The co-expression genes of SKA1 with GO notes

Ontology	ID	Description	Count	P value	P adjust
BP	GO:0006260	DNA replication	94	2.33E-48	1.09E-44
BP	GO:0007059	Chromosome segregation	85	9.61E-38	2.25E-34
BP	GO:0140014	Mitotic nuclear division	75	3.60E-34	5.61E-31
BP	GO:0006261	DNA-dependent DNA replication	56	6.33E-34	7.40E-31
BP	GO:0000280	Nuclear division	90	3.03E-32	2.45E-29
BP	GO:0048285	Organelle fission	95	3.15E-32	2.45E-29
BP	GO:0000819	Sister chromatid segregation	59	9.81E-32	6.55E-29
BP	GO:0098813	Nuclear chromosome segregation	68	2.29E-30	1.34E-27
BP	GO:0000070	Mitotic sister chromatid segregation	53	2.59E-30	1.34E-27
BP	GO:1901990	Regulation of mitotic cell cycle phase transition	93	6.02E-28	2.81E-25
BP	GO:1901987	Regulation of cell cycle phase transition	96	4.34E-27	1.85E-24
BP	GO:0044839	Cell cycle G2/M phase transition	66	2.22E-24	8.66E-22
BP	GO:0000086	G2/M transition of mitotic cell cycle	63	4.29E-24	1.54E-21
BP	GO:0051052	Regulation of DNA metabolic process	82	9.27E-23	3.10E-20
BP	GO:0044843	Cell cycle G1/S phase transition	67	3.96E-22	1.24E-19
BP	GO:0000082	G1/S transition of mitotic cell cycle	64	9.64E-22	2.81E-19
BP	GO:0051983	Regulation of chromosome segregation	37	2.22E-21	6.11E-19
BP	GO:0007051	Spindle organization	46	3.58E-21	9.30E-19
BP	GO:1902749	Regulation of cell cycle G2/M phase transition	54	4.87E-21	1.20E-18
BP	GO:0000075	Cell cycle checkpoint	53	8.24E-21	1.93E-18
BP	GO:0044786	Cell cycle DNA replication	29	1.01E-20	2.25E-18
BP	GO:0010389	Regulation of G2/M transition of mitotic cell cycle	51	1.39E-20	2.94E-18
BP	GO:0006403	RNA localization	54	2.13E-20	4.33E-18
BP	GO:0010948	Negative regulation of cell cycle process	71	3.29E-20	6.41E-18
BP	GO:0000226	Microtubule cytoskeleton organization	84	4.21E-20	7.87E-18
BP	GO:0007093	Mitotic cell cycle checkpoint	44	1.84E-19	3.30E-17
BP	GO:0045930	Negative regulation of mitotic cell cycle	65	4.00E-19	6.93E-17
BP	GO:0072331	Signal transduction by p53 class mediator	59	1.00E-18	1.68E-16
BP	GO:0033260	Nuclear DNA replication	25	1.16E-18	1.86E-16
BP	GO:0000723	Telomere maintenance	44	1.36E-18	2.12E-16
BP	GO:0007088	Regulation of mitotic nuclear division	43	2.92E-18	4.40E-16
BP	GO:1901988	Negative regulation of cell cycle phase transition	57	3.21E-18	4.68E-16

BP	GO:0071103	DNA conformation change	60	3.68E-18	5.21E-16
BP	GO:1901991	Negative regulation of mitotic cell cycle phase transition	54	8.21E-18	1.13E-15
BP	GO:1902850	Microtubule cytoskeleton organization involved in mitosis	37	1.34E-17	1.79E-15
BP	GO:0034502	Protein localization to chromosome	31	2.26E-17	2.93E-15
BP	GO:0032200	Telomere organization	44	4.02E-17	5.08E-15
BP	GO:0051054	Positive regulation of DNA metabolic process	51	6.88E-17	8.46E-15
BP	GO:0006310	DNA recombination	53	2.20E-16	2.63E-14
BP	GO:0034660	Ncrna metabolic process	78	2.86E-16	3.34E-14
BP	GO:0051783	Regulation of nuclear division	43	7.37E-16	8.40E-14
BP	GO:0031145	Anaphase-promoting complex-dependent catabolic process	29	1.33E-15	1.48E-13
BP	GO:0033045	Regulation of sister chromatid segregation	27	1.45E-15	1.58E-13
BP	GO:0007052	Mitotic spindle organization	31	2.80E-15	2.97E-13
BP	GO:0007091	Metaphase/anaphase transition of mitotic cell cycle	22	4.65E-15	4.72E-13
BP	GO:0010965	Regulation of mitotic sister chromatid separation	22	4.65E-15	4.72E-13
BP	GO:0050657	Nucleic acid transport	42	9.33E-15	9.09E-13
BP	GO:0050658	RNA transport	42	9.33E-15	9.09E-13
BP	GO:0033044	Regulation of chromosome organization	58	1.19E-14	1.13E-12
BP	GO:0044784	Metaphase/anaphase transition of cell cycle	22	1.38E-14	1.27E-12
BP	GO:0051306	Mitotic sister chromatid separation	22	1.38E-14	1.27E-12
BP	GO:0051236	Establishment of RNA localization	42	1.75E-14	1.58E-12
BP	GO:0051169	Nuclear transport	57	1.84E-14	1.62E-12
BP	GO:0006405	RNA export from nucleus	34	2.54E-14	2.19E-12
BP	GO:0006275	Regulation of DNA replication	31	2.57E-14	2.19E-12
BP	GO:0090068	Positive regulation of cell cycle process	54	3.72E-14	3.10E-12
BP	GO:0006913	Nucleocytoplasmic transport	56	4.42E-14	3.63E-12
BP	GO:1905818	Regulation of chromosome separation	22	6.33E-14	5.10E-12
BP	GO:0031570	DNA integrity checkpoint	36	8.44E-14	6.68E-12
BP	GO:1901796	Regulation of signal transduction by p53 class mediator	41	8.59E-14	6.69E-12
BP	GO:0045787	Positive regulation of cell cycle	63	1.01E-13	7.62E-12
BP	GO:0006270	DNA replication initiation	17	1.01E-13	7.62E-12
BP	GO:0090329	Regulation of DNA-dependent DNA replication	21	1.05E-13	7.76E-12
BP	GO:0071426	Ribonucleoprotein complex export from nucleus	32	2.00E-13	1.46E-11
BP	GO:0071166	Ribonucleoprotein complex localization	32	2.59E-13	1.86E-11
BP	GO:0006302	Double-strand break repair	44	3.62E-13	2.56E-11
BP	GO:0033047	Regulation of mitotic sister chromatid segregation	22	6.09E-13	4.25E-11

BP	GO:0071897	DNA biosynthetic process	41	1.02E-12	7.00E-11
BP	GO:0051168	Nuclear export	39	1.06E-12	7.21E-11
BP	GO:0000725	Recombinational repair	30	1.21E-12	8.05E-11
BP	GO:0006323	DNA packaging	41	1.46E-12	9.60E-11
BP	GO:0006611	Protein export from nucleus	37	1.87E-12	1.22E-10
BP	GO:0030071	Regulation of mitotic metaphase/anaphase transition	19	2.10E-12	1.35E-10
BP	GO:0051310	Metaphase plate congression	21	2.62E-12	1.66E-10
BP	GO:0032201	Telomere maintenance via semi-conservative replication	15	4.36E-12	2.72E-10
BP	GO:0051304	Chromosome separation	23	4.63E-12	2.85E-10
BP	GO:1902099	Regulation of metaphase/anaphase transition of cell cycle	19	5.52E-12	3.35E-10
BP	GO:0000724	Double-strand break repair via homologous recombination	29	5.63E-12	3.37E-10
BP	GO:1903311	Regulation of mrna metabolic process	49	7.98E-12	4.72E-10
BP	GO:0022613	Ribonucleoprotein complex biogenesis	60	8.45E-12	4.94E-10
BP	GO:0007098	Centrosome cycle	29	1.50E-11	8.68E-10
BP	GO:0050000	Chromosome localization	23	1.78E-11	1.00E-09
BP	GO:0051303	Establishment of chromosome localization	23	1.78E-11	1.00E-09
BP	GO:0072401	Signal transduction involved in DNA integrity checkpoint	23	2.45E-11	1.35E-09
BP	GO:0072422	Signal transduction involved in DNA damage checkpoint	23	2.45E-11	1.35E-09
BP	GO:0015931	Nucleobase-containing compound transport	42	3.00E-11	1.63E-09
BP	GO:0072395	Signal transduction involved in cell cycle checkpoint	23	3.35E-11	1.80E-09
BP	GO:0042770	Signal transduction in response to DNA damage	31	3.76E-11	1.99E-09
BP	GO:0045839	Negative regulation of mitotic nuclear division	18	3.83E-11	2.01E-09
BP	GO:0000077	DNA damage checkpoint	31	5.69E-11	2.96E-09
BP	GO:0051225	Spindle assembly	25	7.29E-11	3.72E-09
BP	GO:1902750	Negative regulation of cell cycle G2/M phase transition	26	7.32E-11	3.72E-09
BP	GO:0043044	ATP-dependent chromatin remodeling	23	8.30E-11	4.17E-09
BP	GO:0031503	Protein-containing complex localization	43	9.65E-11	4.80E-09
BP	GO:1903405	Protein localization to nuclear body	9	1.01E-10	4.89E-09
BP	GO:1904851	Positive regulation of establishment of protein localization to telomere	9	1.01E-10	4.89E-09
BP	GO:1904867	Protein localization to Cajal body	9	1.01E-10	4.89E-09
BP	GO:0045841	Negative regulation of mitotic metaphase/anaphase transition	15	1.06E-10	5.03E-09
BP	GO:2000816	Negative regulation of mitotic sister chromatid separation	15	1.06E-10	5.03E-09
BP	GO:0051321	Meiotic cell cycle	39	1.09E-10	5.08E-09
BP	GO:0033046	Negative regulation of sister chromatid segregation	16	1.15E-10	5.31E-09

BP	GO:0070200	Establishment of protein localization to telomere	11	1.28E-10	5.85E-09
BP	GO:0031023	Microtubule organizing center organization	29	1.43E-10	6.31E-09
BP	GO:0009124	Nucleoside monophosphate biosynthetic process	38	1.43E-10	6.31E-09
BP	GO:0006406	Mrna export from nucleus	27	1.43E-10	6.31E-09
BP	GO:0071427	Mrna-containing ribonucleoprotein complex export from nucleus	27	1.43E-10	6.31E-09
BP	GO:2000573	Positive regulation of DNA biosynthetic process	21	1.46E-10	6.39E-09
BP	GO:0051028	Mrna transport	32	1.55E-10	6.69E-09
BP	GO:0032392	DNA geometric change	24	1.57E-10	6.73E-09
BP	GO:1902100	Negative regulation of metaphase/anaphase transition of cell cycle	15	1.84E-10	7.76E-09
BP	GO:1905819	Negative regulation of chromosome separation	15	1.84E-10	7.76E-09
BP	GO:0051985	Negative regulation of chromosome segregation	16	1.87E-10	7.81E-09
BP	GO:0043486	Histone exchange	19	2.21E-10	9.13E-09
BP	GO:0016072	Rrna metabolic process	37	2.55E-10	1.05E-08
BP	GO:0000083	Regulation of transcription involved in G1/S transition of mitotic cell cycle	14	2.74E-10	1.11E-08
BP	GO:0008608	Attachment of spindle microtubules to kinetochore	14	2.74E-10	1.11E-08
BP	GO:0034404	Nucleobase-containing small molecule biosynthetic process	39	3.59E-10	1.44E-08
BP	GO:0071459	Protein localization to chromosome, centromeric region	12	4.10E-10	1.62E-08
BP	GO:0032508	DNA duplex unwinding	22	4.18E-10	1.64E-08
BP	GO:0044774	Mitotic DNA integrity checkpoint	24	4.40E-10	1.71E-08
BP	GO:0071824	Protein-DNA complex subunit organization	42	4.46E-10	1.72E-08
BP	GO:0000375	RNA splicing, via transesterification reactions	53	4.94E-10	1.89E-08
BP	GO:0033048	Negative regulation of mitotic sister chromatid segregation	15	5.14E-10	1.95E-08
BP	GO:0070203	Regulation of establishment of protein localization to telomere	9	5.28E-10	1.99E-08
BP	GO:0051784	Negative regulation of nuclear division	18	6.35E-10	2.37E-08
BP	GO:0043487	Regulation of RNA stability	33	7.22E-10	2.68E-08
BP	GO:0007080	Mitotic metaphase plate congression	16	7.29E-10	2.68E-08
BP	GO:0010972	Negative regulation of G2/M transition of mitotic cell cycle	23	7.40E-10	2.70E-08
BP	GO:0097064	Ncrna export from nucleus	15	8.33E-10	3.02E-08
BP	GO:0006336	DNA replication-independent nucleosome assembly	18	9.07E-10	3.24E-08
BP	GO:0034724	DNA replication-independent nucleosome organization	18	9.07E-10	3.24E-08
BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	52	9.46E-10	3.32E-08
BP	GO:0000398	Mrna splicing, via spliceosome	52	9.46E-10	3.32E-08

