

Supplementary Table 2. Enriched Gene Ontology terms with DEGs

GO_ID	Description	Type	GeneRatio	BgRatio	p-value	q-value	Count	Enrich_Factor
GO:0009888	tissue development	biological_process	93/456	1779/20791	3.122e-13	1.640e-09	93	2.38
GO:0030154	cell differentiation	biological_process	151/456	3607/20791	9.785e-13	2.570e-09	151	1.91
GO:0009653	anatomical structure morphogenesis	biological_process	113/456	2499/20791	8.036e-12	1.407e-08	113	2.06
GO:0048869	cellular developmental process	biological_process	157/456	3923/20791	9.366e-12	1.230e-08	157	1.82
GO:0032502	developmental process	biological_process	202/456	5542/20791	3.588e-11	3.770e-08	202	1.66
GO:0048513	organ development	biological_process	133/456	3214/20791	4.251e-11	3.722e-08	133	1.89
GO:0048856	anatomical structure development	biological_process	189/456	5171/20791	1.204e-10	9.035e-08	189	1.67
GO:0007275	multicellular organismal development	biological_process	173/456	4645/20791	1.874e-10	1.231e-07	173	1.70
GO:0060173	limb development	biological_process	22/456	180/20791	2.559e-10	1.494e-07	22	5.57
GO:0032403	protein complex binding	molecular_function	55/456	930/20791	2.603e-10	1.367e-07	55	2.70
GO:0072359	circulatory system development	biological_process	56/456	962/20791	3.169e-10	1.513e-07	56	2.65
GO:0072358	cardiovascular system development	biological_process	56/456	962/20791	3.169e-10	1.513e-07	56	2.65
GO:0070062	extracellular vesicular exosome	cellular_component	111/456	2603/20791	3.176e-10	1.283e-07	111	1.94
GO:1903561	extracellular vesicle	cellular_component	111/456	2616/20791	4.157e-10	1.560e-07	111	1.93
GO:0008283	cell proliferation	biological_process	84/456	1785/20791	5.613e-10	1.966e-07	84	2.15
GO:0051726	regulation of cell cycle	biological_process	51/456	849/20791	6.625e-10	2.175e-07	51	2.74
GO:0009790	embryo development	biological_process	58/456	1050/20791	1.024e-09	3.164e-07	58	2.52
GO:0035108	limb morphogenesis	biological_process	20/456	160/20791	1.028e-09	3.000e-07	20	5.70
GO:0042127	regulation of cell proliferation	biological_process	72/456	1459/20791	1.333e-09	3.685e-07	72	2.25
GO:0031012	extracellular matrix	cellular_component	32/456	404/20791	1.690e-09	4.439e-07	32	3.61
GO:0048468	cell development	biological_process	88/456	1966/20791	2.277e-09	5.696e-07	88	2.04
GO:0050793	regulation of developmental process	biological_process	94/456	2177/20791	3.722e-09	8.887e-07	94	1.97
GO:0005576	extracellular region	cellular_component	156/456	4263/20791	4.301e-09	9.823e-07	156	1.67
GO:0006928	cellular component movement	biological_process	73/456	1544/20791	5.783e-09	1.266e-06	73	2.16
GO:0045595	regulation of cell differentiation	biological_process	72/456	1526/20791	7.902e-09	1.660e-06	72	2.15
GO:0030326	embryonic limb morphogenesis	biological_process	17/456	135/20791	1.374e-08	2.776e-06	17	5.74
GO:0031982	vesicle	cellular_component	129/456	3412/20791	1.520e-08	2.957e-06	129	1.72
GO:0009967	positive regulation of signal transduction	biological_process	61/456	1237/20791	2.256e-08	4.232e-06	61	2.25
GO:0002062	chondrocyte differentiation	biological_process	14/456	94/20791	2.859e-08	5.179e-06	14	6.79
GO:0001944	vasculature development	biological_process	38/456	611/20791	3.487e-08	6.106e-06	38	2.84
GO:0001568	blood vessel development	biological_process	37/456	588/20791	3.885e-08	6.583e-06	37	2.87
GO:0051216	cartilage development	biological_process	19/456	182/20791	4.060e-08	6.665e-06	19	4.76
GO:0040007	growth	biological_process	50/456	946/20791	4.989e-08	7.942e-06	50	2.41
GO:0048646	anatomical structure formation involved in morphogenesis	biological_process	57/456	1154/20791	5.941e-08	9.179e-06	57	2.25
GO:0007049	cell cycle	biological_process	66/456	1425/20791	6.111e-08	9.172e-06	66	2.11
GO:0010033	response to organic substance	biological_process	104/456	2657/20791	7.192e-08	1.049e-05	104	1.78
GO:0060429	epithelium development	biological_process	55/456	1110/20791	8.993e-08	1.277e-05	55	2.26
GO:0051128	regulation of cellular component organization	biological_process	85/456	2044/20791	9.450e-08	1.306e-05	85	1.90
GO:0050673	epithelial cell proliferation	biological_process	26/456	342/20791	1.038e-07	1.398e-05	26	3.47
GO:0009887	organ morphogenesis	biological_process	49/456	948/20791	1.279e-07	1.680e-05	49	2.36

GO:0016477	cell migration	biological_process	55/456	1125/20791	1.365e-07	1.749e-05	55	2.23
GO:0048729	tissue morphogenesis	biological_process	38/456	646/20791	1.379e-07	1.725e-05	38	2.68
GO:0048598	embryonic morphogenesis	biological_process	37/456	621/20791	1.457e-07	1.780e-05	37	2.72
GO:0061448	connective tissue development	biological_process	21/456	239/20791	1.501e-07	1.792e-05	21	4.01
GO:0031214	biomineral tissue development	biological_process	15/456	125/20791	1.543e-07	1.801e-05	15	5.47
GO:0040011	locomotion	biological_process	65/456	1433/20791	1.568e-07	1.791e-05	65	2.07
GO:0035295	tube development	biological_process	38/456	651/20791	1.663e-07	1.859e-05	38	2.66
GO:0048870	cell motility	biological_process	58/456	1224/20791	1.757e-07	1.923e-05	58	2.16
GO:0048608	reproductive structure development	biological_process	30/456	451/20791	2.102e-07	2.253e-05	30	3.03
GO:0003006	developmental process involved in reproduction	biological_process	39/456	686/20791	2.237e-07	2.350e-05	39	2.59
GO:0007166	cell surface receptor signaling pathway	biological_process	87/456	2154/20791	2.245e-07	2.312e-05	87	1.84
GO:0006468	protein phosphorylation	biological_process	72/456	1669/20791	2.290e-07	2.313e-05	72	1.97
GO:0000278	mitotic cell cycle	biological_process	41/456	742/20791	2.348e-07	2.327e-05	41	2.52
GO:0035136	forelimb morphogenesis	biological_process	9/456	41/20791	2.369e-07	2.305e-05	9	10.01
GO:0008284	positive regulation of cell proliferation	biological_process	44/456	829/20791	2.626e-07	2.508e-05	44	2.42
GO:0061458	reproductive system development	biological_process	30/456	456/20791	2.636e-07	2.473e-05	30	3.00
GO:0001501	skeletal system development	biological_process	30/456	460/20791	3.152e-07	2.905e-05	30	2.97
GO:0061138	morphogenesis of a branching epithelium	biological_process	19/456	210/20791	3.473e-07	3.145e-05	19	4.13
GO:0035115	embryonic forelimb morphogenesis	biological_process	8/456	32/20791	3.634e-07	3.235e-05	8	11.40
GO:0048514	blood vessel morphogenesis	biological_process	31/456	489/20791	3.726e-07	3.262e-05	31	2.89
GO:0071310	cellular response to organic substance	biological_process	76/456	1840/20791	5.507e-07	4.742e-05	76	1.88
GO:0009966	regulation of signal transduction	biological_process	91/456	2344/20791	6.240e-07	5.287e-05	91	1.77
GO:0010564	regulation of cell cycle process	biological_process	29/456	454/20791	7.274e-07	6.065e-05	29	2.91
GO:0007346	regulation of mitotic cell cycle	biological_process	27/456	406/20791	7.903e-07	6.487e-05	27	3.03
GO:0005578	proteinaceous extracellular matrix	cellular_component	24/456	335/20791	8.404e-07	6.792e-05	24	3.27
GO:0001763	morphogenesis of a branching structure	biological_process	19/456	224/20791	8.948e-07	7.122e-05	19	3.87
GO:0007399	nervous system development	biological_process	80/456	2005/20791	1.046e-06	8.201e-05	80	1.82
GO:0022008	neurogenesis	biological_process	62/456	1423/20791	1.081e-06	8.351e-05	62	1.99
GO:0001649	osteoblast differentiation	biological_process	18/456	207/20791	1.168e-06	8.892e-05	18	3.96
GO:0042325	regulation of phosphorylation	biological_process	58/456	1301/20791	1.170e-06	8.780e-05	58	2.03
GO:0009792	embryo development ending in birth or egg hatching	biological_process	37/456	679/20791	1.173e-06	8.679e-05	37	2.48
GO:0044702	single organism reproductive process	biological_process	56/456	1243/20791	1.289e-06	9.404e-05	56	2.05
GO:0007155	cell adhesion	biological_process	58/456	1308/20791	1.376e-06	9.902e-05	58	2.02
GO:0023014	signal transduction by phosphorylation	biological_process	38/456	713/20791	1.434e-06	1.018e-04	38	2.43
GO:0016310	phosphorylation	biological_process	79/456	1995/20791	1.600e-06	1.121e-04	79	1.81
GO:0098797	plasma membrane protein complex	cellular_component	29/456	473/20791	1.615e-06	1.116e-04	29	2.80
GO:0005515	protein binding	molecular_function	349/456	12166/20791	1.753e-06	1.196e-04	349	1.31
GO:0016043	cellular component organization	biological_process	170/456	5243/20791	1.757e-06	1.183e-04	170	1.48
GO:0048699	generation of neurons	biological_process	58/456	1320/20791	1.811e-06	1.204e-04	58	2.00
GO:0023051	regulation of signaling	biological_process	98/456	2649/20791	1.833e-06	1.204e-04	98	1.69
GO:0050678	regulation of epithelial cell proliferation	biological_process	21/456	282/20791	2.035e-06	1.320e-04	21	3.40
GO:0048754	branching morphogenesis of an epithelial tube	biological_process	16/456	175/20791	2.193e-06	1.405e-04	16	4.17

GO:0043009	chordate embryonic development	biological_process	36/456	670/20791	2.194e-06	1.389e-04	36	2.45
GO:0048568	embryonic organ development	biological_process	28/456	456/20791	2.315e-06	1.448e-04	28	2.80
GO:0051130	positive regulation of cellular component organization	biological_process	49/456	1053/20791	2.372e-06	1.466e-04	49	2.12
GO:0001655	urogenital system development	biological_process	23/456	335/20791	2.760e-06	1.686e-04	23	3.13
GO:0007507	heart development	biological_process	31/456	541/20791	2.913e-06	1.759e-04	31	2.61
GO:0045859	regulation of protein kinase activity	biological_process	34/456	625/20791	3.130e-06	1.868e-04	34	2.48
GO:0071363	cellular response to growth factor stimulus	biological_process	31/456	543/20791	3.134e-06	1.850e-04	31	2.60
GO:0070848	response to growth factor	biological_process	32/456	571/20791	3.238e-06	1.890e-04	32	2.56
GO:0010646	regulation of cell communication	biological_process	98/456	2690/20791	3.420e-06	1.974e-04	98	1.66
GO:0006796	phosphate-containing compound metabolic process	biological_process	101/456	2798/20791	3.578e-06	2.043e-04	101	1.65
GO:0000165	MAPK cascade	biological_process	36/456	686/20791	3.679e-06	2.078e-04	36	2.39
GO:0051174	regulation of phosphorus metabolic process	biological_process	64/456	1546/20791	3.762e-06	2.102e-04	64	1.89
GO:0072001	renal system development	biological_process	21/456	294/20791	3.847e-06	2.127e-04	21	3.26
GO:0030278	regulation of ossification	biological_process	16/456	183/20791	3.849e-06	2.106e-04	16	3.99
GO:0001932	regulation of protein phosphorylation	biological_process	53/456	1206/20791	4.815e-06	2.608e-04	53	2.00
GO:0060341	regulation of cellular localization	biological_process	51/456	1144/20791	4.873e-06	2.612e-04	51	2.03
GO:0048589	developmental growth	biological_process	33/456	611/20791	4.969e-06	2.637e-04	33	2.46
GO:0051270	regulation of cellular component movement	biological_process	37/456	728/20791	5.567e-06	2.924e-04	37	2.32
GO:0045860	positive regulation of protein kinase activity	biological_process	25/456	401/20791	5.779e-06	3.006e-04	25	2.84
GO:0006793	phosphorus metabolic process	biological_process	101/456	2836/20791	6.176e-06	3.181e-04	101	1.62
GO:0045667	regulation of osteoblast differentiation	biological_process	12/456	112/20791	6.681e-06	3.407e-04	12	4.89
GO:0030054	cell junction	cellular_component	50/456	1133/20791	7.802e-06	3.941e-04	50	2.01
GO:0005925	focal adhesion	cellular_component	24/456	384/20791	8.285e-06	4.145e-04	24	2.85
GO:0009986	cell surface	cellular_component	39/456	801/20791	8.489e-06	4.207e-04	39	2.22
GO:0048645	organ formation	biological_process	9/456	64/20791	8.501e-06	4.173e-04	9	6.41
GO:0031589	cell-substrate adhesion	biological_process	20/456	286/20791	8.545e-06	4.156e-04	20	3.19
GO:0016049	cell growth	biological_process	26/456	437/20791	8.721e-06	4.203e-04	26	2.71
GO:0022414	reproductive process	biological_process	57/456	1361/20791	8.791e-06	4.198e-04	57	1.91
GO:0000003	reproduction	biological_process	57/456	1363/20791	9.163e-06	4.336e-04	57	1.91
GO:0001701	in utero embryonic development	biological_process	25/456	413/20791	9.488e-06	4.450e-04	25	2.76
GO:0030282	bone mineralization	biological_process	11/456	98/20791	9.573e-06	4.450e-04	11	5.12
GO:0035239	tube morphogenesis	biological_process	24/456	389/20791	1.023e-05	4.714e-04	24	2.81
GO:0005924	cell-substrate adherens junction	cellular_component	24/456	389/20791	1.023e-05	4.714e-04	24	2.81
GO:0009612	response to mechanical stimulus	biological_process	17/456	221/20791	1.081e-05	4.895e-04	17	3.51
GO:0034097	response to cytokine	biological_process	33/456	637/20791	1.151e-05	5.168e-04	33	2.36
GO:0008285	negative regulation of cell proliferation	biological_process	31/456	581/20791	1.170e-05	5.208e-04	31	2.43
GO:0001503	ossification	biological_process	23/456	367/20791	1.188e-05	5.244e-04	23	2.86
GO:0030055	cell-substrate junction	cellular_component	24/456	393/20791	1.207e-05	5.284e-04	24	2.78
GO:0048523	negative regulation of cellular process	biological_process	132/456	4010/20791	1.210e-05	5.253e-04	132	1.50
GO:0005737	cytoplasm	cellular_component	281/456	9747/20791	1.230e-05	5.296e-04	281	1.31
GO:0002009	morphogenesis of an epithelium	biological_process	28/456	500/20791	1.246e-05	5.321e-04	28	2.55
GO:0060562	epithelial tube morphogenesis	biological_process	22/456	345/20791	1.370e-05	5.804e-04	22	2.91

GO:0033993	response to lipid	biological_process	43/456	941/20791	1.417e-05	5.955e-04	43	2.08
GO:0035556	intracellular signal transduction	biological_process	82/456	2231/20791	1.507e-05	6.283e-04	82	1.68
GO:0009893	positive regulation of metabolic process	biological_process	111/456	3261/20791	1.512e-05	6.254e-04	111	1.55
GO:1902533	positive regulation of intracellular signal transduction	biological_process	39/456	824/20791	1.588e-05	6.517e-04	39	2.16
GO:0007167	enzyme linked receptor protein signaling pathway	biological_process	37/456	765/20791	1.619e-05	6.593e-04	37	2.21
GO:0001822	kidney development	biological_process	19/456	275/20791	1.627e-05	6.574e-04	19	3.15
GO:0045786	negative regulation of cell cycle	biological_process	22/456	350/20791	1.704e-05	6.833e-04	22	2.87
GO:0043549	regulation of kinase activity	biological_process	34/456	679/20791	1.719e-05	6.841e-04	34	2.28
GO:0060284	regulation of cell development	biological_process	40/456	858/20791	1.756e-05	6.936e-04	40	2.13
GO:0045596	negative regulation of cell differentiation	biological_process	33/456	651/20791	1.769e-05	6.935e-04	33	2.31
GO:0007389	pattern specification process	biological_process	26/456	456/20791	1.799e-05	7.000e-04	26	2.60
GO:0019222	regulation of metabolic process	biological_process	189/456	6205/20791	1.878e-05	7.254e-04	189	1.39
GO:0030595	leukocyte chemotaxis	biological_process	14/456	165/20791	1.917e-05	7.350e-04	14	3.87
GO:0001525	angiogenesis	biological_process	24/456	405/20791	1.955e-05	7.442e-04	24	2.70
GO:0033674	positive regulation of kinase activity	biological_process	25/456	432/20791	1.996e-05	7.543e-04	25	2.64
GO:0035137	hindlimb morphogenesis	biological_process	7/456	42/20791	2.161e-05	8.108e-04	7	7.60
GO:1903047	mitotic cell cycle process	biological_process	32/456	630/20791	2.242e-05	8.353e-04	32	2.32
GO:0050900	leukocyte migration	biological_process	18/456	258/20791	2.295e-05	8.490e-04	18	3.18
GO:0050790	regulation of catalytic activity	biological_process	74/456	1982/20791	2.319e-05	8.519e-04	74	1.70
GO:0005912	adherens junction	cellular_component	26/456	463/20791	2.323e-05	8.474e-04	26	2.56
GO:0014031	mesenchymal cell development	biological_process	14/456	168/20791	2.337e-05	8.466e-04	14	3.80
GO:0010573	vascular endothelial growth factor production	biological_process	6/456	30/20791	2.452e-05	8.822e-04	6	9.12
GO:0002376	immune system process	biological_process	76/456	2059/20791	2.632e-05	9.405e-04	76	1.68
GO:0090068	positive regulation of cell cycle process	biological_process	15/456	192/20791	2.698e-05	9.576e-04	15	3.56
GO:0036211	protein modification process	biological_process	114/456	3418/20791	2.712e-05	9.561e-04	114	1.52
GO:0006464	cellular protein modification process	biological_process	114/456	3418/20791	2.712e-05	9.561e-04	114	1.52
GO:0032268	regulation of cellular protein metabolic process	biological_process	82/456	2272/20791	2.798e-05	9.670e-04	82	1.65
GO:0007160	cell-matrix adhesion	biological_process	14/456	172/20791	3.023e-05	1.038e-03	14	3.71
GO:0030334	regulation of cell migration	biological_process	32/456	640/20791	3.025e-05	1.032e-03	32	2.28
GO:0001816	cytokine production	biological_process	29/456	555/20791	3.129e-05	1.060e-03	29	2.38
GO:0048864	stem cell development	biological_process	14/456	174/20791	3.429e-05	1.155e-03	14	3.67
GO:0009605	response to external stimulus	biological_process	77/456	2112/20791	3.488e-05	1.167e-03	77	1.66
GO:2000021	regulation of ion homeostasis	biological_process	14/456	175/20791	3.649e-05	1.213e-03	14	3.65
GO:0070371	ERK1 and ERK2 cascade	biological_process	17/456	245/20791	3.963e-05	1.309e-03	17	3.16
GO:0051246	regulation of protein metabolic process	biological_process	86/456	2440/20791	4.114e-05	1.351e-03	86	1.61
GO:0006954	inflammatory response	biological_process	29/456	564/20791	4.158e-05	1.357e-03	29	2.34
GO:0016482	cytoplasmic transport	biological_process	31/456	623/20791	4.322e-05	1.401e-03	31	2.27
GO:0007568	aging	biological_process	19/456	296/20791	4.396e-05	1.417e-03	19	2.93
GO:0072006	nephron development	biological_process	12/456	136/20791	4.532e-05	1.452e-03	12	4.02
GO:0051050	positive regulation of transport	biological_process	39/456	866/20791	4.625e-05	1.472e-03	39	2.05
GO:0014070	response to organic cyclic compound	biological_process	43/456	991/20791	4.634e-05	1.466e-03	43	1.98
GO:0042327	positive regulation of phosphorylation	biological_process	39/456	867/20791	4.739e-05	1.491e-03	39	2.05

GO:0060602	branch elongation of an epithelium	biological_process	5/456	22/20791	4.903e-05	1.533e-03	5	10.36
GO:0048762	mesenchymal cell differentiation	biological_process	14/456	180/20791	4.949e-05	1.538e-03	14	3.55
GO:0043408	regulation of MAPK cascade	biological_process	31/456	628/20791	5.002e-05	1.546e-03	31	2.25
GO:0030111	regulation of Wnt signaling pathway	biological_process	16/456	226/20791	5.036e-05	1.547e-03	16	3.23
GO:0016055	Wnt signaling pathway	biological_process	21/456	352/20791	5.409e-05	1.652e-03	21	2.72
GO:0005856	cytoskeleton	cellular_component	69/456	1866/20791	5.692e-05	1.728e-03	69	1.69
GO:0030177	positive regulation of Wnt signaling pathway	biological_process	10/456	100/20791	5.863e-05	1.770e-03	10	4.56
GO:0030030	cell projection organization	biological_process	49/456	1195/20791	5.912e-05	1.775e-03	49	1.87
GO:0060039	pericardium development	biological_process	5/456	23/20791	6.069e-05	1.811e-03	5	9.91
GO:0036010	protein localization to endosome	biological_process	4/456	13/20791	6.176e-05	1.833e-03	4	14.03
GO:0060485	mesenchyme development	biological_process	16/456	230/20791	6.192e-05	1.827e-03	16	3.17
GO:0005911	cell-cell junction	cellular_component	23/456	409/20791	6.257e-05	1.836e-03	23	2.56
GO:0005615	extracellular space	cellular_component	55/456	1398/20791	6.514e-05	1.901e-03	55	1.79
GO:0048863	stem cell differentiation	biological_process	18/456	280/20791	6.589e-05	1.912e-03	18	2.93
GO:0030855	epithelial cell differentiation	biological_process	30/456	610/20791	6.939e-05	2.003e-03	30	2.24
GO:0019901	protein kinase binding	molecular_function	27/456	525/20791	7.330e-05	2.104e-03	27	2.34
GO:2000145	regulation of cell motility	biological_process	32/456	672/20791	7.507e-05	2.143e-03	32	2.17
GO:0005794	Golgi apparatus	cellular_component	50/456	1242/20791	7.829e-05	2.223e-03	50	1.84
GO:0045597	positive regulation of cell differentiation	biological_process	37/456	827/20791	8.057e-05	2.275e-03	37	2.04
GO:0019900	kinase binding	molecular_function	29/456	586/20791	8.087e-05	2.272e-03	29	2.26
GO:0001657	ureteric bud development	biological_process	10/456	104/20791	8.153e-05	2.278e-03	10	4.38
GO:0097038	perinuclear endoplasmic reticulum	cellular_component	4/456	14/20791	8.232e-05	2.288e-03	4	13.03
GO:0010035	response to inorganic substance	biological_process	26/456	502/20791	8.716e-05	2.410e-03	26	2.36
GO:0072163	mesonephric epithelium development	biological_process	10/456	105/20791	8.833e-05	2.429e-03	10	4.34
GO:0072164	mesonephric tubule development	biological_process	10/456	105/20791	8.833e-05	2.429e-03	10	4.34
GO:0097367	carbohydrate derivative binding	molecular_function	78/456	2213/20791	9.115e-05	2.481e-03	78	1.61
GO:0030500	regulation of bone mineralization	biological_process	8/456	69/20791	9.263e-05	2.508e-03	8	5.29
GO:0030182	neuron differentiation	biological_process	48/456	1185/20791	9.283e-05	2.501e-03	48	1.85
GO:0048732	gland development	biological_process	25/456	476/20791	9.386e-05	2.516e-03	25	2.39
GO:2000027	regulation of organ morphogenesis	biological_process	13/456	169/20791	9.656e-05	2.575e-03	13	3.51
GO:0051960	regulation of nervous system development	biological_process	35/456	773/20791	9.740e-05	2.584e-03	35	2.06
GO:0015631	tubulin binding	molecular_function	17/456	264/20791	9.882e-05	2.609e-03	17	2.94
GO:0050767	regulation of neurogenesis	biological_process	32/456	683/20791	1.009e-04	2.650e-03	32	2.14
GO:0032147	activation of protein kinase activity	biological_process	16/456	240/20791	1.017e-04	2.658e-03	16	3.04
GO:0034236	protein kinase A catalytic subunit binding	molecular_function	4/456	15/20791	1.078e-04	2.803e-03	4	12.16
GO:0097305	response to alcohol	biological_process	22/456	397/20791	1.084e-04	2.805e-03	22	2.53
GO:0031175	neuron projection development	biological_process	35/456	779/20791	1.129e-04	2.907e-03	35	2.05
GO:0030279	negative regulation of ossification	biological_process	8/456	71/20791	1.134e-04	2.906e-03	8	5.14
GO:0038127	ERBB signaling pathway	biological_process	9/456	89/20791	1.134e-04	2.906e-03	9	4.61
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	biological_process	25/456	482/20791	1.140e-04	2.893e-03	25	2.36
GO:0043412	macromolecule modification	biological_process	114/456	3545/20791	1.140e-04	2.893e-03	114	1.47
GO:0043410	positive regulation of MAPK cascade	biological_process	23/456	426/20791	1.143e-04	2.873e-03	23	2.46

