

Table SVII. GO Functional enrichment list.

ONT	ID	Description	P-value	Count
BP	GO:0043062	extracellular structure organization	1.13×10^{-10}	37
BP	GO:0030198	extracellular matrix organization	5.04×10^{-10}	33
BP	GO:0001501	skeletal system development	3.90×10^{-07}	35
BP	GO:0030335	positive regulation of cell migration	1.65×10^{-06}	32
BP	GO:0051272	positive regulation of cellular component movement	1.87×10^{-06}	33
BP	GO:2000147	positive regulation of cell motility	3.01×10^{-06}	32
BP	GO:0040017	positive regulation of locomotion	4.15×10^{-06}	33
BP	GO:0003007	heart morphogenesis	4.20×10^{-06}	21
BP	GO:0001704	formation of primary germ layer	6.07×10^{-06}	14
BP	GO:0001525	angiogenesis	1.01×10^{-05}	32
BP	GO:0071229	cellular response to acid chemical	1.13×10^{-05}	18
BP	GO:0007389	pattern specification process	1.74×10^{-05}	28
BP	GO:0050804	modulation of chemical synaptic transmission	1.79×10^{-05}	24
BP	GO:0099177	regulation of trans ^{syn} aptic signaling	1.79×10^{-05}	24
BP	GO:0001707	mesoderm formation	1.83×10^{-05}	10
BP	GO:0048332	mesoderm morphogenesis	2.38×10^{-05}	10
BP	GO:0060485	mesenchyme development	2.50×10^{-05}	20
BP	GO:0060562	epithelial tube morphogenesis	2.63×10^{-05}	23
BP	GO:0050890	cognition	3.00×10^{-05}	21
BP	GO:0072132	mesenchyme morphogenesis	3.09×10^{-05}	8
BP	GO:0048706	embryonic skeletal system development	3.78×10^{-05}	13
BP	GO:0061448	connective tissue development	3.85×10^{-05}	19
BP	GO:0001503	ossification	4.01×10^{-05}	25
BP	GO:0001101	response to acid chemical	4.09×10^{-05}	23
BP	GO:0072001	renal system development	4.13×10^{-05}	21
BP	GO:0050678	regulation of epithelial cell proliferation	4.29×10^{-05}	23
BP	GO:0003018	vascular process in circulatory system	4.46×10^{-05}	15
BP	GO:0050679	positive regulation of epithelial cell proliferation	4.49×10^{-05}	16
BP	GO:0007611	learning or memory	4.57×10^{-05}	19
BP	GO:0061564	axon development	4.70×10^{-05}	30
BP	GO:0010463	mesenchymal cell proliferation	5.03×10^{-05}	8
BP	GO:0050885	neuromuscular process controlling balance	5.03×10^{-05}	8
BP	GO:0042698	ovulation cycle	6.08×10^{-05}	9
BP	GO:0015837	amine transport	6.90×10^{-05}	10
BP	GO:0051480	regulation of cytosolic calcium ion concentration	6.92×10^{-05}	22
BP	GO:0001936	regulation of endothelial cell proliferation	7.36×10^{-05}	13
BP	GO:0003341	cilium movement	8.82×10^{-05}	9

BP	GO:0051968	positive regulation of synaptic transmission, glutamatergic	0.000104	6
BP	GO:0048736	appendage development	0.000109	15
BP	GO:0060173	limb development	0.000109	15
BP	GO:0050808	synapse organization	0.000111	21
BP	GO:0008217	regulation of blood pressure	0.000116	15
BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	0.000142	20
BP	GO:0050673	epithelial cell proliferation	0.000156	24
BP	GO:0007369	gastrulation	0.000159	15
BP	GO:0042476	odontogenesis	0.000162	12
BP	GO:0048562	embryonic organ morphogenesis	0.000163	20
BP	GO:0038166	angiotensin ^{-activated} signaling pathway	0.000172	4
BP	GO:0051952	regulation of amine transport	0.000175	9
BP	GO:0051216	cartilage development	0.00018	15
BP	GO:0007498	mesoderm development	0.000189	12
BP	GO:0019933	cAMP ^{-mediated} signaling	0.000194	13
BP	GO:0001935	endothelial cell proliferation	0.000208	13
BP	GO:0051962	positive regulation of nervous system development	0.000217	28
BP	GO:0001655	urogenital system development	0.000229	21
BP	GO:0071677	positive regulation of mononuclear cell migration	0.000237	5
BP	GO:0031623	receptor internalization	0.00025	10
BP	GO:0035282	segmentation	0.00025	10
BP	GO:0048511	rhythmic process	0.000251	19
BP	GO:0030326	embryonic limb morphogenesis	0.000255	12
BP	GO:0035113	embryonic appendage morphogenesis	0.000255	12
BP	GO:0035107	appendage morphogenesis	0.000255	13
BP	GO:0035108	limb morphogenesis	0.000255	13
BP	GO:0007188	adenylate cyclase ^{-modulating} G ^{-protein} coupled receptor signaling pathway	0.000306	15
BP	GO:0051966	regulation of synaptic transmission, glutamatergic	0.000358	8
BP	GO:0050905	neuromuscular process	0.000385	10
BP	GO:0007409	axonogenesis	0.000391	26
BP	GO:0051965	positive regulation of synapse assembly	0.000399	8
BP	GO:0019935	cyclic ^{-nucleotide-} mediated signaling	0.000401	13
BP	GO:0007368	determination of left/right symmetry	0.000414	11
BP	GO:0007189	adenylate cyclase ^{-activating} G ^{-protein} coupled receptor signaling pathway	0.000418	10
BP	GO:0050880	regulation of blood vessel size	0.000445	12
BP	GO:0010464	regulation of mesenchymal cell proliferation	0.000446	6

