

Sheet1

GO_Category	genes	nsSNVs	sSNVs	mean rdnsv	sd rdnsv	rdnsv0	rdnsv1
GO:0007169:transmembrane_receptor_tyrosine_kinase_signaling	313	365	636	0.120522	0.0113	0.385	0.072
GO:0007167:enzyme_linked_receptor_protein_signaling_pathway	394	466	771	0.127987	0.0102	0.397	0.095
GO:0006935:chemotaxis	337	405	669	0.136293	0.0104	0.401	0.094
GO:0048812:neuron_projection_morphogenesis	326	445	703	0.13896	0.0114	0.396	0.11
GO:0007409:axonogenesis	303	420	664	0.141014	0.0115	0.397	0.11
GO:0031175:neuron_projection_development	368	510	795	0.143313	0.0109	0.4	0.119
GO:0048667:cell_morphogenesis_involved_in_neuron_differentia	322	446	694	0.145977	0.0118	0.397	0.12
GO:0043005:neuron_projection	411	587	831	0.149634	0.0104	0.484	0.1
GO:0045202:synapse	326	477	633	0.151173	0.0134	0.544	0.089
GO:0048666:neuron_development	436	578	890	0.152631	0.0107	0.399	0.126
GO:0030182:neuron_differentiation	516	667	999	0.153033	0.0098	0.423	0.127
GO:0000904:cell_morphogenesis_involved_in_differentiation	367	543	791	0.155903	0.0113	0.433	0.125
GO:0007268:synaptic_transmission	367	456	698	0.157652	0.0121	0.399	0.155
GO:0048699:generation_of_neurons	664	863	1266	0.161579	0.0083	0.417	0.149
GO:0019226:transmission_of_nerve_impulse	411	503	759	0.163673	0.012	0.394	0.166
GO:0035637:multicellular_organismal_signaling	411	503	759	0.163673	0.012	0.394	0.166
GO:0040011:locomotion	605	872	1180	0.165124	0.0091	0.483	0.125
GO:0030054:cell_junction	412	704	876	0.166789	0.0123	0.577	0.101
GO:0060589:nucleoside-triphosphatase_regulator_activity	325	553	730	0.166863	0.0129	0.499	0.118
GO:0009605:response_to_external_stimulus	703	972	1288	0.167815	0.0091	0.52	0.117
GO:0030695:GTPase_regulator_activity	317	552	723	0.16895	0.013	0.502	0.119
GO:0007267:cell-cell_signaling	568	638	909	0.169132	0.011	0.443	0.147
GO:0022008:neurogenesis	702	948	1346	0.169413	0.0081	0.429	0.154
GO:0001775:cell_activation	350	482	627	0.170157	0.0131	0.51	0.125
GO:0016773:phosphotransferase_activity_alcohol_group_as_acc	577	842	1121	0.173484	0.0112	0.467	0.139
GO:0009719:response_to_endogenous_stimulus	569	692	913	0.175052	0.0116	0.471	0.144
GO:0051056:regulation_of_small_GTPase_mediated_signal_tran	249	479	609	0.176382	0.0158	0.504	0.118
GO:0045859:regulation_of_protein_kinase_activity	360	471	624	0.177153	0.0139	0.499	0.133
GO:0016310:phosphorylation	481	588	837	0.178544	0.0128	0.392	0.156
GO:0048468:cell_development	737	1010	1340	0.178923	0.0098	0.466	0.14
GO:0030001:metal_ion_transport	323	460	634	0.179418	0.014	0.484	0.134
GO:0031399:regulation_of_protein_modification_process	578	715	918	0.18	0.0122	0.493	0.137
GO:0043549:regulation_of_kinase_activity	381	515	676	0.181032	0.0141	0.497	0.139
GO:0001932:regulation_of_protein_phosphorylation	466	585	753	0.181724	0.0134	0.511	0.136
GO:0016477:cell_migration	340	499	633	0.182463	0.0146	0.504	0.154
GO:0004672:protein_kinase_activity	483	722	949	0.183206	0.0127	0.465	0.146
GO:0010646:regulation_of_cell_communication	768	957	1282	0.183792	0.0107	0.453	0.154
GO:0048858:cell_projection_morphogenesis	375	595	790	0.184192	0.0118	0.448	0.161
GO:0032268:regulation_of_cellular_protein_metabolic_process	709	810	1072	0.184493	0.0111	0.452	0.146
GO:0051338:regulation_of_transferase_activity	390	524	679	0.18504	0.0142	0.502	0.143
GO:0010647:positive_regulation_of_cell_communication	379	482	644	0.185201	0.0152	0.451	0.144
GO:0032990:cell_part_morphogenesis	379	597	791	0.18557	0.0118	0.448	0.162
GO:0023056:positive_regulation_of_signaling	381	486	650	0.185964	0.0156	0.456	0.142
GO:0016301:kinase_activity	652	984	1249	0.186251	0.0111	0.488	0.147
GO:0007399:nervous_system_development	1083	1550	1988	0.186352	0.008	0.475	0.172
GO:0006812:cation_transport	390	564	730	0.186553	0.0135	0.507	0.147
GO:0003779:actin_binding	240	511	593	0.186623	0.0167	0.563	0.14

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GO:0007420:brain_development	312	430	572	0.188126	0.0157	0.446	0.212
GO:0010942:positive_regulation_of_cell_death	363	510	624	0.188133	0.0143	0.526	0.171
GO:0043085:positive_regulation_of_catalytic_activity	552	703	926	0.188169	0.0129	0.462	0.151
GO:0008324:cation_transmembrane_transporter_activity	418	585	802	0.188688	0.0128	0.45	0.144
GO:0006915:apoptosis	467	587	776	0.188762	0.0137	0.449	0.146