GO:0003002	regionalization	biological_process	20/456	345/20791	1.159e-04	2.899e-03	20	2.64
GO:0001823	mesonephros development	biological_process	10/456	109/20791	1.206e-04	3.002e-03	10	4.18
GO:1901990	regulation of mitotic cell cycle phase transition	biological_process	14/456	196/20791	1.225e-04	3.035e-03	14	3.26
GO:0008092	cytoskeletal protein binding	molecular_function	35/456	783/20791	1.245e-04	3.042e-03	35	2.04
GO:0008017	microtubule binding	molecular_function	14/456	197/20791	1.293e-04	3.145e-03	14	3.24
GO:0070555	response to interleukin-1	biological_process	10/456	110/20791	1.301e-04	3.149e-03	10	4.14
GO:0000281	mitotic cytokinesis	biological_process	5/456	27/20791	1.315e-04	3.169e-03	5	8.44
GO:0031401	positive regulation of protein modification process	biological_process	42/456	1008/20791	1.345e-04	3.226e-03	42	1.90
GO:2000045	regulation of G1/S transition of mitotic cell cycle	biological_process	9/456	91/20791	1.346e-04	3.214e-03	9	4.51
GO:0032386	regulation of intracellular transport	biological_process	27/456	545/20791	1.348e-04	3.204e-03	27	2.26
GO:0006950	response to stress	biological_process	105/456	3226/20791	1.356e-04	3.209e-03	105	1.48
GO:0031325	positive regulation of cellular metabolic process	biological_process	90/456	2675/20791	1.360e-04	3.204e-03	90	1.53
GO:0097435	fibril organization	biological_process	4/456	16/20791	1.390e-04	3.260e-03	4	11.40
GO:1902531	regulation of intracellular signal transduction	biological_process	54/456	1407/20791	1.395e-04	3.257e-03	54	1.75
GO:0043227	membrane-bounded organelle	cellular_component	306/456	11131/20791	1.435e-04	3.335e-03	306	1.25
GO:0070925	organelle assembly	biological_process	27/456	549/20791	1.516e-04	3.508e-03	27	2.24
GO:0010574	regulation of vascular endothelial growth factor production	biological_process	5/456	28/20791	1.567e-04	3.610e-03	5	8.14
GO:0010628	positive regulation of gene expression	biological_process	61/456	1655/20791	1.606e-04	3.684e-03	61	1.68
GO:0019838	growth factor binding	molecular_function	10/456	113/20791	1.626e-04	3.714e-03	10	4.03
GO:0045668	negative regulation of osteoblast differentiation	biological_process	6/456	42/20791	1.634e-04	3.716e-03	6	6.51
GO:0001934	positive regulation of protein phosphorylation	biological_process	36/456	827/20791	1.684e-04	3.813e-03	36	1.98
GO:0071902	positive regulation of protein serine/threonine kinase activity	biological_process	16/456	251/20791	1.701e-04	3.835e-03	16	2.91
GO:0071900	regulation of protein serine/threonine kinase activity	biological_process	22/456	410/20791	1.709e-04	3.836e-03	22	2.45
GO:0031344	regulation of cell projection organization	biological_process	26/456	525/20791	1.767e-04	3.950e-03	26	2.26
GO:0001933	negative regulation of protein phosphorylation	biological_process	20/456	357/20791	1.824e-04	4.060e-03	20	2.55
GO:0072132	mesenchyme morphogenesis	biological_process	6/456	43/20791	1.864e-04	4.114e-03	6	6.36
GO:0007219	Notch signaling pathway	biological_process	12/456	158/20791	1.888e-04	4.150e-03	12	3.46
GO:0009743	response to carbohydrate	biological_process	15/456	229/20791	1.935e-04	4.183e-03	15	2.99
GO:0045121	membrane raft	cellular_component	17/456	280/20791	1.994e-04	4.293e-03	17	2.77
GO:0034612	response to tumor necrosis factor	biological_process	12/456	159/20791	2.002e-04	4.292e-03	12	3.44
GO:0001890	placenta development	biological_process	12/456	159/20791	2.002e-04	4.292e-03	12	3.44
GO:0032270	positive regulation of cellular protein metabolic process	biological_process	49/456	1261/20791	2.079e-04	4.421e-03	49	1.77
GO:0001819	positive regulation of cytokine production	biological_process	19/456	335/20791	2.193e-04	4.645e-03	19	2.59
GO:0043085	positive regulation of catalytic activity	biological_process	48/456	1231/20791	2.216e-04	4.675e-03	48	1.78
GO:0060707	trophoblast giant cell differentiation	biological_process	4/456	18/20791	2.218e-04	4.660e-03	4	10.13
GO:0015630	microtubule cytoskeleton	cellular_component	42/456	1034/20791	2.290e-04	4.793e-03	42	1.85
GO:0031323	regulation of cellular metabolic process	biological_process	163/456	5495/20791	2.335e-04	4.867e-03	163	1.35
GO:0060627	regulation of vesicle-mediated transport	biological_process	21/456	392/20791	2.388e-04	4.958e-03	21	2.44
GO:0042326	negative regulation of phosphorylation	biological_process	21/456	392/20791	2.388e-04	4.958e-03	21	2.44
GO:0044267	cellular protein metabolic process	biological_process	135/456	4417/20791	2.440e-04	5.026e-03	135	1.39
GO:0050680	negative regulation of epithelial cell proliferation	biological_process	10/456	119/20791	2.485e-04	5.099e-03	10	3.83
GO:0009952	anterior/posterior pattern specification	biological_process	14/456	210/20791	2.511e-04	5.132e-03	14	3.04

GO:0015629	actin cytoskeleton	cellular_component	22/456	422/20791	2.553e-04	5.198e-03	22	2.38
GO:1902806	regulation of cell cycle G1/S phase transition	biological_process	9/456	99/20791	2.558e-04	5.188e-03	9	4.14
GO:0060706	cell differentiation involved in embryonic placenta development	biological_process	5/456	31/20791	2.564e-04	5.180e-03	5	7.35
GO:0060740	prostate gland epithelium morphogenesis	biological_process	5/456	31/20791	2.564e-04	5.180e-03	5	7.35
GO:0003197	endocardial cushion development	biological_process	5/456	31/20791	2.564e-04	5.180e-03	5	7.35
GO:0045335	phagocytic vesicle	cellular_component	7/456	62/20791	2.599e-04	5.191e-03	7	5.15
GO:0007173	epidermal growth factor receptor signaling pathway	biological_process	8/456	80/20791	2.614e-04	5.201e-03	8	4.56
GO:0060828	regulation of canonical Wnt signaling pathway	biological_process	12/456	164/20791	2.669e-04	5.291e-03	12	3.34
GO:0031098	stress-activated protein kinase signaling cascade	biological_process	15/456	236/20791	2.679e-04	5.291e-03	15	2.90
GO:0060326	cell chemotaxis	biological_process	15/456	237/20791	2.803e-04	5.515e-03	15	2.89
GO:0045931	positive regulation of mitotic cell cycle	biological_process	10/456	121/20791	2.847e-04	5.580e-03	10	3.77
GO:0019899	enzyme binding	molecular_function	60/456	1658/20791	2.885e-04	5.634e-03	60	1.65
GO:0060541	respiratory system development	biological_process	15/456	238/20791	2.932e-04	5.704e-03	15	2.87
GO:0001837	epithelial to mesenchymal transition	biological_process	9/456	101/20791	2.975e-04	5.767e-03	9	4.06
GO:0001892	embryonic placenta development	biological_process	9/456	101/20791	2.975e-04	5.767e-03	9	4.06
GO:0045216	cell-cell junction organization	biological_process	12/456	166/20791	2.985e-04	5.744e-03	12	3.30
GO:0060512	prostate gland morphogenesis	biological_process	5/456	32/20791	2.990e-04	5.732e-03	5	7.12
GO:0060441	epithelial tube branching involved in lung morphogenesis	biological_process	5/456	32/20791	2.990e-04	5.732e-03	5	7.12
GO:0005921	gap junction	cellular_component	5/456	32/20791	2.990e-04	5.732e-03	5	7.12
GO:1901987	regulation of cell cycle phase transition	biological_process	14/456	214/20791	3.046e-04	5.776e-03	14	2.98
GO:0040008	regulation of growth	biological_process	28/456	604/20791	3.052e-04	5.767e-03	28	2.11
GO:0030666	endocytic vesicle membrane	cellular_component	6/456	47/20791	3.068e-04	5.776e-03	6	5.82
GO:0072073	kidney epithelium development	biological_process	11/456	144/20791	3.095e-04	5.806e-03	11	3.48
GO:0001658	branching involved in ureteric bud morphogenesis	biological_process	7/456	64/20791	3.173e-04	5.932e-03	7	4.99
GO:0004674	protein serine/threonine kinase activity	molecular_function	22/456	429/20791	3.200e-04	5.961e-03	22	2.34
GO:0005768	endosome	cellular_component	30/456	668/20791	3.285e-04	6.098e-03	30	2.05
GO:0005922	connexon complex	cellular_component	4/456	20/20791	3.379e-04	6.250e-03	4	9.12
GO:0003094	glomerular filtration	biological_process	4/456	20/20791	3.379e-04	6.250e-03	4	9.12
GO:0040012	regulation of locomotion	biological_process	32/456	732/20791	3.431e-04	6.302e-03	32	1.99
GO:0048666	neuron development	biological_process	38/456	924/20791	3.465e-04	6.342e-03	38	1.88
GO:0003401	axis elongation	biological_process	5/456	33/20791	3.469e-04	6.327e-03	5	6.91
GO:0042733	embryonic digit morphogenesis	biological_process	7/456	65/20791	3.497e-04	6.356e-03	7	4.91
GO:0090263	positive regulation of canonical Wnt signaling pathway	biological_process	7/456	65/20791	3.497e-04	6.356e-03	7	4.91
GO:0051247	positive regulation of protein metabolic process	biological_process	51/456	1360/20791	3.570e-04	6.444e-03	51	1.71
GO:0007067	mitosis	biological_process	20/456	376/20791	3.576e-04	6.389e-03	20	2.43
GO:0042542	response to hydrogen peroxide	biological_process	10/456	125/20791	3.705e-04	6.597e-03	10	3.65
GO:0006935	chemotaxis	biological_process	24/456	493/20791	3.851e-04	6.743e-03	24	2.22
GO:0019904	protein domain specific binding	molecular_function	28/456	613/20791	3.859e-04	6.735e-03	28	2.08
GO:0030155	regulation of cell adhesion	biological_process	27/456	583/20791	3.900e-04	6.784e-03	27	2.11
GO:0043406	positive regulation of MAP kinase activity	biological_process	12/456	171/20791	3.918e-04	6.792e-03	12	3.20
GO:0004672	protein kinase activity	molecular_function	28/456	614/20791	3.959e-04	6.841e-03	28	2.08
GO:0000187	activation of MAPK activity	biological_process	9/456	105/20791	3.983e-04	6.860e-03	9	3.91

GO:0003158	endothelium development	biological_process	9/456	105/20791	3.983e-04	6.860e-03	9	3.91
GO:0001935	endothelial cell proliferation	biological_process	9/456	105/20791	3.983e-04	6.860e-03	9	3.91
GO:0001817	regulation of cytokine production	biological_process	24/456	495/20791	4.080e-04	6.959e-03	24	2.21
GO:0055026	negative regulation of cardiac muscle tissue development	biological_process	4/456	21/20791	4.109e-04	6.985e-03	4	8.68
GO:0003203	endocardial cushion morphogenesis	biological_process	4/456	21/20791	4.109e-04	6.985e-03	4	8.68
GO:0097205	renal filtration	biological_process	4/456	21/20791	4.109e-04	6.985e-03	4	8.68
GO:0043168	anion binding	molecular_function	86/456	2622/20791	4.171e-04	7.023e-03	86	1.50
GO:0048705	skeletal system morphogenesis	biological_process	14/456	221/20791	4.224e-04	7.089e-03	14	2.89
GO:0060070	canonical Wnt signaling pathway	biological_process	14/456	221/20791	4.224e-04	7.089e-03	14	2.89
GO:0051279	regulation of release of sequestered calcium ion into cytosol	biological_process	7/456	67/20791	4.226e-04	7.047e-03	7	4.76
GO:0030335	positive regulation of cell migration	biological_process	20/456	381/20791	4.233e-04	7.037e-03	20	2.39
GO:0002685	regulation of leukocyte migration	biological_process	11/456	150/20791	4.400e-04	7.291e-03	11	3.34
GO:0090002	establishment of protein localization to plasma membrane	biological_process	10/456	129/20791	4.772e-04	7.883e-03	10	3.53
GO:0030850	prostate gland development	biological_process	6/456	51/20791	4.834e-04	7.813e-03	6	5.36
GO:1900744	regulation of p38MAPK cascade	biological_process	4/456	22/20791	4.954e-04	7.983e-03	4	8.29
GO:0061061	muscle structure development	biological_process	26/456	562/20791	4.984e-04	8.006e-03	26	2.11
GO:0045444	fat cell differentiation	biological_process	13/456	200/20791	5.040e-04	8.072e-03	13	2.96
GO:0042995	cell projection	cellular_component	62/456	1768/20791	5.146e-04	8.216e-03	62	1.60
GO:0005874	microtubule	cellular_component	19/456	359/20791	5.180e-04	8.246e-03	19	2.41
GO:0012505	endomembrane system	cellular_component	105/456	3354/20791	5.256e-04	8.341e-03	105	1.43
GO:1902115	regulation of organelle assembly	biological_process	9/456	109/20791	5.263e-04	8.327e-03	9	3.76
GO:0003156	regulation of organ formation	biological_process	5/456	36/20791	5.280e-04	8.329e-03	5	6.33
GO:0010038	response to metal ion	biological_process	18/456	332/20791	5.310e-04	8.351e-03	18	2.47
GO:0050766	positive regulation of phagocytosis	biological_process	6/456	52/20791	5.383e-04	8.441e-03	6	5.26
GO:0006939	smooth muscle contraction	biological_process	8/456	89/20791	5.449e-04	8.519e-03	8	4.10
GO:0060349	bone morphogenesis	biological_process	8/456	89/20791	5.449e-04	8.519e-03	8	4.10
GO:0098727	maintenance of cell number	biological_process	11/456	154/20791	5.509e-04	8.562e-03	11	3.26
GO:0060675	ureteric bud morphogenesis	biological_process	7/456	70/20791	5.549e-04	8.598e-03	7	4.56
GO:0002687	positive regulation of leukocyte migration	biological_process	9/456	110/20791	5.632e-04	8.701e-03	9	3.73
GO:0071417	cellular response to organonitrogen compound	biological_process	21/456	419/20791	5.748e-04	8.855e-03	21	2.29
GO:0045787	positive regulation of cell cycle	biological_process	16/456	280/20791	5.751e-04	8.833e-03	16	2.61
GO:0045927	positive regulation of growth	biological_process	14/456	228/20791	5.775e-04	8.844e-03	14	2.80
GO:0008219	cell death	biological_process	63/456	1813/20791	5.863e-04	8.953e-03	63	1.58
GO:0033688	regulation of osteoblast proliferation	biological_process	4/456	23/20791	5.924e-04	9.020e-03	4	7.93
GO:0007010	cytoskeleton organization	biological_process	40/456	1017/20791	5.926e-04	8.997e-03	40	1.79
GO:0060348	bone development	biological_process	12/456	179/20791	5.930e-04	8.977e-03	12	3.06
GO:0048562	embryonic organ morphogenesis	biological_process	17/456	308/20791	5.993e-04	9.046e-03	17	2.52
GO:0021696	cerebellar cortex morphogenesis	biological_process	5/456	37/20791	6.025e-04	9.069e-03	5	6.16
GO:0030670	phagocytic vesicle membrane	cellular_component	5/456	37/20791	6.025e-04	9.069e-03	5	6.16
GO:0003007	heart morphogenesis	biological_process	14/456	229/20791	6.033e-04	9.029e-03	14	2.79
GO:2000147	positive regulation of cell motility	biological_process	20/456	392/20791	6.062e-04	9.047e-03	20	2.33
GO:0072659	protein localization to plasma membrane	biological_process	13/456	204/20791	6.084e-04	9.054e-03	13	2.91

GO:0000302	response to reactive oxygen species	biological_process	13/456	204/20791	6.084e-04	9.054e-03	13	2.91
GO:0030198	extracellular matrix organization	biological_process	13/456	205/20791	6.373e-04	9.274e-03	13	2.89
GO:0051649	establishment of localization in cell	biological_process	62/456	1785/20791	6.521e-04	9.258e-03	62	1.58
GO:0070372	regulation of ERK1 and ERK2 cascade	biological_process	14/456	231/20791	6.578e-04	9.314e-03	14	2.76
GO:0051145	smooth muscle cell differentiation	biological_process	6/456	54/20791	6.633e-04	9.366e-03	6	5.07
GO:0002520	immune system development	biological_process	35/456	858/20791	6.634e-04	9.343e-03	35	1.86
GO:0019538	protein metabolic process	biological_process	150/456	5117/20791	6.634e-04	9.343e-03	150	1.34
GO:1990778	protein localization to cell periphery	biological_process	13/456	206/20791	6.673e-04	9.348e-03	13	2.88
GO:0016337	single organismal cell-cell adhesion	biological_process	29/456	667/20791	6.796e-04	9.495e-03	29	1.98
GO:0061098	positive regulation of protein tyrosine kinase activity	biological_process	5/456	38/20791	6.850e-04	9.545e-03	5	6.00
GO:0010575	positive regulation vascular endothelial growth factor production	biological_process	4/456	24/20791	7.032e-04	9.772e-03	4	7.60
GO:2000406	positive regulation of T cell migration	biological_process	4/456	24/20791	7.032e-04	9.772e-03	4	7.60
GO:0005520	insulin-like growth factor binding	molecular_function	4/456	24/20791	7.032e-04	9.772e-03	4	7.60
GO:0046332	SMAD binding	molecular_function	7/456	73/20791	7.193e-04	9.917e-03	7	4.37
GO:0071322	cellular response to carbohydrate stimulus	biological_process	10/456	136/20791	7.266e-04	9.992e-03	10	3.35
GO:0051403	stress-activated MAPK cascade	biological_process	13/456	208/20791	7.309e-04	1.002e-02	13	2.85
GO:0051641	cellular localization	biological_process	81/456	2488/20791	7.483e-04	1.024e-02	81	1.48
GO:0010631	epithelial cell migration	biological_process	13/456	209/20791	7.646e-04	1.043e-02	13	2.84
GO:0030324	lung development	biological_process	13/456	209/20791	7.646e-04	1.043e-02	13	2.84
GO:0040018	positive regulation of multicellular organism growth	biological_process	5/456	39/20791	7.761e-04	1.053e-02	5	5.85
GO:0043065	positive regulation of apoptotic process	biological_process	24/456	519/20791	7.943e-04	1.075e-02	24	2.11
GO:0005518	collagen binding	molecular_function	6/456	56/20791	8.104e-04	1.092e-02	6	4.89
GO:0021695	cerebellar cortex development	biological_process	6/456	56/20791	8.104e-04	1.092e-02	6	4.89
GO:0060537	muscle tissue development	biological_process	19/456	373/20791	8.223e-04	1.102e-02	19	2.32
GO:0051272	positive regulation of cellular component movement	biological_process	20/456	402/20791	8.291e-04	1.108e-02	20	2.27
GO:0007417	central nervous system development	biological_process	36/456	902/20791	8.303e-04	1.107e-02	36	1.82
GO:0051282	regulation of sequestering of calcium ion	biological_process	8/456	95/20791	8.484e-04	1.128e-02	8	3.84
GO:0060993	kidney morphogenesis	biological_process	8/456	95/20791	8.484e-04	1.128e-02	8	3.84
GO:0030323	respiratory tube development	biological_process	13/456	212/20791	8.739e-04	1.156e-02	13	2.80
GO:0090132	epithelium migration	biological_process	13/456	212/20791	8.739e-04	1.156e-02	13	2.80
GO:2000401	regulation of lymphocyte migration	biological_process	5/456	40/20791	8.763e-04	1.154e-02	5	5.70
GO:0003779	actin binding	molecular_function	19/456	375/20791	8.765e-04	1.151e-02	19	2.31
GO:0001558	regulation of cell growth	biological_process	18/456	347/20791	8.884e-04	1.164e-02	18	2.37
GO:0008217	regulation of blood pressure	biological_process	11/456	163/20791	8.896e-04	1.162e-02	11	3.08
GO:0010942	positive regulation of cell death	biological_process	25/456	554/20791	8.938e-04	1.165e-02	25	2.06
GO:0043068	positive regulation of programmed cell death	biological_process	24/456	524/20791	9.066e-04	1.179e-02	24	2.09
GO:0051208	sequestering of calcium ion	biological_process	8/456	96/20791	9.104e-04	1.181e-02	8	3.80
GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	biological_process	17/456	320/20791	9.191e-04	1.189e-02	17	2.42
GO:0050839	cell adhesion molecule binding	molecular_function	11/456	164/20791	9.362e-04	1.208e-02	11	3.06
GO:0071407	cellular response to organic cyclic compound	biological_process	23/456	495/20791	9.382e-04	1.208e-02	23	2.12
GO:0048489	synaptic vesicle transport	biological_process	9/456	118/20791	9.435e-04	1.212e-02	9	3.48
GO:0002682	regulation of immune system process	biological_process	41/456	1077/20791	9.578e-04	1.227e-02	41	1.74

GO:0045664	regulation of neuron differentiation	biological_process	25/456	557/20791	9.644e-04	1.233e-02	25	2.05
GO:0043542	endothelial cell migration	biological_process	10/456	141/20791	9.651e-04	1.231e-02	10	3.23
GO:0002063	chondrocyte development	biological_process	4/456	26/20791	9.709e-04	1.235e-02	4	7.01
GO:0042481	regulation of odontogenesis	biological_process	4/456	26/20791	9.709e-04	1.235e-02	4	7.01
GO:0033687	osteoblast proliferation	biological_process	4/456	26/20791	9.709e-04	1.235e-02	4	7.01
GO:0070266	necroptotic process	biological_process	4/456	26/20791	9.709e-04	1.235e-02	4	7.01
GO:0038066	p38MAPK cascade	biological_process	4/456	26/20791	9.709e-04	1.235e-02	4	7.01
GO:0001556	oocyte maturation	biological_process	4/456	26/20791	9.709e-04	1.235e-02	4	7.01
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	biological_process	4/456	26/20791	9.709e-04	1.235e-02	4	7.01
GO:0048247	lymphocyte chemotaxis	biological_process	5/456	41/20791	9.864e-04	1.234e-02	5	5.56
GO:0007017	microtubule-based process	biological_process	26/456	591/20791	1.040e-03	1.244e-02	26	2.01
GO:0009749	response to glucose	biological_process	12/456	191/20791	1.056e-03	1.261e-02	12	2.86
GO:0000902	cell morphogenesis	biological_process	43/456	1151/20791	1.059e-03	1.261e-02	43	1.70
GO:0009880	embryonic pattern specification	biological_process	6/456	59/20791	1.079e-03	1.282e-02	6	4.64
GO:0061035	regulation of cartilage development	biological_process	6/456	59/20791	1.079e-03	1.282e-02	6	4.64
GO:0016079	synaptic vesicle exocytosis	biological_process	7/456	78/20791	1.080e-03	1.278e-02	7	4.09
GO:0071260	cellular response to mechanical stimulus	biological_process	7/456	78/20791	1.080e-03	1.278e-02	7	4.09
GO:0072078	nephron tubule morphogenesis	biological_process	7/456	78/20791	1.080e-03	1.278e-02	7	4.09
GO:0040017	positive regulation of locomotion	biological_process	20/456	411/20791	1.088e-03	1.279e-02	20	2.22
GO:0032330	regulation of chondrocyte differentiation	biological_process	5/456	42/20791	1.107e-03	1.298e-02	5	5.43
GO:0021697	cerebellar cortex formation	biological_process	4/456	27/20791	1.130e-03	1.322e-02	4	6.75
GO:2000404	regulation of T cell migration	biological_process	4/456	27/20791	1.130e-03	1.322e-02	4	6.75
GO:0008016	regulation of heart contraction	biological_process	10/456	144/20791	1.137e-03	1.324e-02	10	3.17
GO:0032844	regulation of homeostatic process	biological_process	19/456	384/20791	1.161e-03	1.349e-02	19	2.26
GO:0010522	regulation of calcium ion transport into cytosol	biological_process	7/456	79/20791	1.167e-03	1.353e-02	7	4.04
GO:0035265	organ growth	biological_process	10/456	145/20791	1.200e-03	1.388e-02	10	3.14
GO:0033043	regulation of organelle organization	biological_process	37/456	957/20791	1.253e-03	1.447e-02	37	1.76
GO:0010468	regulation of gene expression	biological_process	117/456	3910/20791	1.283e-03	1.468e-02	117	1.36
GO:0060425	lung morphogenesis	biological_process	6/456	61/20791	1.294e-03	1.478e-02	6	4.48
GO:0048545	response to steroid hormone	biological_process	24/456	538/20791	1.299e-03	1.480e-02	24	2.03
GO:0061036	positive regulation of cartilage development	biological_process	4/456	28/20791	1.309e-03	1.488e-02	4	6.51
GO:0060351	cartilage development involved in endochondral bone morphogenesis	biological_process	4/456	28/20791	1.309e-03	1.488e-02	4	6.51
GO:0060571	morphogenesis of an epithelial fold	biological_process	4/456	28/20791	1.309e-03	1.488e-02	4	6.51
GO:0002027	regulation of heart rate	biological_process	7/456	81/20791	1.358e-03	1.534e-02	7	3.94
GO:0040014	regulation of multicellular organism growth	biological_process	7/456	81/20791	1.358e-03	1.534e-02	7	3.94
GO:0061333	renal tubule morphogenesis	biological_process	7/456	81/20791	1.358e-03	1.534e-02	7	3.94
GO:0072028	nephron morphogenesis	biological_process	7/456	81/20791	1.358e-03	1.534e-02	7	3.94
GO:0051656	establishment of organelle localization	biological_process	17/456	332/20791	1.377e-03	1.542e-02	17	2.33
GO:0005539	glycosaminoglycan binding	molecular_function	11/456	172/20791	1.389e-03	1.552e-02	11	2.92
GO:0009611	response to wounding	biological_process	28/456	667/20791	1.400e-03	1.561e-02	28	1.91
GO:0043234	protein complex	cellular_component	116/456	3882/20791	1.408e-03	1.567e-02	116	1.36
GO:0061097	regulation of protein tyrosine kinase activity	biological_process	6/456	62/20791	1.414e-03	1.570e-02	6	4.41

GO:0046907	intracellular transport	biological_process	55/456	1592/20791	1.436e-03	1.591e-02	55	1.58
GO:0010720	positive regulation of cell development	biological_process	22/456	481/20791	1.450e-03	1.604e-02	22	2.09
GO:0048659	smooth muscle cell proliferation	biological_process	8/456	103/20791	1.457e-03	1.608e-02	8	3.54
GO:0035270	endocrine system development	biological_process	10/456	149/20791	1.481e-03	1.631e-02	10	3.06
GO:0071345	cellular response to cytokine stimulus	biological_process	23/456	513/20791	1.504e-03	1.653e-02	23	2.04
GO:0030261	chromosome condensation	biological_process	4/456	29/20791	1.507e-03	1.653e-02	4	6.29
GO:0030496	midbody	cellular_component	9/456	126/20791	1.516e-03	1.609e-02	9	3.26
GO:0051302	regulation of cell division	biological_process	14/456	252/20791	1.536e-03	1.627e-02	14	2.53
GO:1902117	positive regulation of organelle assembly	biological_process	5/456	45/20791	1.538e-03	1.626e-02	5	5.07
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	biological_process	5/456	45/20791	1.538e-03	1.626e-02	5	5.07
GO:0021587	cerebellum morphogenesis	biological_process	5/456	45/20791	1.538e-03	1.626e-02	5	5.07
GO:0006810	transport	biological_process	123/456	4166/20791	1.551e-03	1.629e-02	123	1.35
GO:0005923	tight junction	cellular_component	9/456	127/20791	1.604e-03	1.665e-02	9	3.23
GO:0007548	sex differentiation	biological_process	15/456	281/20791	1.634e-03	1.693e-02	15	2.43
GO:0045666	positive regulation of neuron differentiation	biological_process	16/456	309/20791	1.640e-03	1.696e-02	16	2.36
GO:0070509	calcium ion import	biological_process	10/456	151/20791	1.641e-03	1.694e-02	10	3.02
GO:0019827	stem cell maintenance	biological_process	10/456	151/20791	1.641e-03	1.694e-02	10	3.02
GO:0045598	regulation of fat cell differentiation	biological_process	8/456	105/20791	1.654e-03	1.700e-02	8	3.47
GO:0012501	programmed cell death	biological_process	58/456	1711/20791	1.664e-03	1.707e-02	58	1.55
GO:0007267	cell-cell signaling	biological_process	34/456	872/20791	1.669e-03	1.709e-02	34	1.78
GO:0043005	neuron projection	cellular_component	37/456	973/20791	1.671e-03	1.708e-02	37	1.73
GO:0051384	response to glucocorticoid	biological_process	11/456	176/20791	1.676e-03	1.710e-02	11	2.85
GO:0030234	enzyme regulator activity	molecular_function	33/456	840/20791	1.711e-03	1.742e-02	33	1.79
GO:0010941	regulation of cell death	biological_process	51/456	1462/20791	1.716e-03	1.744e-02	51	1.59
GO:0001726	ruffle	cellular_component	10/456	152/20791	1.726e-03	1.750e-02	10	3.00
GO:0090004	positive regulation of establishment of protein localization to plasma membrane	biological_process	4/456	30/20791	1.728e-03	1.749e-02	4	6.08
GO:0043405	regulation of MAP kinase activity	biological_process	15/456	283/20791	1.754e-03	1.772e-02	15	2.42
GO:0031406	carboxylic acid binding	molecular_function	11/456	177/20791	1.756e-03	1.770e-02	11	2.83
GO:0022607	cellular component assembly	biological_process	69/456	2118/20791	1.756e-03	1.770e-02	69	1.49
GO:1903169	regulation of calcium ion transmembrane transport	biological_process	8/456	106/20791	1.761e-03	1.769e-02	8	3.44
GO:0009953	dorsal/ventral pattern formation	biological_process	8/456	106/20791	1.761e-03	1.769e-02	8	3.44
GO:0022407	regulation of cell-cell adhesion	biological_process	17/456	340/20791	1.780e-03	1.781e-02	17	2.28
GO:0051301	cell division	biological_process	25/456	583/20791	1.812e-03	1.810e-02	25	1.96
GO:0007163	establishment or maintenance of cell polarity	biological_process	10/456	153/20791	1.814e-03	1.808e-02	10	2.98
GO:0043177	organic acid binding	molecular_function	11/456	178/20791	1.838e-03	1.829e-02	11	2.82
GO:0017156	calcium ion-dependent exocytosis	biological_process	8/456	107/20791	1.873e-03	1.860e-02	8	3.41
GO:0010463	mesenchymal cell proliferation	biological_process	5/456	47/20791	1.891e-03	1.874e-02	5	4.85
GO:0042060	wound healing	biological_process	18/456	371/20791	1.891e-03	1.874e-02	18	2.21
GO:0050679	positive regulation of epithelial cell proliferation	biological_process	10/456	154/20791	1.907e-03	1.876e-02	10	2.96
GO:0016301	kinase activity	molecular_function	32/456	813/20791	1.929e-03	1.894e-02	32	1.79
GO:0034284	response to monosaccharide	biological_process	12/456	205/20791	1.952e-03	1.913e-02	12	2.67
GO:0017124	SH3 domain binding	molecular_function	8/456	108/20791	1.991e-03	1.948e-02	8	3.38