BP	GO:0048762	mesenchymal cell differentiation	0.00045	15
BP	GO:0060632	regulation of microtubule ^{ba} sed movement	0.000462	5
BP	GO:0001822	kidney development	0.000462	18
BP	GO:0007187	G ^P rotein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	0.000465	16
BP	GO:0035150	regulation of tube size	0.000476	12
BP	GO:0072006	nephron development	0.000476	12
BP	GO:0002040	sprouting angiogenesis	0.000479	11
BP	GO:0003352	regulation of cilium movement	0.000487	4
BP	GO:0050930	induction of positive chemotaxis	0.000487	4
BP	GO:0006874	cellular calcium ion homeostasis	0.000499	24
BP	GO:0032526	response to retinoic acid	0.000533	10
BP	GO:0071300	cellular response to retinoic acid	0.000547	8
BP	GO:0060326	cell chemotaxis	0.000553	18
BP	GO:0007631	feeding behavior	0.000576	10
BP	GO:0007548	sex differentiation	0.00063	18
BP	GO:1901652	response to peptide	0.000635	27
BP	GO:0003197	endocardial cushion development	0.000697	6
BP	GO:0032941	secretion by tissue	0.000697	6
BP	GO:0055074	calcium ion homeostasis	0.000728	24
BP	GO:0019226	transmission of nerve impulse	0.000736	8
BP	GO:0009855	determination of bilateral symmetry	0.000779	11
BP	GO:0060537	muscle tissue development	0.000784	22
BP	GO:0001706	endoderm formation	0.000822	7
BP	GO:0009799	specification of symmetry	0.000833	11
BP	GO:0035249	synaptic transmission, glutamatergic	0.00086	9
BP	GO:0003002	regionalization	0.000881	20
BP	GO:0043434	response to peptide hormone	0.000917	24
BP	GO:0001938	positive regulation of endothelial cell proliferation	0.000932	9
BP	GO:0035296	regulation of tube diameter	0.000949	11
BP	GO:0097746	regulation of blood vessel diameter	0.000949	11
BP	GO:0007416	synapse assembly	0.001005	12
BP	GO:0015850	organic hydroxy compound transport	0.001008	15
BP	GO:0007586	digestion	0.001012	11
BP	GO:0002042	cell migration involved in sprouting angiogenesis	0.00102	7
BP	GO:0007613	memory	0.001041	10
BP	GO:0090026	positive regulation of monocyte chemotaxis	0.001083	4
BP	GO:0007589	body fluid secretion	0.001092	9
BP	GO:0031128	developmental induction	0.00115	5
BP	GO:0034698	response to gonadotropin	0.00115	5