GO:0070727:cellular_macromolecule_localization	390	522	630	0.189018	0.0149	0.501	0.112
GO:0010604:positive_regulation_of_macromolecule_metabolic_p	903	998	1350	0.18929	0.0114	0.424	0.147
GO:0012501:programmed_cell_death	477	595	788	0.189632	0.0137	0.444	0.146
GO:0042325:regulation_of_phosphorylation	497	648	825	0.189865	0.0134	0.498	0.149
GO:0051674:localization_of_cell	376	613	718	0.189947	0.0134	0.557	0.149
GO:0048870:cell_motility	376	613	718	0.189947	0.0134	0.557	0.149
GO:0019725:cellular_homeostasis	389	487	636	0.189994	0.0139	0.462	0.2
GO:0030030:cell_projection_organization	482	776	1004	0.190529	0.0112	0.453	0.167
GO:0051174:regulation_of_phosphorus_metabolic_process	513	665	842	0.190972	0.0137	0.504	0.151
GO:0019220:regulation_of_phosphate_metabolic_process	513	665	842	0.190972	0.0137	0.504	0.151
GO:0023057:negative_regulation_of_signaling	329	417	591	0.190974	0.015	0.409	0.163
GO:0072359:circulatory_system_development	392	561	775	0.191049	0.0143	0.425	0.162
GO:0072358:cardiovascular_system_development	392	561	775	0.191049	0.0143	0.425	0.162
GO:0010648:negative_regulation_of_cell_communication	329	418	591	0.191081	0.015	0.412	0.163
GO:0006468:protein_phosphorylation	401	511	716	0.1912	0.0133	0.388	0.17
GO:0042995:cell_projection	749	1418	1608	0.19135	0.0089	0.602	0.144
GO:0010557:positive_regulation_of_macromolecule_biosynthetic	643	714	926	0.191482	0.014	0.453	0.152
GO:0044451:nucleoplasm_part	457	456	596	0.191537	0.0165	0.477	0.161
GO:0043065:positive_regulation_of_apoptosis	353	499	594	0.191548	0.0148	0.545	0.172
GO:0043068:positive_regulation_of_programmed_cell_death	354	500	596	0.191668	0.0147	0.545	0.172
GO:0008284:positive_regulation_of_cell_proliferation	388	427	586	0.191713	0.0168	0.412	0.134
GO:0034613:cellular_protein_localization	387	521	621	0.191797	0.0151	0.506	0.113
GO:0061024:membrane_organization	316	535	644	0.191893	0.0141	0.545	0.148
GO:0016044:cellular_membrane_organization	315	535	644	0.191893	0.0141	0.545	0.148
GO:0007417:central_nervous_system_development	428	591	764	0.192519	0.0133	0.468	0.194
GO:0016265:death	566	719	923	0.192707	0.0129	0.456	0.16
GO:0042127:regulation_of_cell_proliferation	686	803	1068	0.193078	0.0122	0.415	0.16
GO:0008219:cell_death	563	719	922	0.193437	0.0129	0.455	0.163
GO:0031325:positive_regulation_of_cellular_metabolic_process	934	1041	1353	0.193644	0.0116	0.439	0.151
GO:0045595:regulation_of_cell_differentiation	553	687	869	0.193818	0.0128	0.488	0.185
GO:0016772:transferase_activity,_transferring_phosphorus-conta	751	1155	1398	0.194148	0.0102	0.501	0.16
GO:0009967:positive_regulation_of_signal_transduction	356	468	594	0.194435	0.0163	0.48	0.15
GO:0007186:G-protein_coupled_receptor_signaling_pathway	385	508	675	0.19452	0.0142	0.456	0.141
GO:0000902:cell_morphogenesis	456	741	937	0.194902	0.0112	0.476	0.167
GO:0015075:ion_transmembrane_transporter_activity	547	853	1114	0.195177	0.0105	0.486	0.148
GO:0009725:response_to_hormone_stimulus	475	609	747	0.195188	0.014	0.493	0.171
GO:0009891:positive_regulation_of_biosynthetic_process	714	796	1022	0.195661	0.013	0.453	0.155
GO:0035556:intracellular_signal_transduction	933	1246	1539	0.196455	0.0093	0.509	0.154
GO:0005216:ion_channel_activity	313	506	690	0.196637	0.0126	0.455	0.139
GO:0009893:positive_regulation_of_metabolic_process	975	1108	1457	0.196734	0.0113	0.432	0.151
GO:0031324:negative_regulation_of_cellular_metabolic_process	653	670	890	0.197214	0.0137	0.403	0.169
GO:0048585:negative_regulation_of_response_to_stimulus	375	483	647	0.197368	0.0146	0.451	0.173
GO:0031328:positive_regulation_of_cellular_biosynthetic_proces	706	794	1012	0.197489	0.0133	0.459	0.156
GO:0022891:substrate-specific_transmembrane_transporter_acti	632	954	1241	0.197576	0.0105	0.489	0.153

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GO:0044092:negative_regulation_of_molecular_function	383	445	584	0.19871	0.0165	0.426	0.173
GO:0023051:regulation_of_signaling	1119	1584	1980	0.198962	0.0091	0.483	0.164
GO:0004674:protein_serine/threonine_kinase_activity	335	503	599	0.199132	0.0147	0.525	0.161
GO:0051246:regulation_of_protein_metabolic_process	795	962	1216	0.199198	0.0107	0.463	0.162
GO:0009966:regulation_of_signal_transduction	960	1394	1736	0.200048	0.0098	0.488	0.16