BP	GO:0044773	Mitotic DNA damage checkpoint	23	9.53E-10	3.32E-08
BP	GO:0034508	Centromere complex assembly	18	1.28E-09	4.44E-08
BP	GO:0043488	Regulation of mrna stability	32	1.29E-09	4.44E-08
BP	GO:1904874	Positive regulation of telomerase RNA localization to Cajal body	10	1.46E-09	4.99E-08
BP	GO:0006399	Trna metabolic process	32	1.80E-09	6.09E-08
BP	GO:0061013	Regulation of mrna catabolic process	34	1.99E-09	6.57E-08
BP	GO:0070202	Regulation of establishment of protein localization to chromosome	9	2.00E-09	6.57E-08
BP	GO:1904816	Positive regulation of protein localization to chromosome, telomeric region	9	2.00E-09	6.57E-08
BP	GO:1990173	Protein localization to nucleoplasm	9	2.00E-09	6.57E-08
BP	GO:0006409	Trna export from nucleus	14	2.30E-09	7.42E-08
BP	GO:0051031	Trna transport	14	2.30E-09	7.42E-08
BP	GO:0071431	Trna-containing ribonucleoprotein complex export from nucleus	14	2.30E-09	7.42E-08
BP	GO:0031571	Mitotic G1 DNA damage checkpoint	19	3.03E-09	9.64E-08
BP	GO:0044819	Mitotic G1/S transition checkpoint	19	3.03E-09	9.64E-08
BP	GO:2000278	Regulation of DNA biosynthetic process	25	3.14E-09	9.91E-08
BP	GO:0072431	Signal transduction involved in mitotic G1 DNA damage checkpoint	18	3.46E-09	1.08E-07
BP	GO:1902400	Intracellular signal transduction involved in G1 DNA damage checkpoint	18	3.46E-09	1.08E-07
BP	GO:0034501	Protein localization to kinetochore	10	3.69E-09	1.14E-07
BP	GO:0031123	RNA 3'-end processing	25	3.86E-09	1.19E-07
BP	GO:0051383	Kinetochore organization	11	3.92E-09	1.20E-07
BP	GO:0044783	G1 DNA damage checkpoint	19	4.07E-09	1.24E-07
BP	GO:0042254	Ribosome biogenesis	36	4.72E-09	1.42E-07
BP	GO:0031055	Chromatin remodeling at centromere	16	5.26E-09	1.58E-07
BP	GO:2001251	Negative regulation of chromosome organization	27	5.82E-09	1.73E-07
BP	GO:0007094	Mitotic spindle assembly checkpoint	13	6.33E-09	1.83E-07
BP	GO:0031577	Spindle checkpoint	13	6.33E-09	1.83E-07
BP	GO:0071173	Spindle assembly checkpoint	13	6.33E-09	1.83E-07
BP	GO:0071174	Mitotic spindle checkpoint	13	6.33E-09	1.83E-07
BP	GO:0072413	Signal transduction involved in mitotic cell cycle checkpoint	18	6.42E-09	1.83E-07
BP	GO:1902402	Signal transduction involved in mitotic DNA damage checkpoint	18	6.42E-09	1.83E-07
BP	GO:1902403	Signal transduction involved in mitotic DNA integrity checkpoint	18	6.42E-09	1.83E-07

BP	GO:0009156	Ribonucleoside monophosphate biosynthetic process	34	8.58E-09	2.43E-07
BP	GO:0006401	RNA catabolic process	52	1.01E-08	2.85E-07
BP	GO:0006397	Mrna processing	64	1.02E-08	2.85E-07
BP	GO:0006369	Termination of RNA polymerase II transcription	13	1.03E-08	2.87E-07
BP	GO:0034080	CENP-A containing nucleosome assembly	15	1.05E-08	2.87E-07
BP	GO:0061641	CENP-A containing chromatin organization	15	1.05E-08	2.87E-07
BP	GO:0031124	Mrna 3'-end processing	22	1.09E-08	2.97E-07
BP	GO:0065004	Protein-DNA complex assembly	36	1.37E-08	3.71E-07
BP	GO:0006338	Chromatin remodeling	30	1.49E-08	4.03E-07
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	24	1.53E-08	4.09E-07
BP	GO:0034728	Nucleosome organization	31	1.53E-08	4.09E-07
BP	GO:1904814	Regulation of protein localization to chromosome, telomeric region	9	1.63E-08	4.32E-07
BP	GO:1904872	Regulation of telomerase RNA localization to Cajal body	10	1.80E-08	4.76E-07
BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	17	1.84E-08	4.83E-07
BP	GO:1901293	Nucleoside phosphate biosynthetic process	51	2.05E-08	5.35E-07
BP	GO:0034470	Ncrna processing	44	2.27E-08	5.88E-07
BP	GO:1903046	Meiotic cell cycle process	29	2.67E-08	6.89E-07
BP	GO:2001252	Positive regulation of chromosome organization	31	2.74E-08	7.05E-07
BP	GO:0070198	Protein localization to chromosome, telomeric region	12	2.85E-08	7.29E-07
BP	GO:0070316	Regulation of G0 to G1 transition	15	3.08E-08	7.81E-07
BP	GO:0070507	Regulation of microtubule cytoskeleton organization	31	3.17E-08	8.00E-07
BP	GO:0009123	Nucleoside monophosphate metabolic process	49	3.32E-08	8.35E-07
BP	GO:0009165	Nucleotide biosynthetic process	50	3.43E-08	8.57E-07
BP	GO:0090670	RNA localization to Cajal body	10	3.60E-08	8.80E-07
BP	GO:0090671	Telomerase RNA localization to Cajal body	10	3.60E-08	8.80E-07
BP	GO:0090672	Telomerase RNA localization	10	3.60E-08	8.80E-07
BP	GO:0090685	RNA localization to nucleus	10	3.60E-08	8.80E-07
BP	GO:0070199	Establishment of protein localization to chromosome	11	4.64E-08	1.13E-06
BP	GO:0019882	Antigen processing and presentation	36	4.73E-08	1.14E-06
BP	GO:0009127	Purine nucleoside monophosphate biosynthetic process	31	5.53E-08	1.33E-06
BP	GO:0009168	Purine ribonucleoside monophosphate biosynthetic process	31	5.53E-08	1.33E-06
BP	GO:0045740	Positive regulation of DNA replication	13	5.87E-08	1.40E-06
BP	GO:0045023	G0 to G1 transition	15	5.98E-08	1.42E-06

BP	GO:0070317	Negative regulation of G0 to G1 transition	14	6.27E-08	1.48E-06
BP	GO:0022616	DNA strand elongation	9	8.32E-08	1.95E-06
BP	GO:0006333	Chromatin assembly or disassembly	31	9.47E-08	2.21E-06
BP	GO:0140013	Meiotic nuclear division	27	9.93E-08	2.31E-06
BP	GO:0008380	RNA splicing	56	1.12E-07	2.58E-06
BP	GO:0006364	Rrna processing	28	1.55E-07	3.55E-06
BP	GO:0045931	Positive regulation of mitotic cell cycle	28	1.55E-07	3.55E-06
BP	GO:0030261	Chromosome condensation	12	1.69E-07	3.85E-06
BP	GO:0060249	Anatomical structure homeostasis	53	1.87E-07	4.24E-06
BP	GO:0061640	Cytoskeleton-dependent cytokinesis	19	3.24E-07	7.29E-06
BP	GO:0071158	Positive regulation of cell cycle arrest	19	3.24E-07	7.29E-06
BP	GO:0090305	Nucleic acid phosphodiester bond hydrolysis	39	3.27E-07	7.31E-06
BP	GO:0009260	Ribonucleotide biosynthetic process	40	3.45E-07	7.69E-06
BP	GO:0006297	Nucleotide-excision repair, DNA gap filling	10	3.56E-07	7.89E-06
BP	GO:0032212	Positive regulation of telomere maintenance via telomerase	12	3.66E-07	8.07E-06
BP	GO:0006301	Postreplication repair	14	4.32E-07	9.47E-06
BP	GO:0051302	Regulation of cell division	28	4.60E-07	1.00E-05
BP	GO:0006520	Cellular amino acid metabolic process	46	4.76E-07	1.03E-05
BP	GO:0031497	Chromatin assembly	27	4.79E-07	1.04E-05
BP	GO:0006334	Nucleosome assembly	25	4.94E-07	1.06E-05
BP	GO:0009163	Nucleoside biosynthetic process	13	4.98E-07	1.07E-05
BP	GO:0000281	Mitotic cytokinesis	17	5.29E-07	1.13E-05
BP	GO:0046390	Ribose phosphate biosynthetic process	40	5.53E-07	1.18E-05
BP	GO:0006402	Mrna catabolic process	45	5.61E-07	1.19E-05
BP	GO:0046653	Tetrahydrofolate metabolic process	9	5.69E-07	1.20E-05
BP	GO:0008334	Histone mrna metabolic process	10	5.78E-07	1.20E-05
BP	GO:0051984	Positive regulation of chromosome segregation	10	5.78E-07	1.20E-05
BP	GO:0002478	Antigen processing and presentation of exogenous peptide antigen	29	6.34E-07	1.32E-05
BP	GO:1901659	Glycosyl compound biosynthetic process	13	6.82E-07	1.41E-05
BP	GO:0010639	Negative regulation of organelle organization	46	7.17E-07	1.48E-05
BP	GO:0000910	Cytokinesis	26	7.43E-07	1.52E-05
BP	GO:0009161	Ribonucleoside monophosphate metabolic process	44	7.80E-07	1.58E-05
BP	GO:0007076	Mitotic chromosome condensation	8	7.81E-07	1.58E-05
BP	GO:0000076	DNA replication checkpoint	7	7.86E-07	1.58E-05