GO:0030139	endocytic vesicle	cellular_component	9/456	131/20791	2.000e-03	1.953e-02	9	3.13
GO:0048706	embryonic skeletal system development	biological_process	9/456	131/20791	2.000e-03	1.953e-02	9	3.13
GO:0010243	response to organonitrogen compound	biological_process	31/456	782/20791	2.010e-03	1.955e-02	31	1.81
GO:0060047	heart contraction	biological_process	11/456	180/20791	2.012e-03	1.954e-02	11	2.79
GO:0006979	response to oxidative stress	biological_process	18/456	374/20791	2.067e-03	2.003e-02	18	2.19
GO:0045926	negative regulation of growth	biological_process	13/456	233/20791	2.078e-03	2.010e-02	13	2.54
GO:0003014	renal system process	biological_process	7/456	87/20791	2.088e-03	2.016e-02	7	3.67
GO:0045600	positive regulation of fat cell differentiation	biological_process	5/456	48/20791	2.089e-03	2.013e-02	5	4.75
GO:1902807	negative regulation of cell cycle G1/S phase transition	biological_process	5/456	48/20791	2.089e-03	2.013e-02	5	4.75
GO:0048639	positive regulation of developmental growth	biological_process	10/456	156/20791	2.103e-03	2.020e-02	10	2.92
GO:0001667	ameboidal cell migration	biological_process	16/456	317/20791	2.134e-03	1.991e-02	16	2.30
GO:0002237	response to molecule of bacterial origin	biological_process	17/456	346/20791	2.146e-03	1.999e-02	17	2.24
GO:0008201	heparin binding	molecular_function	9/456	133/20791	2.227e-03	2.071e-02	9	3.09
GO:0009798	axis specification	biological_process	7/456	88/20791	2.236e-03	2.075e-02	7	3.63
GO:0001772	immunological synapse	cellular_component	4/456	32/20791	2.239e-03	2.074e-02	4	5.70
GO:0002053	positive regulation of mesenchymal cell proliferation	biological_process	4/456	32/20791	2.239e-03	2.074e-02	4	5.70
GO:0010638	positive regulation of organelle organization	biological_process	22/456	498/20791	2.243e-03	2.071e-02	22	2.01
GO:0002684	positive regulation of immune system process	biological_process	28/456	689/20791	2.245e-03	2.069e-02	28	1.85
GO:0071277	cellular response to calcium ion	biological_process	5/456	49/20791	2.302e-03	2.110e-02	5	4.65
GO:0060428	lung epithelium development	biological_process	5/456	49/20791	2.302e-03	2.110e-02	5	4.65
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	biological_process	5/456	49/20791	2.302e-03	2.110e-02	5	4.65
GO:0021575	hindbrain morphogenesis	biological_process	5/456	49/20791	2.302e-03	2.110e-02	5	4.65
GO:0061630	ubiquitin protein ligase activity	molecular_function	12/456	209/20791	2.302e-03	2.110e-02	12	2.62
GO:0070997	neuron death	biological_process	15/456	291/20791	2.308e-03	2.098e-02	15	2.35
GO:0006909	phagocytosis	biological_process	10/456	158/20791	2.316e-03	2.101e-02	10	2.89
GO:0072089	stem cell proliferation	biological_process	10/456	158/20791	2.316e-03	2.101e-02	10	2.89
GO:0048708	astrocyte differentiation	biological_process	6/456	68/20791	2.327e-03	2.104e-02	6	4.02
GO:0032872	regulation of stress-activated MAPK cascade	biological_process	11/456	184/20791	2.401e-03	2.167e-02	11	2.73
GO:0018108	peptidyl-tyrosine phosphorylation	biological_process	16/456	321/20791	2.425e-03	2.185e-02	16	2.27
GO:0006029	proteoglycan metabolic process	biological_process	6/456	69/20791	2.516e-03	2.263e-02	6	3.96
GO:0030513	positive regulation of BMP signaling pathway	biological_process	4/456	33/20791	2.533e-03	2.275e-02	4	5.53
GO:0060043	regulation of cardiac muscle cell proliferation	biological_process	4/456	33/20791	2.533e-03	2.275e-02	4	5.53
GO:1903078	positive regulation of protein localization to plasma membrane	biological_process	4/456	33/20791	2.533e-03	2.275e-02	4	5.53
GO:0035116	embryonic hindlimb morphogenesis	biological_process	4/456	33/20791	2.533e-03	2.275e-02	4	5.53
GO:0005201	extracellular matrix structural constituent	molecular_function	4/456	33/20791	2.533e-03	2.275e-02	4	5.53
GO:0042803	protein homodimerization activity	molecular_function	28/456	697/20791	2.647e-03	2.357e-02	28	1.83
GO:0007159	leukocyte cell-cell adhesion	biological_process	20/456	443/20791	2.652e-03	2.357e-02	20	2.06
GO:0001936	regulation of endothelial cell proliferation	biological_process	7/456	91/20791	2.728e-03	2.024e-02	7	3.51
GO:0045446	endothelial cell differentiation	biological_process	7/456	91/20791	2.728e-03	2.024e-02	7	3.51
GO:0031960	response to corticosteroid	biological_process	11/456	187/20791	2.733e-03	2.022e-02	11	2.68
GO:0030239	myofibril assembly	biological_process	5/456	51/20791	2.779e-03	2.053e-02	5	4.47
GO:0003229	ventricular cardiac muscle tissue development	biological_process	5/456	51/20791	2.779e-03	2.053e-02	5	4.47

GO:0005102	receptor binding	molecular_function	51/456	1498/20791	2.818e-03	2.076e-02	51	1.55
GO:0034405	response to fluid shear stress	biological_process	4/456	34/20791	2.854e-03	2.100e-02	4	5.36
GO:0046579	positive regulation of Ras protein signal transduction	biological_process	4/456	34/20791	2.854e-03	2.100e-02	4	5.36
GO:0045214	sarcomere organization	biological_process	4/456	34/20791	2.854e-03	2.100e-02	4	5.36
GO:0010092	specification of organ identity	biological_process	4/456	34/20791	2.854e-03	2.100e-02	4	5.36
GO:0038179	neurotrophin signaling pathway	biological_process	4/456	34/20791	2.854e-03	2.100e-02	4	5.36
GO:0097300	programmed necrotic cell death	biological_process	4/456	34/20791	2.854e-03	2.100e-02	4	5.36
GO:0009892	negative regulation of metabolic process	biological_process	78/456	2500/20791	2.862e-03	2.088e-02	78	1.42
GO:0045177	apical part of cell	cellular_component	17/456	356/20791	2.897e-03	2.062e-02	17	2.18
GO:0070486	leukocyte aggregation	biological_process	19/456	416/20791	2.907e-03	2.066e-02	19	2.08
GO:0005622	intracellular	cellular_component	344/456	13301/20791	2.908e-03	2.064e-02	344	1.18
GO:0090279	regulation of calcium ion import	biological_process	7/456	92/20791	2.910e-03	2.063e-02	7	3.47
GO:0050769	positive regulation of neurogenesis	biological_process	18/456	386/20791	2.919e-03	2.067e-02	18	2.13
GO:0042692	muscle cell differentiation	biological_process	17/456	357/20791	2.983e-03	2.109e-02	17	2.17
GO:0031346	positive regulation of cell projection organization	biological_process	15/456	299/20791	3.004e-03	2.121e-02	15	2.29
GO:0022612	gland morphogenesis	biological_process	9/456	139/20791	3.034e-03	2.139e-02	9	2.95
GO:0071356	cellular response to tumor necrosis factor	biological_process	9/456	139/20791	3.034e-03	2.139e-02	9	2.95
GO:1901184	regulation of ERBB signaling pathway	biological_process	5/456	52/20791	3.044e-03	2.141e-02	5	4.38
GO:0060711	labyrinthine layer development	biological_process	5/456	52/20791	3.044e-03	2.141e-02	5	4.38
GO:0055024	regulation of cardiac muscle tissue development	biological_process	5/456	52/20791	3.044e-03	2.141e-02	5	4.38
GO:2000738	positive regulation of stem cell differentiation	biological_process	5/456	52/20791	3.044e-03	2.141e-02	5	4.38
GO:0044237	cellular metabolic process	biological_process	250/456	9400/20791	3.061e-03	2.141e-02	250	1.21
GO:0005938	cell cortex	cellular_component	13/456	244/20791	3.131e-03	2.187e-02	13	2.43
GO:0006915	apoptotic process	biological_process	56/456	1688/20791	3.137e-03	2.188e-02	56	1.51
GO:0014032	neural crest cell development	biological_process	6/456	72/20791	3.156e-03	2.199e-02	6	3.80
GO:0008585	female gonad development	biological_process	8/456	116/20791	3.166e-03	2.203e-02	8	3.14
GO:0030308	negative regulation of cell growth	biological_process	10/456	165/20791	3.204e-03	2.223e-02	10	2.76
GO:0032496	response to lipopolysaccharide	biological_process	16/456	330/20791	3.204e-03	2.223e-02	16	2.21
GO:0009954	proximal/distal pattern formation	biological_process	4/456	35/20791	3.205e-03	2.218e-02	4	5.21
GO:0035088	establishment or maintenance of apical/basal cell polarity	biological_process	4/456	35/20791	3.205e-03	2.218e-02	4	5.21
GO:0014069	postsynaptic density	cellular_component	11/456	191/20791	3.232e-03	2.231e-02	11	2.63
GO:0005819	spindle	cellular_component	14/456	273/20791	3.254e-03	2.243e-02	14	2.34
GO:0051209	release of sequestered calcium ion into cytosol	biological_process	7/456	94/20791	3.303e-03	2.274e-02	7	3.40
GO:0002688	regulation of leukocyte chemotaxis	biological_process	7/456	94/20791	3.303e-03	2.274e-02	7	3.40
GO:0060350	endochondral bone morphogenesis	biological_process	5/456	53/20791	3.327e-03	2.285e-02	5	4.30
GO:0045930	negative regulation of mitotic cell cycle	biological_process	10/456	166/20791	3.352e-03	2.299e-02	10	2.75
GO:0050764	regulation of phagocytosis	biological_process	6/456	73/20791	3.395e-03	2.325e-02	6	3.75
GO:0098609	cell-cell adhesion	biological_process	32/456	845/20791	3.493e-03	2.389e-02	32	1.73
GO:0045785	positive regulation of cell adhesion	biological_process	16/456	333/20791	3.507e-03	2.396e-02	16	2.19
GO:0043296	apical junction complex	cellular_component	9/456	142/20791	3.518e-03	2.400e-02	9	2.89
GO:0042476	odontogenesis	biological_process	8/456	118/20791	3.534e-03	2.408e-02	8	3.09
GO:0051592	response to calcium ion	biological_process	8/456	118/20791	3.534e-03	2.408e-02	8	3.09

GO:2000736	regulation of stem cell differentiation	biological_process	8/456	118/20791	3.534e-03	2.408e-02	8	3.09
GO:1990090	cellular response to nerve growth factor stimulus	biological_process	4/456	36/20791	3.586e-03	2.434e-02	4	5.07
GO:0030857	negative regulation of epithelial cell differentiation	biological_process	4/456	36/20791	3.586e-03	2.434e-02	4	5.07
GO:0016831	carboxy-lyase activity	molecular_function	4/456	36/20791	3.586e-03	2.434e-02	4	5.07
GO:0042063	gliogenesis	biological_process	13/456	248/20791	3.611e-03	2.441e-02	13	2.39
GO:0051493	regulation of cytoskeleton organization	biological_process	18/456	394/20791	3.638e-03	2.456e-02	18	2.08
GO:0016324	apical plasma membrane	cellular_component	14/456	277/20791	3.718e-03	2.507e-02	14	2.30
GO:0051015	actin filament binding	molecular_function	8/456	119/20791	3.729e-03	2.511e-02	8	3.07
GO:0072080	nephron tubule development	biological_process	7/456	96/20791	3.737e-03	2.514e-02	7	3.32
GO:0043167	ion binding	molecular_function	165/456	5962/20791	3.794e-03	2.479e-02	165	1.26
GO:0090287	regulation of cellular response to growth factor stimulus	biological_process	12/456	222/20791	3.819e-03	2.492e-02	12	2.46
GO:0007088	regulation of mitosis	biological_process	8/456	120/20791	3.934e-03	2.564e-02	8	3.04
GO:1901992	positive regulation of mitotic cell cycle phase transition	biological_process	5/456	55/20791	3.954e-03	2.574e-02	5	4.14
GO:0070373	negative regulation of ERK1 and ERK2 cascade	biological_process	5/456	55/20791	3.954e-03	2.574e-02	5	4.14
GO:0044772	mitotic cell cycle phase transition	biological_process	14/456	279/20791	3.970e-03	2.578e-02	14	2.29
GO:0003012	muscle system process	biological_process	15/456	308/20791	3.989e-03	2.587e-02	15	2.22
GO:0019902	phosphatase binding	molecular_function	10/456	170/20791	3.996e-03	2.588e-02	10	2.68
GO:0035924	cellular response to vascular endothelial growth factor stimulus	biological_process	4/456	37/20791	3.999e-03	2.587e-02	4	4.93
GO:0071548	response to dexamethasone	biological_process	4/456	37/20791	3.999e-03	2.587e-02	4	4.93
GO:0005769	early endosome	cellular_component	13/456	251/20791	4.009e-03	2.587e-02	13	2.36
GO:0010256	endomembrane system organization	biological_process	20/456	460/20791	4.081e-03	2.630e-02	20	1.98
GO:0051924	regulation of calcium ion transport	biological_process	11/456	197/20791	4.121e-03	2.653e-02	11	2.55
GO:0030029	actin filament-based process	biological_process	24/456	588/20791	4.140e-03	2.662e-02	24	1.86
GO:0046545	development of primary female sexual characteristics	biological_process	8/456	121/20791	4.147e-03	2.663e-02	8	3.01
GO:0002690	positive regulation of leukocyte chemotaxis	biological_process	6/456	76/20791	4.198e-03	2.693e-02	6	3.60
GO:0048704	embryonic skeletal system morphogenesis	biological_process	7/456	98/20791	4.215e-03	2.700e-02	7	3.26
GO:0010976	positive regulation of neuron projection development	biological_process	12/456	225/20791	4.266e-03	2.730e-02	12	2.43
GO:0034103	regulation of tissue remodeling	biological_process	5/456	56/20791	4.299e-03	2.747e-02	5	4.07
GO:0016773	phosphotransferase activity, alcohol group as acceptor	molecular_function	28/456	722/20791	4.331e-03	2.764e-02	28	1.77
GO:0048638	regulation of developmental growth	biological_process	15/456	311/20791	4.372e-03	2.774e-02	15	2.20
GO:0051402	neuron apoptotic process	biological_process	12/456	226/20791	4.424e-03	2.803e-02	12	2.42
GO:0031252	cell leading edge	cellular_component	16/456	341/20791	4.434e-03	2.806e-02	16	2.14
GO:0031128	developmental induction	biological_process	4/456	38/20791	4.446e-03	2.810e-02	4	4.80
GO:0045843	negative regulation of striated muscle tissue development	biological_process	4/456	38/20791	4.446e-03	2.810e-02	4	4.80
GO:0010828	positive regulation of glucose transport	biological_process	4/456	38/20791	4.446e-03	2.810e-02	4	4.80
GO:0003170	heart valve development	biological_process	4/456	38/20791	4.446e-03	2.810e-02	4	4.80
GO:0072678	T cell migration	biological_process	4/456	38/20791	4.446e-03	2.810e-02	4	4.80
GO:0061028	establishment of endothelial barrier	biological_process	4/456	38/20791	4.446e-03	2.810e-02	4	4.80
GO:0000082	G1/S transition of mitotic cell cycle	biological_process	9/456	147/20791	4.463e-03	2.801e-02	9	2.79
GO:0034329	cell junction assembly	biological_process	9/456	147/20791	4.463e-03	2.801e-02	9	2.79
GO:0070301	cellular response to hydrogen peroxide	biological_process	6/456	77/20791	4.496e-03	2.815e-02	6	3.55
GO:0010975	regulation of neuron projection development	biological_process	18/456	402/20791	4.502e-03	2.815e-02	18	2.04

GO:0017076	purine nucleotide binding	molecular_function	60/456	1867/20791	4.552e-03	2.843e-02	60	1.47
GO:0019898	extrinsic component of membrane	cellular_component	13/456	255/20791	4.596e-03	2.867e-02	13	2.32
GO:0051781	positive regulation of cell division	biological_process	8/456	123/20791	4.601e-03	2.867e-02	8	2.97
GO:0007269	neurotransmitter secretion	biological_process	8/456	123/20791	4.601e-03	2.867e-02	8	2.97
GO:0001885	endothelial cell development	biological_process	5/456	57/20791	4.666e-03	2.901e-02	5	4.00
GO:0032835	glomerulus development	biological_process	5/456	57/20791	4.666e-03	2.901e-02	5	4.00
GO:0060688	regulation of morphogenesis of a branching structure	biological_process	5/456	57/20791	4.666e-03	2.901e-02	5	4.00
GO:0072686	mitotic spindle	cellular_component	5/456	57/20791	4.666e-03	2.901e-02	5	4.00
GO:0045184	establishment of protein localization	biological_process	58/456	1795/20791	4.676e-03	2.893e-02	58	1.47
GO:0009725	response to hormone	biological_process	34/456	931/20791	4.711e-03	2.911e-02	34	1.67
GO:0061326	renal tubule development	biological_process	7/456	100/20791	4.739e-03	2.925e-02	7	3.19
GO:0005604	basement membrane	cellular_component	7/456	100/20791	4.739e-03	2.925e-02	7	3.19
GO:1901214	regulation of neuron death	biological_process	13/456	256/20791	4.754e-03	2.928e-02	13	2.32
GO:0034332	adherens junction organization	biological_process	6/456	78/20791	4.810e-03	2.959e-02	6	3.51
GO:0043523	regulation of neuron apoptotic process	biological_process	11/456	201/20791	4.817e-03	2.922e-02	11	2.50
GO:0019887	protein kinase regulator activity	molecular_function	8/456	124/20791	4.843e-03	2.934e-02	8	2.94
GO:0051248	negative regulation of protein metabolic process	biological_process	36/456	1003/20791	4.899e-03	2.965e-02	36	1.64
GO:0060603	mammary gland duct morphogenesis	biological_process	4/456	39/20791	4.929e-03	2.980e-02	4	4.68
GO:1990089	response to nerve growth factor	biological_process	4/456	39/20791	4.929e-03	2.980e-02	4	4.68
GO:0070169	positive regulation of biomineral tissue development	biological_process	4/456	39/20791	4.929e-03	2.980e-02	4	4.68
GO:0032873	negative regulation of stress-activated MAPK cascade	biological_process	4/456	39/20791	4.929e-03	2.980e-02	4	4.68
GO:0010464	regulation of mesenchymal cell proliferation	biological_process	4/456	39/20791	4.929e-03	2.980e-02	4	4.68
GO:0042110	T cell activation	biological_process	18/456	406/20791	4.995e-03	3.002e-02	18	2.02
GO:0015758	glucose transport	biological_process	7/456	101/20791	5.020e-03	2.990e-02	7	3.16
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	biological_process	5/456	58/20791	5.057e-03	3.008e-02	5	3.93
GO:0071593	lymphocyte aggregation	biological_process	18/456	407/20791	5.125e-03	3.045e-02	18	2.02
GO:0014033	neural crest cell differentiation	biological_process	6/456	79/20791	5.140e-03	3.051e-02	6	3.46
GO:0050794	regulation of cellular process	biological_process	278/456	10672/20791	5.168e-03	3.064e-02	278	1.19
GO:0032991	macromolecular complex	cellular_component	130/456	4603/20791	5.220e-03	3.091e-02	130	1.29
GO:0022604	regulation of cell morphogenesis	biological_process	21/456	502/20791	5.222e-03	3.089e-02	21	1.91
GO:0043588	skin development	biological_process	13/456	259/20791	5.252e-03	3.103e-02	13	2.29
GO:0001664	G-protein coupled receptor binding	molecular_function	13/456	259/20791	5.252e-03	3.103e-02	13	2.29
GO:0046903	secretion	biological_process	34/456	938/20791	5.280e-03	3.113e-02	34	1.65
GO:0008406	gonad development	biological_process	12/456	231/20791	5.290e-03	3.115e-02	12	2.37
GO:0051271	negative regulation of cellular component movement	biological_process	12/456	231/20791	5.290e-03	3.115e-02	12	2.37
GO:0001889	liver development	biological_process	9/456	151/20791	5.357e-03	3.148e-02	9	2.72
GO:1901215	negative regulation of neuron death	biological_process	10/456	177/20791	5.364e-03	3.148e-02	10	2.58
GO:0060076	excitatory synapse	cellular_component	11/456	204/20791	5.400e-03	2.759e-02	11	2.46
GO:0046850	regulation of bone remodeling	biological_process	4/456	40/20791	5.448e-03	2.781e-02	4	4.56
GO:0048635	negative regulation of muscle organ development	biological_process	4/456	40/20791	5.448e-03	2.781e-02	4	4.56
GO:0051057	positive regulation of small GTPase mediated signal transduction	biological_process	4/456	40/20791	5.448e-03	2.781e-02	4	4.56
GO:0051148	negative regulation of muscle cell differentiation	biological_process	5/456	59/20791	5.471e-03	2.785e-02	5	3.86

GO:1901989	positive regulation of cell cycle phase transition	biological_process	5/456	59/20791	5.471e-03	2.785e-02	5	3.86
GO:0050920	regulation of chemotaxis	biological_process	10/456	178/20791	5.587e-03	2.838e-02	10	2.56
GO:0034111	negative regulation of homotypic cell-cell adhesion	biological_process	7/456	103/20791	5.620e-03	2.852e-02	7	3.10
GO:0032269	negative regulation of cellular protein metabolic process	biological_process	34/456	942/20791	5.631e-03	2.855e-02	34	1.65
GO:0051899	membrane depolarization	biological_process	6/456	81/20791	5.853e-03	2.951e-02	6	3.38
GO:0005884	actin filament	cellular_component	6/456	81/20791	5.853e-03	2.951e-02	6	3.38
GO:0009898	cytoplasmic side of plasma membrane	cellular_component	9/456	153/20791	5.855e-03	2.946e-02	9	2.68
GO:0048771	tissue remodeling	biological_process	9/456	153/20791	5.855e-03	2.946e-02	9	2.68
GO:0005798	Golgi-associated vesicle	cellular_component	5/456	60/20791	5.910e-03	2.968e-02	5	3.80
GO:0043067	regulation of programmed cell death	biological_process	46/456	1374/20791	5.980e-03	3.000e-02	46	1.53
GO:0061005	cell differentiation involved in kidney development	biological_process	4/456	41/20791	6.005e-03	3.010e-02	4	4.45
GO:0001990	regulation of systemic arterial blood pressure by hormone	biological_process	4/456	41/20791	6.005e-03	3.010e-02	4	4.45
GO:1901862	negative regulation of muscle tissue development	biological_process	4/456	41/20791	6.005e-03	3.010e-02	4	4.45
GO:0043627	response to estrogen	biological_process	12/456	235/20791	6.078e-03	2.987e-02	12	2.33
GO:0036094	small molecule binding	molecular_function	80/456	2655/20791	6.107e-03	2.998e-02	80	1.37
GO:0008152	metabolic process	biological_process	293/456	11338/20791	6.127e-03	3.005e-02	293	1.18
GO:0000904	cell morphogenesis involved in differentiation	biological_process	27/456	707/20791	6.137e-03	3.007e-02	27	1.74
GO:0071248	cellular response to metal ion	biological_process	8/456	129/20791	6.205e-03	3.038e-02	8	2.83
GO:0034614	cellular response to reactive oxygen species	biological_process	8/456	129/20791	6.205e-03	3.038e-02	8	2.83
GO:0033554	cellular response to stress	biological_process	53/456	1634/20791	6.213e-03	3.036e-02	53	1.48
GO:0042310	vasoconstriction	biological_process	6/456	82/20791	6.237e-03	3.045e-02	6	3.34
GO:0030163	protein catabolic process	biological_process	28/456	742/20791	6.273e-03	3.060e-02	28	1.72
GO:0045137	development of primary sexual characteristics	biological_process	12/456	236/20791	6.289e-03	3.065e-02	12	2.32
GO:0007420	brain development	biological_process	27/456	709/20791	6.368e-03	3.100e-02	27	1.74
GO:0048661	positive regulation of smooth muscle cell proliferation	biological_process	5/456	61/20791	6.375e-03	3.101e-02	5	3.74
GO:0045669	positive regulation of osteoblast differentiation	biological_process	5/456	61/20791	6.375e-03	3.101e-02	5	3.74
GO:0032886	regulation of microtubule-based process	biological_process	9/456	155/20791	6.389e-03	3.102e-02	9	2.65
GO:0005802	trans-Golgi network	cellular_component	9/456	155/20791	6.389e-03	3.102e-02	9	2.65
GO:0044297	cell body	cellular_component	21/456	511/20791	6.390e-03	3.097e-02	21	1.87
GO:0000226	microtubule cytoskeleton organization	biological_process	18/456	416/20791	6.427e-03	3.112e-02	18	1.97
GO:0036477	somatodendritic compartment	cellular_component	26/456	676/20791	6.445e-03	3.117e-02	26	1.75
GO:0016772	transferase activity, transferring phosphorus-containing groups	molecular_function	34/456	952/20791	6.598e-03	3.168e-02	34	1.63
GO:0001569	patterning of blood vessels	biological_process	4/456	42/20791	6.603e-03	3.168e-02	4	4.34
GO:0051046	regulation of secretion	biological_process	25/456	644/20791	6.625e-03	3.175e-02	25	1.77
GO:0045893	positive regulation of transcription, DNA-templated	biological_process	46/456	1382/20791	6.630e-03	3.175e-02	46	1.52
GO:0032355	response to estradiol	biological_process	9/456	156/20791	6.671e-03	3.192e-02	9	2.63
GO:0002683	negative regulation of immune system process	biological_process	16/456	356/20791	6.724e-03	3.214e-02	16	2.05
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	biological_process	11/456	210/20791	6.737e-03	3.217e-02	11	2.39
GO:0008643	carbohydrate transport	biological_process	8/456	131/20791	6.827e-03	3.257e-02	8	2.78
GO:0003281	ventricular septum development	biological_process	5/456	62/20791	6.867e-03	3.273e-02	5	3.68
GO:0055017	cardiac muscle tissue growth	biological_process	5/456	62/20791	6.867e-03	3.273e-02	5	3.68
GO:0014706	striated muscle tissue development	biological_process	16/456	357/20791	6.907e-03	3.286e-02	16	2.04