GO:0022838:substrate-specific_channel_activity	321	520	702	0.200089	0.0128	0.463	0.142
GO:0044093:positive_regulation_of_molecular_function	649	824	1033	0.200122	0.0126	0.485	0.159
GO:0065008:regulation_of_biological_quality	1392	2000	2390	0.200235	0.0076	0.511	0.181
GO:0019899:enzyme_binding	588	887	1023	0.200511	0.0121	0.534	0.161
GO:0010605:negative_regulation_of_macromolecule_metabolic_	668	704	919	0.200531	0.0146	0.414	0.165
GO:0071822:protein_complex_subunit_organization	418	529	670	0.200659	0.0169	0.467	0.175
GO:0009892:negative_regulation_of_metabolic_process	713	736	969	0.200827	0.0137	0.403	0.171
GO:0015267:channel_activity	332	533	710	0.201019	0.0128	0.474	0.141
GO:0022803:passive_transmembrane_transporter_activity	332	533	710	0.201019	0.0128	0.474	0.141
GO:0010941:regulation_of_cell_death	762	986	1184	0.201134	0.0115	0.514	0.162
GO:0070271:protein_complex_biogenesis	347	504	623	0.201332	0.0171	0.488	0.175
GO:0006928:cellular_component_movement	532	920	1050	0.201386	0.0124	0.56	0.141
GO:0006793:phosphorus_metabolic_process	577	758	997	0.201441	0.0129	0.412	0.183
GO:0006796:phosphate-containing_compound_metabolic_proces	577	758	997	0.201441	0.0129	0.412	0.183
GO:0008092:cytoskeletal_protein_binding	400	767	857	0.201502	0.0136	0.541	0.166
GO:0050878:regulation_of_body_fluid_levels	394	524	704	0.201524	0.0145	0.429	0.197
GO:0005829:cytosol	1418	1788	2228	0.201573	0.0079	0.465	0.174
GO:0007166:cell_surface_receptor_linked_signaling_pathway	1190	1659	2128	0.201971	0.0084	0.446	0.168
GO:0051173:positive_regulation_of_nitrogen_compound_metabo	671	733	938	0.201979	0.0139	0.444	0.158
GO:0007010:cytoskeleton_organization	374	658	757	0.202404	0.0146	0.537	0.17
GO:0043067:regulation_of_programmed_cell_death	739	953	1138	0.202407	0.0116	0.519	0.165
GO:0006461:protein_complex_assembly	345	503	621	0.202427	0.0172	0.488	0.176
GO:0051254:positive_regulation_of_RNA_metabolic_process	594	630	817	0.202828	0.0151	0.44	0.165
GO:0042981:regulation_of_apoptosis	733	946	1126	0.202993	0.0117	0.52	0.165
GO:0045935:positive_regulation_of_nucleobase-containing_comf	655	716	917	0.203097	0.0142	0.444	0.161
GO:0007599:hemostasis	334	462	619	0.204117	0.015	0.413	0.21
GO:0051172:negative_regulation_of_nitrogen_compound_metabr	487	518	660	0.204261	0.0153	0.437	0.174
GO:0007596:blood_coagulation	331	461	615	0.204366	0.015	0.415	0.21
GO:0050817:coagulation	331	461	615	0.204366	0.015	0.415	0.21
GO:0051049:regulation_of_transport	540	718	889	0.204599	0.0138	0.481	0.153
GO:0022892:substrate-specific_transporter_activity	742	1178	1446	0.204718	0.01	0.531	0.158
GO:0051094:positive_regulation_of_developmental_process	390	486	590	0.204832	0.0158	0.513	0.165
GO:0042060:wound_healing	408	599	747	0.206088	0.0136	0.465	0.202
GO:0065003:macromolecular_complex_assembly	464	632	771	0.206849	0.0153	0.476	0.167
GO:0032989:cellular_component_morphogenesis	490	809	985	0.206885	0.0118	0.493	0.177
GO:0032879:regulation_of_localization	742	1083	1305	0.207358	0.0119	0.488	0.178
GO:0045934:negative_regulation_of_nucleobase-containing_com	482	514	650	0.207878	0.0155	0.437	0.175
GO:0042592:homeostatic_process	646	925	1076	0.208832	0.0113	0.531	0.181
GO:0006357:regulation_of_transcription_from_RNA_polymerase_	652	658	837	0.208942	0.0149	0.452	0.169
GO:0046907:intracellular_transport	508	691	782	0.209389	0.0131	0.531	0.14
GO:0048878:chemical_homeostasis	450	625	759	0.209576	0.0147	0.501	0.196
GO:0051253:negative_regulation_of_RNA_metabolic_process	450	471	605	0.20991	0.0163	0.427	0.177
GO:2000113:negative_regulation_of_cellular_macromolecule_bio	483	506	642	0.209948	0.0174	0.426	0.183
GO:0048523:negative_regulation_of_cellular_process	1545	1956	2411	0.209978	0.0091	0.463	0.183

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GO:0010629:negative_regulation_of_gene_expression	483	509	661	0.210373	0.0164	0.413	0.178
GO:0045893:positive_regulation_of_transcription,_DNA-depende	566	619	778	0.210427	0.016	0.449	0.17
GO:0022857:transmembrane_transporter_activity	700	1099	1343	0.21087	0.0105	0.521	0.166
GO:0055086:nucleobase-containing_small_molecule_metabolic_	397	495	572	0.2109	0.0185	0.519	0.168
GO:0031327:negative_regulation_of_cellular_biosynthetic_proces	518	540	685	0.210986	0.0167	0.423	0.183