BP	GO:2000105	Positive regulation of DNA-dependent DNA replication	7	7.86E-07	1.58E-05
BP	GO:0019884	Antigen processing and presentation of exogenous antigen	29	8.10E-07	1.62E-05
BP	GO:0010833	Telomere maintenance via telomere lengthening	18	8.60E-07	1.72E-05
BP	GO:0075733	Intracellular transport of virus	15	9.89E-07	1.97E-05
BP	GO:0036297	Interstrand cross-link repair	14	9.99E-07	1.98E-05
BP	GO:1904358	Positive regulation of telomere maintenance via telomere lengthening	12	1.04E-06	2.05E-05
BP	GO:0072522	Purine-containing compound biosynthetic process	40	1.04E-06	2.05E-05
BP	GO:0048002	Antigen processing and presentation of peptide antigen	30	1.06E-06	2.07E-05
BP	GO:1901989	Positive regulation of cell cycle phase transition	20	1.18E-06	2.29E-05
BP	GO:0032886	Regulation of microtubule-based process	31	1.20E-06	2.32E-05
BP	GO:0044766	Multi-organism transport	17	1.24E-06	2.39E-05
BP	GO:1902579	Multi-organism localization	17	1.24E-06	2.39E-05
BP	GO:0009141	Nucleoside triphosphate metabolic process	44	1.28E-06	2.45E-05
BP	GO:0032206	Positive regulation of telomere maintenance	14	1.30E-06	2.48E-05
BP	GO:0006284	Base-excision repair	12	1.44E-06	2.74E-05
BP	GO:0043161	Proteasome-mediated ubiquitin-dependent protein catabolic process	43	1.51E-06	2.85E-05
BP	GO:0043039	Trna aminoacylation	13	1.64E-06	3.10E-05
BP	GO:0090307	Mitotic spindle assembly	14	1.68E-06	3.15E-05
BP	GO:0007004	Telomere maintenance via telomerase	16	1.78E-06	3.31E-05
BP	GO:0046112	Nucleobase biosynthetic process	7	1.79E-06	3.31E-05
BP	GO:0051988	Regulation of attachment of spindle microtubules to kinetochore	7	1.79E-06	3.31E-05
BP	GO:0018205	Peptidyl-lysine modification	47	1.94E-06	3.58E-05
BP	GO:0046794	Transport of virus	15	2.01E-06	3.70E-05
BP	GO:0006298	Mismatch repair	10	2.10E-06	3.82E-05
BP	GO:0006760	Folic acid-containing compound metabolic process	10	2.10E-06	3.82E-05
BP	GO:0009112	Nucleobase metabolic process	10	2.10E-06	3.82E-05
BP	GO:0032210	Regulation of telomere maintenance via telomerase	14	2.16E-06	3.90E-05
BP	GO:0043038	Amino acid activation	13	2.17E-06	3.90E-05
BP	GO:0045005	DNA-dependent DNA replication maintenance of fidelity	11	2.17E-06	3.90E-05
BP	GO:0000018	Regulation of DNA recombination	18	2.23E-06	3.99E-05
BP	GO:0009142	Nucleoside triphosphate biosynthetic process	28	2.27E-06	4.03E-05
BP	GO:1901292	Nucleoside phosphate catabolic process	28	2.27E-06	4.03E-05
BP	GO:1904666	Regulation of ubiquitin protein ligase activity	9	2.59E-06	4.59E-05

BP	GO:0006164	Purine nucleotide biosynthetic process	38	2.64E-06	4.65E-05
BP	GO:0006353	DNA-templated transcription, termination	16	2.71E-06	4.75E-05
BP	GO:0046605	Regulation of centrosome cycle	14	2.75E-06	4.82E-05
BP	GO:0006165	Nucleoside diphosphate phosphorylation	23	2.77E-06	4.82E-05
BP	GO:1902807	Negative regulation of cell cycle G1/S phase transition	23	3.17E-06	5.51E-05
BP	GO:0006282	Regulation of DNA repair	21	3.24E-06	5.61E-05
BP	GO:0016925	Protein sumoylation	17	3.31E-06	5.71E-05
BP	GO:0097711	Ciliary basal body-plasma membrane docking	19	3.50E-06	6.01E-05
BP	GO:0009166	Nucleotide catabolic process	27	3.53E-06	6.03E-05
BP	GO:0046939	Nucleotide phosphorylation	23	3.63E-06	6.19E-05
BP	GO:0009167	Purine ribonucleoside monophosphate metabolic process	41	3.70E-06	6.30E-05
BP	GO:0009126	Purine nucleoside monophosphate metabolic process	41	4.01E-06	6.79E-05
BP	GO:1901657	Glycosyl compound metabolic process	23	4.15E-06	7.00E-05
BP	GO:2001020	Regulation of response to DNA damage stimulus	30	4.34E-06	7.28E-05
BP	GO:0009116	Nucleoside metabolic process	21	4.35E-06	7.28E-05
BP	GO:0031297	Replication fork processing	10	4.46E-06	7.45E-05
BP	GO:0051782	Negative regulation of cell division	8	4.50E-06	7.49E-05
BP	GO:0006418	Trna aminoacylation for protein translation	12	4.70E-06	7.79E-05
BP	GO:2000134	Negative regulation of G1/S transition of mitotic cell cycle	22	4.92E-06	8.12E-05
BP	GO:0034504	Protein localization to nucleus	32	4.94E-06	8.12E-05
BP	GO:0006732	Coenzyme metabolic process	45	4.95E-06	8.12E-05
BP	GO:0051656	Establishment of organelle localization	52	5.11E-06	8.33E-05
BP	GO:0009152	Purine ribonucleotide biosynthetic process	36	5.12E-06	8.33E-05
BP	GO:0007062	Sister chromatid cohesion	13	6.02E-06	9.77E-05
BP	GO:0009303	Rrna transcription	10	6.33E-06	0.000102392
BP	GO:0071156	Regulation of cell cycle arrest	20	6.72E-06	0.000108293
BP	GO:0010498	Proteasomal protein catabolic process	46	6.80E-06	0.000108898
BP	GO:1901992	Positive regulation of mitotic cell cycle phase transition	17	6.80E-06	0.000108898
BP	GO:0006278	RNA-dependent DNA biosynthetic process	16	7.14E-06	0.000113556
BP	GO:1900182	Positive regulation of protein localization to nucleus	16	7.14E-06	0.000113556
BP	GO:0032465	Regulation of cytokinesis	17	8.08E-06	0.000127993
BP	GO:0006188	IMP biosynthetic process	6	8.33E-06	0.000131017
BP	GO:0046040	IMP metabolic process	6	8.33E-06	0.000131017
BP	GO:0051298	Centrosome duplication	14	8.49E-06	0.000133061
BP	GO:0006096	Glycolytic process	20	8.96E-06	0.00014007

BP	GO:0140053	Mitochondrial gene expression	24	9.32E-06	0.000145173
BP	GO:0036294	Cellular response to decreased oxygen levels	31	1.01E-05	0.000156172
BP	GO:0042769	DNA damage response, detection of DNA damage	11	1.02E-05	0.00015777
BP	GO:0006757	ATP generation from ADP	20	1.03E-05	0.000159139
BP	GO:0006289	Nucleotide-excision repair	19	1.04E-05	0.000159683
BP	GO:0071456	Cellular response to hypoxia	30	1.06E-05	0.000162092
BP	GO:0046031	ADP metabolic process	21	1.14E-05	0.000174636
BP	GO:0000966	RNA 5'-end processing	8	1.16E-05	0.000176981
BP	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	15	1.28E-05	0.000193898
BP	GO:1904356	Regulation of telomere maintenance via telomere lengthening	14	1.28E-05	0.000193898
BP	GO:0042866	Pyruvate biosynthetic process	20	1.56E-05	0.000234666
BP	GO:0042558	Pteridine-containing compound metabolic process	10	1.65E-05	0.000248085
BP	GO:0009132	Nucleoside diphosphate metabolic process	24	1.66E-05	0.000248115
BP	GO:0032204	Regulation of telomere maintenance	16	1.72E-05	0.000256931
BP	GO:0007100	Mitotic centrosome separation	6	1.74E-05	0.000258601
BP	GO:0071453	Cellular response to oxygen levels	32	1.77E-05	0.000262127
BP	GO:0010212	Response to ionizing radiation	23	1.83E-05	0.000270696
BP	GO:0009201	Ribonucleoside triphosphate biosynthetic process	25	1.84E-05	0.000271919
BP	GO:1902751	Positive regulation of cell cycle G2/M phase transition	9	1.85E-05	0.00027255
BP	GO:1902806	Regulation of cell cycle G1/S phase transition	28	1.87E-05	0.000274164
BP	GO:0051382	Kinetochore assembly	7	2.08E-05	0.000302875
BP	GO:0099116	Trna 5'-end processing	7	2.08E-05	0.000302875
BP	GO:0051653	Spindle localization	11	2.26E-05	0.00032847
BP	GO:1900180	Regulation of protein localization to nucleus	20	2.31E-05	0.000334208
BP	GO:0009199	Ribonucleoside triphosphate metabolic process	39	2.37E-05	0.000342143
BP	GO:2000045	Regulation of G1/S transition of mitotic cell cycle	26	2.46E-05	0.000353818
BP	GO:0046394	Carboxylic acid biosynthetic process	48	2.55E-05	0.000365278
BP	GO:0040001	Establishment of mitotic spindle localization	9	2.59E-05	0.000369669
BP	GO:0016053	Organic acid biosynthetic process	48	2.71E-05	0.000385672
BP	GO:0009144	Purine nucleoside triphosphate metabolic process	39	2.73E-05	0.000388429
BP	GO:0009308	Amine metabolic process	21	2.77E-05	0.000391686
BP	GO:1903578	Regulation of ATP metabolic process	19	3.16E-05	0.000446023
BP	GO:0051299	Centrosome separation	6	3.30E-05	0.000464015
BP	GO:0009108	Coenzyme biosynthetic process	32	3.45E-05	0.000484427

BP	GO:0009262	Deoxyribonucleotide metabolic process	9	3.55E-05	0.000495203
BP	GO:0046134	Pyrimidine nucleoside biosynthetic process	9	3.55E-05	0.000495203
BP	GO:0046434	Organophosphate catabolic process	30	3.74E-05	0.000519459
BP	GO:0051973	Positive regulation of telomerase activity	10	3.84E-05	0.000531327
BP	GO:0000729	DNA double-strand break processing	8	3.84E-05	0.000531327
BP	GO:0140056	Organelle localization by membrane tethering	22	4.00E-05	0.000550996
BP	GO:0042398	Cellular modified amino acid biosynthetic process	11	4.65E-05	0.000638574
BP	GO:0007143	Female meiotic nuclear division	9	4.80E-05	0.000657795
BP	GO:0098781	Ncrna transcription	18	4.92E-05	0.000672635
BP	GO:0009135	Purine nucleoside diphosphate metabolic process	21	4.97E-05	0.000674471
BP	GO:0009179	Purine ribonucleoside diphosphate metabolic process	21	4.97E-05	0.000674471
BP	GO:0061418	Regulation of transcription from RNA polymerase II promoter in response to hypoxia	15	5.05E-05	0.000684695
BP	GO:0034471	Ncrna 5'-end processing	7	5.20E-05	0.000702055
BP	GO:0010971	Positive regulation of G2/M transition of mitotic cell cycle	8	5.46E-05	0.000735211
BP	GO:0042559	Pteridine-containing compound biosynthetic process	6	5.81E-05	0.000779906
BP	GO:0006521	Regulation of cellular amino acid metabolic process	13	5.98E-05	0.000801024
BP	GO:0032543	Mitochondrial translation	20	6.15E-05	0.000820473
BP	GO:0006457	Protein folding	25	6.17E-05	0.00082091
BP	GO:0009185	Ribonucleoside diphosphate metabolic process	21	6.21E-05	0.000824738
BP	GO:0051188	Cofactor biosynthetic process	37	6.37E-05	0.000842633
BP	GO:0007099	Centriole replication	9	6.40E-05	0.000845107
BP	GO:0007050	Cell cycle arrest	30	6.67E-05	0.000877589
BP	GO:0006575	Cellular modified amino acid metabolic process	25	8.16E-05	0.001070934
BP	GO:0009205	Purine ribonucleoside triphosphate metabolic process	37	8.34E-05	0.001091317
BP	GO:0051438	Regulation of ubiquitin-protein transferase activity	11	8.93E-05	0.001165005
BP	GO:0009206	Purine ribonucleoside triphosphate biosynthetic process	23	9.02E-05	0.001174055
BP	GO:1902036	Regulation of hematopoietic stem cell differentiation	14	9.12E-05	0.001180622
BP	GO:2000779	Regulation of double-strand break repair	14	9.12E-05	0.001180622
BP	GO:0043618	Regulation of transcription from RNA polymerase II promoter in response to stress	18	9.28E-05	0.001198549
BP	GO:0009145	Purine nucleoside triphosphate biosynthetic process	23	9.94E-05	0.001279853
BP	GO:0019985	Translesion synthesis	10	0.000102555	0.001316598
BP	GO:0006754	ATP biosynthetic process	22	0.000103401	0.001320203
BP	GO:0022406	Membrane docking	22	0.000103401	0.001320203
BP	GO:0061982	Meiosis I cell cycle process	16	0.000104784	0.001334206