BP	GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G ^{pr} protein coupled signaling pathway	0.00115	5
BP	GO:0048704	embryonic skeletal system morphogenesis	0.001179	9
BP	GO:0044060	regulation of endocrine process	0.001184	6
BP	GO:0046717	acid secretion	0.001195	10
BP	GO:0048565	digestive tract development	0.001222	11
BP	GO:0050918	positive chemotaxis	0.001255	7
BP	GO:0042310	vasoconstriction	0.001271	8
BP	GO:0022617	extracellular matrix disassembly	0.001273	9
BP	GO:0001763	morphogenesis of a branching structure	0.001347	14
BP	GO:0051385	response to mineralocorticoid	0.001349	5
BP	GO:0001759	organ induction	0.001362	4
BP	GO:0051412	response to corticosterone	0.001362	4
BP	GO:0060973	cell migration involved in heart development	0.001362	4
BP	GO:0061333	renal tubule morphogenesis	0.001384	8
BP	GO:0007612	learning	0.001467	11
BP	GO:0072503	cellular divalent inorganic cation homeostasis	0.001514	24
BP	GO:0048545	response to steroid hormone	0.001543	22
BP	GO:0007492	endoderm development	0.001635	8
BP	GO:0035987	endodermal cell differentiation	0.001696	6
BP	GO:0048333	mesodermal cell differentiation	0.00182	5
BP	GO:0050769	positive regulation of neurogenesis	0.001846	23
BP	GO:0045444	fat cell differentiation	0.001872	14
BP	GO:0030278	regulation of ossification	0.001888	13
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	0.001998	18
BP	GO:0007517	muscle organ development	0.002003	21
BP	GO:0001756	somitogenesis	0.002027	7
BP	GO:0048705	skeletal system morphogenesis	0.002049	14
BP	GO:0010770	positive regulation of cell morphogenesis involved in differentiation	0.002076	11
BP	GO:0061053	somite development	0.002077	8
BP	GO:0035115	embryonic forelimb morphogenesis	0.002097	5
BP	GO:0006816	calcium ion transport	0.002117	22
BP	GO:0001667	ameboidal-type cell migration	0.002136	21
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.002156	15
BP	GO:0006898	receptor ^{me} diated endocytosis	0.002237	17
BP	GO:0097756	negative regulation of blood vessel diameter	0.002243	8
BP	GO:2001023	regulation of response to drug	0.002243	8

BP	GO:0001823	mesonephros development	0.002253	9
BP	GO:0010838	positive regulation of keratinocyte proliferation	0.002264	3
BP	GO:0051956	negative regulation of amino acid transport	0.002264	3
BP	GO:0050729	positive regulation of inflammatory response	0.002274	10
BP	GO:0010976	positive regulation of neuron projection development	0.002305	16
BP	GO:0055123	digestive system development	0.00232	11
BP	GO:0007190	activation of adenylate cyclase activity	0.002403	5
BP	GO:0006939	smooth muscle contraction	0.002409	9
BP	GO:0003206	cardiac chamber morphogenesis	0.002416	10
BP	GO:0014706	striated muscle tissue development	0.002438	20
BP	GO:0003272	endocardial cushion formation	0.002492	4
BP	GO:0035929	steroid hormone secretion	0.002492	4
BP	GO:0010810	regulation of cell ^{su} strate adhesion	0.002512	13
BP	GO:0072507	divalent inorganic cation homeostasis	0.002559	24
BP	GO:0051963	regulation of synapse assembly	0.002608	8
BP	GO:0060021	roof of mouth development	0.002608	8
BP	GO:0048546	digestive tract morphogenesis	0.002619	6
BP	GO:0050805	negative regulation of synaptic transmission	0.002642	7
BP	GO:0048167	regulation of synaptic plasticity	0.002649	12
BP	GO:0048566	embryonic digestive tract development	0.002739	5
BP	GO:0019932	second ^{me} ssenger ^{me} diated signaling	0.002777	19
BP	GO:0032103	positive regulation of response to external stimulus	0.002792	17
BP	GO:0045666	positive regulation of neuron differentiation	0.00287	19
BP	GO:0030574	collagen catabolic process	0.002876	7
BP	GO:0016331	morphogenesis of embryonic epithelium	0.002878	11
BP	GO:0090025	regulation of monocyte chemotaxis	0.002979	4
BP	GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	0.002979	4
BP	GO:1904385	cellular response to angiotensin	0.002979	4
BP	GO:0010720	positive regulation of cell development	0.00299	25
BP	GO:0086103	G ^{pr} rotein coupled receptor signaling pathway involved in heart process	0.003048	3
BP	GO:0006024	glycosaminoglycan biosynthetic process	0.003122	9
BP	GO:0010811	positive regulation of cell ^{su} strate adhesion	0.003122	9
BP	GO:0006026	aminoglycan catabolic process	0.003125	7
BP	GO:0001942	hair follicle development	0.00324	8