GO:0044092	negative regulation of molecular function	biological_process	34/456	955/20791	6.914e-03	3.287e-02	34	1.62
GO:0001883	purine nucleoside binding	molecular_function	58/456	1830/20791	6.936e-03	3.294e-02	58	1.45
GO:0032549	ribonucleoside binding	molecular_function	58/456	1830/20791	6.936e-03	3.294e-02	58	1.45
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	biological_process	9/456	157/20791	6.961e-03	3.300e-02	9	2.61
GO:0051345	positive regulation of hydrolase activity	biological_process	27/456	714/20791	6.979e-03	3.306e-02	27	1.72
GO:0071347	cellular response to interleukin-1	biological_process	6/456	84/20791	7.062e-03	3.342e-02	6	3.26
GO:0006936	muscle contraction	biological_process	12/456	240/20791	7.194e-03	3.401e-02	12	2.28
GO:0007009	plasma membrane organization	biological_process	13/456	269/20791	7.235e-03	3.418e-02	13	2.20
GO:0060560	developmental growth involved in morphogenesis	biological_process	11/456	212/20791	7.238e-03	3.416e-02	11	2.37
GO:0004712	protein serine/threonine/tyrosine kinase activity	molecular_function	4/456	43/20791	7.242e-03	3.415e-02	4	4.24
GO:0061337	cardiac conduction	biological_process	4/456	43/20791	7.242e-03	3.415e-02	4	4.24
GO:0032154	cleavage furrow	cellular_component	4/456	43/20791	7.242e-03	3.415e-02	4	4.24
GO:0021983	pituitary gland development	biological_process	4/456	43/20791	7.242e-03	3.415e-02	4	4.24
GO:0045604	regulation of epidermal cell differentiation	biological_process	4/456	43/20791	7.242e-03	3.415e-02	4	4.24
GO:0051018	protein kinase A binding	molecular_function	4/456	43/20791	7.242e-03	3.415e-02	4	4.24
GO:0009987	cellular process	biological_process	393/456	15603/20791	7.266e-03	3.408e-02	393	1.15
GO:0000070	mitotic sister chromatid segregation	biological_process	7/456	108/20791	7.365e-03	3.451e-02	7	2.96
GO:0045732	positive regulation of protein catabolic process	biological_process	10/456	185/20791	7.365e-03	3.451e-02	10	2.46
GO:1903076	regulation of protein localization to plasma membrane	biological_process	5/456	63/20791	7.386e-03	3.455e-02	5	3.62
GO:0045682	regulation of epidermis development	biological_process	5/456	63/20791	7.386e-03	3.455e-02	5	3.62
GO:0060322	head development	biological_process	28/456	752/20791	7.493e-03	3.459e-02	28	1.70
GO:0007050	cell cycle arrest	biological_process	8/456	133/20791	7.498e-03	3.458e-02	8	2.74
GO:0005488	binding	molecular_function	398/456	15825/20791	7.517e-03	3.464e-02	398	1.15
GO:0001882	nucleoside binding	molecular_function	58/456	1838/20791	7.568e-03	3.484e-02	58	1.44
GO:0044770	cell cycle phase transition	biological_process	14/456	300/20791	7.580e-03	3.487e-02	14	2.13
GO:0005829	cytosol	cellular_component	57/456	1803/20791	7.782e-03	3.576e-02	57	1.44
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	biological_process	14/456	301/20791	7.803e-03	3.583e-02	14	2.12
GO:0001666	response to hypoxia	biological_process	14/456	301/20791	7.803e-03	3.583e-02	14	2.12
GO:0060038	cardiac muscle cell proliferation	biological_process	4/456	44/20791	7.924e-03	3.632e-02	4	4.14
GO:0060420	regulation of heart growth	biological_process	4/456	44/20791	7.924e-03	3.632e-02	4	4.14
GO:0008543	fibroblast growth factor receptor signaling pathway	biological_process	5/456	64/20791	7.934e-03	3.630e-02	5	3.56
GO:0042981	regulation of apoptotic process	biological_process	45/456	1360/20791	7.978e-03	3.647e-02	45	1.51
GO:0006875	cellular metal ion homeostasis	biological_process	18/456	425/20791	7.995e-03	3.652e-02	18	1.93
GO:0008015	blood circulation	biological_process	17/456	394/20791	8.079e-03	3.687e-02	17	1.97
GO:0050863	regulation of T cell activation	biological_process	12/456	244/20791	8.202e-03	3.740e-02	12	2.24
GO:0006996	organelle organization	biological_process	93/456	3197/20791	8.275e-03	3.770e-02	93	1.33
GO:0030425	dendrite	cellular_component	19/456	459/20791	8.409e-03	3.805e-02	19	1.89
GO:0042475	odontogenesis of dentin-containing tooth	biological_process	6/456	87/20791	8.451e-03	3.820e-02	6	3.14
GO:0070588	calcium ion transmembrane transport	biological_process	12/456	245/20791	8.471e-03	3.826e-02	12	2.23
GO:0000932	cytoplasmic mRNA processing body	cellular_component	5/456	65/20791	8.512e-03	3.841e-02	5	3.51
GO:0060402	calcium ion transport into cytosol	biological_process	7/456	111/20791	8.597e-03	3.876e-02	7	2.88
GO:0010623	developmental programmed cell death	biological_process	4/456	45/20791	8.651e-03	3.897e-02	4	4.05

GO:0051640	organelle localization	biological_process	17/456	397/20791	8.698e-03	3.915e-02	17	1.95
GO:0030036	actin cytoskeleton organization	biological_process	21/456	526/20791	8.819e-03	3.966e-02	21	1.82
GO:0016192	vesicle-mediated transport	biological_process	38/456	1114/20791	8.863e-03	3.565e-02	38	1.56
GO:0005524	ATP binding	molecular_function	48/456	1479/20791	8.872e-03	3.566e-02	48	1.48
GO:0048738	cardiac muscle tissue development	biological_process	10/456	190/20791	8.892e-03	3.571e-02	10	2.40
GO:0003013	circulatory system process	biological_process	17/456	398/20791	8.913e-03	3.577e-02	17	1.95
GO:0007162	negative regulation of cell adhesion	biological_process	11/456	218/20791	8.922e-03	3.578e-02	11	2.30
GO:0031100	organ regeneration	biological_process	6/456	88/20791	8.957e-03	3.589e-02	6	3.11
GO:0045778	positive regulation of ossification	biological_process	6/456	88/20791	8.957e-03	3.589e-02	6	3.11
GO:0003073	regulation of systemic arterial blood pressure	biological_process	6/456	88/20791	8.957e-03	3.589e-02	6	3.11
GO:0007015	actin filament organization	biological_process	14/456	306/20791	9.000e-03	3.560e-02	14	2.09
GO:0000166	nucleotide binding	molecular_function	71/456	2351/20791	9.075e-03	3.587e-02	71	1.38
GO:0010721	negative regulation of cell development	biological_process	14/456	307/20791	9.257e-03	3.656e-02	14	2.08
GO:0048599	oocyte development	biological_process	4/456	46/20791	9.424e-03	3.719e-02	4	3.96
GO:0045840	positive regulation of mitosis	biological_process	4/456	46/20791	9.424e-03	3.719e-02	4	3.96
GO:0016667	oxidoreductase activity, acting on a sulfur group of donors	molecular_function	4/456	46/20791	9.424e-03	3.719e-02	4	3.96
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	biological_process	27/456	731/20791	9.438e-03	3.716e-02	27	1.68
GO:1990266	neutrophil migration	biological_process	6/456	89/20791	9.486e-03	3.710e-02	6	3.07
GO:1903524	positive regulation of blood circulation	biological_process	6/456	89/20791	9.486e-03	3.710e-02	6	3.07
GO:0060401	cytosolic calcium ion transport	biological_process	7/456	113/20791	9.503e-03	3.711e-02	7	2.82
GO:0031324	negative regulation of cellular metabolic process	biological_process	69/456	2279/20791	9.508e-03	3.711e-02	69	1.38
GO:0010557	positive regulation of macromolecule biosynthetic process	biological_process	50/456	1561/20791	9.717e-03	3.789e-02	50	1.46
GO:0072676	lymphocyte migration	biological_process	5/456	67/20791	9.759e-03	3.803e-02	5	3.40
GO:0070098	chemokine-mediated signaling pathway	biological_process	5/456	67/20791	9.759e-03	3.803e-02	5	3.40
GO:0043235	receptor complex	cellular_component	14/456	309/20791	9.788e-03	3.809e-02	14	2.07
GO:0022408	negative regulation of cell-cell adhesion	biological_process	8/456	139/20791	9.823e-03	3.819e-02	8	2.62
GO:0022409	positive regulation of cell-cell adhesion	biological_process	10/456	193/20791	9.922e-03	3.855e-02	10	2.36
GO:0055082	cellular chemical homeostasis	biological_process	24/456	632/20791	9.973e-03	3.872e-02	24	1.73
GO:0008047	enzyme activator activity	molecular_function	16/456	372/20791	1.017e-02	3.946e-02	16	1.96
GO:0031625	ubiquitin protein ligase binding	molecular_function	12/456	251/20791	1.024e-02	3.970e-02	12	2.18
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	biological_process	10/456	194/20791	1.029e-02	3.986e-02	10	2.35
GO:0060419	heart growth	biological_process	5/456	68/20791	1.043e-02	4.037e-02	5	3.35
GO:0001707	mesoderm formation	biological_process	5/456	68/20791	1.043e-02	4.037e-02	5	3.35
GO:0050921	positive regulation of chemotaxis	biological_process	7/456	115/20791	1.048e-02	4.051e-02	7	2.78
GO:0090150	establishment of protein localization to membrane	biological_process	12/456	252/20791	1.056e-02	4.079e-02	12	2.17
GO:0005178	integrin binding	molecular_function	6/456	91/20791	1.061e-02	4.080e-02	6	3.01
GO:0048520	positive regulation of behavior	biological_process	8/456	141/20791	1.071e-02	4.116e-02	8	2.59
GO:2001235	positive regulation of apoptotic signaling pathway	biological_process	9/456	168/20791	1.087e-02	4.138e-02	9	2.44
GO:0050768	negative regulation of neurogenesis	biological_process	12/456	253/20791	1.089e-02	4.142e-02	12	2.16
GO:0090003	regulation of establishment of protein localization to plasma membrane	biological_process	4/456	48/20791	1.111e-02	4.223e-02	4	3.80

GO:0031102	neuron projection regeneration	biological_process	4/456	48/20791	1.111e-02	4.223e-02	4	3.80
GO:0032940	secretion by cell	biological_process	29/456	810/20791	1.111e-02	4.223e-02	29	1.63
GO:0060415	muscle tissue morphogenesis	biological_process	5/456	69/20791	1.113e-02	4.221e-02	5	3.30
GO:0034109	homotypic cell-cell adhesion	biological_process	14/456	314/20791	1.122e-02	4.252e-02	14	2.03
GO:0046983	protein dimerization activity	molecular_function	39/456	1168/20791	1.129e-02	4.276e-02	39	1.52
GO:0000910	cytokinesis	biological_process	7/456	117/20791	1.153e-02	4.364e-02	7	2.73
GO:0044389	small conjugating protein ligase binding	molecular_function	12/456	255/20791	1.157e-02	4.376e-02	12	2.15
GO:0016032	viral process	biological_process	11/456	226/20791	1.164e-02	4.399e-02	11	2.22
GO:0043409	negative regulation of MAPK cascade	biological_process	8/456	143/20791	1.166e-02	4.403e-02	8	2.55
GO:0051495	positive regulation of cytoskeleton organization	biological_process	9/456	170/20791	1.174e-02	4.430e-02	9	2.41
GO:0007043	cell-cell junction assembly	biological_process	5/456	70/20791	1.187e-02	4.470e-02	5	3.26
GO:0051047	positive regulation of secretion	biological_process	15/456	347/20791	1.188e-02	4.470e-02	15	1.97
GO:0006952	defense response	biological_process	42/456	1282/20791	1.192e-02	4.482e-02	42	1.49
GO:0002064	epithelial cell development	biological_process	11/456	227/20791	1.202e-02	4.517e-02	11	2.21
GO:0018193	peptidyl-amino acid modification	biological_process	35/456	1028/20791	1.202e-02	4.517e-02	35	1.55
GO:0071320	cellular response to cAMP	biological_process	4/456	49/20791	1.204e-02	4.518e-02	4	3.72
GO:0090398	cellular senescence	biological_process	4/456	49/20791	1.204e-02	4.518e-02	4	3.72
GO:0043524	negative regulation of neuron apoptotic process	biological_process	8/456	144/20791	1.216e-02	4.556e-02	8	2.53
GO:0048565	digestive tract development	biological_process	8/456	144/20791	1.216e-02	4.556e-02	8	2.53
GO:0051650	establishment of vesicle localization	biological_process	9/456	171/20791	1.219e-02	4.561e-02	9	2.40
GO:0006469	negative regulation of protein kinase activity	biological_process	10/456	199/20791	1.226e-02	4.584e-02	10	2.29
GO:1903038	negative regulation of leukocyte cell-cell adhesion	biological_process	6/456	94/20791	1.249e-02	4.666e-02	6	2.91
GO:0032587	ruffle membrane	cellular_component	5/456	71/20791	1.265e-02	4.723e-02	5	3.21
GO:0002088	lens development in camera-type eye	biological_process	5/456	71/20791	1.265e-02	4.723e-02	5	3.21
GO:0055085	transmembrane transport	biological_process	41/456	1250/20791	1.265e-02	4.723e-02	41	1.50
GO:0003231	cardiac ventricle development	biological_process	7/456	119/20791	1.266e-02	4.717e-02	7	2.68
GO:0019207	kinase regulator activity	molecular_function	8/456	145/20791	1.267e-02	4.717e-02	8	2.52
GO:0042593	glucose homeostasis	biological_process	11/456	229/20791	1.282e-02	4.713e-02	11	2.19
GO:0044089	positive regulation of cellular component biogenesis	biological_process	16/456	382/20791	1.297e-02	4.764e-02	16	1.91
GO:0050840	extracellular matrix binding	molecular_function	4/456	50/20791	1.301e-02	4.776e-02	4	3.65
GO:0009994	oocyte differentiation	biological_process	4/456	50/20791	1.301e-02	4.776e-02	4	3.65
GO:0071944	cell periphery	cellular_component	148/456	5477/20791	1.313e-02	4.435e-02	148	1.23
GO:0045055	regulated secretory pathway	biological_process	9/456	173/20791	1.314e-02	4.436e-02	9	2.37
GO:0035264	multicellular organism growth	biological_process	9/456	173/20791	1.314e-02	4.436e-02	9	2.37
GO:0005770	late endosome	cellular_component	9/456	173/20791	1.314e-02	4.436e-02	9	2.37
GO:0030136	clathrin-coated vesicle	cellular_component	6/456	95/20791	1.317e-02	4.438e-02	6	2.88
GO:0004725	protein tyrosine phosphatase activity	molecular_function	6/456	95/20791	1.317e-02	4.438e-02	6	2.88
GO:0032388	positive regulation of intracellular transport	biological_process	14/456	320/20791	1.317e-02	4.438e-02	14	1.99
GO:0031032	actomyosin structure organization	biological_process	8/456	146/20791	1.320e-02	4.439e-02	8	2.50
GO:0048812	neuron projection morphogenesis	biological_process	20/456	513/20791	1.328e-02	4.463e-02	20	1.78
GO:0048471	perinuclear region of cytoplasm	cellular_component	23/456	614/20791	1.336e-02	4.487e-02	23	1.71
GO:0048332	mesoderm morphogenesis	biological_process	5/456	72/20791	1.346e-02	4.518e-02	5	3.17

GO:0019842	vitamin binding	molecular_function	5/456	72/20791	1.346e-02	4.518e-02	5	3.17
GO:0023057	negative regulation of signaling	biological_process	37/456	1109/20791	1.353e-02	4.536e-02	37	1.52
GO:0051056	regulation of small GTPase mediated signal transduction	biological_process	10/456	202/20791	1.359e-02	4.553e-02	10	2.26
GO:0071704	organic substance metabolic process	biological_process	256/456	9972/20791	1.359e-02	4.553e-02	256	1.17
GO:0016874	ligase activity	molecular_function	16/456	384/20791	1.360e-02	4.550e-02	16	1.90
GO:0046879	hormone secretion	biological_process	13/456	291/20791	1.376e-02	4.601e-02	13	2.04
GO:0043025	neuronal cell body	cellular_component	18/456	449/20791	1.378e-02	4.605e-02	18	1.83
GO:0003279	cardiac septum development	biological_process	6/456	96/20791	1.387e-02	4.632e-02	6	2.85
GO:0042383	sarcolemma	cellular_component	7/456	121/20791	1.387e-02	4.632e-02	7	2.64
GO:0045807	positive regulation of endocytosis	biological_process	7/456	121/20791	1.387e-02	4.632e-02	7	2.64
GO:0006816	calcium ion transport	biological_process	15/456	354/20791	1.414e-02	4.713e-02	15	1.93
GO:0006066	alcohol metabolic process	biological_process	13/456	292/20791	1.415e-02	4.713e-02	13	2.03
GO:0002526	acute inflammatory response	biological_process	7/456	122/20791	1.451e-02	4.821e-02	7	2.62
GO:0030856	regulation of epithelial cell differentiation	biological_process	7/456	122/20791	1.451e-02	4.821e-02	7	2.62
GO:1901991	negative regulation of mitotic cell cycle phase transition	biological_process	6/456	97/20791	1.460e-02	4.845e-02	6	2.82
GO:0032880	regulation of protein localization	biological_process	30/456	864/20791	1.487e-02	4.882e-02	30	1.58
GO:0006801	superoxide metabolic process	biological_process	4/456	52/20791	1.512e-02	4.961e-02	4	3.51
GO:0016830	carbon-carbon lyase activity	molecular_function	4/456	52/20791	1.512e-02	4.961e-02	4	3.51
GO:0007051	spindle organization	biological_process	7/456	123/20791	1.517e-02	4.971e-02	7	2.59
GO:2000648	positive regulation of stem cell proliferation	biological_process	5/456	74/20791	1.519e-02	4.975e-02	5	3.08
GO:0007423	sensory organ development	biological_process	21/456	554/20791	1.540e-02	5.040e-02	21	1.73
GO:0060548	negative regulation of cell death	biological_process	31/456	902/20791	1.540e-02	5.040e-02	31	1.57
GO:0071241	cellular response to inorganic substance	biological_process	8/456	150/20791	1.550e-02	5.067e-02	8	2.43
GO:0015031	protein transport	biological_process	52/456	1680/20791	1.570e-02	5.129e-02	52	1.41
GO:0042698	ovulation cycle	biological_process	7/456	124/20791	1.585e-02	5.175e-02	7	2.57
GO:0007264	small GTPase mediated signal transduction	biological_process	19/456	489/20791	1.598e-02	5.182e-02	19	1.77
GO:0007154	cell communication	biological_process	171/456	6460/20791	1.603e-02	5.195e-02	171	1.21
GO:0008104	protein localization	biological_process	66/456	2220/20791	1.605e-02	5.198e-02	66	1.36
GO:0048660	regulation of smooth muscle cell proliferation	biological_process	6/456	99/20791	1.615e-02	5.227e-02	6	2.76
GO:0046883	regulation of hormone secretion	biological_process	11/456	237/20791	1.641e-02	5.308e-02	11	2.12
GO:0071333	cellular response to glucose stimulus	biological_process	7/456	125/20791	1.656e-02	5.353e-02	7	2.55
GO:0030097	hemopoiesis	biological_process	27/456	765/20791	1.656e-02	5.353e-02	27	1.61
GO:1903829	positive regulation of cellular protein localization	biological_process	13/456	298/20791	1.662e-02	5.366e-02	13	1.99
GO:0002790	peptide secretion	biological_process	11/456	238/20791	1.691e-02	5.456e-02	11	2.11
GO:0061180	mammary gland epithelium development	biological_process	5/456	76/20791	1.707e-02	5.505e-02	5	3.00
GO:0070507	regulation of microtubule cytoskeleton organization	biological_process	7/456	126/20791	1.728e-02	5.515e-02	7	2.53
GO:0055001	muscle cell development	biological_process	8/456	153/20791	1.741e-02	5.553e-02	8	2.38
GO:0006874	cellular calcium ion homeostasis	biological_process	14/456	331/20791	1.742e-02	5.553e-02	14	1.93
GO:0048546	digestive tract morphogenesis	biological_process	4/456	54/20791	1.746e-02	5.562e-02	4	3.38
GO:0071230	cellular response to amino acid stimulus	biological_process	4/456	54/20791	1.746e-02	5.562e-02	4	3.38
GO:0008328	ionotropic glutamate receptor complex	cellular_component	4/456	54/20791	1.746e-02	5.562e-02	4	3.38
GO:0032970	regulation of actin filament-based process	biological_process	13/456	300/20791	1.751e-02	5.568e-02	13	1.98

GO:0007517	muscle organ development	biological_process	14/456	332/20791	1.786e-02	5.655e-02	14	1.92
GO:0044265	cellular macromolecule catabolic process	biological_process	27/456	770/20791	1.791e-02	5.668e-02	27	1.60
GO:0017048	Rho GTPase binding	molecular_function	5/456	77/20791	1.808e-02	5.387e-02	5	2.96
GO:0051668	localization within membrane	biological_process	5/456	77/20791	1.808e-02	5.387e-02	5	2.96
GO:0048644	muscle organ morphogenesis	biological_process	5/456	77/20791	1.808e-02	5.387e-02	5	2.96
GO:0051092	positive regulation of NF-kappaB transcription factor activity	biological_process	6/456	102/20791	1.869e-02	5.559e-02	6	2.68
GO:0004860	protein kinase inhibitor activity	molecular_function	4/456	55/20791	1.871e-02	5.562e-02	4	3.32
GO:0005871	kinesin complex	cellular_component	4/456	55/20791	1.871e-02	5.562e-02	4	3.32
GO:0046578	regulation of Ras protein signal transduction	biological_process	9/456	183/20791	1.875e-02	5.568e-02	9	2.24
GO:0003824	catalytic activity	molecular_function	152/456	5707/20791	1.893e-02	5.618e-02	152	1.21
GO:0051171	regulation of nitrogen compound metabolic process	biological_process	109/456	3952/20791	1.918e-02	5.689e-02	109	1.26
GO:0051648	vesicle localization	biological_process	9/456	184/20791	1.940e-02	5.738e-02	9	2.23
GO:0008022	protein C-terminus binding	molecular_function	9/456	184/20791	1.940e-02	5.738e-02	9	2.23
GO:0010594	regulation of endothelial cell migration	biological_process	6/456	103/20791	1.960e-02	5.791e-02	6	2.66
GO:0005788	endoplasmic reticulum lumen	cellular_component	6/456	103/20791	1.960e-02	5.791e-02	6	2.66
GO:0019903	protein phosphatase binding	molecular_function	7/456	129/20791	1.961e-02	5.787e-02	7	2.47
GO:0005815	microtubule organizing center	cellular_component	22/456	602/20791	1.986e-02	5.831e-02	22	1.67
GO:0042246	tissue regeneration	biological_process	4/456	56/20791	2.003e-02	5.878e-02	4	3.26
GO:0050795	regulation of behavior	biological_process	11/456	244/20791	2.015e-02	5.910e-02	11	2.06
GO:0010632	regulation of epithelial cell migration	biological_process	8/456	157/20791	2.023e-02	5.930e-02	8	2.32
GO:0070374	positive regulation of ERK1 and ERK2 cascade	biological_process	8/456	157/20791	2.023e-02	5.930e-02	8	2.32
GO:0031256	leading edge membrane	cellular_component	7/456	130/20791	2.044e-02	5.985e-02	7	2.46
GO:0032526	response to retinoic acid	biological_process	6/456	104/20791	2.054e-02	6.011e-02	6	2.63
GO:0030203	glycosaminoglycan metabolic process	biological_process	6/456	104/20791	2.054e-02	6.011e-02	6	2.63
GO:0016202	regulation of striated muscle tissue development	biological_process	6/456	104/20791	2.054e-02	6.011e-02	6	2.63
GO:0051591	response to cAMP	biological_process	6/456	104/20791	2.054e-02	6.011e-02	6	2.63
GO:0009991	response to extracellular stimulus	biological_process	20/456	536/20791	2.072e-02	6.050e-02	20	1.70
GO:0090276	regulation of peptide hormone secretion	biological_process	9/456	186/20791	2.075e-02	6.056e-02	9	2.21
GO:0005886	plasma membrane	cellular_component	143/456	5355/20791	2.096e-02	6.113e-02	143	1.22
GO:2001236	regulation of extrinsic apoptotic signaling pathway	biological_process	8/456	158/20791	2.098e-02	6.106e-02	8	2.31
GO:0055123	digestive system development	biological_process	8/456	158/20791	2.098e-02	6.106e-02	8	2.31
GO:0000819	sister chromatid segregation	biological_process	7/456	131/20791	2.129e-02	6.189e-02	7	2.44
GO:0007204	positive regulation of cytosolic calcium ion concentration	biological_process	10/456	216/20791	2.130e-02	6.189e-02	10	2.11
GO:0046849	bone remodeling	biological_process	5/456	80/20791	2.134e-02	6.197e-02	5	2.85
GO:0046620	regulation of organ growth	biological_process	5/456	80/20791	2.134e-02	6.197e-02	5	2.85
GO:0060443	mammary gland morphogenesis	biological_process	4/456	57/20791	2.141e-02	6.210e-02	4	3.20
GO:0019210	kinase inhibitor activity	molecular_function	4/456	57/20791	2.141e-02	6.210e-02	4	3.20
GO:0019882	antigen processing and presentation	biological_process	6/456	105/20791	2.151e-02	6.232e-02	6	2.61
GO:0042176	regulation of protein catabolic process	biological_process	15/456	372/20791	2.159e-02	6.252e-02	15	1.84
GO:0003205	cardiac chamber development	biological_process	8/456	159/20791	2.176e-02	6.298e-02	8	2.29
GO:0033673	negative regulation of kinase activity	biological_process	10/456	217/20791	2.196e-02	6.352e-02	10	2.10
GO:0030509	BMP signaling pathway	biological_process	7/456	132/20791	2.216e-02	6.407e-02	7	2.42