BP	GO:0051972	Regulation of telomerase activity	11	0.000109508	0.001389706
BP	GO:0042455	Ribonucleoside biosynthetic process	9	0.000109737	0.001389706
BP	GO:0001666	Response to hypoxia	40	0.000110477	0.0013953
BP	GO:0070498	Interleukin-1-mediated signaling pathway	17	0.000113108	0.001424677
BP	GO:0070646	Protein modification by small protein removal	33	0.000121816	0.001530233
BP	GO:0000079	Regulation of cyclin-dependent protein serine/threonine kinase activity	15	0.000123959	0.001548826
BP	GO:0060218	Hematopoietic stem cell differentiation	15	0.000123959	0.001548826
BP	GO:0002479	Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	14	0.000144412	0.001794781
BP	GO:0006110	Regulation of glycolytic process	14	0.000144412	0.001794781
BP	GO:0006144	Purine nucleobase metabolic process	6	0.000152478	0.001885001
BP	GO:0046931	Pore complex assembly	6	0.000152478	0.001885001
BP	GO:0031109	Microtubule polymerization or depolymerization	16	0.00015563	0.001918895
BP	GO:0051231	Spindle elongation	5	0.000158202	0.00193528
BP	GO:0051315	Attachment of mitotic spindle microtubules to kinetochore	5	0.000158202	0.00193528
BP	GO:1901838	Positive regulation of transcription of nucleolar large rrna by RNA polymerase I	5	0.000158202	0.00193528
BP	GO:2000104	Negative regulation of DNA-dependent DNA replication	7	0.000161732	0.001970831
BP	GO:0000731	DNA synthesis involved in DNA repair	11	0.000161951	0.001970831
BP	GO:0002200	Somatic diversification of immune receptors	13	0.00016485	0.001999901
BP	GO:0022618	Ribonucleoprotein complex assembly	27	0.000165196	0.001999901
BP	GO:0071826	Ribonucleoprotein complex subunit organization	28	0.000176107	0.002123828
BP	GO:0072525	Pyridine-containing compound biosynthetic process	21	0.000176356	0.002123828
BP	GO:0072527	Pyrimidine-containing compound metabolic process	16	0.000176796	0.002123828
BP	GO:0007339	Binding of sperm to zona pellucida	9	0.000180037	0.002151697
BP	GO:0098534	Centriole assembly	9	0.000180037	0.002151697
BP	GO:0006220	Pyrimidine nucleotide metabolic process	12	0.000183015	0.002181713
BP	GO:0043620	Regulation of DNA-templated transcription in response to stress	18	0.000187511	0.002229613
BP	GO:0009150	Purine ribonucleotide metabolic process	51	0.000189141	0.002243294
BP	GO:0030811	Regulation of nucleotide catabolic process	14	0.000193235	0.002286045
BP	GO:0006213	Pyrimidine nucleoside metabolic process	11	0.00019531	0.002304755
BP	GO:0036293	Response to decreased oxygen levels	40	0.000211899	0.002494217
BP	GO:1904029	Regulation of cyclin-dependent protein kinase activity	15	0.000213749	0.002508418
BP	GO:0006090	Pyruvate metabolic process	21	0.000214179	0.002508418

BP	GO:0002562	Somatic diversification of immune receptors via germline recombination within a single locus	12	0.000216318	0.002520828
BP	GO:0016444	Somatic cell DNA recombination	12	0.000216318	0.002520828
BP	GO:0042590	Antigen processing and presentation of exogenous peptide antigen via MHC class I	14	0.000222572	0.002583523
BP	GO:0002244	Hematopoietic progenitor cell differentiation	22	0.000222803	0.002583523
BP	GO:0045943	Positive regulation of transcription by RNA polymerase I	7	0.000224856	0.002600874
BP	GO:0008156	Negative regulation of DNA replication	9	0.000227255	0.00261567
BP	GO:0051293	Establishment of spindle localization	9	0.000227255	0.00261567
BP	GO:0043174	Nucleoside salvage	6	0.000231482	0.002657777
BP	GO:0072528	Pyrimidine-containing compound biosynthetic process	11	0.000234307	0.002683622
BP	GO:0007127	Meiosis I	15	0.000243471	0.00278176
BP	GO:0016579	Protein deubiquitination	31	0.000246891	0.002813959
BP	GO:0006733	Oxidoreduction coenzyme metabolic process	25	0.000251073	0.002854657
BP	GO:1900542	Regulation of purine nucleotide metabolic process	19	0.000255503	0.002892726
BP	GO:1900034	Regulation of cellular response to heat	14	0.000255659	0.002892726
BP	GO:0001682	Trna 5'-leader removal	5	0.000275556	0.003102827
BP	GO:0016446	Somatic hypermutation of immunoglobulin genes	5	0.000275556	0.003102827
BP	GO:0006296	Nucleotide-excision repair, DNA incision, 5'-to lesion	9	0.000284306	0.003193658
BP	GO:0033238	Regulation of cellular amine metabolic process	14	0.000292884	0.003282123
BP	GO:0046034	ATP metabolic process	33	0.000310564	0.003471932
BP	GO:0016571	Histone methylation	19	0.000312934	0.003482563
BP	GO:0051196	Regulation of coenzyme metabolic process	15	0.000313746	0.003482563
BP	GO:0031572	G2 DNA damage checkpoint	8	0.000313751	0.003482563
BP	GO:0072524	Pyridine-containing compound metabolic process	24	0.000322318	0.003569172
BP	GO:0044106	Cellular amine metabolic process	18	0.000357671	0.003951292
BP	GO:0019359	Nicotinamide nucleotide biosynthetic process	20	0.000362596	0.003986845
BP	GO:0019363	Pyridine nucleotide biosynthetic process	20	0.000362596	0.003986845
BP	GO:0006140	Regulation of nucleotide metabolic process	19	0.000381299	0.004182655
BP	GO:0016445	Somatic diversification of immunoglobulins	11	0.000392872	0.004299514
BP	GO:0006283	Transcription-coupled nucleotide-excision repair	13	0.000400078	0.004368138
BP	GO:0070482	Response to oxygen levels	41	0.000402271	0.004381846
BP	GO:0002204	Somatic recombination of immunoglobulin genes involved in immune response	10	0.000425595	0.00460372
BP	GO:0002208	Somatic diversification of immunoglobulins involved in immune response	10	0.000425595	0.00460372
BP	GO:0045190	Isotype switching	10	0.000425595	0.00460372

BP	GO:0033683	Nucleotide-excision repair, DNA incision	9	0.000434134	0.004683273
BP	GO:0022411	Cellular component disassembly	49	0.000434954	0.004683273
BP	GO:0043467	Regulation of generation of precursor metabolites and energy	20	0.000436486	0.004688961
BP	GO:0000212	Meiotic spindle organization	5	0.000448834	0.004766823
BP	GO:0002566	Somatic diversification of immune receptors via somatic mutation	5	0.000448834	0.004766823
BP	GO:0006999	Nuclear pore organization	5	0.000448834	0.004766823
BP	GO:0007077	Mitotic nuclear envelope disassembly	5	0.000448834	0.004766823
BP	GO:1904668	Positive regulation of ubiquitin protein ligase activity	5	0.000448834	0.004766823
BP	GO:0072330	Monocarboxylic acid biosynthetic process	35	0.000473602	0.00500711
BP	GO:1903829	Positive regulation of cellular protein localization	35	0.000473602	0.00500711
BP	GO:0006312	Mitotic recombination	6	0.000483202	0.005074165
BP	GO:0042276	Error-prone translesion synthesis	6	0.000483202	0.005074165
BP	GO:0042772	DNA damage response, signal transduction resulting in transcription	6	0.000483202	0.005074165
BP	GO:0043470	Regulation of carbohydrate catabolic process	14	0.000491887	0.005153784
BP	GO:0031100	Animal organ regeneration	13	0.000524783	0.005486159
BP	GO:0019362	Pyridine nucleotide metabolic process	23	0.000527298	0.005487893
BP	GO:0046496	Nicotinamide nucleotide metabolic process	23	0.000527298	0.005487893
BP	GO:0010824	Regulation of centrosome duplication	9	0.000530399	0.005507901
BP	GO:0070585	Protein localization to mitochondrion	18	0.000534557	0.005538764
BP	GO:1900739	Regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	7	0.000540026	0.005570729
BP	GO:1900740	Positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	7	0.000540026	0.005570729
BP	GO:0016570	Histone modification	43	0.000542214	0.005580979
BP	GO:0016569	Covalent chromatin modification	44	0.000550323	0.005652
BP	GO:1901532	Regulation of hematopoietic progenitor cell differentiation	14	0.000556623	0.005704165
BP	GO:0008033	Trna processing	16	0.000568264	0.005810713
BP	GO:0002474	Antigen processing and presentation of peptide antigen via MHC class I	15	0.000569842	0.00581413
BP	GO:0006479	Protein methylation	22	0.000577067	0.005862245
BP	GO:0008213	Protein alkylation	22	0.000577067	0.005862245
BP	GO:0016447	Somatic recombination of immunoglobulin gene segments	10	0.000604987	0.006129425
BP	GO:0009314	Response to radiation	44	0.000605991	0.006129425
BP	GO:0032984	Protein-containing complex disassembly	33	0.0006091	0.006147564
BP	GO:0009411	Response to UV	19	0.000611586	0.006159355

BP	GO:0045132	Meiotic chromosome segregation	12	0.000627013	0.006301148
BP	GO:0043094	Cellular metabolic compound salvage	8	0.000632867	0.00634633
BP	GO:0010569	Regulation of double-strand break repair via homologous recombination	9	0.000643479	0.006425168
BP	GO:0090224	Regulation of spindle organization	9	0.000643479	0.006425168
BP	GO:0046655	Folic acid metabolic process	6	0.000670215	0.006677859
BP	GO:0034605	Cellular response to heat	17	0.000679612	0.006757078
BP	GO:0001833	Inner cell mass cell proliferation	5	0.000693056	0.006847039
BP	GO:0042790	Nucleolar large rrna transcription by RNA polymerase I	5	0.000693056	0.006847039
BP	GO:1901836	Regulation of transcription of nucleolar large rrna by RNA polymerase I	5	0.000693056	0.006847039
BP	GO:0019886	Antigen processing and presentation of exogenous peptide antigen via MHC class II	15	0.00071353	0.007034442
BP	GO:0000387	Spliceosomal snrnp assembly	10	0.000715745	0.007041428
BP	GO:0006997	Nucleus organization	17	0.000750118	0.007364077
BP	GO:0000959	Mitochondrial RNA metabolic process	8	0.000784126	0.007665735
BP	GO:0007019	Microtubule depolymerization	8	0.000784126	0.007665735
BP	GO:0034968	Histone lysine methylation	16	0.000863096	0.008402603
BP	GO:0090175	Regulation of establishment of planar polarity	16	0.000863096	0.008402603
BP	GO:0051053	Negative regulation of DNA metabolic process	19	0.000874093	0.008491971
BP	GO:0001824	Blastocyst development	15	0.000886883	0.008598347
BP	GO:0009119	Ribonucleoside metabolic process	14	0.000892777	0.008623725
BP	GO:0009394	2'-deoxyribonucleotide metabolic process	7	0.000896882	0.008623725
BP	GO:0015949	Nucleobase-containing small molecule interconversion	7	0.000896882	0.008623725
BP	GO:0042273	Ribosomal large subunit biogenesis	7	0.000896882	0.008623725
BP	GO:0031398	Positive regulation of protein ubiquitination	16	0.000954391	0.009157838
BP	GO:1901998	Toxin transport	8	0.000963115	0.009222619
BP	GO:0002495	Antigen processing and presentation of peptide antigen via MHC class II	15	0.000986134	0.009423735
BP	GO:2001169	Regulation of ATP biosynthetic process	14	0.000999441	0.009531404
BP	GO:0000963	Mitochondrial RNA processing	5	0.001024516	0.009691426
BP	GO:0090231	Regulation of spindle checkpoint	5	0.001024516	0.009691426
BP	GO:0090266	Regulation of mitotic cell cycle spindle assembly checkpoint	5	0.001024516	0.009691426
BP	GO:1903504	Regulation of mitotic spindle checkpoint	5	0.001024516	0.009691426
BP	GO:0090501	RNA phosphodiester bond hydrolysis	18	0.001027312	0.009698237
BP	GO:1903747	Regulation of establishment of protein localization to mitochondrion	12	0.001071209	0.010092259