BP	GO:0031589	cell ^{su} bsstrate adhesion	0.003265	18
BP	GO:0045137	development of primary sexual characteristics	0.003434	14
BP	GO:0050900	leukocyte migration	0.003505	22
BP	GO:0015872	dopamine transport	0.003514	5
BP	GO:0051953	negative regulation of amine transport	0.003527	4
BP	GO:0072012	glomerulus vasculature development	0.003527	4
BP	GO:2000209	regulation of anoikis	0.003527	4
BP	GO:0070371	ERK1 and ERK2 cascade	0.003609	18
BP	GO:0050921	positive regulation of chemotaxis	0.003611	10
BP	GO:0022404	molting cycle process	0.003723	8
BP	GO:0022405	hair cycle process	0.003723	8
BP	GO:0098773	skin epidermis development	0.003723	8
BP	GO:0071675	regulation of mononuclear cell migration	0.003955	5
BP	GO:0006936	muscle contraction	0.003957	19
BP	GO:0042340	keratan sulfate catabolic process	0.00398	3
BP	GO:0043116	negative regulation of vascular permeability	0.00398	3
BP	GO:0060272	embryonic skeletal joint morphogenesis	0.00398	3
BP	GO:0060536	cartilage morphogenesis	0.00398	3
BP	GO:0060707	trophoblast giant cell differentiation	0.00398	3
BP	GO:2000052	positive regulation of non ^{ca} nonical Wnt signaling pathway	0.00398	3
BP	GO:0014046	dopamine secretion	0.00414	4
BP	GO:0014059	regulation of dopamine secretion	0.00414	4
BP	GO:0006023	aminoglycan biosynthetic process	0.004235	9
BP	GO:0033627	cell adhesion mediated by integrin	0.00425	6
BP	GO:0043536	positive regulation of blood vessel endothelial cell migration	0.00425	6
BP	GO:0060993	kidney morphogenesis	0.00426	8
BP	GO:0048568	embryonic organ development	0.004266	22
BP	GO:0072078	nephron tubule morphogenesis	0.00429	7
BP	GO:0010634	positive regulation of epithelial cell migration	0.004479	10
BP	GO:0022600	digestive system process	0.00455	8
BP	GO:0001649	osteoblast differentiation	0.00464	13
BP	GO:0003205	cardiac chamber development	0.004751	11
BP	GO:1903510	mucopolysaccharide metabolic process	0.004758	9
BP	GO:0003012	muscle system process	0.00476	22
BP	GO:0045992	negative regulation of embryonic development	0.004821	4
BP	GO:0050927	positive regulation of positive chemotaxis	0.004821	4
BP	GO:0061437	renal system vasculature development	0.004821	4
BP	GO:0061440	kidney vasculature development	0.004821	4

BP	GO:1990776	response to angiotensin	0.004821	4
BP	GO:0051048	negative regulation of secretion	0.004835	13
BP	GO:0061326	renal tubule development	0.004854	8
BP	GO:1901653	cellular response to peptide	0.004906	19
BP	GO:0044058	regulation of digestive system process	0.004953	5
BP	GO:0030534	adult behavior	0.004972	10
BP	GO:0003151	outflow tract morphogenesis	0.004983	7
BP	GO:0072088	nephron epithelium morphogenesis	0.004983	7
BP	GO:0050727	regulation of inflammatory response	0.005055	19
BP	GO:0030157	pancreatic juice secretion	0.005068	3
BP	GO:0034374	low-density lipoprotein particle remodeling	0.005068	3
BP	GO:0048934	peripheral nervous system neuron differentiation	0.005068	3
BP	GO:0048935	peripheral nervous system neuron development	0.005068	3
BP	GO:2000095	regulation of Wnt signaling pathway, planar cell polarity pathway	0.005068	3
BP	GO:1901654	response to ketone	0.005072	12
BP	GO:0007218	neuropeptide signaling pathway	0.005175	8
BP	GO:0046661	male sex differentiation	0.005222	11
BP	GO:0007519	skeletal muscle tissue development	0.00547	11
BP	GO:0035136	forelimb morphogenesis	0.005514	5
BP	GO:1903672	positive regulation of sprouting angiogenesis	0.005514	5
BP	GO:0050926	regulation of positive chemotaxis	0.005574	4
BP	GO:0061311	cell surface receptor signaling pathway involved in heart development	0.005574	4
BP	GO:0050807	regulation of synapse organization	0.005728	11
BP	GO:0072028	nephron morphogenesis	0.005758	7
BP	GO:0061138	morphogenesis of a branching epithelium	0.00577	12
BP	GO:0001657	ureteric bud development	0.005863	8
BP	GO:1903522	regulation of blood circulation	0.00591	16
BP	GO:0048645	animal organ formation	0.006016	6
BP	GO:0051937	catecholamine transport	0.006016	6
BP	GO:0007018	microtubule-based movement	0.006079	17
BP	GO:0022602	ovulation cycle process	0.006118	5
BP	GO:0030857	negative regulation of epithelial cell differentiation	0.006118	5
BP	GO:0071674	mononuclear cell migration	0.006177	7
BP	GO:1903670	regulation of sprouting angiogenesis	0.006177	7
BP	GO:0072163	mesonephric epithelium development	0.006233	8
BP	GO:0072164	mesonephric tubule development	0.006233	8
BP	GO:0003214	cardiac left ventricle morphogenesis	0.006317	3
BP	GO:0030238	male sex determination	0.006317	3

