]
ENSG00000172845	SP3	Sp3 transcription factor [Source:HGNC Symbol;Acc:HGNC:11208]
ENSG00000173039	RELA	v-rel avian reticuloendotheliosis viral oncogene homolog A [Source:HGNC Symbol;Acc:HGNC:9955]
ENSG00000173273	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase [Source:HGNC Symbol;Acc:HGNC:11941]
ENSG00000173673	HES3	hes family bHLH transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:26226]
ENSG00000173757	STAT5B	signal transducer and activator of transcription 5B [Source:HGNC Symbol;Acc:HGNC:11367]
ENSG00000174156	GSTA3	glutathione S-transferase alpha 3 [Source:HGNC Symbol;Acc:HGNC:4628]
ENSG00000174175	SELP	selectin P (granule membrane protein 140kDa, antigen CD62) [Source:HGNC Symbol;Acc:HGNC:10721]
ENSG00000174697	LEP	leptin [Source:HGNC Symbol;Acc:HGNC:6553]
ENSG00000175084	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
ENSG00000175387	SMAD2	SMAD family member 2 [Source:HGNC Symbol;Acc:HGNC:6768]
ENSG00000175445	LPL	lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677]
ENSG00000176165	FOXG1	forkhead box G1 [Source:HGNC Symbol;Acc:HGNC:3811]
ENSG00000176387	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2 [Source:HGNC Symbol;Acc:HGNC:5209]
ENSG00000177283	FZD8	frizzled class receptor 8 [Source:HGNC Symbol;Acc:HGNC:4046]
ENSG00000177302	TOP3A	topoisomerase (DNA) III alpha [Source:HGNC Symbol;Acc:HGNC:11992]
ENSG00000177455	CD19	CD19 molecule [Source:HGNC Symbol;Acc:HGNC:1633]
ENSG00000177606	JUN	jun proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6204]
ENSG00000177889	UBE2N	ubiquitin-conjugating enzyme E2N [Source:HGNC Symbol;Acc:HGNC:12492]
ENSG00000178568	ERBB4	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 4 [Source:HGNC Symbol;Acc:HGNC:3432]
ENSG00000178573	MAF	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog [Source:HGNC Symbol;Acc:HGNC:6776]
ENSG00000178726	THBD	thrombomodulin [Source:HGNC Symbol;Acc:HGNC:11784]
ENSG00000178764	ZHX2	zinc fingers and homeoboxes 2 [Source:HGNC Symbol;Acc:HGNC:18513]
ENSG00000179348	GATA2	GATA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:4171]
ENSG00000179776	CDH5	cadherin 5, type 2 (vascular endothelium) [Source:HGNC Symbol;Acc:HGNC:1764]
ENSG00000179914	ITLN1	intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;Acc:HGNC:18259]

ENSG00000180176	TH	tyrosine hydroxylase [Source:HGNC Symbol;Acc:HGNC:11782]
ENSG00000180210	F2	coagulation factor II (thrombin) [Source:HGNC Symbol;Acc:HGNC:3535]
ENSG00000180817	PPA1	pyrophosphatase (inorganic) 1 [Source:HGNC Symbol;Acc:HGNC:9226]
ENSG00000181019	NQO1	NAD(P)H dehydrogenase, quinone 1 [Source:HGNC Symbol;Acc:HGNC:2874]
ENSG00000181026	AEN	apoptosis enhancing nuclease [Source:HGNC Symbol;Acc:HGNC:25722]
ENSG00000182054	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Source:HGNC Symbol;Acc:HGNC:5383]
ENSG00000182866	LCK	LCK proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:6524]
ENSG00000182985	CADM1	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:5951]
ENSG00000183734	ASCL2	achaete-scute family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:739]
ENSG00000183765	CHEK2	checkpoint kinase 2 [Source:HGNC Symbol;Acc:HGNC:16627]