BP	GO:0002504	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	15	0.001094605	0.010291925
BP	GO:0045739	Positive regulation of DNA repair	11	0.00113231	0.010576754
BP	GO:0045737	Positive regulation of cyclin-dependent protein serine/threonine kinase activity	7	0.001133951	0.010576754
BP	GO:0051443	Positive regulation of ubiquitin-protein transferase activity	7	0.001133951	0.010576754
BP	GO:0071168	Protein localization to chromatin	7	0.001133951	0.010576754
BP	GO:0007063	Regulation of sister chromatid cohesion	6	0.001207488	0.011240219
BP	GO:0032259	Methylation	35	0.001269178	0.011790996
BP	GO:0002223	Stimulatory C-type lectin receptor signaling pathway	16	0.0012789	0.011857737
BP	GO:0006414	Translational elongation	17	0.00131823	0.012198198
BP	GO:0000209	Protein polyubiquitination	31	0.001393572	0.012869885
BP	GO:0051193	Regulation of cofactor metabolic process	16	0.001405892	0.012947658
BP	GO:0001844	Protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	7	0.001417472	0.012947658
BP	GO:0019692	Deoxyribose phosphate metabolic process	7	0.001417472	0.012947658
BP	GO:0032467	Positive regulation of cytokinesis	8	0.001418618	0.012947658
BP	GO:0032506	Cytokinetic process	8	0.001418618	0.012947658
BP	GO:0060236	Regulation of mitotic spindle organization	8	0.001418618	0.012947658
BP	GO:0051170	Import into nucleus	17	0.001441586	0.013131643
BP	GO:0002381	Immunoglobulin production involved in immunoglobulin mediated immune response	10	0.001548626	0.014079236
BP	GO:0002220	Innate immune response activating cell surface receptor signaling pathway	16	0.00169189	0.015292461
BP	GO:0007569	Cell aging	16	0.00169189	0.015292461
BP	GO:2000736	Regulation of stem cell differentiation	16	0.00169189	0.015292461
BP	GO:0016572	Histone phosphorylation	8	0.00170286	0.015361901
BP	GO:0043624	Cellular protein complex disassembly	23	0.001707077	0.015370267
BP	GO:0031396	Regulation of protein ubiquitination	23	0.001826083	0.016410161
BP	GO:0060968	Regulation of gene silencing	18	0.001864148	0.016720079
BP	GO:0016052	Carbohydrate catabolic process	22	0.001916102	0.017153154
BP	GO:0070125	Mitochondrial translational elongation	13	0.001949811	0.017421542
BP	GO:0060071	Wnt signaling pathway, planar cell polarity pathway	15	0.001978483	0.017643994
BP	GO:0007096	Regulation of exit from mitosis	5	0.002019196	0.017836866
BP	GO:0009219	Pyrimidine deoxyribonucleotide metabolic process	5	0.002019196	0.017836866
BP	GO:0030397	Membrane disassembly	5	0.002019196	0.017836866
BP	GO:0033262	Regulation of nuclear cell cycle DNA replication	5	0.002019196	0.017836866

BP	GO:0051081	Nuclear envelope disassembly	5	0.002019196	0.017836866
BP	GO:0044818	Mitotic G2/M transition checkpoint	6	0.002024054	0.017846042
BP	GO:0009162	Deoxyribonucleoside monophosphate metabolic process	4	0.002099971	0.01834236
BP	GO:0009263	Deoxyribonucleotide biosynthetic process	4	0.002099971	0.01834236
BP	GO:0042023	DNA endoreduplication	4	0.002099971	0.01834236
BP	GO:0051255	Spindle midzone assembly	4	0.002099971	0.01834236
BP	GO:0075522	IRES-dependent viral translational initiation	4	0.002099971	0.01834236
BP	GO:0045840	Positive regulation of mitotic nuclear division	9	0.002104689	0.018349276
BP	GO:0051204	Protein insertion into mitochondrial membrane	7	0.002147947	0.018656793
BP	GO:1901976	Regulation of cell cycle checkpoint	7	0.002147947	0.018656793
BP	GO:0050684	Regulation of mrna processing	15	0.002171895	0.018829805
BP	GO:0002377	Immunoglobulin production	14	0.002302965	0.019929176
BP	GO:0072594	Establishment of protein localization to organelle	43	0.00230725	0.01992935
BP	GO:0062012	Regulation of small molecule metabolic process	42	0.002322712	0.02002589
BP	GO:0070126	Mitochondrial translational termination	13	0.002405801	0.020704068
BP	GO:0035690	Cellular response to drug	36	0.002432453	0.020894953
BP	GO:0035036	Sperm-egg recognition	9	0.002442122	0.020901166
BP	GO:1902369	Negative regulation of RNA catabolic process	9	0.002442122	0.020901166
BP	GO:0000132	Establishment of mitotic spindle orientation	6	0.002562035	0.021887367
BP	GO:0048511	Rhythmic process	30	0.002581189	0.022010762
BP	GO:0006356	Regulation of transcription by RNA polymerase I	7	0.002607678	0.022155783
BP	GO:1904031	Positive regulation of cyclin-dependent protein kinase activity	7	0.002607678	0.022155783
BP	GO:0072655	Establishment of protein localization to mitochondrion	16	0.002626511	0.022275291
BP	GO:0000726	Non-recombinational repair	13	0.002664608	0.02255745
BP	GO:0006379	Mrna cleavage	5	0.002719085	0.022771118
BP	GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	5	0.002719085	0.022771118
BP	GO:0009148	Pyrimidine nucleoside triphosphate biosynthetic process	5	0.002719085	0.022771118
BP	GO:0009264	Deoxyribonucleotide catabolic process	5	0.002719085	0.022771118
BP	GO:0034629	Cellular protein-containing complex localization	5	0.002719085	0.022771118
BP	GO:0097329	Response to antimetabolite	5	0.002719085	0.022771118
BP	GO:0009988	Cell-cell recognition	11	0.002761108	0.023040462
BP	GO:1903312	Negative regulation of mrna metabolic process	11	0.002761108	0.023040462
BP	GO:0006415	Translational termination	14	0.002788539	0.02322788
BP	GO:0043414	Macromolecule methylation	29	0.002793902	0.023231147

BP	GO:0002639	Positive regulation of immunoglobulin production	8	0.002832335	0.023467204
BP	GO:0043489	RNA stabilization	8	0.002832335	0.023467204
BP	GO:0018022	Peptidyl-lysine methylation	16	0.00285721	0.023631406
BP	GO:0050852	T cell receptor signaling pathway	21	0.003022715	0.024956088
BP	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	11	0.003100429	0.025495618
BP	GO:0001736	Establishment of planar polarity	16	0.003104431	0.025495618
BP	GO:0007164	Establishment of tissue polarity	16	0.003104431	0.025495618
BP	GO:0008655	Pyrimidine-containing compound salvage	4	0.003142493	0.025583398
BP	GO:0035404	Histone-serine phosphorylation	4	0.003142493	0.025583398
BP	GO:0043097	Pyrimidine nucleoside salvage	4	0.003142493	0.025583398
BP	GO:0048875	Chemical homeostasis within a tissue	4	0.003142493	0.025583398
BP	GO:0051573	Negative regulation of histone H3-K9 methylation	4	0.003142493	0.025583398
BP	GO:0006730	One-carbon metabolic process	6	0.003200564	0.02596569
BP	GO:0045830	Positive regulation of isotype switching	6	0.003200564	0.02596569
BP	GO:0090263	Positive regulation of canonical Wnt signaling pathway	17	0.003306864	0.026781586
BP	GO:0006221	Pyrimidine nucleotide biosynthetic process	8	0.003316295	0.0268115
BP	GO:0009408	Response to heat	19	0.003327174	0.026852996
BP	GO:0006303	Double-strand break repair via nonhomologous end joining	12	0.003397029	0.027369511
BP	GO:0030177	Positive regulation of Wnt signaling pathway	20	0.003403807	0.027376921
BP	GO:0031099	Regeneration	22	0.003465216	0.027785566
BP	GO:0000245	Spliceosomal complex assembly	11	0.003472452	0.027785566
BP	GO:0002312	B cell activation involved in immune response	11	0.003472452	0.027785566
BP	GO:2001022	Positive regulation of response to DNA damage stimulus	13	0.003580613	0.028602061
BP	GO:1901030	Positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	7	0.003749974	0.029903801
BP	GO:0001676	Long-chain fatty acid metabolic process	13	0.004322137	0.034407748
BP	GO:0001738	Morphogenesis of a polarized epithelium	17	0.004472759	0.035546264
BP	GO:0000722	Telomere maintenance via recombination	4	0.004489323	0.035556957
BP	GO:0051095	Regulation of helicase activity	4	0.004489323	0.035556957
BP	GO:1903320	Regulation of protein modification by small protein conjugation or removal	24	0.004577645	0.036103114
BP	GO:0001832	Blastocyst growth	5	0.004617906	0.036103114
BP	GO:0009147	Pyrimidine nucleoside triphosphate metabolic process	5	0.004617906	0.036103114
BP	GO:0032069	Regulation of nuclease activity	5	0.004617906	0.036103114
BP	GO:0046386	Deoxyribose phosphate catabolic process	5	0.004617906	0.036103114
BP	GO:0046599	Regulation of centriole replication	5	0.004617906	0.036103114

BP	GO:0070987	Error-free translesion synthesis	5	0.004617906	0.036103114
BP	GO:1903322	Positive regulation of protein modification by small protein conjugation or removal	16	0.004620086	0.036103114
BP	GO:0060147	Regulation of posttranscriptional gene silencing	15	0.004724928	0.036799315
BP	GO:0060966	Regulation of gene silencing by RNA	15	0.004724928	0.036799315
BP	GO:0006735	NADH regeneration	6	0.004823009	0.037314492
BP	GO:0061621	Canonical glycolysis	6	0.004823009	0.037314492
BP	GO:0061718	Glucose catabolic process to pyruvate	6	0.004823009	0.037314492
BP	GO:0000380	Alternative mrna splicing, via spliceosome	9	0.004823016	0.037314492
BP	GO:0097327	Response to antineoplastic agent	13	0.005182717	0.040031138
BP	GO:0045911	Positive regulation of DNA recombination	7	0.005236802	0.04031561
BP	GO:0048255	Mrna stabilization	7	0.005236802	0.04031561
BP	GO:0007623	Circadian rhythm	22	0.00529827	0.040721736
BP	GO:0006919	Activation of cysteine-type endopeptidase activity involved in apoptotic process	11	0.005332444	0.040917096
BP	GO:0001889	Liver development	16	0.005374806	0.041174536
BP	GO:1901568	Fatty acid derivative metabolic process	18	0.005662122	0.04330458
BP	GO:0010458	Exit from mitosis	6	0.005829116	0.044219899
BP	GO:0051294	Establishment of spindle orientation	6	0.005829116	0.044219899
BP	GO:0061615	Glycolytic process through fructose-6-phosphate	6	0.005829116	0.044219899
BP	GO:0061620	Glycolytic process through glucose-6-phosphate	6	0.005829116	0.044219899
BP	GO:0070979	Protein K11-linked ubiquitination	6	0.005829116	0.044219899
BP	GO:0070584	Mitochondrion morphogenesis	5	0.005854308	0.044339026
BP	GO:1900371	Regulation of purine nucleotide biosynthetic process	14	0.006121146	0.046259767
BP	GO:0051567	Histone H3-K9 methylation	7	0.006127711	0.046259767
BP	GO:0002921	Negative regulation of humoral immune response	4	0.006176552	0.0463291
BP	GO:0006206	Pyrimidine nucleobase metabolic process	4	0.006176552	0.0463291
BP	GO:0009130	Pyrimidine nucleoside monophosphate biosynthetic process	4	0.006176552	0.0463291
BP	GO:0035563	Positive regulation of chromatin binding	4	0.006176552	0.0463291
BP	GO:0007568	Aging	31	0.006232365	0.04667282
BP	GO:0071347	Cellular response to interleukin-1	18	0.006467623	0.048357121
BP	GO:0030808	Regulation of nucleotide biosynthetic process	14	0.006633778	0.049520198
BP	GO:0061008	Hepaticobiliary system development	16	0.00669172	0.049873058
CC	GO:0098687	Chromosomal region	104	3.85E-46	2.23E-43
CC	GO:0000775	Chromosome, centromeric region	68	8.32E-36	2.41E-33
CC	GO:0000793	Condensed chromosome	70	2.14E-35	4.13E-33