BP	GO:0032105	negative regulation of response to extracellular stimulus	0.006317	3
BP	GO:0032108	negative regulation of response to nutrient levels	0.006317	3
BP	GO:0035589	G ^{pr} rotein coupled purinergic nucleotide receptor signaling pathway	0.006317	3
BP	GO:0021537	telencephalon development	0.006383	14
BP	GO:0060402	calcium ion transport into cytosol	0.006388	10
BP	GO:0002675	positive regulation of acute inflammatory response	0.006401	4
BP	GO:0090130	tissue migration	0.006524	16
BP	GO:0019229	regulation of vasoconstriction	0.00653	6
BP	GO:0035082	axoneme assembly	0.00653	6
BP	GO:0003231	cardiac ventricle development	0.006634	9
BP	GO:0032963	collagen metabolic process	0.006634	9
BP	GO:0071375	cellular response to peptide hormone stimulus	0.006678	17
BP	GO:0050433	regulation of catecholamine secretion	0.006767	5
BP	GO:0008406	gonad development	0.006904	13
BP	GO:0043534	blood vessel endothelial cell migration	0.006995	9
BP	GO:0002548	monocyte chemotaxis	0.007076	6
BP	GO:0032835	glomerulus development	0.007076	6
BP	GO:0050772	positive regulation of axonogenesis	0.007083	7
BP	GO:0060560	developmental growth involved in morphogenesis	0.007172	13
BP	GO:0002053	positive regulation of mesenchymal cell proliferation	0.007305	4
BP	GO:0071709	membrane assembly	0.007305	4
BP	GO:0070838	divalent metal ion transport	0.007418	22
BP	GO:0010817	regulation of hormone levels	0.00754	24
BP	GO:0006027	glycosaminoglycan catabolic process	0.007653	6
BP	GO:0006940	regulation of smooth muscle contraction	0.007653	6
BP	GO:0061371	determination of heart left/right asymmetry	0.007653	6
BP	GO:0010766	negative regulation of sodium ion transport	0.007734	3
BP	GO:0050961	detection of temperature stimulus involved in sensory perception	0.007734	3
BP	GO:0050965	detection of temperature stimulus involved in sensory perception of pain	0.007734	3
BP	GO:0060026	convergent extension	0.007734	3
BP	GO:0072498	embryonic skeletal joint development	0.007734	3
BP	GO:2000846	regulation of corticosteroid hormone secretion	0.007734	3

BP	GO:0002687	positive regulation of leukocyte migration	0.007762	9
BP	GO:0060538	skeletal muscle organ development	0.007813	11
BP	GO:0060840	artery development	0.008084	7
BP	GO:0072511	divalent inorganic cation transport	0.008193	22
BP	GO:0051932	synaptic transmission, GABAergic	0.008207	5
BP	GO:0071230	cellular response to amino acid stimulus	0.008264	6
BP	GO:0003203	endocardial cushion morphogenesis	0.00829	4
BP	GO:0007205	protein kinase C-activating G ^{pr} protein coupled receptor signaling pathway	0.00829	4
BP	GO:0010092	specification of animal organ identity	0.00829	4
BP	GO:0018146	keratan sulfate biosynthetic process	0.00829	4
BP	GO:0035116	embryonic hindlimb morphogenesis	0.00829	4
BP	GO:0051955	regulation of amino acid transport	0.00829	4
BP	GO:0042391	regulation of membrane potential	0.008396	21
BP	GO:0007411	axon guidance	0.008477	14
BP	GO:0048608	reproductive structure development	0.008611	21
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	0.008764	17
BP	GO:0006022	aminoglycan metabolic process	0.008869	11
BP	GO:0048844	artery morphogenesis	0.00891	6
BP	GO:0045765	regulation of angiogenesis	0.008954	16
BP	GO:0030199	collagen fibril organization	0.009001	5
BP	GO:0050432	catecholamine secretion	0.009001	5
BP	GO:0060986	endocrine hormone secretion	0.009001	5
BP	GO:1901342	regulation of vasculature development	0.009024	17
BP	GO:0097485	neuron projection guidance	0.009078	14
BP	GO:0090066	regulation of anatomical structure size	0.009182	23
BP	GO:0050803	regulation of synapse structure or activity	0.009244	11
BP	GO:0061458	reproductive system development	0.009283	21
BP	GO:0003198	epithelial to mesenchymal transition involved in endocardial cushion formation	0.009323	3
BP	GO:0007158	neuron cell-cell adhesion	0.009323	3
BP	GO:0007625	grooming behavior	0.009323	3
BP	GO:0035930	corticosteroid hormone secretion	0.009323	3
BP	GO:0036342	post-anal tail morphogenesis	0.009323	3
BP	GO:2000380	regulation of mesoderm development	0.009323	3
BP	GO:2000811	negative regulation of anoikis	0.009323	3
BP	GO:0048873	homeostasis of number of cells within a tissue	0.009358	4
BP	GO:1903523	negative regulation of blood circulation	0.009358	4
BP	GO:0023061	signal release	0.009517	21
BP	GO:0072171	mesonephric tubule morphogenesis	0.00959	6
BP	GO:0001578	microtubule bundle formation	0.010394	7
BP	GO:0031214	biomineral tissue development	0.010451	9