ENSG00000184144	CNTN2	contactin 2 (axonal) [Source:HGNC Symbol;Acc:HGNC:2172]
ENSG00000184216	IRAK1	interleukin-1 receptor-associated kinase 1 [Source:HGNC Symbol;Acc:HGNC:6112]
ENSG00000184557	SOCS3	suppressor of cytokine signaling 3 [Source:HGNC Symbol;Acc:HGNC:19391]
ENSG00000184678	HIST2H2BE	histone cluster 2, H2be [Source:HGNC Symbol;Acc:HGNC:4760]
ENSG00000184895	SRY	sex determining region Y [Source:HGNC Symbol;Acc:HGNC:11311]
ENSG00000184900	SUMO3	small ubiquitin-like modifier 3 [Source:HGNC Symbol;Acc:HGNC:11124]
ENSG00000185010	F8	coagulation factor VIII, procoagulant component [Source:HGNC Symbol;Acc:HGNC:3546]
ENSG00000185303	SFTPA2	surfactant protein A2 [Source:HGNC Symbol;Acc:HGNC:10799]
ENSG00000185345	PARK2	parkin RBR E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:8607]
ENSG00000185532	PRKG1	protein kinase, cGMP-dependent, type I [Source:HGNC Symbol;Acc:HGNC:9414]
ENSG00000185591	SP1	Sp1 transcription factor [Source:HGNC Symbol;Acc:HGNC:11205]
ENSG00000185920	PTCH1	patched 1 [Source:HGNC Symbol;Acc:HGNC:9585]
ENSG00000185928	PAGR1	PAXIP1 associated glutamate-rich protein 1 [Source:HGNC Symbol;Acc:HGNC:28707]

ENSG00000185960	SHOX	short stature homeobox [Source:HGNC Symbol;Acc:HGNC:10853]
ENSG00000186377	CYP4X1	cytochrome P450, family 4, subfamily X, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:20244]
ENSG00000186790	FOXE3	forkhead box E3 [Source:HGNC Symbol;Acc:HGNC:3808]
ENSG00000186951	PPARA	peroxisome proliferator-activated receptor alpha [Source:HGNC Symbol;Acc:HGNC:9232]
ENSG00000187678	SPRY4	sprouty homolog 4 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:15533]
ENSG00000187758	ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide [Source:HGNC Symbol;Acc:HGNC:249]
ENSG00000187837	HIST1H1C	histone cluster 1, H1c [Source:HGNC Symbol;Acc:HGNC:4716]
ENSG00000187840	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1 [Source:HGNC Symbol;Acc:HGNC:3288]
ENSG00000188379	IFNA2	interferon, alpha 2 [Source:HGNC Symbol;Acc:HGNC:5423]
ENSG00000188486	H2AFX	H2A histone family, member X [Source:HGNC Symbol;Acc:HGNC:4739]
ENSG00000196139	AKR1C3	aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:HGNC:386]
ENSG00000196230	TUBB	tubulin, beta class I [Source:HGNC Symbol;Acc:HGNC:20778]
ENSG00000196305	IARS	isoleucyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:5330]
ENSG00000196405	EVL	Enah/Vasp-like [Source:HGNC Symbol;Acc:HGNC:20234]
ENSG00000196611	MMP1	matrix metallopeptidase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:HGNC:7155]
ENSG00000196712	NF1	neurofibromin 1 [Source:HGNC Symbol;Acc:HGNC:7765]
ENSG00000197061	HIST1H4C	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:4787]
ENSG00000197081	IGF2R	insulin-like growth factor 2 receptor [Source:HGNC Symbol;Acc:HGNC:5467]
ENSG00000197122	SRC	SRC proto-oncogene, non-receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:11283]
ENSG00000197238	HIST1H4J	histone cluster 1, H4j [Source:HGNC Symbol;Acc:HGNC:4785]
ENSG00000197299	BLM	Bloom syndrome, RecQ helicase-like [Source:HGNC Symbol;Acc:HGNC:1058]
ENSG00000197408	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6 [Source:HGNC Symbol;Acc:HGNC:2615]