GO:0006790	sulfur compound metabolic process	biological_process	12/456	278/20791	2.216e-02	6.407e-02	12	1.97
GO:0071396	cellular response to lipid	biological_process	19/456	506/20791	2.228e-02	6.434e-02	19	1.71
GO:0004843	ubiquitin-specific protease activity	molecular_function	5/456	81/20791	2.251e-02	6.444e-02	5	2.81
GO:0030593	neutrophil chemotaxis	biological_process	5/456	81/20791	2.251e-02	6.444e-02	5	2.81
GO:0019905	syntaxin binding	molecular_function	5/456	81/20791	2.251e-02	6.444e-02	5	2.81
GO:0032640	tumor necrosis factor production	biological_process	6/456	106/20791	2.252e-02	6.436e-02	6	2.58
GO:0055074	calcium ion homeostasis	biological_process	14/456	342/20791	2.270e-02	6.484e-02	14	1.87
GO:0006461	protein complex assembly	biological_process	37/456	1150/20791	2.275e-02	6.495e-02	37	1.47
GO:0010595	positive regulation of endothelial cell migration	biological_process	4/456	58/20791	2.285e-02	6.499e-02	4	3.14
GO:0072341	modified amino acid binding	molecular_function	4/456	58/20791	2.285e-02	6.499e-02	4	3.14
GO:0048306	calcium-dependent protein binding	molecular_function	4/456	58/20791	2.285e-02	6.499e-02	4	3.14
GO:0008360	regulation of cell shape	biological_process	7/456	133/20791	2.307e-02	6.551e-02	7	2.40
GO:1903827	regulation of cellular protein localization	biological_process	18/456	475/20791	2.347e-02	6.661e-02	18	1.73
GO:0021549	cerebellum development	biological_process	6/456	107/20791	2.356e-02	6.683e-02	6	2.56
GO:0043010	camera-type eye development	biological_process	13/456	312/20791	2.372e-02	6.429e-02	13	1.90
GO:0044236	multicellular organismal metabolic process	biological_process	5/456	82/20791	2.373e-02	6.429e-02	5	2.78
GO:0016311	dephosphorylation	biological_process	16/456	409/20791	2.373e-02	6.429e-02	16	1.78
GO:0051146	striated muscle cell differentiation	biological_process	11/456	250/20791	2.387e-02	6.460e-02	11	2.01
GO:0016791	phosphatase activity	molecular_function	11/456	250/20791	2.387e-02	6.460e-02	11	2.01
GO:0043086	negative regulation of catalytic activity	biological_process	25/456	718/20791	2.391e-02	6.464e-02	25	1.59
GO:0048878	chemical homeostasis	biological_process	32/456	970/20791	2.395e-02	6.472e-02	32	1.50
GO:0030424	axon	cellular_component	16/456	410/20791	2.424e-02	6.547e-02	16	1.78
GO:0055008	cardiac muscle tissue morphogenesis	biological_process	4/456	59/20791	2.436e-02	6.576e-02	4	3.09
GO:0048146	positive regulation of fibroblast proliferation	biological_process	4/456	59/20791	2.436e-02	6.576e-02	4	3.09
GO:0014896	muscle hypertrophy	biological_process	4/456	59/20791	2.436e-02	6.576e-02	4	3.09
GO:0045892	negative regulation of transcription, DNA-templated	biological_process	38/456	1194/20791	2.468e-02	6.652e-02	38	1.45
GO:0030003	cellular cation homeostasis	biological_process	18/456	478/20791	2.487e-02	6.693e-02	18	1.72
GO:0007265	Ras protein signal transduction	biological_process	14/456	346/20791	2.490e-02	6.697e-02	14	1.84
GO:0043433	negative regulation of sequence-specific DNA binding transcription factor activity	biological_process	7/456	135/20791	2.495e-02	6.707e-02	7	2.36
GO:0005783	endoplasmic reticulum	cellular_component	44/456	1421/20791	2.506e-02	6.734e-02	44	1.41
GO:0030902	hindbrain development	biological_process	8/456	163/20791	2.508e-02	6.735e-02	8	2.24
GO:0072657	protein localization to membrane	biological_process	15/456	379/20791	2.521e-02	6.767e-02	15	1.80
GO:0071560	cellular response to transforming growth factor beta stimulus	biological_process	9/456	192/20791	2.522e-02	6.766e-02	9	2.14
GO:0010469	regulation of receptor activity	biological_process	6/456	109/20791	2.574e-02	6.843e-02	6	2.51
GO:0006887	exocytosis	biological_process	12/456	284/20791	2.588e-02	6.876e-02	12	1.93
GO:0043507	positive regulation of JUN kinase activity	biological_process	4/456	60/20791	2.594e-02	6.889e-02	4	3.04
GO:0046683	response to organophosphorus	biological_process	7/456	136/20791	2.594e-02	6.889e-02	7	2.35
GO:0004713	protein tyrosine kinase activity	molecular_function	7/456	136/20791	2.594e-02	6.889e-02	7	2.35
GO:0030336	negative regulation of cell migration	biological_process	9/456	194/20791	2.687e-02	7.125e-02	9	2.12
GO:0045995	regulation of embryonic development	biological_process	6/456	110/20791	2.689e-02	7.127e-02	6	2.49
GO:0034765	regulation of ion transmembrane transport	biological_process	15/456	382/20791	2.689e-02	7.127e-02	15	1.79

GO:0019897	extrinsic component of plasma membrane	cellular_component	7/456	137/20791	2.695e-02	7.121e-02	7	2.33
GO:0043269	regulation of ion transport	biological_process	20/456	551/20791	2.715e-02	7.170e-02	20	1.65
GO:1901888	regulation of cell junction assembly	biological_process	4/456	61/20791	2.758e-02	7.280e-02	4	2.99
GO:0030864	cortical actin cytoskeleton	cellular_component	4/456	61/20791	2.758e-02	7.280e-02	4	2.99
GO:0032760	positive regulation of tumor necrosis factor production	biological_process	4/456	61/20791	2.758e-02	7.280e-02	4	2.99
GO:0048857	neural nucleus development	biological_process	4/456	61/20791	2.758e-02	7.280e-02	4	2.99
GO:0006836	neurotransmitter transport	biological_process	8/456	166/20791	2.781e-02	7.326e-02	8	2.20
GO:0007268	synaptic transmission	biological_process	19/456	518/20791	2.782e-02	7.325e-02	19	1.67
GO:0030001	metal ion transport	biological_process	26/456	764/20791	2.796e-02	7.358e-02	26	1.55
GO:0001678	cellular glucose homeostasis	biological_process	7/456	138/20791	2.799e-02	7.363e-02	7	2.31
GO:0007498	mesoderm development	biological_process	6/456	111/20791	2.807e-02	7.380e-02	6	2.46
GO:0071383	cellular response to steroid hormone stimulus	biological_process	11/456	256/20791	2.808e-02	7.379e-02	11	1.96
GO:0071559	response to transforming growth factor beta	biological_process	9/456	196/20791	2.859e-02	7.461e-02	9	2.09
GO:0019725	cellular homeostasis	biological_process	25/456	730/20791	2.870e-02	7.486e-02	25	1.56
GO:0001505	regulation of neurotransmitter levels	biological_process	8/456	167/20791	2.877e-02	7.500e-02	8	2.18
GO:0051716	cellular response to stimulus	biological_process	189/456	7333/20791	2.894e-02	7.541e-02	189	1.18
GO:0002695	negative regulation of leukocyte activation	biological_process	7/456	139/20791	2.906e-02	7.568e-02	7	2.30
GO:0030833	regulation of actin filament polymerization	biological_process	7/456	139/20791	2.906e-02	7.568e-02	7	2.30
GO:0051147	regulation of muscle cell differentiation	biological_process	7/456	139/20791	2.906e-02	7.568e-02	7	2.30
GO:0044344	cellular response to fibroblast growth factor stimulus	biological_process	5/456	86/20791	2.907e-02	7.560e-02	5	2.65
GO:0001708	cell fate specification	biological_process	5/456	86/20791	2.907e-02	7.560e-02	5	2.65
GO:0036459	ubiquitinyl hydrolase activity	molecular_function	5/456	86/20791	2.907e-02	7.560e-02	5	2.65
GO:0001938	positive regulation of endothelial cell proliferation	biological_process	4/456	62/20791	2.929e-02	7.598e-02	4	2.94
GO:0015833	peptide transport	biological_process	12/456	289/20791	2.933e-02	7.605e-02	12	1.89
GO:0009968	negative regulation of signal transduction	biological_process	32/456	987/20791	2.982e-02	7.728e-02	32	1.48
GO:0030162	regulation of proteolysis	biological_process	24/456	697/20791	2.986e-02	7.734e-02	24	1.57
GO:0043229	intracellular organelle	cellular_component	276/456	11021/20791	2.992e-02	7.746e-02	276	1.14
GO:0007610	behavior	biological_process	26/456	769/20791	3.007e-02	7.479e-02	26	1.54
GO:0006897	endocytosis	biological_process	19/456	523/20791	3.042e-02	7.563e-02	19	1.66
GO:0050868	negative regulation of T cell activation	biological_process	5/456	87/20791	3.053e-02	7.586e-02	5	2.62
GO:0044853	plasma membrane raft	cellular_component	5/456	87/20791	3.053e-02	7.586e-02	5	2.62
GO:0046887	positive regulation of hormone secretion	biological_process	6/456	113/20791	3.054e-02	7.582e-02	6	2.42
GO:0042107	cytokine metabolic process	biological_process	6/456	113/20791	3.054e-02	7.582e-02	6	2.42
GO:0050878	regulation of body fluid levels	biological_process	13/456	323/20791	3.080e-02	7.639e-02	13	1.84
GO:0017038	protein import	biological_process	12/456	291/20791	3.081e-02	7.638e-02	12	1.88
GO:0010629	negative regulation of gene expression	biological_process	45/456	1479/20791	3.085e-02	7.644e-02	45	1.39
GO:0019229	regulation of vasoconstriction	biological_process	4/456	63/20791	3.107e-02	7.695e-02	4	2.89
GO:0010717	regulation of epithelial to mesenchymal transition	biological_process	4/456	63/20791	3.107e-02	7.695e-02	4	2.89
GO:0010827	regulation of glucose transport	biological_process	4/456	63/20791	3.107e-02	7.695e-02	4	2.89
GO:0031267	small GTPase binding	molecular_function	10/456	229/20791	3.111e-02	7.694e-02	10	1.99
GO:0097191	extrinsic apoptotic signaling pathway	biological_process	10/456	229/20791	3.111e-02	7.694e-02	10	1.99
GO:0001654	eye development	biological_process	14/456	356/20791	3.114e-02	7.694e-02	14	1.79

GO:0009617	response to bacterium	biological_process	20/456	559/20791	3.118e-02	7.700e-02	20	1.63
GO:0023052	signaling	biological_process	165/456	6345/20791	3.118e-02	7.700e-02	165	1.19
GO:0031345	negative regulation of cell projection organization	biological_process	7/456	141/20791	3.129e-02	7.720e-02	7	2.26
GO:0006873	cellular ion homeostasis	biological_process	18/456	491/20791	3.171e-02	7.809e-02	18	1.67
GO:1903364	positive regulation of cellular protein catabolic process	biological_process	6/456	114/20791	3.183e-02	7.835e-02	6	2.40
GO:0007249	I-kappaB kinase/NF-kappaB signaling	biological_process	10/456	230/20791	3.199e-02	7.809e-02	10	1.98
GO:0030072	peptide hormone secretion	biological_process	10/456	230/20791	3.199e-02	7.809e-02	10	1.98
GO:0042802	identical protein binding	molecular_function	37/456	1179/20791	3.199e-02	7.809e-02	37	1.43
GO:0008289	lipid binding	molecular_function	21/456	597/20791	3.283e-02	8.003e-02	21	1.60
GO:0050896	response to stimulus	biological_process	221/456	8711/20791	3.285e-02	8.004e-02	221	1.16
GO:0043087	regulation of GTPase activity	biological_process	18/456	493/20791	3.289e-02	8.010e-02	18	1.66
GO:0051117	ATPase binding	molecular_function	4/456	64/20791	3.292e-02	8.013e-02	4	2.85
GO:0051304	chromosome separation	biological_process	4/456	64/20791	3.292e-02	8.013e-02	4	2.85
GO:0044291	cell-cell contact zone	cellular_component	4/456	64/20791	3.292e-02	8.013e-02	4	2.85
GO:0017158	regulation of calcium ion-dependent exocytosis	biological_process	4/456	64/20791	3.292e-02	8.013e-02	4	2.85
GO:0071385	cellular response to glucocorticoid stimulus	biological_process	4/456	64/20791	3.292e-02	8.013e-02	4	2.85
GO:0090288	negative regulation of cellular response to growth factor stimulus	biological_process	6/456	115/20791	3.316e-02	8.053e-02	6	2.38
GO:0007584	response to nutrient	biological_process	9/456	201/20791	3.325e-02	8.071e-02	9	2.04
GO:0002793	positive regulation of peptide secretion	biological_process	5/456	89/20791	3.359e-02	8.150e-02	5	2.56
GO:0007569	cell aging	biological_process	5/456	89/20791	3.359e-02	8.150e-02	5	2.56
GO:0048145	regulation of fibroblast proliferation	biological_process	5/456	89/20791	3.359e-02	8.150e-02	5	2.56
GO:0045619	regulation of lymphocyte differentiation	biological_process	7/456	143/20791	3.364e-02	8.151e-02	7	2.23
GO:0030135	coated vesicle	cellular_component	7/456	143/20791	3.364e-02	8.151e-02	7	2.23
GO:0043209	myelin sheath	cellular_component	9/456	202/20791	3.424e-02	8.281e-02	9	2.03
GO:1903507	negative regulation of nucleic acid-templated transcription	biological_process	38/456	1223/20791	3.434e-02	8.301e-02	38	1.42
GO:0048015	phosphatidylinositol-mediated signaling	biological_process	6/456	116/20791	3.453e-02	8.343e-02	6	2.36
GO:0030695	GTPase regulator activity	molecular_function	10/456	233/20791	3.472e-02	8.385e-02	10	1.96
GO:0032963	collagen metabolic process	biological_process	4/456	65/20791	3.484e-02	8.411e-02	4	2.81
GO:2001057	reactive nitrogen species metabolic process	biological_process	4/456	65/20791	3.484e-02	8.411e-02	4	2.81
GO:0002367	cytokine production involved in immune response	biological_process	4/456	65/20791	3.484e-02	8.411e-02	4	2.81
GO:0034644	cellular response to UV	biological_process	4/456	65/20791	3.484e-02	8.411e-02	4	2.81
GO:0007179	transforming growth factor beta receptor signaling pathway	biological_process	7/456	144/20791	3.486e-02	8.400e-02	7	2.22
GO:0030175	filopodium	cellular_component	5/456	90/20791	3.520e-02	8.478e-02	5	2.53
GO:0030863	cortical cytoskeleton	cellular_component	5/456	90/20791	3.520e-02	8.478e-02	5	2.53
GO:2000146	negative regulation of cell motility	biological_process	9/456	203/20791	3.526e-02	8.485e-02	9	2.02
GO:0006955	immune response	biological_process	35/456	1113/20791	3.550e-02	8.539e-02	35	1.43
GO:0042592	homeostatic process	biological_process	44/456	1455/20791	3.563e-02	8.527e-02	44	1.38
GO:0031328	positive regulation of cellular biosynthetic process	biological_process	50/456	1690/20791	3.678e-02	8.766e-02	50	1.35
GO:0045087	innate immune response	biological_process	19/456	534/20791	3.682e-02	8.772e-02	19	1.62
GO:0006970	response to osmotic stress	biological_process	4/456	66/20791	3.683e-02	8.770e-02	4	2.76
GO:0016209	antioxidant activity	molecular_function	4/456	66/20791	3.683e-02	8.770e-02	4	2.76
GO:0051017	actin filament bundle assembly	biological_process	6/456	118/20791	3.739e-02	8.626e-02	6	2.32

GO:0071901	negative regulation of protein serine/threonine kinase activity	biological_process	6/456	118/20791	3.739e-02	8.626e-02	6	2.32
GO:0071773	cellular response to BMP stimulus	biological_process	7/456	146/20791	3.739e-02	8.626e-02	7	2.19
GO:0010817	regulation of hormone levels	biological_process	16/456	432/20791	3.761e-02	8.665e-02	16	1.69
GO:0051252	regulation of RNA metabolic process	biological_process	93/456	3408/20791	3.761e-02	8.665e-02	93	1.24
GO:0050727	regulation of inflammatory response	biological_process	10/456	236/20791	3.763e-02	8.662e-02	10	1.93
GO:0048858	cell projection morphogenesis	biological_process	25/456	749/20791	3.782e-02	8.702e-02	25	1.52
GO:0006355	regulation of transcription, DNA-templated	biological_process	90/456	3289/20791	3.830e-02	8.809e-02	90	1.25
GO:0044257	cellular protein catabolic process	biological_process	21/456	607/20791	3.853e-02	8.858e-02	21	1.58
GO:0048144	fibroblast proliferation	biological_process	5/456	92/20791	3.857e-02	8.863e-02	5	2.48
GO:0007589	body fluid secretion	biological_process	5/456	92/20791	3.857e-02	8.863e-02	5	2.48
GO:0018105	peptidyl-serine phosphorylation	biological_process	10/456	237/20791	3.864e-02	8.871e-02	10	1.92
GO:0007266	Rho protein signal transduction	biological_process	7/456	147/20791	3.871e-02	8.884e-02	7	2.17
GO:0030879	mammary gland development	biological_process	7/456	147/20791	3.871e-02	8.884e-02	7	2.17
GO:0022037	metencephalon development	biological_process	6/456	119/20791	3.887e-02	8.912e-02	6	2.30
GO:0071384	cellular response to corticosteroid stimulus	biological_process	4/456	67/20791	3.890e-02	8.915e-02	4	2.72
GO:0043292	contractile fiber	cellular_component	9/456	207/20791	3.955e-02	8.978e-02	9	1.98
GO:1902679	negative regulation of RNA biosynthetic process	biological_process	38/456	1237/20791	3.999e-02	9.074e-02	38	1.40
GO:0048609	multicellular organismal reproductive process	biological_process	27/456	826/20791	4.004e-02	9.082e-02	27	1.49
GO:0030099	myeloid cell differentiation	biological_process	13/456	335/20791	4.025e-02	9.125e-02	13	1.77
GO:0071621	granulocyte chemotaxis	biological_process	5/456	93/20791	4.033e-02	9.139e-02	5	2.45
GO:0035335	peptidyl-tyrosine dephosphorylation	biological_process	5/456	93/20791	4.033e-02	9.139e-02	5	2.45
GO:0071774	response to fibroblast growth factor	biological_process	5/456	93/20791	4.033e-02	9.139e-02	5	2.45
GO:1904591	positive regulation of protein import	biological_process	5/456	93/20791	4.033e-02	9.139e-02	5	2.45
GO:0000922	spindle pole	cellular_component	6/456	120/20791	4.040e-02	9.140e-02	6	2.28
GO:0048017	inositol lipid-mediated signaling	biological_process	6/456	120/20791	4.040e-02	9.140e-02	6	2.28
GO:0051250	negative regulation of lymphocyte activation	biological_process	6/456	120/20791	4.040e-02	9.140e-02	6	2.28
GO:0001818	negative regulation of cytokine production	biological_process	8/456	178/20791	4.095e-02	9.252e-02	8	2.05
GO:0034333	adherens junction assembly	biological_process	4/456	68/20791	4.104e-02	9.268e-02	4	2.68
GO:0003208	cardiac ventricle morphogenesis	biological_process	4/456	68/20791	4.104e-02	9.268e-02	4	2.68
GO:0050852	T cell receptor signaling pathway	biological_process	4/456	68/20791	4.104e-02	9.268e-02	4	2.68
GO:0051480	cytosolic calcium ion homeostasis	biological_process	10/456	240/20791	4.178e-02	9.423e-02	10	1.90
GO:0016050	vesicle organization	biological_process	9/456	209/20791	4.184e-02	9.405e-02	9	1.96
GO:0033365	protein localization to organelle	biological_process	23/456	684/20791	4.193e-02	9.421e-02	23	1.53
GO:0061572	actin filament bundle organization	biological_process	6/456	121/20791	4.197e-02	9.426e-02	6	2.26
GO:0019221	cytokine-mediated signaling pathway	biological_process	13/456	337/20791	4.201e-02	9.431e-02	13	1.76
GO:0051297	centrosome organization	biological_process	5/456	94/20791	4.215e-02	9.458e-02	5	2.43
GO:1903506	regulation of nucleic acid-templated transcription	biological_process	90/456	3304/20791	4.217e-02	9.459e-02	90	1.24
GO:0061564	axon development	biological_process	15/456	405/20791	4.293e-02	9.625e-02	15	1.69
GO:0010467	gene expression	biological_process	128/456	4871/20791	4.324e-02	9.690e-02	128	1.20
GO:0051341	regulation of oxidoreductase activity	biological_process	4/456	69/20791	4.326e-02	9.691e-02	4	2.64
GO:0002521	leukocyte differentiation	biological_process	17/456	474/20791	4.333e-02	9.702e-02	17	1.64
GO:0005795	Golgi stack	cellular_component	6/456	122/20791	4.359e-02	9.694e-02	6	2.24

GO:2001141	regulation of RNA biosynthetic process	biological_process	90/456	3310/20791	4.380e-02	9.737e-02	90	1.24
GO:0014013	regulation of gliogenesis	biological_process	5/456	95/20791	4.403e-02	9.784e-02	5	2.40
GO:0010634	positive regulation of epithelial cell migration	biological_process	5/456	95/20791	4.403e-02	9.784e-02	5	2.40
GO:0016597	amino acid binding	molecular_function	5/456	95/20791	4.403e-02	9.784e-02	5	2.40
GO:0043069	negative regulation of programmed cell death	biological_process	27/456	835/20791	4.505e-02	9.667e-02	27	1.47
GO:0007409	axonogenesis	biological_process	14/456	374/20791	4.531e-02	9.719e-02	14	1.71
GO:0019217	regulation of fatty acid metabolic process	biological_process	4/456	70/20791	4.556e-02	9.768e-02	4	2.61
GO:0007052	mitotic spindle organization	biological_process	4/456	70/20791	4.556e-02	9.768e-02	4	2.61
GO:0042035	regulation of cytokine biosynthetic process	biological_process	5/456	96/20791	4.595e-02	9.844e-02	5	2.37
GO:0006351	transcription, DNA-templated	biological_process	91/456	3360/20791	4.640e-02	9.936e-02	91	1.23
GO:0072594	establishment of protein localization to organelle	biological_process	17/456	478/20791	4.647e-02	9.947e-02	17	1.62
GO:0019722	calcium-mediated signaling	biological_process	6/456	124/20791	4.694e-02	1.004e-01	6	2.21
GO:0006357	regulation of transcription from RNA polymerase II promoter	biological_process	50/456	1718/20791	4.730e-02	1.012e-01	50	1.33
GO:0045862	positive regulation of proteolysis	biological_process	11/456	277/20791	4.738e-02	1.013e-01	11	1.81
GO:0048588	developmental cell growth	biological_process	8/456	183/20791	4.757e-02	1.017e-01	8	1.99
GO:0009890	negative regulation of biosynthetic process	biological_process	44/456	1485/20791	4.770e-02	1.012e-01	44	1.35
GO:0046427	positive regulation of JAK-STAT cascade	biological_process	4/456	71/20791	4.793e-02	1.017e-01	4	2.57
GO:0022602	ovulation cycle process	biological_process	5/456	97/20791	4.794e-02	1.017e-01	5	2.35
GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	cellular_component	5/456	97/20791	4.794e-02	1.017e-01	5	2.35
GO:0017157	regulation of exocytosis	biological_process	7/456	154/20791	4.886e-02	1.035e-01	7	2.07
GO:0030041	actin filament polymerization	biological_process	7/456	154/20791	4.886e-02	1.035e-01	7	2.07
GO:0007369	gastrulation	biological_process	8/456	184/20791	4.898e-02	1.037e-01	8	1.98
GO:0070201	regulation of establishment of protein localization	biological_process	24/456	732/20791	4.948e-02	1.047e-01	24	1.49
GO:0003682	chromatin binding	molecular_function	17/456	482/20791	4.978e-02	1.053e-01	17	1.61
GO:0007338	single fertilization	biological_process	5/456	98/20791	4.998e-02	1.057e-01	5	2.33
GO:0032273	positive regulation of protein polymerization	biological_process	5/456	98/20791	4.998e-02	1.057e-01	5	2.33
GO:0034613	cellular protein localization	biological_process	42/456	1413/20791	5.026e-02	1.062e-01	42	1.36
GO:0050870	positive regulation of T cell activation	biological_process	7/456	155/20791	5.045e-02	1.066e-01	7	2.06
GO:0060491	regulation of cell projection assembly	biological_process	6/456	126/20791	5.046e-02	1.065e-01	6	2.17
GO:0005096	GTPase activator activity	molecular_function	9/456	216/20791	5.059e-02	1.068e-01	9	1.90
GO:0034599	cellular response to oxidative stress	biological_process	9/456	216/20791	5.059e-02	1.068e-01	9	1.90
GO:0017016	Ras GTPase binding	molecular_function	9/456	216/20791	5.059e-02	1.068e-01	9	1.90
GO:0004842	ubiquitin-protein ligase activity	molecular_function	14/456	380/20791	5.098e-02	1.073e-01	14	1.68
GO:0051707	response to other organism	biological_process	28/456	882/20791	5.108e-02	1.075e-01	28	1.45
GO:0007165	signal transduction	biological_process	154/456	5992/20791	5.133e-02	1.079e-01	154	1.17
GO:0046649	lymphocyte activation	biological_process	20/456	590/20791	5.138e-02	1.080e-01	20	1.55
GO:0043207	response to external biotic stimulus	biological_process	28/456	883/20791	5.171e-02	1.087e-01	28	1.45
GO:0006886	intracellular protein transport	biological_process	30/456	958/20791	5.185e-02	1.089e-01	30	1.43
GO:0046777	protein autophosphorylation	biological_process	9/456	217/20791	5.194e-02	1.090e-01	9	1.89
GO:0043231	intracellular membrane-bounded organelle	cellular_component	247/456	9940/20791	5.207e-02	1.093e-01	247	1.13
GO:0008064	regulation of actin polymerization or depolymerization	biological_process	7/456	156/20791	5.208e-02	1.093e-01	7	2.05
GO:0010921	regulation of phosphatase activity	biological_process	6/456	127/20791	5.229e-02	1.093e-01	6	2.15