BP	GO:0010837	regulation of keratinocyte proliferation	0.010512	4
BP	GO:0032228	regulation of synaptic transmission, GABAergic	0.010512	4
BP	GO:0048754	branching morphogenesis of an epithelial tube	0.010599	10
BP	GO:0007528	neuromuscular junction development	0.010745	5
BP	GO:0009952	anterior/posterior pattern specification	0.010876	12
BP	GO:0002690	positive regulation of leukocyte chemotaxis	0.01104	7
BP	GO:0060401	cytosolic calcium ion transport	0.011066	10
BP	GO:0017085	response to insecticide	0.011089	3
BP	GO:0021756	striatum development	0.011089	3
BP	GO:0022010	central nervous system myelination	0.011089	3
BP	GO:0032291	axon ensheathment in central nervous system	0.011089	3
BP	GO:0032354	response to follicle-stimulating hormone	0.011089	3
BP	GO:0032891	negative regulation of organic acid transport	0.011089	3
BP	GO:0043951	negative regulation of cAMP-mediated signaling	0.011089	3
BP	GO:0048871	multicellular organismal homeostasis	0.011342	17
BP	GO:0072009	nephron epithelium development	0.011556	8
BP	GO:0044273	sulfur compound catabolic process	0.011698	5
BP	GO:0046879	hormone secretion	0.011712	16
BP	GO:0009954	proximal/distal pattern formation	0.011753	4
BP	GO:0043276	anoikis	0.011753	4
BP	GO:0060317	cardiac epithelial to mesenchymal transition	0.011753	4
BP	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	0.011853	6
BP	GO:0051047	positive regulation of secretion	0.011911	19
BP	GO:0090287	regulation of cellular response to growth factor stimulus	0.012205	14
BP	GO:0050878	regulation of body fluid levels	0.012339	23
BP	GO:0001837	epithelial to mesenchymal transition	0.012598	9
BP	GO:0035051	cardiocyte differentiation	0.012598	9
BP	GO:0031279	regulation of cyclase activity	0.012707	5
BP	GO:0032890	regulation of organic acid transport	0.012707	5
BP	GO:0051339	regulation of lyase activity	0.012707	5
BP	GO:0042303	molting cycle	0.012803	8
BP	GO:0042633	hair cycle	0.012803	8
BP	GO:0001710	mesodermal cell fate commitment	0.013034	3
BP	GO:0016048	detection of temperature stimulus	0.013034	3
BP	GO:0071371	cellular response to gonadotropin stimulus	0.013034	3