GO:0043933:macromolecular_complex_subunit_organization	564	709	864	0.211059	0.0153	0.467	0.177
GO:0000267:cell_fraction	811	1328	1538	0.211105	0.0098	0.552	0.174
GO:0006811:ion_transport	591	979	1205	0.211152	0.0109	0.51	0.162
GO:0006996:organelle_organization	1078	1604	1810	0.211289	0.0095	0.538	0.172
GO:0005626:insoluble_fraction	610	1085	1246	0.211392	0.0108	0.565	0.169
GO:0045892:negative_regulation_of_transcription,_DNA-depende	440	458	592	0.212085	0.0166	0.415	0.182
GO:0009890:negative_regulation_of_biosynthetic_process	529	555	696	0.212097	0.0167	0.429	0.181
GO:0005654:nucleoplasm	855	971	1180	0.212153	0.0118	0.479	0.175
GO:0050790:regulation_of_catalytic_activity	866	1151	1383	0.212214	0.0118	0.493	0.17
GO:0031975:envelope	507	639	748	0.212384	0.0168	0.479	0.176
GO:0051641:cellular_localization	846	1266	1402	0.212522	0.0098	0.543	0.164
GO:0030234:enzyme_regulator_activity	648	1002	1153	0.212706	0.0115	0.534	0.161
GO:0016070:RNA_metabolic_process	822	935	1055	0.212885	0.0137	0.557	0.171
GO:0006464:protein_modification_process	1116	1478	1779	0.212917	0.009	0.47	0.182
GO:0044267:cellular_protein_metabolic_process	1558	1965	2291	0.213473	0.008	0.497	0.18
GO:0050793:regulation_of_developmental_process	787	1075	1278	0.213508	0.0109	0.503	0.202
GO:0065009:regulation_of_molecular_function	1063	1375	1631	0.213999	0.0102	0.503	0.175
GO:0048522:positive_regulation_of_cellular_process	1750	2222	2666	0.214074	0.0087	0.484	0.174
GO:0051276:chromosome_organization	380	577	600	0.214198	0.0172	0.628	0.174
GO:0048518:positive_regulation_of_biological_process	1927	2471	2939	0.214277	0.0083	0.49	0.183
GO:0010558:negative_regulation_of_macromolecule_biosynthetic	503	537	670	0.214311	0.0173	0.434	0.183
GO:0005624:membrane_fraction	587	1067	1225	0.21492	0.011	0.56	0.174
GO:2000026:regulation_of_multicellular_organismal_developmen	617	772	957	0.215249	0.0125	0.476	0.209
GO:0016043:cellular_component_organization	2173	3361	3861	0.215321	0.0068	0.519	0.186
GO:0071842:cellular_component_organization_at_cellular_level	1765	2680	3055	0.215434	0.0073	0.52	0.183
GO:0044431:Golgi_apparatus_part	409	491	596	0.215459	0.0169	0.456	0.179
GO:0009057:macromolecule_catabolic_process	377	494	540	0.215998	0.0187	0.533	0.208
GO:0051336:regulation_of_hydrolase_activity	416	536	675	0.216314	0.0157	0.453	0.161
GO:0030554:adenyl_nucleotide_binding	1172	2292	2444	0.216788	0.0085	0.602	0.172
GO:0032559:adenyl_ribonucleotide_binding	1165	2290	2439	0.21689	0.0085	0.603	0.171
GO:0016023:cytoplasmic_membrane-bounded_vesicle	498	786	898	0.216929	0.0151	0.551	0.192
GO:0007154:cell_communication	2634	3667	4325	0.217105	0.0062	0.501	0.179
GO:0019904:protein_domain_specific_binding	324	504	597	0.217243	0.0151	0.495	0.164
GO:0048519:negative_regulation_of_biological_process	1705	2196	2655	0.217574	0.0089	0.469	0.186
GO:0044463:cell_projection_part	391	799	836	0.217609	0.0134	0.637	0.185
GO:0048583:regulation_of_response_to_stimulus	1288	1858	2220	0.21818	0.0087	0.486	0.195
GO:0046483:heterocycle_metabolic_process	484	655	714	0.218251	0.0157	0.568	0.191
GO:0007165:signal_transduction	2245	3141	3689	0.218292	0.0067	0.5	0.177
GO:0043412:macromolecule_modification	1187	1611	1882	0.218371	0.0092	0.486	0.184
GO:0023052:signaling	2530	3537	4163	0.218855	0.0064	0.496	0.182
GO:0043234:protein_complex	2051	2948	3312	0.218863	0.0084	0.525	0.186
GO:0071310:cellular_response_to_organic_substance	543	687	815	0.218995	0.014	0.473	0.229
GO:0008283:cell_proliferation	321	495	551	0.219151	0.0182	0.597	0.148
GO:0032553:ribonucleotide_binding	1433	2560	2758	0.219178	0.0079	0.589	0.173

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GO:0032555:purine_ribonucleotide_binding	1432	2559	2757	0.219185	0.0079	0.589	0.173
GO:0017076:purine_nucleotide_binding	1441	2566	2763	0.219372	0.0079	0.589	0.173
GO:0005524:ATP_binding	1145	2254	2399	0.219975	0.0087	0.598	0.175
GO:0005215:transporter_activity	912	1497	1739	0.220082	0.0094	0.554	0.173
GO:0051128:regulation_of_cellular_component_organization	662	967	1088	0.22018	0.0132	0.522	0.191
GO:0031410:cytoplasmic_vesicle	531	841	951	0.220713	0.0148	0.552	0.192
GO:0051649:establishment_of_localization_in_cell	718	1057	1142	0.220887	0.0119	0.554	0.161