CC	GO:0000776	Kinetochore	50	1.61E-27	2.32E-25
CC	GO:0005819	Spindle	78	1.52E-26	1.76E-24
CC	GO:0000779	Condensed chromosome, centromeric region	44	2.30E-25	2.22E-23
CC	GO:0000777	Condensed chromosome kinetochore	41	3.20E-24	2.65E-22
CC	GO:0044454	Nuclear chromosome part	83	4.28E-19	3.10E-17
CC	GO:0000922	Spindle pole	42	2.75E-17	1.77E-15
CC	GO:0005813	Centrosome	79	1.01E-16	5.87E-15
CC	GO:0072686	Mitotic spindle	30	3.56E-14	1.88E-12
CC	GO:0000781	Chromosome, telomeric region	38	7.66E-14	3.70E-12
CC	GO:0005874	Microtubule	58	4.37E-12	1.94E-10
CC	GO:0000785	Chromatin	70	3.49E-11	1.44E-09
CC	GO:0000794	Condensed nuclear chromosome	23	4.17E-11	1.61E-09
CC	GO:0000784	Nuclear chromosome, telomeric region	29	1.04E-10	3.76E-09
CC	GO:0042555	MCM complex	9	5.06E-10	1.72E-08
CC	GO:0030496	Midbody	34	5.90E-10	1.90E-08
CC	GO:0005657	Replication fork	18	1.20E-09	3.64E-08
CC	GO:0000940	Condensed chromosome outer kinetochore	9	1.92E-09	5.55E-08
CC	GO:0005876	Spindle microtubule	17	6.74E-09	1.86E-07
CC	GO:0005635	Nuclear envelope	57	7.58E-09	2.00E-07
CC	GO:0101031	Chaperone complex	10	3.44E-08	8.67E-07
CC	GO:0000792	Heterochromatin	19	6.59E-08	1.59E-06
CC	GO:0000790	Nuclear chromatin	44	9.77E-08	2.26E-06
CC	GO:0005643	Nuclear pore	16	2.59E-07	5.77E-06
CC	GO:0005681	Spliceosomal complex	28	3.23E-07	6.93E-06
CC	GO:0031965	Nuclear membrane	40	3.74E-07	7.73E-06
CC	GO:0005732	Small nucleolar ribonucleoprotein complex	10	1.34E-06	2.65E-05
CC	GO:0000152	Nuclear ubiquitin ligase complex	12	1.37E-06	2.65E-05
CC	GO:0034709	Methylosome	7	1.73E-06	2.98E-05
CC	GO:0044215	Other organism	17	1.75E-06	2.98E-05
CC	GO:0044216	Other organism cell	17	1.75E-06	2.98E-05
CC	GO:0044217	Other organism part	17	1.75E-06	2.98E-05
CC	GO:0018995	Host	16	2.55E-06	4.10E-05
CC	GO:0043657	Host cell	16	2.55E-06	4.10E-05
CC	GO:0034708	Methyltransferase complex	18	4.22E-06	6.61E-05
CC	GO:0005721	Pericentric heterochromatin	8	1.12E-05	0.000171206

CC	GO:0045120	Pronucleus	7	1.20E-05	0.000176214
CC	GO:0000502	Proteasome complex	14	1.22E-05	0.000176214
CC	GO:0097431	Mitotic spindle pole	9	1.26E-05	0.000177733
CC	GO:1905369	Endopeptidase complex	14	1.49E-05	0.000204854
CC	GO:0005720	Nuclear heterochromatin	10	1.59E-05	0.000213527
CC	GO:1905368	Peptidase complex	15	2.09E-05	0.000274463
CC	GO:0090734	Site of DNA damage	14	2.63E-05	0.000338493
CC	GO:0044450	Microtubule organizing center part	25	3.19E-05	0.00040137
CC	GO:0000307	Cyclin-dependent protein kinase holoenzyme complex	9	3.42E-05	0.000421596
CC	GO:0071007	U2-type catalytic step 2 spliceosome	9	4.63E-05	0.000554023
CC	GO:0046540	U4/U6 x U5 tri-snrnp complex	10	4.78E-05	0.000554023
CC	GO:0097526	Spliceosomal tri-snrnp complex	10	4.78E-05	0.000554023
CC	GO:0034399	Nuclear periphery	20	6.48E-05	0.000735287
CC	GO:0005759	Mitochondrial matrix	48	8.12E-05	0.000903949
CC	GO:0000800	Lateral element	6	9.39E-05	0.001007249
CC	GO:0010369	Chromocenter	6	9.39E-05	0.001007249
CC	GO:0071013	Catalytic step 2 spliceosome	15	0.000102132	0.001075174
CC	GO:0044452	Nucleolar part	22	0.000107009	0.001106396
CC	GO:0051233	Spindle midzone	8	0.000135548	0.001376883
CC	GO:0005680	Anaphase-promoting complex	7	0.000157081	0.001564703
CC	GO:0005684	U2-type spliceosomal complex	14	0.000159443	0.001564703
CC	GO:0017101	Aminoacyl-trna synthetase multienzyme complex	5	0.000269548	0.002601136
CC	GO:0022624	Proteasome accessory complex	7	0.000297753	0.002826211
CC	GO:0000780	Condensed nuclear chromosome, centromeric region	6	0.000330951	0.002994072
CC	GO:0034719	SMN-Sm protein complex	6	0.000330951	0.002994072
CC	GO:0042599	Lamellar body	6	0.000330951	0.002994072
CC	GO:0031970	Organelle envelope lumen	14	0.00036408	0.003243109
CC	GO:0005814	Centriole	18	0.00045888	0.003965544
CC	GO:1904813	Ficolin-1-rich granule lumen	18	0.00045888	0.003965544
CC	GO:0015030	Cajal body	13	0.000502336	0.004277244
CC	GO:0061695	Transferase complex, transferring phosphorus-containing groups	23	0.000579815	0.004865402
CC	GO:0120114	Sm-like protein family complex	15	0.000608572	0.005033762
CC	GO:0042575	DNA polymerase complex	5	0.000678268	0.005479163
CC	GO:1990752	Microtubule end	7	0.000681347	0.005479163

CC	GO:0031519	Pcg protein complex	9	0.000750026	0.005948838
CC	GO:0098798	Mitochondrial protein complex	27	0.00087306	0.006831101
CC	GO:0030894	Replisome	6	0.000886562	0.006844255
CC	GO:0030677	Ribonuclease P complex	5	0.001002895	0.007640473
CC	GO:0005758	Mitochondrial intermembrane space	12	0.001322908	0.00994758
CC	GO:1990391	DNA repair complex	7	0.001379414	0.010239497
CC	GO:0000313	Organellar ribosome	13	0.001503858	0.010884169
CC	GO:0005761	Mitochondrial ribosome	13	0.001503858	0.010884169
CC	GO:1902554	Serine/threonine protein kinase complex	11	0.001628062	0.011637631
CC	GO:0000803	Sex chromosome	7	0.001706724	0.01205114
CC	GO:0030532	Small nuclear ribonucleoprotein complex	13	0.001871521	0.013055553
CC	GO:0035098	ESC/E(Z) complex	5	0.001977517	0.013275925
CC	GO:0035371	Microtubule plus-end	5	0.001977517	0.013275925
CC	GO:0071005	U2-type precatalytic spliceosome	9	0.002038547	0.013275925
CC	GO:0071011	Precatalytic spliceosome	9	0.002038547	0.013275925
CC	GO:0005838	Proteasome regulatory particle	4	0.002063615	0.013275925
CC	GO:0030681	Multimeric ribonuclease P complex	4	0.002063615	0.013275925
CC	GO:0031080	Nuclear pore outer ring	4	0.002063615	0.013275925
CC	GO:0097525	Spliceosomal snrnp complex	12	0.002370467	0.015082425
CC	GO:0000178	Exosome (rnase complex)	6	0.002502019	0.015577084
CC	GO:1905354	Exoribonuclease complex	6	0.002502019	0.015577084
CC	GO:0031968	Organelle outer membrane	22	0.002706912	0.016673423
CC	GO:0019867	Outer membrane	22	0.003078942	0.018249116
CC	GO:0005652	Nuclear lamina	4	0.003088797	0.018249116
CC	GO:0005687	U4 snrnp	4	0.003088797	0.018249116
CC	GO:1990023	Mitotic spindle midzone	4	0.003088797	0.018249116
CC	GO:0035861	Site of double-strand break	9	0.003145353	0.018291475
CC	GO:0019866	Organelle inner membrane	45	0.003208815	0.018291475
CC	GO:0009295	Nucleoid	8	0.003222332	0.018291475
CC	GO:0042645	Mitochondrial nucleoid	8	0.003222332	0.018291475
CC	GO:0046930	Pore complex	5	0.003506812	0.019713049
CC	GO:0000795	Synaptonemal complex	7	0.003653702	0.020147557
CC	GO:0099086	Synaptonemal structure	7	0.003653702	0.020147557
CC	GO:0005637	Nuclear inner membrane	8	0.0037535	0.020502606

CC	GO:0005847	Mrna cleavage and polyadenylation specificity factor complex	4	0.004413619	0.023822008
CC	GO:0005697	Telomerase holoenzyme complex	5	0.00452577	0.023822008
CC	GO:0035145	Exon-exon junction complex	5	0.00452577	0.023822008
CC	GO:0043073	Germ cell nucleus	5	0.00452577	0.023822008
CC	GO:0016363	Nuclear matrix	14	0.004580921	0.023895073
CC	GO:0043596	Nuclear replication fork	6	0.004713392	0.024366554
CC	GO:0000315	Organellar large ribosomal subunit	9	0.005300988	0.026752764
CC	GO:0005762	Mitochondrial large ribosomal subunit	9	0.005300988	0.026752764
CC	GO:0035097	Histone methyltransferase complex	10	0.005313589	0.026752764
CC	GO:0001650	Fibrillar center	16	0.00554177	0.027661077
CC	GO:0005685	U1 snrnp	6	0.00569798	0.027922589
CC	GO:0090543	Flemming body	6	0.00569798	0.027922589
CC	GO:0005839	Proteasome core complex	5	0.00573884	0.027922589
CC	GO:0005741	Mitochondrial outer membrane	19	0.006188199	0.02985806
CC	GO:1902911	Protein kinase complex	11	0.006300412	0.030148251
CC	GO:0032153	Cell division site	9	0.006737066	0.031713507
CC	GO:0032155	Cell division site part	9	0.006737066	0.031713507
CC	GO:0005775	Vacuolar lumen	19	0.007456468	0.034816894
CC	GO:0005849	Mrna cleavage factor complex	4	0.008102127	0.037231202
CC	GO:0030684	Preribosome	4	0.008102127	0.037231202
CC	GO:0101002	Ficolin-1-rich granule	20	0.008275693	0.037729339
CC	GO:0035578	Azurophil granule lumen	12	0.008425079	0.038110318
CC	GO:0000151	Ubiquitin ligase complex	23	0.008961341	0.040221834
CC	GO:0044798	Nuclear transcription factor complex	16	0.010347972	0.046088276
CC	GO:0001673	Male germ cell nucleus	4	0.010528336	0.046533639
MF	GO:0140097	Catalytic activity, acting on DNA	41	1.19E-15	9.25E-13
MF	GO:0008094	DNA-dependent atpase activity	25	8.91E-13	3.46E-10
MF	GO:0016887	Atpase activity	52	2.54E-12	6.58E-10
MF	GO:0003684	Damaged DNA binding	21	5.00E-11	9.71E-09
MF	GO:0043142	Single-stranded DNA-dependent atpase activity	9	3.19E-09	4.96E-07
MF	GO:0003697	Single-stranded DNA binding	23	6.87E-09	7.97E-07
MF	GO:0004386	Helicase activity	28	7.19E-09	7.97E-07
MF	GO:0042623	Atpase activity, coupled	38	1.40E-08	1.36E-06
MF	GO:0003682	Chromatin binding	58	9.19E-08	7.92E-06