BP	GO:0099054	presynapse assembly	0.013034	3
BP	GO:2000831	regulation of steroid hormone secretion	0.013034	3
BP	GO:0001894	tissue homeostasis	0.013035	12
BP	GO:0003156	regulation of animal organ formation	0.013085	4
BP	GO:0044091	membrane biogenesis	0.013085	4
BP	GO:0070286	axonemal dynein complex assembly	0.013085	4
BP	GO:0030900	forebrain development	0.013488	18
BP	GO:0015844	monoamine transport	0.013555	6
BP	GO:0031644	regulation of neurological system process	0.013555	6
BP	GO:0010975	regulation of neuron projection development	0.013622	21
BP	GO:0030203	glycosaminoglycan metabolic process	0.013643	10
BP	GO:0010524	positive regulation of calcium ion transport into cytosol	0.013773	5
BP	GO:0030817	regulation of cAMP biosynthetic process	0.013773	5
BP	GO:0060070	canonical Wnt signaling pathway	0.014287	16
BP	GO:0008584	male gonad development	0.014412	9
BP	GO:0030802	regulation of cyclic nucleotide biosynthetic process	0.014468	6
BP	GO:0007616	long-term memory	0.01451	4
BP	GO:0042339	keratan sulfate metabolic process	0.01451	4
BP	GO:0045761	regulation of adenylate cyclase activity	0.01451	4
BP	GO:0072080	nephron tubule development	0.014709	7
BP	GO:0031960	response to corticosteroid	0.014791	10
BP	GO:0048168	regulation of neuronal synaptic plasticity	0.014897	5
BP	GO:0046546	development of primary male sexual characteristics	0.015058	9
BP	GO:0023019	signal transduction involved in regulation of gene expression	0.015162	3
BP	GO:0048557	embryonic digestive tract morphogenesis	0.015162	3
BP	GO:0060008	Sertoli cell differentiation	0.015162	3
BP	GO:0071625	vocalization behavior	0.015162	3
BP	GO:0046883	regulation of hormone secretion	0.015172	14
BP	GO:0002027	regulation of heart rate	0.015536	7
BP	GO:0001654	eye development	0.015674	17
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	0.016042	12
BP	GO:0009914	hormone transport	0.016382	16
BP	GO:0010522	regulation of calcium ion transport into cytosol	0.016396	7
BP	GO:0003208	cardiac ventricle morphogenesis	0.016419	6
BP	GO:0035050	embryonic heart tube development	0.016419	6
BP	GO:0070509	calcium ion import	0.016419	6

BP	GO:0052547	regulation of peptidase activity	0.016596	20
BP	GO:0072073	kidney epithelium development	0.017121	9
BP	GO:0010595	positive regulation of endothelial cell migration	0.017288	7
BP	GO:0019233	sensory perception of pain	0.017288	7
BP	GO:0051279	regulation of release of sequestered calcium ion into cytosol	0.017459	6
BP	GO:0019373	epoxygenase P450 pathway	0.017474	3
BP	GO:0030325	adrenal gland development	0.017474	3
BP	GO:0036120	cellular response to platelet ^{de} rived growth factor stimulus	0.017474	3
BP	GO:0072087	renal vesicle development	0.017474	3
BP	GO:0099172	presynapse organization	0.017474	3
BP	GO:1903587	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	0.017474	3
BP	GO:0045995	regulation of embryonic development	0.017948	8
BP	GO:0010959	regulation of metal ion transport	0.018276	17
BP	GO:0031346	positive regulation of cell projection organization	0.019213	17
BP	GO:0010470	regulation of gastrulation	0.019356	4
BP	GO:0035137	hindlimb morphogenesis	0.019356	4
BP	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	0.019356	4
BP	GO:0051384	response to glucocorticoid	0.019385	9
BP	GO:0007422	peripheral nervous system development	0.019674	6
BP	GO:0036119	response to platelet ^{de} rived growth factor	0.019971	3
BP	GO:0044321	response to leptin	0.019971	3
BP	GO:0050855	regulation of B cell receptor signaling pathway	0.019971	3
BP	GO:0050951	sensory perception of temperature stimulus	0.019971	3
BP	GO:0030282	bone mineralization	0.020171	7
BP	GO:0043112	receptor metabolic process	0.020863	10
BP	GO:0050806	positive regulation of synaptic transmission	0.021009	9
BP	GO:0001947	heart looping	0.021442	5
BP	GO:0071559	response to transforming growth factor beta	0.021499	12
BP	GO:2000027	regulation of organ morphogenesis	0.021631	13
BP	GO:0051924	regulation of calcium ion transport	0.022181	12
BP	GO:0021761	limbic system development	0.022269	7
BP	GO:0035637	multicellular organismal signaling	0.022484	11
BP	GO:0030539	male genitalia development	0.022654	3