GO:0010628:positive_regulation_of_gene_expression	604	677	856	0.22089	0.0155	0.432	0.173
GO:0035639:purine_ribonucleoside_triphosphate_binding	1409	2514	2712	0.220916	0.008	0.584	0.175
GO:0051726:regulation_of_cell_cycle	453	608	673	0.221173	0.0188	0.5	0.179
GO:0031967:organelle_envelope	496	611	695	0.221443	0.0179	0.484	0.185
GO:0071841:cellular_component_organization_or_biogenesis_at	1826	2817	3153	0.22161	0.0071	0.526	0.186
GO:0010033:response_to_organic_substance	996	1332	1528	0.222207	0.0104	0.514	0.201
GO:0071840:cellular_component_organization_or_biogenesis	2249	3522	3972	0.222241	0.0067	0.525	0.19
GO:0048731:system_development	2046	3090	3614	0.222675	0.0067	0.498	0.205
GO:0016192:vesicle-mediated_transport	484	782	860	0.222896	0.0135	0.579	0.183
GO:0031988:membrane-bounded_vesicle	509	812	922	0.223037	0.0149	0.549	0.196
GO:0031982:vesicle	554	890	996	0.224303	0.0142	0.563	0.192
GO:0030154:cell_differentiation	1457	2117	2537	0.224457	0.0073	0.475	0.211
GO:0042623:ATPase_activity,_coupled	221	501	526	0.224688	0.0205	0.573	0.192
GO:0032991:macromolecular_complex	2450	3393	3738	0.224789	0.0078	0.537	0.19
GO:0051179:localization	2410	3777	4179	0.224922	0.0069	0.555	0.185
GO:0010467:gene_expression	906	1018	1114	0.225655	0.0129	0.575	0.173
GO:0051239:regulation_of_multicellular_organismal_process	1025	1334	1616	0.225808	0.0101	0.462	0.211
GO:0000166:nucleotide_binding	1822	3033	3227	0.226313	0.0083	0.582	0.18
GO:0070887:cellular_response_to_chemical_stimulus	782	1004	1134	0.227288	0.0121	0.535	0.214
GO:0055085:transmembrane_transport	527	879	1033	0.227346	0.0132	0.527	0.195
GO:0008104:protein_localization	715	1088	1174	0.227617	0.0128	0.535	0.185
GO:0016740:transferase_activity	1386	2043	2261	0.227651	0.009	0.541	0.194
GO:0003700:sequence-specific_DNA_binding_transcription_factc	665	584	739	0.228105	0.0173	0.452	0.169
GO:0001071:nucleic_acid_binding_transcription_factor_activity	667	585	741	0.228318	0.0172	0.452	0.168
GO:0051716:cellular_response_to_stimulus	2814	4085	4502	0.229533	0.0064	0.539	0.191
GO:0009611:response_to_wounding	623	922	1075	0.23078	0.0123	0.5	0.197
GO:0051234:establishment_of_localization	2011	3049	3399	0.23107	0.0076	0.539	0.192
GO:0046983:protein_dimerization_activity	476	621	665	0.231154	0.0186	0.582	0.185
GO:0005794:Golgi_apparatus	690	914	1054	0.231344	0.0119	0.471	0.215
GO:0019538:protein_metabolic_process	1950	2700	2978	0.231454	0.0077	0.531	0.201
GO:0006810:transport	1981	2985	3339	0.231589	0.0076	0.537	0.193
GO:0031981:nuclear_lumen	1488	1974	2157	0.232298	0.0092	0.547	0.198
GO:0042221:response_to_chemical_stimulus	1689	2394	2696	0.232877	0.0087	0.531	0.206
GO:0044428:nuclear_part	1682	2230	2439	0.232908	0.0088	0.538	0.196
GO:0003008:system_process	983	1520	1731	0.233115	0.0107	0.52	0.221
GO:0012505:endomembrane_system	1038	1410	1562	0.233675	0.0113	0.523	0.213
GO:0009059:macromolecule_biosynthetic_process	857	1131	1119	0.233921	0.0146	0.638	0.177
GO:0048584:positive_regulation_of_response_to_stimulus	568	760	893	0.234049	0.015	0.466	0.238
GO:0007275:multicellular_organismal_development	2438	3758	4242	0.23469	0.0067	0.509	0.214
GO:0042802:identical_protein_binding	480	598	681	0.23482	0.0185	0.529	0.191
GO:0048513:organ_development	1445	2145	2453	0.234858	0.009	0.501	0.216
GO:0051171:regulation_of_nitrogen_compound_metabolic_proce	2191	2625	3026	0.235373	0.0081	0.477	0.201

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GO:0009653:anatomical_structure_morphogenesis	1120	1728	2039	0.235593	0.0097	0.468	0.209
GO:0048869:cellular_developmental_process	1503	2262	2624	0.235675	0.0075	0.488	0.221
GO:0048856:anatomical_structure_development	2263	3473	3946	0.235684	0.0067	0.498	0.219
GO:0005730:nucleolus	748	1047	1118	0.236454	0.0124	0.567	0.194
GO:0009790:embryo_development	530	714	808	0.236583	0.0173	0.49	0.189
GO:0044260:cellular_macromolecule_metabolic_process	2621	3657	3792	0.236643	0.0075	0.571	0.199
GO:0031323:regulation_of_cellular_metabolic_process	2703	3252	3741	0.23721	0.0074	0.475	0.203
GO:0022607:cellular_component_assembly	729	1138	1268	0.237565	0.0133	0.51	0.199
GO:0031090:organelle_membrane	1387	1767	1934	0.237624	0.0109	0.531	0.202