MF	GO:0051082	Unfolded protein binding	19	8.86E-07	6.88E-05
MF	GO:0016874	Ligase activity	25	1.13E-06	7.97E-05
MF	GO:0003678	DNA helicase activity	13	1.24E-06	8.02E-05
MF	GO:0042393	Histone binding	28	5.55E-06	0.000331307
MF	GO:0000217	DNA secondary structure binding	9	6.23E-06	0.000345469
MF	GO:0140098	Catalytic activity, acting on RNA	37	7.90E-06	0.000408452
MF	GO:0004003	ATP-dependent DNA helicase activity	10	1.41E-05	0.000683718
MF	GO:0008026	ATP-dependent helicase activity	13	1.70E-05	0.000731679
MF	GO:0070035	Purine NTP-dependent helicase activity	13	1.70E-05	0.000731679
MF	GO:0000400	Four-way junction DNA binding	7	2.94E-05	0.001200221
MF	GO:0000287	Magnesium ion binding	29	6.68E-05	0.002583064
MF	GO:0015631	Tubulin binding	33	6.99E-05	0.002583064
MF	GO:0042054	Histone methyltransferase activity	12	8.34E-05	0.002940974
MF	GO:0016893	Endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	10	0.000126462	0.004266714
MF	GO:0043021	Ribonucleoprotein complex binding	18	0.00014167	0.004443619
MF	GO:0000049	Trna binding	11	0.000143158	0.004443619
MF	GO:0030515	Snorna binding	7	0.000158762	0.004571126
MF	GO:0016879	Ligase activity, forming carbon-nitrogen bonds	10	0.000159047	0.004571126
MF	GO:0140101	Catalytic activity, acting on a trna	17	0.00016615	0.004604736
MF	GO:0004518	Nuclease activity	24	0.00023083	0.006176702
MF	GO:0004812	Aminoacyl-trna ligase activity	9	0.000268277	0.006715587
MF	GO:0016875	Ligase activity, forming carbon-oxygen bonds	9	0.000268277	0.006715587
MF	GO:0008187	Poly-pyrimidine tract binding	7	0.000311978	0.00756547
MF	GO:0003727	Single-stranded RNA binding	13	0.000323342	0.007603433
MF	GO:0008017	Microtubule binding	23	0.000372876	0.00851035
MF	GO:0070182	DNA polymerase binding	6	0.000452267	0.010027416
MF	GO:0016741	Transferase activity, transferring one-carbon groups	26	0.000477785	0.010298931
MF	GO:0016891	Endoribonuclease activity, producing 5'-phosphomonoesters	8	0.000571824	0.011992853
MF	GO:0004540	Ribonuclease activity	15	0.000877377	0.016802756
MF	GO:0016646	Oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	5	0.00088385	0.016802756
MF	GO:0019104	DNA N-glycosylase activity	5	0.00088385	0.016802756
MF	GO:0008327	Methyl-cpg binding	6	0.000887775	0.016802756
MF	GO:0004536	Deoxyribonuclease activity	9	0.00094171	0.017399213

MF	GO:0004527	Exonuclease activity	12	0.000999314	0.018034128
MF	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	19	0.001052061	0.01855453
MF	GO:0008266	Poly(U) RNA binding	6	0.001200209	0.020606767
MF	GO:0016810	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	15	0.001221535	0.020606767
MF	GO:0035173	Histone kinase activity	5	0.001302878	0.02151134
MF	GO:0018024	Histone-lysine N-methyltransferase activity	9	0.001351129	0.02184325
MF	GO:0004521	Endoribonuclease activity	10	0.001476827	0.023388117
MF	GO:0008536	Ran gtpase binding	7	0.001545822	0.023481463
MF	GO:0016814	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	6	0.001590267	0.023481463
MF	GO:0070717	Poly-purine tract binding	6	0.001590267	0.023481463
MF	GO:0016796	Exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	9	0.00160376	0.023481463
MF	GO:0008409	5'-3' exonuclease activity	5	0.002553442	0.034193131
MF	GO:0004523	RNA-DNA hybrid ribonuclease activity	4	0.002555672	0.034193131
MF	GO:0030983	Mismatched DNA binding	4	0.002555672	0.034193131
MF	GO:0033204	Ribonuclease P RNA binding	4	0.002555672	0.034193131
MF	GO:0097617	Annealing activity	4	0.002555672	0.034193131
MF	GO:0140142	Nucleocytoplasmic carrier activity	6	0.002650475	0.034860483
MF	GO:0044389	Ubiquitin-like protein ligase binding	31	0.002818111	0.036447572
MF	GO:0008170	N-methyltransferase activity	13	0.003097149	0.039399802
MF	GO:0048037	Cofactor binding	43	0.00338871	0.042413535
MF	GO:0034061	DNA polymerase activity	7	0.003513832	0.043281483
MF	GO:0032404	Mismatch repair complex binding	4	0.003814105	0.046246024
MF	GO:0050661	NADP binding	9	0.00401982	0.047990464

The co-expression genes of SKA2 with GO notes

Ontology	ID	Description	Count	P value	P adjust
BP	GO:0007059	Chromosome segregation	68	7.90E-54	2.15E-50
BP	GO:0006260	DNA replication	65	9.44E-52	1.28E-48
BP	GO:0000280	Nuclear division	71	3.47E-49	3.15E-46
BP	GO:0048285	Organelle fission	72	4.05E-47	2.75E-44
BP	GO:0140014	Mitotic nuclear division	58	1.49E-45	8.09E-43
BP	GO:0000819	Sister chromatid segregation	47	1.89E-41	8.54E-39
BP	GO:0098813	Nuclear chromosome segregation	53	3.08E-41	1.20E-38
BP	GO:0000070	Mitotic sister chromatid segregation	43	9.33E-40	3.17E-37
BP	GO:0006261	DNA-dependent DNA replication	38	3.42E-33	1.03E-30
BP	GO:0051983	Regulation of chromosome segregation	32	1.13E-30	3.07E-28
BP	GO:0071103	DNA conformation change	47	4.01E-29	9.90E-27
BP	GO:1901990	Regulation of mitotic cell cycle phase transition	56	9.81E-29	2.22E-26
BP	GO:1901987	Regulation of cell cycle phase transition	58	1.09E-28	2.29E-26
BP	GO:0007088	Regulation of mitotic nuclear division	36	3.86E-28	7.50E-26
BP	GO:0000226	Microtubule cytoskeleton organization	57	5.38E-28	9.75E-26
BP	GO:0051783	Regulation of nuclear division	36	6.66E-26	1.13E-23
BP	GO:0007051	Spindle organization	33	7.25E-25	1.16E-22
BP	GO:0033045	Regulation of sister chromatid segregation	25	1.13E-24	1.71E-22
BP	GO:0044839	Cell cycle G2/M phase transition	41	1.52E-24	2.18E-22
BP	GO:0044843	Cell cycle G1/S phase transition	42	1.51E-23	2.05E-21
BP	GO:1902850	Microtubule cytoskeleton organization involved in mitosis	29	2.05E-23	2.53E-21
BP	GO:0007091	Metaphase/anaphase transition of mitotic cell cycle	21	2.14E-23	2.53E-21
BP	GO:0010965	Regulation of mitotic sister chromatid separation	21	2.14E-23	2.53E-21
BP	GO:0044784	Metaphase/anaphase transition of cell cycle	21	6.40E-23	6.96E-21
BP	GO:0051306	Mitotic sister chromatid separation	21	6.40E-23	6.96E-21
BP	GO:0000086	G2/M transition of mitotic cell cycle	38	7.98E-23	8.35E-21
BP	GO:0000082	G1/S transition of mitotic cell cycle	40	8.66E-23	8.72E-21
BP	GO:0000075	Cell cycle checkpoint	35	1.08E-22	1.05E-20
BP	GO:1905818	Regulation of chromosome separation	21	2.97E-22	2.79E-20
BP	GO:0051304	Chromosome separation	23	3.68E-22	3.34E-20
BP	GO:0010948	Negative regulation of cell cycle process	43	2.13E-21	1.87E-19
BP	GO:0033047	Regulation of mitotic sister chromatid segregation	21	3.00E-21	2.55E-19

BP	GO:0051321	Meiotic cell cycle	34	3.26E-21	2.69E-19
BP	GO:0090068	Positive regulation of cell cycle process	39	5.08E-21	4.06E-19
BP	GO:0045787	Positive regulation of cell cycle	44	7.25E-21	5.63E-19
BP	GO:0006323	DNA packaging	33	7.75E-21	5.85E-19
BP	GO:0007093	Mitotic cell cycle checkpoint	29	2.62E-20	1.93E-18
BP	GO:0044786	Cell cycle DNA replication	20	8.48E-20	6.07E-18
BP	GO:0007052	Mitotic spindle organization	24	1.08E-19	7.50E-18
BP	GO:0051052	Regulation of DNA metabolic process	44	1.54E-19	1.05E-17
BP	GO:0030071	Regulation of mitotic metaphase/anaphase transition	18	2.26E-19	1.50E-17
BP	GO:1902099	Regulation of metaphase/anaphase transition of cell cycle	18	5.97E-19	3.86E-17
BP	GO:0033260	Nuclear DNA replication	18	9.49E-19	6.00E-17
BP	GO:1902749	Regulation of cell cycle G2/M phase transition	31	2.71E-18	1.67E-16
BP	GO:0045930	Negative regulation of mitotic cell cycle	37	5.93E-18	3.58E-16
BP	GO:1903046	Meiotic cell cycle process	27	7.86E-18	4.65E-16
BP	GO:0033044	Regulation of chromosome organization	37	8.21E-18	4.75E-16
BP	GO:0006275	Regulation of DNA replication	23	1.00E-17	5.68E-16
BP	GO:0034508	Centromere complex assembly	18	1.76E-17	9.78E-16
BP	GO:0010389	Regulation of G2/M transition of mitotic cell cycle	28	1.79E-16	9.76E-15
BP	GO:0140013	Meiotic nuclear division	25	1.97E-16	1.05E-14
BP	GO:0033046	Negative regulation of sister chromatid segregation	15	2.80E-16	1.46E-14
BP	GO:1901988	Negative regulation of cell cycle phase transition	32	2.84E-16	1.46E-14
BP	GO:0045839	Negative regulation of mitotic nuclear division	16	3.39E-16	1.71E-14
BP	GO:0051985	Negative regulation of chromosome segregation	15	4.54E-16	2.25E-14
BP	GO:0031055	Chromatin remodeling at centromere	16	5.10E-16	2.47E-14
BP	GO:0051310	Metaphase plate congression	17	6.01E-16	2.87E-14
BP	GO:0006310	DNA recombination	31	6.65E-16	3.12E-14
BP	GO:0045841	Negative regulation of mitotic metaphase/anaphase transition	14	7.59E-16	3.44E-14
BP	GO:2000816	Negative regulation of mitotic sister chromatid separation	14	7.59E-16	3.44E-14
BP	GO:1902100	Negative regulation of metaphase/anaphase transition of cell cycle	14	1.29E-15	5.67E-14
BP	GO:1905819	Negative regulation of chromosome separation	14	1.29E-15	5.67E-14
BP	GO:1901991	Negative regulation of mitotic cell cycle phase transition	30	1.74E-15	7.52E-14
BP	GO:0034080	CENP-A containing nucleosome assembly	15	2.69E-15	1.12E-13