GO:0003777	microtubule motor activity	molecular_function	4/456	73/20791	5.291e-02	1.078e-01	4	2.50
GO:0043547	positive regulation of GTPase activity	biological_process	16/456	451/20791	5.318e-02	1.083e-01	16	1.62
GO:0040013	negative regulation of locomotion	biological_process	10/456	250/20791	5.362e-02	1.092e-01	10	1.82
GO:0030832	regulation of actin filament length	biological_process	7/456	157/20791	5.374e-02	1.094e-01	7	2.03
GO:0009411	response to UV	biological_process	6/456	128/20791	5.417e-02	1.098e-01	6	2.14
GO:0032874	positive regulation of stress-activated MAPK cascade	biological_process	6/456	128/20791	5.417e-02	1.098e-01	6	2.14
GO:0005057	receptor signaling protein activity	molecular_function	6/456	128/20791	5.417e-02	1.098e-01	6	2.14
GO:1903706	regulation of hemopoiesis	biological_process	12/456	316/20791	5.437e-02	1.101e-01	12	1.73
GO:0051020	GTPase binding	molecular_function	10/456	251/20791	5.492e-02	1.111e-01	10	1.82
GO:0097159	organic cyclic compound binding	molecular_function	153/456	5966/20791	5.517e-02	1.116e-01	153	1.17
GO:0016525	negative regulation of angiogenesis	biological_process	4/456	74/20791	5.552e-02	1.123e-01	4	2.46
GO:0045638	negative regulation of myeloid cell differentiation	biological_process	4/456	74/20791	5.552e-02	1.123e-01	4	2.46
GO:0005902	microvillus	cellular_component	4/456	74/20791	5.552e-02	1.123e-01	4	2.46
GO:0035690	cellular response to drug	biological_process	4/456	74/20791	5.552e-02	1.123e-01	4	2.46
GO:0006812	cation transport	biological_process	31/456	1002/20791	5.578e-02	1.126e-01	31	1.41
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	biological_process	6/456	129/20791	5.609e-02	1.132e-01	6	2.12
GO:0032990	cell part morphogenesis	biological_process	25/456	779/20791	5.669e-02	1.144e-01	25	1.46
GO:0032774	RNA biosynthetic process	biological_process	91/456	3394/20791	5.705e-02	1.146e-01	91	1.22
GO:0034112	positive regulation of homotypic cell-cell adhesion	biological_process	7/456	159/20791	5.717e-02	1.148e-01	7	2.01
GO:0019953	sexual reproduction	biological_process	25/456	781/20791	5.817e-02	1.164e-01	25	1.46
GO:0035023	regulation of Rho protein signal transduction	biological_process	5/456	102/20791	5.872e-02	1.175e-01	5	2.24
GO:0016579	protein deubiquitination	biological_process	5/456	102/20791	5.872e-02	1.175e-01	5	2.24
GO:0034220	ion transmembrane transport	biological_process	30/456	969/20791	5.888e-02	1.177e-01	30	1.41
GO:0043279	response to alkaloid	biological_process	7/456	160/20791	5.894e-02	1.178e-01	7	1.99
GO:0045165	cell fate commitment	biological_process	10/456	254/20791	5.897e-02	1.178e-01	10	1.80
GO:0006470	protein dephosphorylation	biological_process	12/456	320/20791	5.911e-02	1.180e-01	12	1.71
GO:0051222	positive regulation of protein transport	biological_process	15/456	423/20791	5.986e-02	1.195e-01	15	1.62
GO:1903039	positive regulation of leukocyte cell-cell adhesion	biological_process	7/456	161/20791	6.074e-02	1.212e-01	7	1.98
GO:0046661	male sex differentiation	biological_process	7/456	161/20791	6.074e-02	1.212e-01	7	1.98
GO:1903409	reactive oxygen species biosynthetic process	biological_process	4/456	76/20791	6.097e-02	1.212e-01	4	2.40
GO:0035050	embryonic heart tube development	biological_process	4/456	76/20791	6.097e-02	1.212e-01	4	2.40
GO:0043066	negative regulation of apoptotic process	biological_process	26/456	823/20791	6.182e-02	1.194e-01	26	1.44
GO:0005126	cytokine receptor binding	molecular_function	11/456	289/20791	6.203e-02	1.198e-01	11	1.74
GO:0008544	epidermis development	biological_process	11/456	289/20791	6.203e-02	1.198e-01	11	1.74
GO:0030216	keratinocyte differentiation	biological_process	6/456	132/20791	6.212e-02	1.199e-01	6	2.07
GO:0036464	cytoplasmic ribonucleoprotein granule	cellular_component	6/456	132/20791	6.212e-02	1.199e-01	6	2.07
GO:0009056	catabolic process	biological_process	53/456	1869/20791	6.214e-02	1.198e-01	53	1.29
GO:0014074	response to purine-containing compound	biological_process	7/456	162/20791	6.259e-02	1.207e-01	7	1.97
GO:0009913	epidermal cell differentiation	biological_process	8/456	193/20791	6.302e-02	1.214e-01	8	1.89
GO:0031023	microtubule organizing center organization	biological_process	5/456	104/20791	6.344e-02	1.222e-01	5	2.19
GO:0016651	oxidoreductase activity, acting on NAD(P)H	molecular_function	4/456	77/20791	6.382e-02	1.229e-01	4	2.37
GO:0015696	ammonium transport	biological_process	4/456	77/20791	6.382e-02	1.229e-01	4	2.37

GO:0010769	regulation of cell morphogenesis involved in differentiation	biological_process	12/456	324/20791	6.414e-02	1.234e-01	12	1.69
GO:0030307	positive regulation of cell growth	biological_process	6/456	133/20791	6.422e-02	1.235e-01	6	2.06
GO:0004857	enzyme inhibitor activity	molecular_function	13/456	358/20791	6.425e-02	1.235e-01	13	1.66
GO:0004721	phosphoprotein phosphatase activity	molecular_function	7/456	163/20791	6.447e-02	1.239e-01	7	1.96
GO:0030246	carbohydrate binding	molecular_function	10/456	258/20791	6.469e-02	1.241e-01	10	1.77
GO:0043583	ear development	biological_process	9/456	226/20791	6.526e-02	1.251e-01	9	1.82
GO:0050801	ion homeostasis	biological_process	21/456	643/20791	6.564e-02	1.258e-01	21	1.49
GO:0032680	regulation of tumor necrosis factor production	biological_process	5/456	105/20791	6.590e-02	1.262e-01	5	2.17
GO:0004866	endopeptidase inhibitor activity	molecular_function	8/456	195/20791	6.648e-02	1.273e-01	8	1.87
GO:0043506	regulation of JUN kinase activity	biological_process	4/456	78/20791	6.676e-02	1.278e-01	4	2.34
GO:0019787	small conjugating protein ligase activity	molecular_function	14/456	395/20791	6.742e-02	1.285e-01	14	1.62
GO:0001894	tissue homeostasis	biological_process	8/456	196/20791	6.826e-02	1.296e-01	8	1.86
GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	biological_process	5/456	106/20791	6.841e-02	1.299e-01	5	2.15
GO:0098655	cation transmembrane transport	biological_process	22/456	683/20791	6.869e-02	1.304e-01	22	1.47
GO:0043266	regulation of potassium ion transport	biological_process	4/456	79/20791	6.977e-02	1.324e-01	4	2.31
GO:0030100	regulation of endocytosis	biological_process	8/456	197/20791	7.008e-02	1.329e-01	8	1.85
GO:0032412	regulation of ion transmembrane transporter activity	biological_process	7/456	166/20791	7.035e-02	1.334e-01	7	1.92
GO:0001948	glycoprotein binding	molecular_function	5/456	107/20791	7.098e-02	1.315e-01	5	2.13
GO:0072091	regulation of stem cell proliferation	biological_process	5/456	107/20791	7.098e-02	1.315e-01	5	2.13
GO:0016331	morphogenesis of embryonic epithelium	biological_process	7/456	167/20791	7.239e-02	1.333e-01	7	1.91
GO:0008610	lipid biosynthetic process	biological_process	17/456	505/20791	7.239e-02	1.333e-01	17	1.53
GO:0030901	midbrain development	biological_process	4/456	80/20791	7.287e-02	1.341e-01	4	2.28
GO:0021536	diencephalon development	biological_process	4/456	80/20791	7.287e-02	1.341e-01	4	2.28
GO:0071482	cellular response to light stimulus	biological_process	4/456	80/20791	7.287e-02	1.341e-01	4	2.28
GO:0048477	oogenesis	biological_process	4/456	80/20791	7.287e-02	1.341e-01	4	2.28
GO:0006366	transcription from RNA polymerase II promoter	biological_process	50/456	1770/20791	7.307e-02	1.343e-01	50	1.29
GO:0003774	motor activity	molecular_function	6/456	137/20791	7.310e-02	1.343e-01	6	2.00
GO:0031333	negative regulation of protein complex assembly	biological_process	5/456	108/20791	7.362e-02	1.352e-01	5	2.11
GO:0010565	regulation of cellular ketone metabolic process	biological_process	5/456	108/20791	7.362e-02	1.352e-01	5	2.11
GO:0030010	establishment of cell polarity	biological_process	5/456	108/20791	7.362e-02	1.352e-01	5	2.11
GO:0007292	female gamete generation	biological_process	5/456	108/20791	7.362e-02	1.352e-01	5	2.11
GO:0032870	cellular response to hormone stimulus	biological_process	19/456	579/20791	7.440e-02	1.365e-01	19	1.50
GO:0000775	chromosome, centromeric region	cellular_component	7/456	168/20791	7.447e-02	1.365e-01	7	1.90
GO:0031667	response to nutrient levels	biological_process	17/456	507/20791	7.466e-02	1.368e-01	17	1.53
GO:0042578	phosphoric ester hydrolase activity	molecular_function	12/456	332/20791	7.512e-02	1.376e-01	12	1.65
GO:0031988	membrane-bounded vesicle	cellular_component	29/456	953/20791	7.524e-02	1.378e-01	29	1.39
GO:0010822	positive regulation of mitochondrion organization	biological_process	6/456	138/20791	7.544e-02	1.381e-01	6	1.98
GO:0055002	striated muscle cell development	biological_process	6/456	138/20791	7.544e-02	1.381e-01	6	1.98
GO:0035770	ribonucleoprotein granule	cellular_component	6/456	138/20791	7.544e-02	1.381e-01	6	1.98
GO:0019208	phosphatase regulator activity	molecular_function	4/456	81/20791	7.605e-02	1.387e-01	4	2.25
GO:0001570	vasculogenesis	biological_process	4/456	81/20791	7.605e-02	1.387e-01	4	2.25

GO:0033077	T cell differentiation in thymus	biological_process	4/456	81/20791	7.605e-02	1.387e-01	4	2.25
GO:0042089	cytokine biosynthetic process	biological_process	5/456	109/20791	7.631e-02	1.390e-01	5	2.09
GO:0002757	immune response-activating signal transduction	biological_process	9/456	233/20791	7.716e-02	1.405e-01	9	1.76
GO:0006082	organic acid metabolic process	biological_process	29/456	957/20791	7.860e-02	1.425e-01	29	1.38
GO:0007254	JNK cascade	biological_process	7/456	170/20791	7.874e-02	1.427e-01	7	1.88
GO:0045637	regulation of myeloid cell differentiation	biological_process	7/456	170/20791	7.874e-02	1.427e-01	7	1.88
GO:0022898	regulation of transmembrane transporter activity	biological_process	7/456	170/20791	7.874e-02	1.427e-01	7	1.88
GO:0001775	cell activation	biological_process	25/456	806/20791	7.917e-02	1.433e-01	25	1.41
GO:0046872	metal ion binding	molecular_function	103/456	3949/20791	7.918e-02	1.433e-01	103	1.19
GO:0030510	regulation of BMP signaling pathway	biological_process	4/456	82/20791	7.931e-02	1.435e-01	4	2.22
GO:0032956	regulation of actin cytoskeleton organization	biological_process	10/456	268/20791	8.070e-02	1.422e-01	10	1.70
GO:0098588	bounding membrane of organelle	cellular_component	54/456	1943/20791	8.082e-02	1.424e-01	54	1.27
GO:0042180	cellular ketone metabolic process	biological_process	7/456	171/20791	8.094e-02	1.425e-01	7	1.87
GO:0005509	calcium ion binding	molecular_function	22/456	696/20791	8.139e-02	1.433e-01	22	1.44
GO:1902532	negative regulation of intracellular signal transduction	biological_process	14/456	406/20791	8.172e-02	1.438e-01	14	1.57
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function	5/456	111/20791	8.189e-02	1.441e-01	5	2.05
GO:0046330	positive regulation of JNK cascade	biological_process	5/456	111/20791	8.189e-02	1.441e-01	5	2.05
GO:0009607	response to biotic stimulus	biological_process	28/456	923/20791	8.224e-02	1.446e-01	28	1.38
GO:0043254	regulation of protein complex assembly	biological_process	12/456	337/20791	8.262e-02	1.452e-01	12	1.62
GO:0019955	cytokine binding	molecular_function	4/456	83/20791	8.266e-02	1.452e-01	4	2.20
GO:0050729	positive regulation of inflammatory response	biological_process	4/456	83/20791	8.266e-02	1.452e-01	4	2.20
GO:1903825	organic acid transmembrane transport	biological_process	4/456	83/20791	8.266e-02	1.452e-01	4	2.20
GO:0051048	negative regulation of secretion	biological_process	8/456	204/20791	8.369e-02	1.464e-01	8	1.79
GO:0048667	cell morphogenesis involved in neuron differentiation	biological_process	16/456	479/20791	8.430e-02	1.474e-01	16	1.52
GO:0090316	positive regulation of intracellular protein transport	biological_process	9/456	237/20791	8.459e-02	1.478e-01	9	1.73
GO:0000149	SNARE binding	molecular_function	5/456	112/20791	8.477e-02	1.480e-01	5	2.04
GO:0006323	DNA packaging	biological_process	6/456	142/20791	8.530e-02	1.489e-01	6	1.93
GO:0030426	growth cone	cellular_component	6/456	142/20791	8.530e-02	1.489e-01	6	1.93
GO:0009566	fertilization	biological_process	6/456	142/20791	8.530e-02	1.489e-01	6	1.93
GO:0090257	regulation of muscle system process	biological_process	7/456	173/20791	8.545e-02	1.490e-01	7	1.84
GO:0007018	microtubule-based movement	biological_process	8/456	205/20791	8.577e-02	1.495e-01	8	1.78
GO:0019932	second-messenger-mediated signaling	biological_process	8/456	205/20791	8.577e-02	1.495e-01	8	1.78
GO:0016887	ATPase activity	molecular_function	14/456	409/20791	8.597e-02	1.498e-01	14	1.56
GO:0035249	synaptic transmission, glutamatergic	biological_process	4/456	84/20791	8.610e-02	1.500e-01	4	2.17
GO:0030838	positive regulation of actin filament polymerization	biological_process	4/456	84/20791	8.610e-02	1.500e-01	4	2.17
GO:1902911	protein kinase complex	cellular_component	4/456	84/20791	8.610e-02	1.500e-01	4	2.17
GO:0046888	negative regulation of hormone secretion	biological_process	4/456	84/20791	8.610e-02	1.500e-01	4	2.17
GO:2001233	regulation of apoptotic signaling pathway	biological_process	13/456	374/20791	8.617e-02	1.499e-01	13	1.58
GO:0010608	posttranscriptional regulation of gene expression	biological_process	12/456	340/20791	8.737e-02	1.519e-01	12	1.61
GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	molecular_function	5/456	113/20791	8.772e-02	1.525e-01	5	2.02
GO:0071375	cellular response to peptide hormone stimulus	biological_process	9/456	239/20791	8.848e-02	1.537e-01	9	1.72

GO:0016787	hydrolase activity	molecular_function	66/456	2443/20791	8.910e-02	1.547e-01	66	1.23
GO:0090277	positive regulation of peptide hormone secretion	biological_process	4/456	85/20791	8.961e-02	1.551e-01	4	2.15
GO:0022405	hair cycle process	biological_process	4/456	85/20791	8.961e-02	1.551e-01	4	2.15
GO:0001942	hair follicle development	biological_process	4/456	85/20791	8.961e-02	1.551e-01	4	2.15
GO:0030414	peptidase inhibitor activity	molecular_function	8/456	207/20791	9.004e-02	1.557e-01	8	1.76
GO:0051258	protein polymerization	biological_process	9/456	240/20791	9.047e-02	1.564e-01	9	1.71
GO:0072655	establishment of protein localization to mitochondrion	biological_process	6/456	144/20791	9.052e-02	1.564e-01	6	1.90
GO:0050880	regulation of blood vessel size	biological_process	6/456	144/20791	9.052e-02	1.564e-01	6	1.90
GO:0031410	cytoplasmic vesicle	cellular_component	31/456	1049/20791	9.201e-02	1.563e-01	31	1.35
GO:0030659	cytoplasmic vesicle membrane	cellular_component	12/456	343/20791	9.231e-02	1.568e-01	12	1.60
GO:0004540	ribonuclease activity	molecular_function	4/456	86/20791	9.321e-02	1.579e-01	4	2.12
GO:0005581	collagen	cellular_component	4/456	86/20791	9.321e-02	1.579e-01	4	2.12
GO:0060021	palate development	biological_process	4/456	86/20791	9.321e-02	1.579e-01	4	2.12
GO:0001952	regulation of cell-matrix adhesion	biological_process	4/456	86/20791	9.321e-02	1.579e-01	4	2.12
GO:0035150	regulation of tube size	biological_process	6/456	145/20791	9.321e-02	1.579e-01	6	1.89
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	biological_process	30/456	1012/20791	9.358e-02	1.583e-01	30	1.35
GO:0072562	blood microparticle	cellular_component	5/456	115/20791	9.380e-02	1.586e-01	5	1.98
GO:0051100	negative regulation of binding	biological_process	5/456	115/20791	9.380e-02	1.586e-01	5	1.98
GO:0001227	RNA polymerase II transcription regulatory region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	molecular_function	7/456	177/20791	9.497e-02	1.605e-01	7	1.80
GO:0006605	protein targeting	biological_process	18/456	560/20791	9.527e-02	1.610e-01	18	1.47
GO:0016023	cytoplasmic membrane-bounded vesicle	cellular_component	28/456	938/20791	9.661e-02	1.626e-01	28	1.36
GO:1901342	regulation of vasculature development	biological_process	8/456	210/20791	9.670e-02	1.627e-01	8	1.74
GO:0061053	somite development	biological_process	4/456	87/20791	9.690e-02	1.629e-01	4	2.10
GO:0051153	regulation of striated muscle cell differentiation	biological_process	4/456	87/20791	9.690e-02	1.629e-01	4	2.10
GO:0098773	skin epidermis development	biological_process	4/456	87/20791	9.690e-02	1.629e-01	4	2.10
GO:0061041	regulation of wound healing	biological_process	5/456	116/20791	9.694e-02	1.628e-01	5	1.97
GO:0045580	regulation of T cell differentiation	biological_process	5/456	116/20791	9.694e-02	1.628e-01	5	1.97
GO:0008154	actin polymerization or depolymerization	biological_process	7/456	178/20791	9.746e-02	1.636e-01	7	1.79
GO:0017111	nucleoside-triphosphatase activity	molecular_function	23/456	749/20791	9.844e-02	1.652e-01	23	1.40
GO:0030427	site of polarized growth	cellular_component	6/456	147/20791	9.874e-02	1.656e-01	6	1.86
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	biological_process	8/456	211/20791	9.899e-02	1.660e-01	8	1.73
GO:0043169	cation binding	molecular_function	104/456	4037/20791	9.994e-02	1.675e-01	104	1.17
GO:0031334	positive regulation of protein complex assembly	biological_process	7/456	179/20791	9.998e-02	1.675e-01	7	1.78
GO:0001704	formation of primary germ layer	biological_process	5/456	117/20791	1.001e-01	1.677e-01	5	1.95
GO:0050851	antigen receptor-mediated signaling pathway	biological_process	5/456	117/20791	1.001e-01	1.677e-01	5	1.95
GO:0007229	integrin-mediated signaling pathway	biological_process	4/456	88/20791	1.007e-01	1.686e-01	4	2.07
GO:0000956	nuclear-transcribed mRNA catabolic process	biological_process	4/456	88/20791	1.007e-01	1.686e-01	4	2.07
GO:0032535	regulation of cellular component size	biological_process	12/456	348/20791	1.010e-01	1.690e-01	12	1.57
GO:0002443	leukocyte mediated immunity	biological_process	10/456	279/20791	1.013e-01	1.654e-01	10	1.63
GO:0002253	activation of immune response	biological_process	10/456	279/20791	1.013e-01	1.654e-01	10	1.63

GO:0050776	regulation of immune response	biological_process	17/456	528/20791	1.017e-01	1.660e-01	17	1.47
GO:0000981	sequence-specific DNA binding RNA polymerase II transcription factor activity	molecular_function	20/456	639/20791	1.017e-01	1.660e-01	20	1.43
GO:1903531	negative regulation of secretion by cell	biological_process	7/456	180/20791	1.026e-01	1.667e-01	7	1.77
GO:0006606	protein import into nucleus	biological_process	9/456	246/20791	1.030e-01	1.673e-01	9	1.67
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	molecular_function	5/456	118/20791	1.034e-01	1.678e-01	5	1.93
GO:0051897	positive regulation of protein kinase B signaling	biological_process	4/456	89/20791	1.045e-01	1.696e-01	4	2.05
GO:0035304	regulation of protein dephosphorylation	biological_process	6/456	149/20791	1.045e-01	1.696e-01	6	1.84
GO:0050778	positive regulation of immune response	biological_process	14/456	421/20791	1.045e-01	1.696e-01	14	1.52
GO:0071456	cellular response to hypoxia	biological_process	5/456	119/20791	1.067e-01	1.730e-01	5	1.92
GO:0060041	retina development in camera-type eye	biological_process	6/456	150/20791	1.074e-01	1.740e-01	6	1.82
GO:0070585	protein localization to mitochondrion	biological_process	6/456	150/20791	1.074e-01	1.740e-01	6	1.82
GO:0002764	immune response-regulating signaling pathway	biological_process	9/456	248/20791	1.075e-01	1.740e-01	9	1.65
GO:0051170	nuclear import	biological_process	9/456	248/20791	1.075e-01	1.740e-01	9	1.65
GO:0007283	spermatogenesis	biological_process	15/456	459/20791	1.077e-01	1.742e-01	15	1.49
GO:0030098	lymphocyte differentiation	biological_process	11/456	317/20791	1.083e-01	1.752e-01	11	1.58
GO:0042307	positive regulation of protein import into nucleus	biological_process	4/456	90/20791	1.085e-01	1.754e-01	4	2.03
GO:0043204	perikaryon	cellular_component	4/456	90/20791	1.085e-01	1.754e-01	4	2.03
GO:0043648	dicarboxylic acid metabolic process	biological_process	4/456	90/20791	1.085e-01	1.754e-01	4	2.03
GO:0048232	male gamete generation	biological_process	15/456	460/20791	1.093e-01	1.761e-01	15	1.49
GO:0015711	organic anion transport	biological_process	12/456	353/20791	1.101e-01	1.774e-01	12	1.55
GO:0048592	eye morphogenesis	biological_process	6/456	151/20791	1.104e-01	1.778e-01	6	1.81
GO:0072593	reactive oxygen species metabolic process	biological_process	8/456	216/20791	1.110e-01	1.787e-01	8	1.69
GO:0007276	gamete generation	biological_process	20/456	646/20791	1.111e-01	1.788e-01	20	1.41
GO:0001656	metanephros development	biological_process	4/456	91/20791	1.125e-01	1.779e-01	4	2.00
GO:0030217	T cell differentiation	biological_process	8/456	217/20791	1.135e-01	1.794e-01	8	1.68
GO:1903828	negative regulation of cellular protein localization	biological_process	5/456	121/20791	1.136e-01	1.795e-01	5	1.88
GO:0051223	regulation of protein transport	biological_process	21/456	687/20791	1.157e-01	1.823e-01	21	1.39
GO:0046328	regulation of JNK cascade	biological_process	6/456	153/20791	1.165e-01	1.836e-01	6	1.79
GO:0035303	regulation of dephosphorylation	biological_process	6/456	153/20791	1.165e-01	1.836e-01	6	1.79
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	biological_process	6/456	153/20791	1.165e-01	1.836e-01	6	1.79
GO:0051291	protein heterooligomerization	biological_process	4/456	92/20791	1.166e-01	1.835e-01	4	1.98
GO:0030165	PDZ domain binding	molecular_function	4/456	92/20791	1.166e-01	1.835e-01	4	1.98
GO:0007059	chromosome segregation	biological_process	9/456	252/20791	1.167e-01	1.836e-01	9	1.63
GO:0043200	response to amino acid	biological_process	5/456	122/20791	1.171e-01	1.842e-01	5	1.87
GO:0030178	negative regulation of Wnt signaling pathway	biological_process	5/456	122/20791	1.171e-01	1.842e-01	5	1.87
GO:0005088	Ras guanyl-nucleotide exchange factor activity	molecular_function	5/456	122/20791	1.171e-01	1.842e-01	5	1.87
GO:0016788	hydrolase activity, acting on ester bonds	molecular_function	21/456	689/20791	1.184e-01	1.858e-01	21	1.39
GO:0019058	viral life cycle	biological_process	7/456	186/20791	1.188e-01	1.864e-01	7	1.72
GO:0010212	response to ionizing radiation	biological_process	6/456	154/20791	1.197e-01	1.878e-01	6	1.78
GO:0006811	ion transport	biological_process	40/456	1433/20791	1.198e-01	1.879e-01	40	1.27

GO:0010008	endosome membrane	cellular_component	10/456	288/20791	1.205e-01	1.889e-01	10	1.58
GO:0046425	regulation of JAK-STAT cascade	biological_process	5/456	123/20791	1.207e-01	1.892e-01	5	1.85
GO:0003705	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity	molecular_function	4/456	93/20791	1.208e-01	1.893e-01	4	1.96
GO:0009408	response to heat	biological_process	4/456	93/20791	1.208e-01	1.893e-01	4	1.96
GO:0036294	cellular response to decreased oxygen levels	biological_process	5/456	124/20791	1.243e-01	1.918e-01	5	1.84
GO:0051603	proteolysis involved in cellular protein catabolic process	biological_process	18/456	580/20791	1.244e-01	1.919e-01	18	1.41
GO:0005813	centrosome	cellular_component	15/456	469/20791	1.247e-01	1.923e-01	15	1.46
GO:0043434	response to peptide hormone	biological_process	12/456	361/20791	1.260e-01	1.943e-01	12	1.52
GO:0042594	response to starvation	biological_process	6/456	156/20791	1.261e-01	1.944e-01	6	1.75
GO:1901653	cellular response to peptide	biological_process	9/456	256/20791	1.265e-01	1.949e-01	9	1.60
GO:0070646	protein modification by small protein removal	biological_process	5/456	125/20791	1.281e-01	1.971e-01	5	1.82
GO:0006937	regulation of muscle contraction	biological_process	5/456	125/20791	1.281e-01	1.971e-01	5	1.82
GO:1901652	response to peptide	biological_process	13/456	398/20791	1.282e-01	1.971e-01	13	1.49
GO:0015297	antiporter activity	molecular_function	4/456	95/20791	1.294e-01	1.989e-01	4	1.92
GO:0014065	phosphatidylinositol 3-kinase signaling	biological_process	4/456	95/20791	1.294e-01	1.989e-01	4	1.92
GO:0030674	protein binding, bridging	molecular_function	4/456	95/20791	1.294e-01	1.989e-01	4	1.92
GO:0090090	negative regulation of canonical Wnt signaling pathway	biological_process	4/456	95/20791	1.294e-01	1.989e-01	4	1.92
GO:0031985	Golgi cisterna	cellular_component	4/456	95/20791	1.294e-01	1.989e-01	4	1.92
GO:0012506	vesicle membrane	cellular_component	12/456	363/20791	1.302e-01	1.993e-01	12	1.51
GO:0000793	condensed chromosome	cellular_component	7/456	190/20791	1.306e-01	1.998e-01	7	1.68
GO:0002573	myeloid leukocyte differentiation	biological_process	7/456	190/20791	1.306e-01	1.998e-01	7	1.68
GO:0043623	cellular protein complex assembly	biological_process	15/456	473/20791	1.320e-01	2.019e-01	15	1.45
GO:0035282	segmentation	biological_process	4/456	96/20791	1.339e-01	2.046e-01	4	1.90
GO:0045211	postsynaptic membrane	cellular_component	7/456	192/20791	1.367e-01	2.065e-01	7	1.66
GO:0060048	cardiac muscle contraction	biological_process	4/456	97/20791	1.384e-01	2.088e-01	4	1.88
GO:0043491	protein kinase B signaling	biological_process	6/456	160/20791	1.397e-01	2.103e-01	6	1.71
GO:0042306	regulation of protein import into nucleus	biological_process	6/456	160/20791	1.397e-01	2.103e-01	6	1.71
GO:0050770	regulation of axonogenesis	biological_process	6/456	160/20791	1.397e-01	2.103e-01	6	1.71
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	biological_process	6/456	160/20791	1.397e-01	2.103e-01	6	1.71
GO:0045665	negative regulation of neuron differentiation	biological_process	7/456	193/20791	1.398e-01	2.102e-01	7	1.65
GO:0050865	regulation of cell activation	biological_process	14/456	441/20791	1.413e-01	2.124e-01	14	1.45
GO:0050804	regulation of synaptic transmission	biological_process	10/456	297/20791	1.420e-01	2.134e-01	10	1.54
GO:0042470	melanosome	cellular_component	4/456	98/20791	1.430e-01	2.149e-01	4	1.86
GO:0051261	protein depolymerization	biological_process	4/456	98/20791	1.430e-01	2.149e-01	4	1.86
GO:0000209	protein polyubiquitination	biological_process	6/456	161/20791	1.432e-01	2.150e-01	6	1.70
GO:0030027	lamellipodium	cellular_component	6/456	161/20791	1.432e-01	2.150e-01	6	1.70
GO:0015718	monocarboxylic acid transport	biological_process	5/456	129/20791	1.436e-01	2.155e-01	5	1.77
GO:0042471	ear morphogenesis	biological_process	5/456	129/20791	1.436e-01	2.155e-01	5	1.77
GO:0052547	regulation of peptidase activity	biological_process	13/456	406/20791	1.447e-01	2.159e-01	13	1.46
GO:0000287	magnesium ion binding	molecular_function	7/456	195/20791	1.462e-01	2.181e-01	7	1.64
GO:0000077	DNA damage checkpoint	biological_process	4/456	99/20791	1.477e-01	2.202e-01	4	1.84