GO:0045184:establishment_of_protein_localization	566	811	874	0.23803	0.0154	0.516	0.193
GO:0033036:macromolecule_localization	859	1415	1439	0.238077	0.0115	0.592	0.195
GO:0034645:cellular_macromolecule_biosynthetic_process	840	1107	1087	0.238483	0.015	0.636	0.182
GO:0050794:regulation_of_cellular_process	4960	6866	7585	0.238704	0.0054	0.519	0.199
GO:0080090:regulation_of_primary_metabolic_process	2680	3295	3752	0.239051	0.0073	0.483	0.203
GO:0019219:regulation_of_nucleobase-containing_compound_m	2141	2584	2951	0.239358	0.0083	0.482	0.204
GO:0060255:regulation_of_macromolecule_metabolic_process	2562	3114	3560	0.23973	0.0078	0.481	0.204
GO:0065007:biological_regulation	5554	7945	8623	0.239733	0.0052	0.532	0.203
GO:0007155:cell_adhesion	464	1100	1213	0.240373	0.0123	0.545	0.222
GO:0022610:biological_adhesion	464	1100	1213	0.240373	0.0123	0.545	0.222
GO:0009628:response_to_abiotic_stimulus	370	609	625	0.240543	0.0174	0.624	0.21
GO:0005515:protein_binding	4128	6043	6474	0.240993	0.0056	0.544	0.206
GO:0015031:protein_transport	557	793	847	0.241062	0.0156	0.523	0.197
GO:0044429:mitochondrial_part	453	546	542	0.241774	0.0195	0.615	0.177
GO:0005634:nucleus	3650	4751	5028	0.241798	0.0066	0.552	0.198
GO:0005102:receptor_binding	739	979	1022	0.241871	0.014	0.572	0.218
GO:0070013:intracellular_organelle_lumen	1734	2356	2498	0.242056	0.0096	0.564	0.202
GO:0050789:regulation_of_biological_process	5255	7414	8072	0.242179	0.0054	0.525	0.203
GO:0050877:neurological_system_process	755	1149	1296	0.242368	0.012	0.515	0.239
GO:0032501:multicellular_organismal_process	3362	5273	5854	0.242856	0.0061	0.517	0.221
GO:0009889:regulation_of_biosynthetic_process	2125	2567	2914	0.243318	0.0089	0.479	0.212
GO:0006508:proteolysis	588	920	951	0.243395	0.0148	0.589	0.206
GO:0032502:developmental_process	2662	4097	4565	0.243491	0.0066	0.505	0.226
GO:0031974:membrane-enclosed_lumen	1784	2449	2584	0.243969	0.0096	0.564	0.206
GO:0006139:nucleobase-containing_compound_metabolic_proce	1616	2225	2224	0.2442	0.0104	0.607	0.198
GO:0044459:plasma_membrane_part	1296	2358	2625	0.244269	0.0086	0.53	0.219
GO:0031326:regulation_of_cellular_biosynthetic_process	2109	2539	2884	0.244398	0.0091	0.476	0.214
GO:0043233:organelle_lumen	1757	2427	2561	0.244423	0.0096	0.565	0.206
GO:0019222:regulation_of_metabolic_process	2965	3718	4160	0.244557	0.0071	0.491	0.207
GO:0044444:cytoplasmic_part	4151	5736	6037	0.245252	0.0063	0.56	0.205
GO:0010556:regulation_of_macromolecule_biosynthetic_process	1991	2390	2703	0.246205	0.0093	0.476	0.217
GO:0044085:cellular_component_biogenesis	816	1285	1391	0.24838	0.0124	0.518	0.204
GO:0034641:cellular_nitrogen_compound_metabolic_process	1931	2677	2678	0.248763	0.0097	0.601	0.209
GO:0043170:macromolecule_metabolic_process	3074	4495	4572	0.248833	0.0072	0.582	0.211
GO:2000112:regulation_of_cellular_macromolecule_biosynthetic_	1951	2336	2631	0.249026	0.0096	0.476	0.22
GO:0044237:cellular_metabolic_process	3947	5532	5717	0.249179	0.0065	0.564	0.214
GO:0009987:cellular_process	7681	11623	12113	0.249603	0.0044	0.566	0.211
GO:0009058:biosynthetic_process	1455	1959	1977	0.250098	0.0113	0.59	0.213
GO:0051252:regulation_of_RNA_metabolic_process	1872	2211	2491	0.250145	0.0093	0.478	0.222
GO:2001141:regulation_of_RNA_biosynthetic_process	1835	2184	2461	0.250468	0.0096	0.476	0.223

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GO:0044446:intracellular_organelle_part	3893	5466	5689	0.250566	0.0067	0.56	0.208
GO:0016887:ATPase_activity	281	776	712	0.250663	0.0175	0.698	0.2
GO:0010468:regulation_of_gene_expression	2059	2467	2784	0.250936	0.0093	0.476	0.218
GO:0044249:cellular_biosynthetic_process	1385	1828	1854	0.251064	0.0117	0.58	0.217
GO:0016817:hydrolase_activity_acting_on_acid_anhydrides	619	1325	1282	0.251066	0.0135	0.631	0.207
GO:0016462:pyrophosphatase_activity	613	1325	1279	0.251238	0.0135	0.634	0.207
GO:0016818:hydrolase_activity_acting_on_acid_anhydrides_in	616	1325	1279	0.251238	0.0135	0.634	0.207
GO:0005783:endoplasmic_reticulum	716	1036	1004	0.251474	0.0134	0.662	0.189
GO:0044248:cellular_catabolic_process	785	1108	1160	0.25198	0.0141	0.529	0.236
GO:0006355:regulation_of_transcription_DNA-dependent	1824	2183	2450	0.252119	0.0096	0.477	0.225