ENSG00000197561	ELANE	elastase, neutrophil expressed [Source:HGNC Symbol;Acc:HGNC:3309]
ENSG00000197837	HIST4H4	histone cluster 4, H4 [Source:HGNC Symbol;Acc:HGNC:20510]
ENSG00000197971	MBP	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925]

ENSG00000198668	CALM1	calmodulin 1 (phosphorylase kinase, delta) [Source:HGNC Symbol;Acc:HGNC:1442]
ENSG00000198719	DLL1	delta-like 1 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:2908]
ENSG00000198793	MTOR	mechanistic target of rapamycin (serine/threonine kinase) [Source:HGNC Symbol;Acc:HGNC:3942]
ENSG00000198900	TOP1	topoisomerase (DNA) I [Source:HGNC Symbol;Acc:HGNC:11986]
ENSG00000203782	LOR	loricrin [Source:HGNC Symbol;Acc:HGNC:6663]
ENSG00000203857	HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 [Source:HGNC Symbol;Acc:HGNC:5217]
ENSG00000204941	PSG5	pregnancy specific beta-1-glycoprotein 5 [Source:HGNC Symbol;Acc:HGNC:9522]
ENSG00000213281	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog [Source:HGNC Symbol;Acc:HGNC:7989]
ENSG00000213741	RPS29	ribosomal protein S29 [Source:HGNC Symbol;Acc:HGNC:10419]
ENSG00000214274	ANG	angiogenin, ribonuclease, RNase A family, 5 [Source:HGNC Symbol;Acc:HGNC:483]
ENSG00000215021	PHB2	prohibitin 2 [Source:HGNC Symbol;Acc:HGNC:30306]
ENSG00000224156	TUBB	tubulin, beta class I [Source:HGNC Symbol;Acc:HGNC:20778]
ENSG00000224586	GPX5	glutathione peroxidase 5 [Source:HGNC Symbol;Acc:HGNC:4557]
ENSG00000224740	FLOT1	flotillin 1 [Source:HGNC Symbol;Acc:HGNC:3757]
ENSG00000228321	TNF	tumor necrosis factor [Source:HGNC Symbol;Acc:HGNC:11892]
ENSG00000228978	TNF	tumor necrosis factor [Source:HGNC Symbol;Acc:HGNC:11892]
ENSG00000232280	FLOT1	flotillin 1 [Source:HGNC Symbol;Acc:HGNC:3757]
ENSG00000232575	TUBB	tubulin, beta class I [Source:HGNC Symbol;Acc:HGNC:20778]
ENSG00000232810	TNF	tumor necrosis factor [Source:HGNC Symbol;Acc:HGNC:11892]
ENSG00000233276	GPX1	glutathione peroxidase 1 [Source:HGNC Symbol;Acc:HGNC:4553]
ENSG00000233608	TWIST2	twist family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:20670]
ENSG00000234745	HLA-B	major histocompatibility complex, class I, B [Source:HGNC Symbol;Acc:HGNC:4932]
ENSG00000235067	TUBB	tubulin, beta class I [Source:HGNC Symbol;Acc:HGNC:20778]
ENSG00000242252	BGLAP	bone gamma-carboxyglutamate (gla) protein [Source:HGNC Symbol;Acc:HGNC:1043]
ENSG00000242950	ERVW-1	endogenous retrovirus group W, member 1 [Source:HGNC Symbol;Acc:HGNC:13525]
ENSG00000243955	GSTA1	glutathione S-transferase alpha 1 [Source:HGNC

		Symbol;Acc:HGNC:4626]
ENSG00000244067	GSTA2	glutathione S-transferase alpha 2 [Source:HGNC Symbol;Acc:HGNC:4627]
ENSG00000244482	LILRA6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 [Source:HGNC Symbol;Acc:HGNC:15495]
ENSG00000244734	HBB	hemoglobin, beta [Source:HGNC Symbol;Acc:HGNC:4827]
ENSG00000255974	CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6 [Source:HGNC Symbol;Acc:HGNC:2610]
ENSG00000256269	HMBS	hydroxymethylbilane synthase [Source:HGNC Symbol;Acc:HGNC:4982]
ENSG00000261857	MIA	melanoma inhibitory activity [Source:HGNC Symbol;Acc:HGNC:7076]
ENSG00000278705	HIST1H4B	histone cluster 1, H4b [Source:HGNC Symbol;Acc:HGNC:4789]