GO:0042391	regulation of membrane potential	biological_process	12/456	371/20791	1.478e-01	2.203e-01	12	1.47
GO:0045765	regulation of angiogenesis	biological_process	7/456	196/20791	1.494e-01	2.196e-01	7	1.63
GO:0051346	negative regulation of hydrolase activity	biological_process	13/456	409/20791	1.513e-01	2.222e-01	13	1.45
GO:0050792	regulation of viral process	biological_process	5/456	131/20791	1.517e-01	2.227e-01	5	1.74
GO:0051051	negative regulation of transport	biological_process	14/456	446/20791	1.517e-01	2.227e-01	14	1.43
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function	4/456	100/20791	1.525e-01	2.234e-01	4	1.82
GO:0044325	ion channel binding	molecular_function	4/456	100/20791	1.525e-01	2.234e-01	4	1.82
GO:0050728	negative regulation of inflammatory response	biological_process	4/456	100/20791	1.525e-01	2.234e-01	4	1.82
GO:0030016	myofibril	cellular_component	7/456	197/20791	1.527e-01	2.235e-01	7	1.62
GO:0006508	proteolysis	biological_process	43/456	1586/20791	1.529e-01	2.237e-01	43	1.24
GO:0009897	external side of plasma membrane	cellular_component	10/456	302/20791	1.549e-01	2.266e-01	10	1.51
GO:0051098	regulation of binding	biological_process	9/456	267/20791	1.559e-01	2.280e-01	9	1.54
GO:0016462	pyrophosphatase activity	molecular_function	23/456	791/20791	1.563e-01	2.284e-01	23	1.33
GO:1903305	regulation of regulated secretory pathway	biological_process	4/456	101/20791	1.574e-01	2.299e-01	4	1.81
GO:0071453	cellular response to oxygen levels	biological_process	5/456	133/20791	1.601e-01	2.333e-01	5	1.71
GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	molecular_function	23/456	794/20791	1.612e-01	2.331e-01	23	1.32
GO:0034622	cellular macromolecular complex assembly	biological_process	23/456	794/20791	1.612e-01	2.331e-01	23	1.32
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	biological_process	4/456	102/20791	1.623e-01	2.344e-01	4	1.79
GO:0048839	inner ear development	biological_process	7/456	200/20791	1.629e-01	2.352e-01	7	1.60
GO:0051896	regulation of protein kinase B signaling	biological_process	5/456	134/20791	1.644e-01	2.373e-01	5	1.70
GO:0006626	protein targeting to mitochondrion	biological_process	5/456	134/20791	1.644e-01	2.373e-01	5	1.70
GO:0016817	hydrolase activity, acting on acid anhydrides	molecular_function	23/456	796/20791	1.645e-01	2.373e-01	23	1.32
GO:0008134	transcription factor binding	molecular_function	17/456	565/20791	1.649e-01	2.378e-01	17	1.37
GO:0010810	regulation of cell-substrate adhesion	biological_process	6/456	167/20791	1.653e-01	2.384e-01	6	1.64
GO:0006457	protein folding	biological_process	6/456	167/20791	1.653e-01	2.384e-01	6	1.64
GO:0042633	hair cycle	biological_process	4/456	103/20791	1.674e-01	2.412e-01	4	1.77
GO:0010811	positive regulation of cell-substrate adhesion	biological_process	4/456	103/20791	1.674e-01	2.412e-01	4	1.77
GO:0019216	regulation of lipid metabolic process	biological_process	9/456	271/20791	1.676e-01	2.414e-01	9	1.51
GO:0031253	cell projection membrane	cellular_component	9/456	271/20791	1.676e-01	2.414e-01	9	1.51
GO:0006694	steroid biosynthetic process	biological_process	5/456	135/20791	1.687e-01	2.422e-01	5	1.69
GO:0002429	immune response-activating cell surface receptor signaling pathway	biological_process	5/456	135/20791	1.687e-01	2.422e-01	5	1.69
GO:0002761	regulation of myeloid leukocyte differentiation	biological_process	4/456	104/20791	1.725e-01	2.475e-01	4	1.75
GO:0006402	mRNA catabolic process	biological_process	4/456	104/20791	1.725e-01	2.475e-01	4	1.75
GO:1900182	positive regulation of protein localization to nucleus	biological_process	4/456	104/20791	1.725e-01	2.475e-01	4	1.75
GO:0031503	protein complex localization	biological_process	4/456	104/20791	1.725e-01	2.475e-01	4	1.75
GO:0002244	hematopoietic progenitor cell differentiation	biological_process	6/456	169/20791	1.731e-01	2.481e-01	6	1.62
GO:0008514	organic anion transmembrane transporter activity	molecular_function	6/456	169/20791	1.731e-01	2.481e-01	6	1.62
GO:0006633	fatty acid biosynthetic process	biological_process	5/456	136/20791	1.732e-01	2.481e-01	5	1.68
GO:0016485	protein processing	biological_process	9/456	273/20791	1.736e-01	2.459e-01	9	1.50
GO:0048871	multicellular organismal homeostasis	biological_process	10/456	309/20791	1.743e-01	2.468e-01	10	1.48
GO:0052548	regulation of endopeptidase activity	biological_process	12/456	382/20791	1.745e-01	2.466e-01	12	1.43

GO:0031090	organelle membrane	cellular_component	67/456	2600/20791	1.765e-01	2.488e-01	67	1.17
GO:0051321	meiotic cell cycle	biological_process	7/456	204/20791	1.770e-01	2.494e-01	7	1.56
GO:0034504	protein localization to nucleus	biological_process	10/456	310/20791	1.771e-01	2.495e-01	10	1.47
GO:0046546	development of primary male sexual characteristics	biological_process	5/456	137/20791	1.776e-01	2.501e-01	5	1.66
GO:0008584	male gonad development	biological_process	5/456	137/20791	1.776e-01	2.501e-01	5	1.66
GO:0046486	glycerolipid metabolic process	biological_process	9/456	275/20791	1.798e-01	2.531e-01	9	1.49
GO:0031398	positive regulation of protein ubiquitination	biological_process	4/456	106/20791	1.829e-01	2.573e-01	4	1.72
GO:0032635	interleukin-6 production	biological_process	4/456	106/20791	1.829e-01	2.573e-01	4	1.72
GO:0005262	calcium channel activity	molecular_function	4/456	106/20791	1.829e-01	2.573e-01	4	1.72
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	biological_process	4/456	106/20791	1.829e-01	2.573e-01	4	1.72
GO:0042493	response to drug	biological_process	15/456	498/20791	1.839e-01	2.584e-01	15	1.37
GO:0032869	cellular response to insulin stimulus	biological_process	6/456	172/20791	1.852e-01	2.598e-01	6	1.59
GO:0044822	poly(A) RNA binding	molecular_function	32/456	1167/20791	1.860e-01	2.608e-01	32	1.25
GO:0005875	microtubule associated complex	cellular_component	5/456	139/20791	1.868e-01	2.599e-01	5	1.64
GO:0019233	sensory perception of pain	biological_process	4/456	107/20791	1.883e-01	2.617e-01	4	1.70
GO:0046824	positive regulation of nucleocytoplasmic transport	biological_process	4/456	107/20791	1.883e-01	2.617e-01	4	1.70
GO:0042098	T cell proliferation	biological_process	6/456	173/20791	1.893e-01	2.630e-01	6	1.58
GO:0030017	sarcomere	cellular_component	6/456	173/20791	1.893e-01	2.630e-01	6	1.58
GO:1903533	regulation of protein targeting	biological_process	9/456	278/20791	1.893e-01	2.630e-01	9	1.48
GO:0033157	regulation of intracellular protein transport	biological_process	11/456	351/20791	1.902e-01	2.640e-01	11	1.43
GO:0006511	ubiquitin-dependent protein catabolic process	biological_process	15/456	501/20791	1.909e-01	2.649e-01	15	1.37
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	molecular_function	5/456	140/20791	1.915e-01	2.657e-01	5	1.63
GO:0015293	symporter activity	molecular_function	5/456	140/20791	1.915e-01	2.657e-01	5	1.63
GO:0019318	hexose metabolic process	biological_process	7/456	208/20791	1.918e-01	2.660e-01	7	1.53
GO:0006869	lipid transport	biological_process	9/456	279/20791	1.925e-01	2.669e-01	9	1.47
GO:0008203	cholesterol metabolic process	biological_process	4/456	108/20791	1.937e-01	2.679e-01	4	1.69
GO:0042472	inner ear morphogenesis	biological_process	4/456	108/20791	1.937e-01	2.679e-01	4	1.69
GO:0090501	RNA phosphodiester bond hydrolysis	biological_process	4/456	108/20791	1.937e-01	2.679e-01	4	1.69
GO:0005996	monosaccharide metabolic process	biological_process	8/456	244/20791	1.950e-01	2.693e-01	8	1.49
GO:0010952	positive regulation of peptidase activity	biological_process	5/456	141/20791	1.962e-01	2.709e-01	5	1.62
GO:0016070	RNA metabolic process	biological_process	102/456	4103/20791	1.968e-01	2.717e-01	102	1.13
GO:0007596	blood coagulation	biological_process	6/456	175/20791	1.977e-01	2.729e-01	6	1.56
GO:0000139	Golgi membrane	cellular_component	15/456	504/20791	1.981e-01	2.733e-01	15	1.36
GO:0001508	action potential	biological_process	4/456	109/20791	1.992e-01	2.748e-01	4	1.67
GO:0060090	binding, bridging	molecular_function	4/456	109/20791	1.992e-01	2.748e-01	4	1.67
GO:0030258	lipid modification	biological_process	6/456	176/20791	2.020e-01	2.760e-01	6	1.55
GO:0008234	cysteine-type peptidase activity	molecular_function	6/456	176/20791	2.020e-01	2.760e-01	6	1.55
GO:0006006	glucose metabolic process	biological_process	6/456	176/20791	2.020e-01	2.760e-01	6	1.55
GO:0061024	membrane organization	biological_process	22/456	779/20791	2.047e-01	2.795e-01	22	1.29
GO:0030705	cytoskeleton-dependent intracellular transport	biological_process	4/456	110/20791	2.048e-01	2.796e-01	4	1.66
GO:0031638	zymogen activation	biological_process	4/456	110/20791	2.048e-01	2.796e-01	4	1.66
GO:0032182	small conjugating protein binding	molecular_function	4/456	110/20791	2.048e-01	2.796e-01	4	1.66

GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	biological_process	4/456	110/20791	2.048e-01	2.796e-01	4	1.66
GO:0015291	secondary active transmembrane transporter activity	molecular_function	8/456	247/20791	2.057e-01	2.805e-01	8	1.48
GO:0008083	growth factor activity	molecular_function	5/456	143/20791	2.058e-01	2.806e-01	5	1.59
GO:0004518	nuclease activity	molecular_function	6/456	177/20791	2.063e-01	2.812e-01	6	1.55
GO:0007599	hemostasis	biological_process	6/456	177/20791	2.063e-01	2.812e-01	6	1.55
GO:0030900	forebrain development	biological_process	12/456	394/20791	2.069e-01	2.819e-01	12	1.39
GO:0019941	modification-dependent protein catabolic process	biological_process	15/456	508/20791	2.079e-01	2.828e-01	15	1.35
GO:0006275	regulation of DNA replication	biological_process	4/456	111/20791	2.105e-01	2.862e-01	4	1.64
GO:0021510	spinal cord development	biological_process	4/456	111/20791	2.105e-01	2.862e-01	4	1.64
GO:0021953	central nervous system neuron differentiation	biological_process	6/456	178/20791	2.107e-01	2.858e-01	6	1.54
GO:1990138	neuron projection extension	biological_process	5/456	144/20791	2.108e-01	2.859e-01	5	1.58
GO:0007259	JAK-STAT cascade	biological_process	5/456	144/20791	2.108e-01	2.859e-01	5	1.58
GO:0072372	primary cilium	cellular_component	6/456	179/20791	2.151e-01	2.889e-01	6	1.53
GO:0045471	response to ethanol	biological_process	5/456	145/20791	2.157e-01	2.896e-01	5	1.57
GO:2000377	regulation of reactive oxygen species metabolic process	biological_process	5/456	145/20791	2.157e-01	2.896e-01	5	1.57
GO:0030031	cell projection assembly	biological_process	11/456	360/20791	2.168e-01	2.910e-01	11	1.39
GO:0010876	lipid localization	biological_process	10/456	323/20791	2.171e-01	2.913e-01	10	1.41
GO:0007586	digestion	biological_process	4/456	113/20791	2.221e-01	2.971e-01	4	1.61
GO:0050777	negative regulation of immune response	biological_process	4/456	113/20791	2.221e-01	2.971e-01	4	1.61
GO:0007411	axon guidance	biological_process	6/456	181/20791	2.241e-01	2.996e-01	6	1.51
GO:0010951	negative regulation of endopeptidase activity	biological_process	8/456	252/20791	2.243e-01	2.998e-01	8	1.45
GO:0005634	nucleus	cellular_component	150/456	6204/20791	2.243e-01	2.998e-01	150	1.10
GO:0051054	positive regulation of DNA metabolic process	biological_process	5/456	147/20791	2.259e-01	3.018e-01	5	1.55
GO:0006612	protein targeting to membrane	biological_process	4/456	114/20791	2.279e-01	3.022e-01	4	1.60
GO:0004197	cysteine-type endopeptidase activity	molecular_function	4/456	114/20791	2.279e-01	3.022e-01	4	1.60
GO:0006413	translational initiation	biological_process	4/456	114/20791	2.279e-01	3.022e-01	4	1.60
GO:0002218	activation of innate immune response	biological_process	4/456	114/20791	2.279e-01	3.022e-01	4	1.60
GO:0016125	sterol metabolic process	biological_process	4/456	114/20791	2.279e-01	3.022e-01	4	1.60
GO:0048593	camera-type eye morphogenesis	biological_process	4/456	114/20791	2.279e-01	3.022e-01	4	1.60
GO:0004867	serine-type endopeptidase inhibitor activity	molecular_function	4/456	114/20791	2.279e-01	3.022e-01	4	1.60
GO:0097485	neuron projection guidance	biological_process	6/456	182/20791	2.287e-01	3.026e-01	6	1.50
GO:0009058	biosynthetic process	biological_process	134/456	5519/20791	2.297e-01	3.033e-01	134	1.11
GO:0006913	nucleocytoplasmic transport	biological_process	13/456	440/20791	2.304e-01	3.042e-01	13	1.35
GO:0002768	immune response-regulating cell surface receptor signaling pathway	biological_process	5/456	148/20791	2.310e-01	3.049e-01	5	1.54
GO:0008654	phospholipid biosynthetic process	biological_process	5/456	148/20791	2.310e-01	3.049e-01	5	1.54
GO:0009266	response to temperature stimulus	biological_process	5/456	148/20791	2.310e-01	3.049e-01	5	1.54
GO:0006820	anion transport	biological_process	15/456	517/20791	2.310e-01	3.049e-01	15	1.32
GO:1900180	regulation of protein localization to nucleus	biological_process	6/456	183/20791	2.333e-01	3.076e-01	6	1.49
GO:0006417	regulation of translation	biological_process	9/456	291/20791	2.338e-01	3.082e-01	9	1.41
GO:0043624	cellular protein complex disassembly	biological_process	4/456	115/20791	2.339e-01	3.082e-01	4	1.59
GO:0034702	ion channel complex	cellular_component	8/456	255/20791	2.359e-01	3.102e-01	8	1.43

GO:0001764	neuron migration	biological_process	5/456	149/20791	2.362e-01	3.105e-01	5	1.53
GO:0046631	alpha-beta T cell activation	biological_process	4/456	116/20791	2.399e-01	3.147e-01	4	1.57
GO:0051169	nuclear transport	biological_process	13/456	444/20791	2.421e-01	3.156e-01	13	1.33
GO:0010821	regulation of mitochondrion organization	biological_process	6/456	185/20791	2.427e-01	3.159e-01	6	1.48
GO:0005543	phospholipid binding	molecular_function	10/456	331/20791	2.441e-01	3.176e-01	10	1.38
GO:0009267	cellular response to starvation	biological_process	4/456	117/20791	2.461e-01	3.201e-01	4	1.56
GO:0043197	dendritic spine	cellular_component	4/456	117/20791	2.461e-01	3.201e-01	4	1.56
GO:0007281	germ cell development	biological_process	8/456	258/20791	2.478e-01	3.219e-01	8	1.41
GO:0009306	protein secretion	biological_process	13/456	446/20791	2.481e-01	3.222e-01	13	1.33
GO:0001078	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	molecular_function	4/456	118/20791	2.522e-01	3.270e-01	4	1.55
GO:0051604	protein maturation	biological_process	9/456	296/20791	2.523e-01	3.271e-01	9	1.39
GO:0044309	neuron spine	cellular_component	4/456	119/20791	2.585e-01	3.325e-01	4	1.53
GO:0009791	post-embryonic development	biological_process	4/456	119/20791	2.585e-01	3.325e-01	4	1.53
GO:0022618	ribonucleoprotein complex assembly	biological_process	6/456	189/20791	2.621e-01	3.370e-01	6	1.45
GO:0050796	regulation of insulin secretion	biological_process	5/456	154/20791	2.632e-01	3.383e-01	5	1.48
GO:0016567	protein ubiquitination	biological_process	19/456	687/20791	2.645e-01	3.399e-01	19	1.26
GO:0007224	smoothened signaling pathway	biological_process	4/456	120/20791	2.648e-01	3.402e-01	4	1.52
GO:0044070	regulation of anion transport	biological_process	4/456	120/20791	2.648e-01	3.402e-01	4	1.52
GO:2001056	positive regulation of cysteine-type endopeptidase activity	biological_process	4/456	120/20791	2.648e-01	3.402e-01	4	1.52
GO:0010977	negative regulation of neuron projection development	biological_process	4/456	120/20791	2.648e-01	3.402e-01	4	1.52
GO:0005623	cell	cellular_component	378/456	16285/20791	2.656e-01	3.407e-01	378	1.06
GO:0005125	cytokine activity	molecular_function	7/456	227/20791	2.714e-01	3.464e-01	7	1.41
GO:0051259	protein oligomerization	biological_process	12/456	415/20791	2.716e-01	3.465e-01	12	1.32
GO:0010001	glial cell differentiation	biological_process	6/456	191/20791	2.720e-01	3.470e-01	6	1.43
GO:0046651	lymphocyte proliferation	biological_process	8/456	264/20791	2.725e-01	3.475e-01	8	1.38
GO:0061351	neural precursor cell proliferation	biological_process	5/456	156/20791	2.743e-01	3.497e-01	5	1.46
GO:0009100	glycoprotein metabolic process	biological_process	10/456	340/20791	2.766e-01	3.526e-01	10	1.34
GO:0015085	calcium ion transmembrane transporter activity	molecular_function	4/456	122/20791	2.777e-01	3.534e-01	4	1.49
GO:0051251	positive regulation of lymphocyte activation	biological_process	7/456	229/20791	2.806e-01	3.567e-01	7	1.39
GO:0010466	negative regulation of peptidase activity	biological_process	8/456	266/20791	2.811e-01	3.573e-01	8	1.37
GO:0032943	mononuclear cell proliferation	biological_process	8/456	266/20791	2.811e-01	3.573e-01	8	1.37
GO:0019439	aromatic compound catabolic process	biological_process	9/456	304/20791	2.835e-01	3.602e-01	9	1.35
GO:0044798	nuclear transcription factor complex	cellular_component	4/456	123/20791	2.842e-01	3.610e-01	4	1.48
GO:0009314	response to radiation	biological_process	12/456	419/20791	2.850e-01	3.619e-01	12	1.31
GO:0061025	membrane fusion	biological_process	5/456	158/20791	2.857e-01	3.604e-01	5	1.44
GO:0044249	cellular biosynthetic process	biological_process	128/456	5330/20791	2.902e-01	3.650e-01	128	1.09
GO:0051494	negative regulation of cytoskeleton organization	biological_process	4/456	124/20791	2.908e-01	3.656e-01	4	1.47
GO:0071222	cellular response to lipopolysaccharide	biological_process	5/456	159/20791	2.915e-01	3.664e-01	5	1.43
GO:0009059	macromolecule biosynthetic process	biological_process	110/456	4551/20791	2.918e-01	3.667e-01	110	1.10
GO:0045088	regulation of innate immune response	biological_process	6/456	195/20791	2.925e-01	3.675e-01	6	1.40

GO:0007126	meiotic nuclear division	biological_process	5/456	160/20791	2.973e-01	3.723e-01	5	1.42
GO:0035051	cardiocyte differentiation	biological_process	4/456	125/20791	2.975e-01	3.724e-01	4	1.46
GO:0071103	DNA conformation change	biological_process	6/456	196/20791	2.977e-01	3.726e-01	6	1.40
GO:0045834	positive regulation of lipid metabolic process	biological_process	4/456	126/20791	3.042e-01	3.787e-01	4	1.45
GO:0032387	negative regulation of intracellular transport	biological_process	4/456	126/20791	3.042e-01	3.787e-01	4	1.45
GO:0006865	amino acid transport	biological_process	4/456	126/20791	3.042e-01	3.787e-01	4	1.45
GO:0046822	regulation of nucleocytoplasmic transport	biological_process	6/456	198/20791	3.083e-01	3.830e-01	6	1.38
GO:0048193	Golgi vesicle transport	biological_process	6/456	198/20791	3.083e-01	3.830e-01	6	1.38
GO:0016358	dendrite development	biological_process	6/456	198/20791	3.083e-01	3.830e-01	6	1.38
GO:0002699	positive regulation of immune effector process	biological_process	5/456	162/20791	3.091e-01	3.838e-01	5	1.41
GO:0016798	hydrolase activity, acting on glycosyl bonds	molecular_function	4/456	127/20791	3.110e-01	3.860e-01	4	1.44
GO:0008509	anion transmembrane transporter activity	molecular_function	8/456	273/20791	3.119e-01	3.871e-01	8	1.34
GO:0048037	cofactor binding	molecular_function	8/456	273/20791	3.119e-01	3.871e-01	8	1.34
GO:0006644	phospholipid metabolic process	biological_process	9/456	311/20791	3.124e-01	3.873e-01	9	1.32
GO:0005764	lysosome	cellular_component	12/456	427/20791	3.130e-01	3.880e-01	12	1.28
GO:0000323	lytic vacuole	cellular_component	12/456	427/20791	3.130e-01	3.880e-01	12	1.28
GO:0048469	cell maturation	biological_process	5/456	163/20791	3.151e-01	3.904e-01	5	1.40
GO:0006401	RNA catabolic process	biological_process	4/456	128/20791	3.178e-01	3.908e-01	4	1.42
GO:0046890	regulation of lipid biosynthetic process	biological_process	4/456	128/20791	3.178e-01	3.908e-01	4	1.42
GO:0031668	cellular response to extracellular stimulus	biological_process	6/456	200/20791	3.191e-01	3.922e-01	6	1.37
GO:0045089	positive regulation of innate immune response	biological_process	5/456	164/20791	3.211e-01	3.945e-01	5	1.39
GO:0016740	transferase activity	molecular_function	56/456	2254/20791	3.213e-01	3.946e-01	56	1.13
GO:0032561	guanyl ribonucleotide binding	molecular_function	11/456	391/20791	3.241e-01	3.980e-01	11	1.28
GO:0030814	regulation of cAMP metabolic process	biological_process	4/456	129/20791	3.247e-01	3.986e-01	4	1.41
GO:0019001	guanyl nucleotide binding	molecular_function	11/456	392/20791	3.280e-01	4.022e-01	11	1.28
GO:0070661	leukocyte proliferation	biological_process	8/456	277/20791	3.303e-01	4.045e-01	8	1.32
GO:0010950	positive regulation of endopeptidase activity	biological_process	4/456	130/20791	3.317e-01	4.042e-01	4	1.40
GO:0045861	negative regulation of proteolysis	biological_process	10/456	355/20791	3.355e-01	4.087e-01	10	1.28
GO:0003723	RNA binding	molecular_function	40/456	1585/20791	3.361e-01	4.094e-01	40	1.15
GO:0006941	striated muscle contraction	biological_process	4/456	131/20791	3.387e-01	4.122e-01	4	1.39
GO:0071219	cellular response to molecule of bacterial origin	biological_process	5/456	167/20791	3.395e-01	4.131e-01	5	1.37
GO:0019867	outer membrane	cellular_component	5/456	167/20791	3.395e-01	4.131e-01	5	1.37
GO:0008233	peptidase activity	molecular_function	18/456	675/20791	3.416e-01	4.155e-01	18	1.22
GO:0005773	vacuole	cellular_component	14/456	517/20791	3.515e-01	4.247e-01	14	1.23
GO:0016051	carbohydrate biosynthetic process	biological_process	5/456	169/20791	3.520e-01	4.252e-01	5	1.35
GO:0021915	neural tube development	biological_process	5/456	170/20791	3.583e-01	4.325e-01	5	1.34
GO:1902495	transmembrane transporter complex	cellular_component	8/456	283/20791	3.588e-01	4.330e-01	8	1.29
GO:0097060	synaptic membrane	cellular_component	7/456	245/20791	3.597e-01	4.335e-01	7	1.30
GO:0016829	lyase activity	molecular_function	5/456	171/20791	3.646e-01	4.377e-01	5	1.33
GO:0006807	nitrogen compound metabolic process	biological_process	144/456	6108/20791	3.673e-01	4.408e-01	144	1.07
GO:0043241	protein complex disassembly	biological_process	4/456	135/20791	3.674e-01	4.408e-01	4	1.35
GO:0015075	ion transmembrane transporter activity	molecular_function	21/456	807/20791	3.692e-01	4.429e-01	21	1.19