GO:0043228:non-membrane-bounded_organelle	2236	3592	3657	0.253155	0.008	0.572	0.216
GO:0043232:intracellular_non-membrane-bounded_organelle	2236	3592	3657	0.253155	0.008	0.572	0.216
GO:0016874:ligase_activity	334	511	538	0.253245	0.0205	0.54	0.228
GO:0009887:organ_morphogenesis	484	687	773	0.2533	0.0167	0.485	0.211
GO:0044422:organelle_part	3948	5626	5828	0.253338	0.0068	0.563	0.212
GO:0005856:cytoskeleton	1142	2143	2195	0.253416	0.0112	0.558	0.221
GO:0006807:nitrogen_compound_metabolic_process	2017	2829	2806	0.253549	0.0096	0.607	0.217
GO:0005737:cytoplasm	5695	8116	8373	0.254054	0.0055	0.565	0.21
GO:0017111:nucleoside-triphosphatase_activity	589	1295	1246	0.254382	0.0137	0.627	0.213
GO:0043231:intracellular_membrane-bounded_organelle	5940	8092	8225	0.255142	0.0056	0.575	0.212
GO:0043227:membrane-bounded_organelle	5945	8099	8234	0.255291	0.0056	0.575	0.212
GO:0044238:primary_metabolic_process	4098	6023	6096	0.255464	0.0068	0.579	0.221
GO:0048646:anatomical_structure_formation_involved_in_morph	393	626	695	0.257011	0.0189	0.506	0.228
GO:0071844:cellular_component_assembly_at_cellular_level	528	874	893	0.257216	0.0159	0.554	0.219
GO:0044424:intracellular_part	7869	11080	11205	0.257478	0.0049	0.579	0.213
GO:0005622:intracellular	8231	11661	11781	0.257763	0.0049	0.581	0.212
GO:0043229:intracellular_organelle	6692	9419	9502	0.257892	0.0055	0.577	0.215
GO:0043226:organelle	6700	9432	9516	0.257978	0.0055	0.577	0.215
GO:0002376:immune_system_process	885	1169	1261	0.258273	0.0138	0.494	0.249
GO:0008152:metabolic_process	4604	6735	6780	0.259408	0.0063	0.579	0.224
GO:0005975:carbohydrate_metabolic_process	451	737	724	0.260228	0.0188	0.581	0.213
GO:0005887:integral_to_plasma_membrane	762	1341	1519	0.260415	0.0122	0.49	0.234
GO:0031226:intrinsic_to_plasma_membrane	788	1374	1549	0.260551	0.012	0.496	0.233
GO:0090304:nucleic_acid_metabolic_process	1234	1755	1647	0.260817	0.0128	0.645	0.216
GO:0044281:small_molecule_metabolic_process	1272	1944	1922	0.261145	0.0108	0.619	0.229
GO:0009888:tissue_development	672	1054	1174	0.261508	0.0127	0.474	0.261
GO:0009056:catabolic_process	962	1393	1404	0.261989	0.0134	0.558	0.251
GO:0003723:RNA_binding	546	577	623	0.262546	0.0244	0.506	0.216
GO:0046872:metal_ion_binding	2833	4823	4742	0.26318	0.0065	0.61	0.223
GO:0022414:reproductive_process	741	1144	1098	0.26427	0.0141	0.623	0.217
GO:0000278:mitotic_cell_cycle	363	522	592	0.264822	0.0201	0.414	0.265
GO:0071702:organic_substance_transport	272	567	544	0.264906	0.0174	0.624	0.284
GO:0000003:reproduction	744	1146	1104	0.265257	0.0141	0.616	0.218
GO:0005488:binding	8391	12913	12759	0.266124	0.0046	0.594	0.225
GO:0044432:endoplasmic_reticulum_part	481	681	657	0.26626	0.0178	0.639	0.225
GO:0043167:ion_binding	2876	4916	4809	0.266348	0.0065	0.611	0.225
GO:0043169:cation_binding	2870	4910	4797	0.267127	0.0066	0.611	0.225
GO:0042175:nuclear_outer_membrane-endoplasmic_reticulum_n	445	614	598	0.267346	0.0196	0.621	0.24
GO:0005789:endoplasmic_reticulum_membrane	431	597	579	0.267848	0.0199	0.631	0.235

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GO:0003824:catalytic_activity	4151	6849	6751	0.268096	0.006	0.592	0.238
GO:0005739:mitochondrion	980	1169	1117	0.268658	0.0155	0.613	0.21
GO:0044430:cytoskeletal_part	835	1596	1605	0.269157	0.0133	0.562	0.236
GO:0006066:alcohol_metabolic_process	312	526	502	0.269607	0.0208	0.606	0.248
GO:0003676:nucleic_acid_binding	2365	3028	3001	0.269625	0.0097	0.575	0.224
GO:0080134:regulation_of_response_to_stress	390	538	582	0.271493	0.0197	0.479	0.334
GO:0003677:DNA_binding	1595	2062	2025	0.272903	0.0116	0.571	0.244
GO:0007049:cell_cycle	670	1052	1066	0.273023	0.015	0.521	0.23
GO:0009986:cell_surface	282	483	519	0.274604	0.0188	0.516	0.235
GO:0006950:response_to_stress	1611	2375	2401	0.27478	0.0108	0.547	0.266
GO:0002682:regulation_of_immune_system_process	489	611	686	0.276352	0.0179	0.421	0.342
GO:0007017:microtubule-based_process	217	534	492	0.277274	0.0217	0.617	0.236
GO:0008270:zinc_ion_binding	1489	2345	2202	0.27741	0.0101	0.63	0.225
GO:0004175:endorpeptidase_activity	303	522	527	0.278657	0.0193	0.582	0.262
GO:0070011:peptidase_activity_acting_on_L-amino_acid_peptidi	433	763	739	0.279801	0.0163	0.632	0.249
GO:0055114:oxidation-reduction_process	402	608	580	0.280096	0.0224	0.604	0.247