BP	GO:0030728	ovulation	0.022654	3
BP	GO:0035590	purinergic nucleotide receptor signaling pathway	0.022654	3
BP	GO:0045109	intermediate filament organization	0.022654	3
BP	GO:0060487	lung epithelial cell differentiation	0.022654	3
BP	GO:2000050	regulation of non-canonical Wnt signaling pathway	0.022654	3
BP	GO:0010517	regulation of phospholipase activity	0.022943	5
BP	GO:0033628	regulation of cell adhesion mediated by integrin	0.023081	4
BP	GO:0016055	Wnt signaling pathway	0.023252	22
BP	GO:1903532	positive regulation of secretion by cell	0.023337	17
BP	GO:0010631	epithelial cell migration	0.023365	14
BP	GO:0097553	calcium ion transmembrane import into cytosol	0.023415	8
BP	GO:0045165	cell fate commitment	0.023606	13
BP	GO:0198738	cell-cell signaling by wnt	0.024192	22
BP	GO:0046887	positive regulation of hormone secretion	0.024429	8
BP	GO:0060415	muscle tissue morphogenesis	0.024661	6
BP	GO:0032309	icosanoid secretion	0.025095	4
BP	GO:0090132	epithelium migration	0.02534	14
BP	GO:0007530	sex determination	0.025523	3
BP	GO:0021544	subpallium development	0.025523	3
BP	GO:0060479	lung cell differentiation	0.025523	3
BP	GO:0060914	heart formation	0.025523	3
BP	GO:0098868	bone growth	0.025523	3
BP	GO:0001952	regulation of cell-matrix adhesion	0.025692	7
BP	GO:0097529	myeloid leukocyte migration	0.025812	10
BP	GO:0030595	leukocyte chemotaxis	0.026444	11
BP	GO:0043542	endothelial cell migration	0.026444	11
CC	GO:0031012	extracellular matrix	7.01×10^{-18}	53
CC	GO:0005578	proteinaceous extracellular matrix	1.36×10^{-14}	42
CC	GO:0044420	extracellular matrix component	1.76×10^{-07}	16
CC	GO:0043235	receptor complex	4.70×10^{-05}	25
CC	GO:0098644	complex of collagen trimers	0.000188	5
CC	GO:0005604	basement membrane	0.000215	10
CC	GO:0032281	AMPA glutamate receptor complex	0.000694	5
CC	GO:0008328	ionotropic glutamate receptor complex	0.00216	6
CC	GO:0005581	collagen trimer	0.002297	8
CC	GO:0098878	neurotransmitter receptor complex	0.002668	6
CC	GO:0032982	myosin filament	0.003019	4
CC	GO:0031225	anchored component of membrane	0.003643	11
CC	GO:0005583	fibrillar collagen trimer	0.004021	3
CC	GO:0098643	banded collagen fibril	0.004021	3

CC	GO:0005891	voltage-gated calcium channel complex	0.006213	5
CC	GO:0097060	synaptic membrane	0.007376	17
CC	GO:0030016	myofibril	0.008276	13
CC	GO:0046658	anchored component of plasma membrane	0.008333	5
CC	GO:0005930	axoneme	0.011202	8
CC	GO:0031093	platelet alpha granule lumen	0.011252	6
CC	GO:0097014	ciliary plasm	0.011803	8
CC	GO:0016460	myosin II complex	0.011901	4
CC	GO:0098839	postsynaptic density membrane	0.011901	4
CC	GO:0043292	contractile fiber	0.012212	13
CC	GO:0031091	platelet alpha granule	0.013401	7
CC	GO:0031901	early endosome membrane	0.013485	9
CC	GO:0016459	myosin complex	0.013785	6
CC	GO:0099634	postsynaptic specialization membrane	0.014689	4
CC	GO:1902495	transmembrane transporter complex	0.016482	16
CC	GO:0034703	cation channel complex	0.017046	12
CC	GO:0034702	ion channel complex	0.017096	15
CC	GO:0005605	basal lamina	0.017643	3
CC	GO:0045211	postsynaptic membrane	0.018574	13
MF	GO:0005201	extracellular matrix structural constituent	7.11×10^{-6}	11
MF	GO:0005516	calmodulin binding	2.85×10^{-5}	17
MF	GO:0008528	G-protein coupled peptide receptor activity	4.29×10^{-5}	13
MF	GO:0001653	peptide receptor activity	4.66×10^{-5}	13
MF	GO:0043121	neurotrophin binding	9.98×10^{-5}	4
MF	GO:0019838	growth factor binding	0.000279	12
MF	GO:0005518	collagen binding	0.000295	8
MF	GO:0048018	receptor ligand activity	0.000376	26
MF	GO:0008083	growth factor activity	0.000441	13
MF	GO:0030545	receptor regulator activity	0.000904	26
MF	GO:0042056	chemoattractant activity	0.001847	5
MF	GO:0005539	glycosaminoglycan binding	0.002051	14
MF	GO:0048407	platelet-derived growth factor binding	0.002808	3
MF	GO:0008201	heparin binding	0.003649	11
MF	GO:0000982	transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	0.003974	21
MF	GO:0061134	peptidase regulator activity	0.004663	13
MF	GO:0005245	voltage-gated calcium channel activity	0.004884	5
MF	GO:0030594	neurotransmitter receptor activity	0.004944	8
MF	GO:0005262	calcium channel activity	0.00495	9
MF	GO:0001608	G-protein coupled nucleotide receptor activity	0.005829	3
MF	GO:0045028	G-protein coupled purinergic nucleotide receptor activity	0.005829	3

MF	GO:0001664	G-protein coupled receptor binding	0.005964	15
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