GO:0008194	UDP-glycosyltransferase activity	molecular_function	4/456	136/20791	3.747e-01	4.487e-01	4	1.34
GO:0001838	embryonic epithelial tube formation	biological_process	4/456	136/20791	3.747e-01	4.487e-01	4	1.34
GO:0007519	skeletal muscle tissue development	biological_process	5/456	173/20791	3.775e-01	4.497e-01	5	1.32
GO:0032446	protein modification by small protein conjugation	biological_process	19/456	729/20791	3.815e-01	4.539e-01	19	1.19
GO:0072175	epithelial tube formation	biological_process	4/456	137/20791	3.820e-01	4.544e-01	4	1.33
GO:0005777	peroxisome	cellular_component	4/456	137/20791	3.820e-01	4.544e-01	4	1.33
GO:0098656	anion transmembrane transport	biological_process	7/456	250/20791	3.863e-01	4.593e-01	7	1.28
GO:0031225	anchored component of membrane	cellular_component	4/456	138/20791	3.894e-01	4.628e-01	4	1.32
GO:0042129	regulation of T cell proliferation	biological_process	4/456	138/20791	3.894e-01	4.628e-01	4	1.32
GO:0045333	cellular respiration	biological_process	4/456	138/20791	3.894e-01	4.628e-01	4	1.32
GO:0008202	steroid metabolic process	biological_process	7/456	251/20791	3.917e-01	4.646e-01	7	1.27
GO:0048872	homeostasis of number of cells	biological_process	7/456	252/20791	3.971e-01	4.692e-01	7	1.27
GO:0034645	cellular macromolecule biosynthetic process	biological_process	105/456	4429/20791	3.996e-01	4.720e-01	105	1.08
GO:0044255	cellular lipid metabolic process	biological_process	22/456	859/20791	3.997e-01	4.720e-01	22	1.17
GO:0000975	regulatory region DNA binding	molecular_function	20/456	778/20791	4.054e-01	4.776e-01	20	1.17
GO:0097190	apoptotic signaling pathway	biological_process	15/456	573/20791	4.068e-01	4.789e-01	15	1.19
GO:0005525	GTP binding	molecular_function	10/456	373/20791	4.135e-01	4.851e-01	10	1.22
GO:0002696	positive regulation of leukocyte activation	biological_process	7/456	255/20791	4.136e-01	4.851e-01	7	1.25
GO:0055114	oxidation-reduction process	biological_process	25/456	990/20791	4.163e-01	4.877e-01	25	1.15
GO:0016197	endosomal transport	biological_process	6/456	217/20791	4.168e-01	4.882e-01	6	1.26
GO:0007626	locomotory behavior	biological_process	6/456	217/20791	4.168e-01	4.882e-01	6	1.26
GO:0019752	carboxylic acid metabolic process	biological_process	22/456	865/20791	4.172e-01	4.884e-01	22	1.16
GO:0007033	vacuole organization	biological_process	4/456	142/20791	4.195e-01	4.910e-01	4	1.28
GO:0046906	tetrapyrrole binding	molecular_function	5/456	180/20791	4.238e-01	4.939e-01	5	1.27
GO:0000228	nuclear chromosome	cellular_component	12/456	456/20791	4.254e-01	4.955e-01	12	1.20
GO:0046434	organophosphate catabolic process	biological_process	4/456	143/20791	4.272e-01	4.975e-01	4	1.28
GO:0006959	humoral immune response	biological_process	4/456	143/20791	4.272e-01	4.975e-01	4	1.28
GO:0060538	skeletal muscle organ development	biological_process	5/456	181/20791	4.305e-01	5.011e-01	5	1.26
GO:0009615	response to virus	biological_process	9/456	337/20791	4.313e-01	5.019e-01	9	1.22
GO:0005085	guanyl-nucleotide exchange factor activity	molecular_function	5/456	182/20791	4.373e-01	5.082e-01	5	1.25
GO:0008361	regulation of cell size	biological_process	5/456	182/20791	4.373e-01	5.082e-01	5	1.25
GO:0030141	secretory granule	cellular_component	8/456	299/20791	4.397e-01	5.094e-01	8	1.22
GO:0001228	RNA polymerase II transcription regulatory region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	molecular_function	9/456	339/20791	4.412e-01	5.111e-01	9	1.21
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	biological_process	6/456	221/20791	4.413e-01	5.111e-01	6	1.24
GO:0007270	neuron-neuron synaptic transmission	biological_process	4/456	145/20791	4.426e-01	5.122e-01	4	1.26
GO:0048167	regulation of synaptic plasticity	biological_process	4/456	145/20791	4.426e-01	5.122e-01	4	1.26
GO:0046395	carboxylic acid catabolic process	biological_process	5/456	183/20791	4.442e-01	5.138e-01	5	1.25
GO:0005635	nuclear envelope	cellular_component	10/456	380/20791	4.458e-01	5.156e-01	10	1.20
GO:0048511	rhythmic process	biological_process	9/456	340/20791	4.461e-01	5.158e-01	9	1.21
GO:0033218	amide binding	molecular_function	7/456	261/20791	4.473e-01	5.171e-01	7	1.22

GO:0050867	positive regulation of cell activation	biological_process	7/456	264/20791	4.646e-01	5.346e-01	7	1.21
GO:0030073	insulin secretion	biological_process	5/456	187/20791	4.719e-01	5.404e-01	5	1.22
GO:0009755	hormone-mediated signaling pathway	biological_process	5/456	187/20791	4.719e-01	5.404e-01	5	1.22
GO:0032868	response to insulin	biological_process	6/456	226/20791	4.726e-01	5.410e-01	6	1.21
GO:0016853	isomerase activity	molecular_function	4/456	149/20791	4.739e-01	5.424e-01	4	1.22
GO:0046058	cAMP metabolic process	biological_process	4/456	150/20791	4.818e-01	5.507e-01	4	1.22
GO:0019693	ribose phosphate metabolic process	biological_process	12/456	470/20791	4.851e-01	5.543e-01	12	1.16
GO:0042384	cilium assembly	biological_process	5/456	189/20791	4.859e-01	5.551e-01	5	1.21
GO:0043401	steroid hormone mediated signaling pathway	biological_process	4/456	151/20791	4.898e-01	5.579e-01	4	1.21
GO:0007286	spermatid development	biological_process	4/456	151/20791	4.898e-01	5.579e-01	4	1.21
GO:0000982	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity	molecular_function	9/456	350/20791	4.968e-01	5.652e-01	9	1.17
GO:0035148	tube formation	biological_process	4/456	152/20791	4.978e-01	5.663e-01	4	1.20
GO:0050663	cytokine secretion	biological_process	4/456	152/20791	4.978e-01	5.663e-01	4	1.20
GO:0008270	zinc ion binding	molecular_function	27/456	1107/20791	5.076e-01	5.755e-01	27	1.11
GO:0016491	oxidoreductase activity	molecular_function	19/456	768/20791	5.094e-01	5.774e-01	19	1.13
GO:0003924	GTPase activity	molecular_function	6/456	232/20791	5.111e-01	5.792e-01	6	1.18
GO:0097193	intrinsic apoptotic signaling pathway	biological_process	7/456	272/20791	5.116e-01	5.797e-01	7	1.17
GO:0000790	nuclear chromatin	cellular_component	7/456	272/20791	5.116e-01	5.797e-01	7	1.17
GO:0032787	monocarboxylic acid metabolic process	biological_process	14/456	560/20791	5.158e-01	5.838e-01	14	1.14
GO:0009187	cyclic nucleotide metabolic process	biological_process	5/456	194/20791	5.216e-01	5.884e-01	5	1.18
GO:0048515	spermatid differentiation	biological_process	4/456	155/20791	5.219e-01	5.886e-01	4	1.18
GO:0042445	hormone metabolic process	biological_process	4/456	155/20791	5.219e-01	5.886e-01	4	1.18
GO:0006629	lipid metabolic process	biological_process	28/456	1155/20791	5.226e-01	5.891e-01	28	1.11
GO:0006631	fatty acid metabolic process	biological_process	9/456	357/20791	5.334e-01	6.009e-01	9	1.15
GO:0044212	transcription regulatory region DNA binding	molecular_function	19/456	775/20791	5.340e-01	6.014e-01	19	1.12
GO:0003700	sequence-specific DNA binding transcription factor activity	molecular_function	25/456	1031/20791	5.357e-01	6.022e-01	25	1.11
GO:0001071	nucleic acid binding transcription factor activity	molecular_function	25/456	1031/20791	5.357e-01	6.022e-01	25	1.11
GO:0090305	nucleic acid phosphodiester bond hydrolysis	biological_process	5/456	196/20791	5.360e-01	6.023e-01	5	1.16
GO:0005929	cilium	cellular_component	11/456	440/20791	5.364e-01	6.026e-01	11	1.14
GO:0006139	nucleobase-containing compound metabolic process	biological_process	118/456	5106/20791	5.373e-01	6.035e-01	118	1.05
GO:0050708	regulation of protein secretion	biological_process	9/456	358/20791	5.386e-01	6.048e-01	9	1.15
GO:0016758	transferase activity, transferring hexosyl groups	molecular_function	5/456	197/20791	5.433e-01	6.097e-01	5	1.16
GO:0016020	membrane	cellular_component	226/456	9922/20791	5.473e-01	6.138e-01	226	1.04
GO:0022857	transmembrane transporter activity	molecular_function	23/456	950/20791	5.501e-01	6.168e-01	23	1.10
GO:0006650	glycerophospholipid metabolic process	biological_process	5/456	198/20791	5.505e-01	6.171e-01	5	1.15
GO:0043393	regulation of protein binding	biological_process	4/456	159/20791	5.546e-01	6.213e-01	4	1.15
GO:0050714	positive regulation of protein secretion	biological_process	5/456	199/20791	5.578e-01	6.248e-01	5	1.15
GO:0022891	substrate-specific transmembrane transporter activity	molecular_function	21/456	867/20791	5.582e-01	6.251e-01	21	1.10
GO:0002366	leukocyte activation involved in immune response	biological_process	5/456	201/20791	5.725e-01	6.403e-01	5	1.13
GO:0006109	regulation of carbohydrate metabolic process	biological_process	4/456	162/20791	5.793e-01	6.472e-01	4	1.13
GO:0016323	basolateral plasma membrane	cellular_component	5/456	202/20791	5.799e-01	6.477e-01	5	1.13

GO:0002263	cell activation involved in immune response	biological_process	5/456	203/20791	5.873e-01	6.547e-01	5	1.12
GO:0051224	negative regulation of protein transport	biological_process	5/456	203/20791	5.873e-01	6.547e-01	5	1.12
GO:0009636	response to toxic substance	biological_process	5/456	203/20791	5.873e-01	6.547e-01	5	1.12
GO:0045202	synapse	cellular_component	17/456	706/20791	5.937e-01	6.607e-01	17	1.10
GO:0031968	organelle outer membrane	cellular_component	4/456	164/20791	5.959e-01	6.631e-01	4	1.11
GO:0046982	protein heterodimerization activity	molecular_function	12/456	495/20791	5.988e-01	6.657e-01	12	1.11
GO:0006813	potassium ion transport	biological_process	5/456	205/20791	6.021e-01	6.692e-01	5	1.11
GO:0043565	sequence-specific DNA binding	molecular_function	23/456	968/20791	6.095e-01	6.767e-01	23	1.08
GO:0000075	cell cycle checkpoint	biological_process	4/456	166/20791	6.126e-01	6.798e-01	4	1.10
GO:0046483	heterocycle metabolic process	biological_process	120/456	5249/20791	6.131e-01	6.802e-01	120	1.04
GO:0046914	transition metal ion binding	molecular_function	33/456	1405/20791	6.183e-01	6.858e-01	33	1.07
GO:0005975	carbohydrate metabolic process	biological_process	17/456	713/20791	6.212e-01	6.883e-01	17	1.09
GO:0006520	cellular amino acid metabolic process	biological_process	7/456	291/20791	6.285e-01	6.962e-01	7	1.10
GO:0006163	purine nucleotide metabolic process	biological_process	11/456	459/20791	6.290e-01	6.966e-01	11	1.09
GO:0009259	ribonucleotide metabolic process	biological_process	11/456	459/20791	6.290e-01	6.966e-01	11	1.09
GO:0031669	cellular response to nutrient levels	biological_process	4/456	168/20791	6.293e-01	6.967e-01	4	1.09
GO:0004175	endopeptidase activity	molecular_function	12/456	502/20791	6.319e-01	6.991e-01	12	1.09
GO:0006839	mitochondrial transport	biological_process	5/456	210/20791	6.394e-01	7.070e-01	5	1.09
GO:0061136	regulation of proteasomal protein catabolic process	biological_process	5/456	210/20791	6.394e-01	7.070e-01	5	1.09
GO:0050808	synapse organization	biological_process	5/456	211/20791	6.470e-01	7.145e-01	5	1.08
GO:0000151	ubiquitin ligase complex	cellular_component	6/456	253/20791	6.517e-01	7.193e-01	6	1.08
GO:0031965	nuclear membrane	cellular_component	6/456	253/20791	6.517e-01	7.193e-01	6	1.08
GO:0005667	transcription factor complex	cellular_component	8/456	337/20791	6.540e-01	7.216e-01	8	1.08
GO:0006473	protein acetylation	biological_process	4/456	171/20791	6.545e-01	7.220e-01	4	1.07
GO:0020037	heme binding	molecular_function	4/456	172/20791	6.630e-01	7.309e-01	4	1.06
GO:0006725	cellular aromatic compound metabolic process	biological_process	120/456	5285/20791	6.654e-01	7.334e-01	120	1.04
GO:1901360	organic cyclic compound metabolic process	biological_process	124/456	5468/20791	6.715e-01	7.398e-01	124	1.03
GO:0003677	DNA binding	molecular_function	47/456	2041/20791	6.726e-01	7.409e-01	47	1.05
GO:0044782	cilium organization	biological_process	5/456	215/20791	6.771e-01	7.457e-01	5	1.06
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	biological_process	9/456	386/20791	6.923e-01	7.616e-01	9	1.06
GO:0005654	nucleoplasm	cellular_component	55/456	2405/20791	6.950e-01	7.644e-01	55	1.04
GO:0030133	transport vesicle	cellular_component	6/456	260/20791	7.000e-01	7.698e-01	6	1.05
GO:0000987	core promoter proximal region sequence-specific DNA binding	molecular_function	8/456	347/20791	7.137e-01	7.847e-01	8	1.05
GO:0051260	protein homo-oligomerization	biological_process	6/456	262/20791	7.138e-01	7.846e-01	6	1.04
GO:0005215	transporter activity	molecular_function	28/456	1221/20791	7.232e-01	7.948e-01	28	1.05
GO:0001159	core promoter proximal region DNA binding	molecular_function	8/456	349/20791	7.257e-01	7.973e-01	8	1.05
GO:0005882	intermediate filament	cellular_component	4/456	180/20791	7.306e-01	8.026e-01	4	1.01
GO:0031647	regulation of protein stability	biological_process	4/456	180/20791	7.306e-01	8.026e-01	4	1.01
GO:0060271	cilium morphogenesis	biological_process	5/456	223/20791	7.378e-01	8.101e-01	5	1.02
GO:0032993	protein-DNA complex	cellular_component	4/456	181/20791	7.391e-01	8.114e-01	4	1.01
GO:0005198	structural molecule activity	molecular_function	14/456	612/20791	7.431e-01	8.156e-01	14	1.04
GO:0042623	ATPase activity, coupled	molecular_function	7/456	309/20791	7.434e-01	8.158e-01	7	1.03

GO:0043270	positive regulation of ion transport	biological_process	5/456	226/20791	7.607e-01	8.346e-01	5	1.01
GO:0019637	organophosphate metabolic process	biological_process	21/456	931/20791	7.890e-01	8.654e-01	21	1.03
GO:0044262	cellular carbohydrate metabolic process	biological_process	6/456	273/20791	7.904e-01	8.668e-01	6	1.00
GO:0031981	nuclear lumen	cellular_component	69/456	3084/20791	8.096e-01	8.877e-01	69	1.02
GO:0015672	monovalent inorganic cation transport	biological_process	12/456	540/20791	8.176e-01	8.963e-01	12	1.01
GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	cellular_component	18/456	809/20791	8.321e-01	9.120e-01	18	1.01
GO:0005694	chromosome	cellular_component	19/456	854/20791	8.342e-01	9.141e-01	19	1.01
GO:0003676	nucleic acid binding	molecular_function	87/456	3924/20791	8.658e-01	9.485e-01	87	1.01
GO:0008324	cation transmembrane transporter activity	molecular_function	13/456	599/20791	1	1	13	0.99
GO:0007611	learning or memory	biological_process	5/456	230/20791	1	1	5	0.99
GO:0002250	adaptive immune response	biological_process	7/456	321/20791	1	1	7	0.99
GO:0031396	regulation of protein ubiquitination	biological_process	4/456	186/20791	1	1	4	0.98
GO:0045111	intermediate filament cytoskeleton	cellular_component	5/456	233/20791	1	1	5	0.98
GO:0000785	chromatin	cellular_component	10/456	467/20791	1	1	10	0.98
GO:0007565	female pregnancy	biological_process	4/456	187/20791	1	1	4	0.98
GO:0010498	proteasomal protein catabolic process	biological_process	9/456	418/20791	1	1	9	0.98
GO:0005789	endoplasmic reticulum membrane	cellular_component	17/456	794/20791	1	1	17	0.98
GO:0009416	response to light stimulus	biological_process	6/456	283/20791	1	1	6	0.97
GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	molecular_function	7/456	329/20791	1	1	7	0.97
GO:0031301	integral component of organelle membrane	cellular_component	5/456	234/20791	1	1	5	0.97
GO:1901137	carbohydrate derivative biosynthetic process	biological_process	14/456	657/20791	1	1	14	0.97
GO:0042278	purine nucleoside metabolic process	biological_process	6/456	281/20791	1	1	6	0.97
GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	molecular_function	12/456	572/20791	1	1	12	0.96
GO:0009117	nucleotide metabolic process	biological_process	12/456	571/20791	1	1	12	0.96
GO:0042277	peptide binding	molecular_function	5/456	239/20791	1	1	5	0.95
GO:0050803	regulation of synapse structure and activity	biological_process	5/456	239/20791	1	1	5	0.95
GO:0050662	coenzyme binding	molecular_function	4/456	192/20791	1	1	4	0.95
GO:0001012	RNA polymerase II regulatory region DNA binding	molecular_function	12/456	577/20791	1	1	12	0.95
GO:0000976	transcription regulatory region sequence-specific DNA binding	molecular_function	13/456	633/20791	1	1	13	0.94
GO:0008237	metallopeptidase activity	molecular_function	4/456	193/20791	1	1	4	0.94
GO:0006814	sodium ion transport	biological_process	4/456	195/20791	1	1	4	0.94
GO:0001077	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	molecular_function	5/456	242/20791	1	1	5	0.94
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	biological_process	4/456	195/20791	1	1	4	0.94
GO:0006974	cellular response to DNA damage stimulus	biological_process	13/456	637/20791	1	1	13	0.93
GO:0000398	mRNA splicing, via spliceosome	biological_process	4/456	197/20791	1	1	4	0.93
GO:0042742	defense response to bacterium	biological_process	5/456	245/20791	1	1	5	0.93
GO:0044708	single-organism behavior	biological_process	9/456	448/20791	1	1	9	0.92
GO:0000375	RNA splicing, via transesterification reactions	biological_process	4/456	198/20791	1	1	4	0.92

GO:0034976	response to endoplasmic reticulum stress	biological_process	4/456	200/20791	1	1	4	0.91
GO:0046873	metal ion transmembrane transporter activity	molecular_function	8/456	405/20791	1	1	8	0.90
GO:0022890	inorganic cation transmembrane transporter activity	molecular_function	10/456	505/20791	1	1	10	0.90
GO:0021537	telencephalon development	biological_process	5/456	253/20791	1	1	5	0.90
GO:0000988	protein binding transcription factor activity	molecular_function	9/456	456/20791	1	1	9	0.90
GO:2001234	negative regulation of apoptotic signaling pathway	biological_process	4/456	204/20791	1	1	4	0.89
GO:0009116	nucleoside metabolic process	biological_process	6/456	307/20791	1	1	6	0.89
GO:0046390	ribose phosphate biosynthetic process	biological_process	5/456	256/20791	1	1	5	0.89
GO:0006259	DNA metabolic process	biological_process	15/456	769/20791	1	1	15	0.89
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	molecular_function	4/456	205/20791	1	1	4	0.89
GO:0003690	double-stranded DNA binding	molecular_function	14/456	723/20791	1	1	14	0.88
GO:0050890	cognition	biological_process	5/456	259/20791	1	1	5	0.88
GO:0030522	intracellular receptor signaling pathway	biological_process	5/456	262/20791	1	1	5	0.87
GO:1903008	organelle disassembly	biological_process	4/456	210/20791	1	1	4	0.87
GO:0098542	defense response to other organism	biological_process	10/456	523/20791	1	1	10	0.87
GO:0016071	mRNA metabolic process	biological_process	9/456	469/20791	1	1	9	0.87
GO:0005739	mitochondrion	cellular_component	32/456	1682/20791	1	1	32	0.87
GO:0030529	ribonucleoprotein complex	cellular_component	14/456	744/20791	1	1	14	0.86
GO:0031226	intrinsic component of plasma membrane	cellular_component	31/456	1641/20791	1	1	31	0.86
GO:0008380	RNA splicing	biological_process	6/456	319/20791	1	1	6	0.86
GO:0005774	vacuolar membrane	cellular_component	5/456	264/20791	1	1	5	0.86
GO:0005887	integral component of plasma membrane	cellular_component	30/456	1583/20791	1	1	30	0.86
GO:0005765	lysosomal membrane	cellular_component	4/456	215/20791	1	1	4	0.85
GO:0006412	translation	biological_process	11/456	587/20791	1	1	11	0.85
GO:0015267	channel activity	molecular_function	8/456	428/20791	1	1	8	0.85
GO:0016757	transferase activity, transferring glycosyl groups	molecular_function	5/456	271/20791	1	1	5	0.84
GO:0007005	mitochondrion organization	biological_process	11/456	598/20791	1	1	11	0.84
GO:0006518	peptide metabolic process	biological_process	13/456	707/20791	1	1	13	0.84
GO:0051607	defense response to virus	biological_process	5/456	274/20791	1	1	5	0.83
GO:0006914	autophagy	biological_process	7/456	385/20791	1	1	7	0.83
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	biological_process	4/456	220/20791	1	1	4	0.83
GO:0016568	chromatin modification	biological_process	10/456	550/20791	1	1	10	0.83
GO:0051276	chromosome organization	biological_process	17/456	938/20791	1	1	17	0.83
GO:0043043	peptide biosynthetic process	biological_process	11/456	607/20791	1	1	11	0.83
GO:0016570	histone modification	biological_process	7/456	390/20791	1	1	7	0.82
GO:0000989	transcription factor binding transcription factor activity	molecular_function	8/456	452/20791	1	1	8	0.81
GO:0005216	ion channel activity	molecular_function	7/456	394/20791	1	1	7	0.81
GO:0016604	nuclear body	cellular_component	6/456	338/20791	1	1	6	0.81
GO:0006397	mRNA processing	biological_process	7/456	393/20791	1	1	7	0.81
GO:1990234	transferase complex	cellular_component	12/456	686/20791	1	1	12	0.80
GO:0006281	DNA repair	biological_process	7/456	399/20791	1	1	7	0.80

GO:0003712	transcription cofactor activity	molecular_function	7/456	406/20791	1	1	7	0.79
GO:0006486	protein glycosylation	biological_process	4/456	235/20791	1	1	4	0.78
GO:0042113	B cell activation	biological_process	4/456	236/20791	1	1	4	0.77
GO:0009101	glycoprotein biosynthetic process	biological_process	5/456	298/20791	1	1	5	0.77
GO:0009152	purine ribonucleotide biosynthetic process	biological_process	4/456	241/20791	1	1	4	0.76
GO:0070085	glycosylation	biological_process	4/456	244/20791	1	1	4	0.75
GO:0005740	mitochondrial envelope	cellular_component	10/456	606/20791	1	1	10	0.75
GO:0006091	generation of precursor metabolites and energy	biological_process	5/456	305/20791	1	1	5	0.75
GO:0019866	organelle inner membrane	cellular_component	7/456	432/20791	1	1	7	0.74
GO:0006898	receptor-mediated endocytosis	biological_process	4/456	246/20791	1	1	4	0.74
GO:0016021	integral component of membrane	cellular_component	107/456	6631/20791	1	1	107	0.74
GO:0031224	intrinsic component of membrane	cellular_component	110/456	6755/20791	1	1	110	0.74
GO:0031966	mitochondrial membrane	cellular_component	9/456	563/20791	1	1	9	0.73
GO:0006164	purine nucleotide biosynthetic process	biological_process	4/456	249/20791	1	1	4	0.73
GO:0006260	DNA replication	biological_process	4/456	253/20791	1	1	4	0.72
GO:0051186	cofactor metabolic process	biological_process	5/456	321/20791	1	1	5	0.71
GO:0005743	mitochondrial inner membrane	cellular_component	6/456	388/20791	1	1	6	0.71
GO:0016236	macroautophagy	biological_process	4/456	268/20791	1	1	4	0.68
GO:0006325	chromatin organization	biological_process	10/456	668/20791	1	1	10	0.68
GO:0015077	monovalent inorganic cation transmembrane transporter activity	molecular_function	5/456	347/20791	1	1	5	0.66
GO:0006396	RNA processing	biological_process	10/456	702/20791	1	1	10	0.65
GO:0005261	cation channel activity	molecular_function	4/456	287/20791	1	1	4	0.64
GO:0004871	signal transducer activity	molecular_function	36/456	2609/20791	1	1	36	0.63
GO:0009165	nucleotide biosynthetic process	biological_process	4/456	303/20791	1	1	4	0.60
GO:0005730	nucleolus	cellular_component	10/456	812/20791	1	1	10	0.56
GO:0004872	receptor activity	molecular_function	25/456	2555/20791	1	1	25	0.45
GO:0038023	signaling receptor activity	molecular_function	22/456	2355/20791	1	1	22	0.43
GO:0004888	transmembrane signaling receptor activity	molecular_function	21/456	2264/20791	1	1	21	0.42
GO:0050877	neurological system process	biological_process	17/456	1990/20791	1	1	17	0.39
GO:0007186	G-protein coupled receptor signaling pathway	biological_process	19/456	2265/20791	1	1	19	0.38
GO:0007600	sensory perception	biological_process	9/456	1625/20791	1	1	9	0.25
GO:0004930	G-protein coupled receptor activity	molecular_function	6/456	1927/20791	1	1	6	0.14

GO enrichment analysis with DEGs employed three parts including biological process, molecular function and cellular component were performed by clusterProfiler. The details of GO enrichment terms including GO_ID, Description, Type, GeneRatio (the ratio of gene enrichment), BgRatio (background gene ratio), P value, q-value, Count, Genes and Enrich Factor were listed in Table S2, sorted by inverted order with P value.