GO:0008233:peptidase_activity	457	800	762	0.280242	0.016	0.653	0.24
GO:0006974:response_to_DNA_damage_stimulus	332	538	482	0.280322	0.0236	0.636	0.301
GO:0016491:oxidoreductase_activity	554	826	741	0.280546	0.0168	0.66	0.246
GO:0046914:transition_metal_ion_binding	1708	2755	2551	0.281469	0.0092	0.647	0.232
GO:0048609:multicellular_organismal_reproductive_process	391	662	604	0.28321	0.0202	0.637	0.26
GO:0032504:multicellular_organism_reproduction	391	662	604	0.28321	0.0202	0.637	0.26
GO:0022402:cell_cycle_process	535	895	873	0.285577	0.0162	0.529	0.256
GO:0005623:cell	10748	16357	15816	0.28687	0.0045	0.588	0.242
GO:0044464:cell_part	10747	16356	15813	0.286958	0.0045	0.588	0.242
GO:0033554:cellular_response_to_stress	575	867	814	0.287918	0.0177	0.589	0.298
GO:0009308:amine_metabolic_process	390	576	577	0.289057	0.0233	0.55	0.332
GO:0008150:biological_process	10243	16043	15459	0.289405	0.0046	0.587	0.248
GO:0016787:hydrolase_activity	1810	3440	3201	0.290579	0.0089	0.621	0.263
GO:0003674:molecular_function	11210	17637	16817	0.292659	0.0044	0.594	0.252
GO:0005575:cellular_component	11522	17552	16688	0.293881	0.0046	0.596	0.252
GO:0016020:membrane	5195	8539	8324	0.293983	0.0063	0.574	0.258
GO:0022403:cell_cycle_phase	438	738	730	0.296054	0.0185	0.504	0.278
GO:0005509:calcium_ion_binding	492	1107	1021	0.296544	0.0155	0.612	0.254
GO:0015630:microtubule_cytoskeleton	528	1074	1005	0.296609	0.0171	0.57	0.25
GO:0019953:sexual_reproduction	352	675	598	0.298196	0.0198	0.682	0.25
GO:0050896:response_to_stimulus	4220	6821	6620	0.29923	0.007	0.563	0.263
GO:0007276:gamete_generation	304	562	497	0.299358	0.0224	0.651	0.279
GO:0006629:lipid_metabolic_process	657	1064	985	0.301865	0.0168	0.62	0.292
GO:0051704:multi-organism_process	592	824	838	0.304038	0.0198	0.496	0.294
GO:0005615:extracellular_space	526	892	801	0.306037	0.0159	0.651	0.302
GO:0031012:extracellular_matrix	297	744	754	0.307854	0.018	0.532	0.319
GO:0071944:cell_periphery	2714	5061	4943	0.308239	0.0084	0.563	0.283
GO:0005886:plasma_membrane	2666	5006	4891	0.309227	0.0085	0.56	0.287
GO:0005694:chromosome	364	572	548	0.311907	0.0235	0.565	0.259
GO:0043436:oxoacid_metabolic_process	515	814	746	0.313308	0.0201	0.631	0.338
GO:0019752:carboxylic_acid_metabolic_process	515	814	746	0.313308	0.0201	0.631	0.338
GO:0044425:membrane_part	4128	7060	6614	0.313475	0.007	0.588	0.277
GO:0006082:organic_acid_metabolic_process	526	845	766	0.313711	0.0195	0.649	0.333

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GO:0006259:DNA_metabolic_process	485	911	715	0.314683	0.0217	0.751	0.264
GO:0042180:cellular_ketone_metabolic_process	528	833	760	0.316727	0.0206	0.627	0.339
GO:0044421:extracellular_region_part	725	1395	1298	0.319267	0.0133	0.593	0.342
GO:0016788:hydrolase_activity_acting_on_ester_bonds	527	948	847	0.319903	0.0182	0.586	0.376
GO:0005578:proteinaceous_extracellular_matrix	257	684	678	0.320989	0.0203	0.539	0.329
GO:0005198:structural_molecule_activity	464	848	769	0.323	0.0205	0.592	0.307
GO:0000279:M_phase	283	544	488	0.323493	0.0234	0.576	0.284
GO:0030246:carbohydrate_binding	272	534	495	0.327963	0.0256	0.553	0.289
GO:0031224:intrinsic_to_membrane	3569	6168	5655	0.332252	0.008	0.585	0.295
GO:0016021:integral_to_membrane	3497	6088	5558	0.334064	0.008	0.586	0.297
GO:0007600:sensory_perception	313	604	500	0.335213	0.0243	0.719	0.312
GO:0044255:cellular_lipid_metabolic_process	475	714	679	0.339635	0.022	0.519	0.347
GO:0005815:microtubule_organizing_center	277	542	484	0.34376	0.0249	0.5	0.399
GO:0005576:extracellular_region	1322	2281	1948	0.345448	0.0122	0.644	0.341
GO:0006952:defense_response	525	764	691	0.350595	0.0224	0.556	0.345
GO:0006955:immune_response	500	696	625	0.356863	0.0232	0.533	0.393
GO:0004871:signal_transducer_activity	1170	2350	1994	0.400144	0.0161	0.586	0.369
GO:0004872:receptor_activity	1233	2710	2218	0.405647	0.0148	0.615	0.368
GO:0038023:signaling_receptor_activity	913	2046	1583	0.455977	0.0191	0.624	0.43
GO:0004888:transmembrane_signaling_receptor_activity	844	1991	1489	0.465668	0.0198	0.654	0.437
GO:0004930:G-protein_coupled_receptor_activity	604	1469	890	0.60268	0.0293	0.741	0.573
GO:0004984:olfactory_receptor_activity	310	1024	430	0.895853	0.0478	1.011	0.993