BP	GO:0061641	CENP-A containing chromatin organization	15	2.69E-15	1.12E-13
BP	GO:0071824	Protein-DNA complex subunit organization	30	3.11E-15	1.28E-13
BP	GO:0033048	Negative regulation of mitotic sister chromatid segregation	14	3.53E-15	1.43E-13
BP	GO:0051784	Negative regulation of nuclear division	16	4.75E-15	1.90E-13
BP	GO:0065004	Protein-DNA complex assembly	28	5.09E-15	2.01E-13
BP	GO:0050000	Chromosome localization	18	5.36E-15	2.05E-13
BP	GO:0051303	Establishment of chromosome localization	18	5.36E-15	2.05E-13
BP	GO:0006336	DNA replication-independent nucleosome assembly	16	6.68E-15	2.49E-13
BP	GO:0034724	DNA replication-independent nucleosome organization	16	6.68E-15	2.49E-13
BP	GO:0043486	Histone exchange	16	1.29E-14	4.74E-13
BP	GO:0043044	ATP-dependent chromatin remodeling	18	1.92E-14	6.97E-13
BP	GO:0090329	Regulation of DNA-dependent DNA replication	15	2.66E-14	9.42E-13
BP	GO:0051225	Spindle assembly	19	2.67E-14	9.42E-13
BP	GO:0051383	Kinetochore organization	11	3.91E-14	1.36E-12
BP	GO:0006333	Chromatin assembly or disassembly	25	4.55E-14	1.57E-12
BP	GO:0034502	Protein localization to chromosome	18	6.26E-14	2.13E-12
BP	GO:0071459	Protein localization to chromosome, centromeric region	11	8.07E-14	2.71E-12
BP	GO:0022616	DNA strand elongation	10	9.74E-14	3.23E-12
BP	GO:0070507	Regulation of microtubule cytoskeleton organization	24	1.32E-13	4.33E-12
BP	GO:2001251	Negative regulation of chromosome organization	21	1.39E-13	4.49E-12
BP	GO:0072331	Signal transduction by p53 class mediator	29	2.67E-13	8.54E-12
BP	GO:0006302	Double-strand break repair	26	3.25E-13	1.03E-11
BP	GO:0006270	DNA replication initiation	12	3.44E-13	1.03E-11
BP	GO:0007094	Mitotic spindle assembly checkpoint	12	3.44E-13	1.03E-11
BP	GO:0031577	Spindle checkpoint	12	3.44E-13	1.03E-11
BP	GO:0071173	Spindle assembly checkpoint	12	3.44E-13	1.03E-11
BP	GO:0071174	Mitotic spindle checkpoint	12	3.44E-13	1.03E-11
BP	GO:0034728	Nucleosome organization	23	5.68E-13	1.68E-11
BP	GO:0006334	Nucleosome assembly	21	6.64E-13	1.94E-11
BP	GO:0031145	Anaphase-promoting complex-dependent catabolic process	17	6.91E-13	2.00E-11
BP	GO:0031497	Chromatin assembly	22	9.64E-13	2.76E-11
BP	GO:0000723	Telomere maintenance	22	1.10E-12	3.13E-11
BP	GO:0007080	Mitotic metaphase plate congression	13	1.17E-12	3.28E-11

BP	GO:0006338	Chromatin remodeling	22	1.44E-12	4.00E-11
BP	GO:0031570	DNA integrity checkpoint	21	1.59E-12	4.37E-11
BP	GO:0032392	DNA geometric change	17	1.95E-12	5.30E-11
BP	GO:0032201	Telomere maintenance via semi-conservative replication	11	2.67E-12	7.18E-11
BP	GO:0032886	Regulation of microtubule-based process	24	4.33E-12	1.15E-10
BP	GO:0032200	Telomere organization	22	5.83E-12	1.54E-10
BP	GO:0034501	Protein localization to kinetochore	9	6.73E-12	1.76E-10
BP	GO:0045931	Positive regulation of mitotic cell cycle	21	9.09E-12	2.33E-10
BP	GO:0000724	Double-strand break repair via homologous recombination	18	9.09E-12	2.33E-10
BP	GO:0000725	Recombinational repair	18	1.07E-11	2.72E-10
BP	GO:1901989	Positive regulation of cell cycle phase transition	17	1.50E-11	3.78E-10
BP	GO:0030261	Chromosome condensation	11	2.40E-11	6.00E-10
BP	GO:0032508	DNA duplex unwinding	15	4.07E-11	1.00E-09
BP	GO:0061982	Meiosis I cell cycle process	16	5.71E-11	1.40E-09
BP	GO:0007098	Centrosome cycle	17	1.61E-10	3.90E-09
BP	GO:1901796	Regulation of signal transduction by p53 class mediator	21	1.64E-10	3.95E-09
BP	GO:0008608	Attachment of spindle microtubules to kinetochore	10	1.91E-10	4.57E-09
BP	GO:0010639	Negative regulation of organelle organization	29	3.20E-10	7.56E-09
BP	GO:0007127	Meiosis I	15	3.62E-10	8.48E-09
BP	GO:0070317	Negative regulation of G0 to G1 transition	11	4.97E-10	1.16E-08
BP	GO:0090307	Mitotic spindle assembly	12	5.43E-10	1.25E-08
BP	GO:0031023	Microtubule organizing center organization	17	6.35E-10	1.45E-08
BP	GO:0051984	Positive regulation of chromosome segregation	9	6.63E-10	1.50E-08
BP	GO:0061640	Cytoskeleton-dependent cytokinesis	14	1.38E-09	3.07E-08
BP	GO:1901992	Positive regulation of mitotic cell cycle phase transition	14	1.38E-09	3.07E-08
BP	GO:0070316	Regulation of G0 to G1 transition	11	1.48E-09	3.28E-08
BP	GO:0000281	Mitotic cytokinesis	13	1.51E-09	3.32E-08
BP	GO:0051054	Positive regulation of DNA metabolic process	22	1.56E-09	3.39E-08
BP	GO:0045740	Positive regulation of DNA replication	10	1.57E-09	3.39E-08
BP	GO:0000910	Cytokinesis	18	1.69E-09	3.62E-08
BP	GO:0045023	G0 to G1 transition	11	2.45E-09	5.21E-08
BP	GO:0040001	Establishment of mitotic spindle localization	9	3.26E-09	6.86E-08
BP	GO:0036297	Interstrand cross-link repair	11	4.97E-09	1.04E-07

BP	GO:0007143	Female meiotic nuclear division	9	6.50E-09	1.35E-07
BP	GO:0051653	Spindle localization	10	8.58E-09	1.77E-07
BP	GO:0046605	Regulation of centrosome cycle	11	1.18E-08	2.42E-07
BP	GO:0045132	Meiotic chromosome segregation	12	1.19E-08	2.42E-07
BP	GO:1902750	Negative regulation of cell cycle G2/M phase transition	14	1.32E-08	2.66E-07
BP	GO:0051382	Kinetochore assembly	7	1.56E-08	3.12E-07
BP	GO:0000077	DNA damage checkpoint	16	1.77E-08	3.52E-07
BP	GO:0051656	Establishment of organelle localization	30	2.03E-08	3.99E-07
BP	GO:0043161	Proteasome-mediated ubiquitin-dependent protein catabolic process	25	2.63E-08	5.14E-07
BP	GO:0072401	Signal transduction involved in DNA integrity checkpoint	12	3.27E-08	6.30E-07
BP	GO:0072422	Signal transduction involved in DNA damage checkpoint	12	3.27E-08	6.30E-07
BP	GO:0000076	DNA replication checkpoint	6	3.31E-08	6.34E-07
BP	GO:0072395	Signal transduction involved in cell cycle checkpoint	12	3.83E-08	7.23E-07
BP	GO:0051293	Establishment of spindle localization	9	3.83E-08	7.23E-07
BP	GO:1902751	Positive regulation of cell cycle G2/M phase transition	8	5.15E-08	9.66E-07
BP	GO:0000083	Regulation of transcription involved in G1/S transition of mitotic cell cycle	8	9.60E-08	1.79E-06
BP	GO:0031572	G2 DNA damage checkpoint	8	1.29E-07	2.38E-06
BP	GO:0010498	Proteasomal protein catabolic process	26	1.33E-07	2.45E-06
BP	GO:0000079	Regulation of cyclin-dependent protein serine/threonine kinase activity	12	1.43E-07	2.60E-06
BP	GO:0000018	Regulation of DNA recombination	12	1.63E-07	2.96E-06
BP	GO:1904666	Regulation of ubiquitin protein ligase activity	7	2.09E-07	3.76E-06
BP	GO:1904029	Regulation of cyclin-dependent protein kinase activity	12	2.43E-07	4.34E-06
BP	GO:0051302	Regulation of cell division	16	2.87E-07	5.09E-06
BP	GO:0007076	Mitotic chromosome condensation	6	3.34E-07	5.90E-06
BP	GO:0044774	Mitotic DNA integrity checkpoint	12	3.54E-07	6.21E-06
BP	GO:0007050	Cell cycle arrest	19	3.99E-07	6.95E-06
BP	GO:0010971	Positive regulation of G2/M transition of mitotic cell cycle	7	4.09E-07	7.09E-06
BP	GO:0071897	DNA biosynthetic process	17	5.84E-07	1.00E-05
BP	GO:0042770	Signal transduction in response to DNA damage	14	6.10E-07	1.04E-05
BP	GO:0007062	Sister chromatid cohesion	9	7.88E-07	1.34E-05
BP	GO:0051231	Spindle elongation	5	8.81E-07	1.49E-05
BP	GO:0090305	Nucleic acid phosphodiester bond hydrolysis	20	9.28E-07	1.54E-05

BP	GO:0016572	Histone phosphorylation	8	9.29E-07	1.54E-05
BP	GO:0042769	DNA damage response, detection of DNA damage	8	9.29E-07	1.54E-05
BP	GO:0010972	Negative regulation of G2/M transition of mitotic cell cycle	11	1.48E-06	2.44E-05
BP	GO:2000105	Positive regulation of DNA-dependent DNA replication	5	1.59E-06	2.60E-05
BP	GO:0044773	Mitotic DNA damage checkpoint	11	1.67E-06	2.71E-05
BP	GO:0051493	Regulation of cytoskeleton organization	27	2.30E-06	3.73E-05
BP	GO:0000212	Meiotic spindle organization	5	2.68E-06	4.26E-05
BP	GO:0007077	Mitotic nuclear envelope disassembly	5	2.68E-06	4.26E-05
BP	GO:1904668	Positive regulation of ubiquitin protein ligase activity	5	2.68E-06	4.26E-05
BP	GO:0051298	Centrosome duplication	9	3.35E-06	5.30E-05
BP	GO:0031109	Microtubule polymerization or depolymerization	11	4.05E-06	6.37E-05
BP	GO:0045005	DNA-dependent DNA replication maintenance of fidelity	7	4.30E-06	6.72E-05
BP	GO:0006301	Postreplication repair	8	5.07E-06	7.88E-05
BP	GO:0007019	Microtubule depolymerization	7	5.32E-06	8.21E-05
BP	GO:0044818	Mitotic G2/M transition checkpoint	6	5.86E-06	9.00E-05
BP	GO:0090231	Regulation of spindle checkpoint	5	6.54E-06	9.87E-05
BP	GO:0090266	Regulation of mitotic cell cycle spindle assembly checkpoint	5	6.54E-06	9.87E-05
BP	GO:1903504	Regulation of mitotic spindle checkpoint	5	6.54E-06	9.87E-05
BP	GO:0000132	Establishment of mitotic spindle orientation	6	7.67E-06	0.000115256
BP	GO:0051053	Negative regulation of DNA metabolic process	13	8.03E-06	0.000119985
BP	GO:0032465	Regulation of cytokinesis	10	8.56E-06	0.000127144
BP	GO:0010212	Response to ionizing radiation	13	1.01E-05	0.00014935
BP	GO:0070192	Chromosome organization involved in meiotic cell cycle	8	1.11E-05	0.000162915
BP	GO:0030397	Membrane disassembly	5	1.38E-05	0.000200345
BP	GO:0051081	Nuclear envelope disassembly	5	1.38E-05	0.000200345
BP	GO:0010824	Regulation of centrosome duplication	7	1.65E-05	0.000239265
BP	GO:2000779	Regulation of double-strand break repair	9	1.79E-05	0.00025736
BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	8	1.95E-05	0.000278491
BP	GO:0090224	Regulation of spindle organization	7	1.96E-05	0.000278957
BP	GO:0051294	Establishment of spindle orientation	6	2.00E-05	0.000280952
BP	GO:0071168	Protein localization to chromatin	6	2.00E-05	0.000280952
BP	GO:0060249	Anatomical structure homeostasis	23	2.00E-05	0.000280952

BP	GO:0006282	Regulation of DNA repair	11	2.21E-05	0.00030684
BP	GO:0072431	Signal transduction involved in mitotic G1 DNA damage checkpoint	8	2.22E-05	0.00030684
BP	GO:1902400	Intracellular signal transduction involved in G1 DNA damage checkpoint	8	2.22E-05	0.00030684
BP	GO:0031297	Replication fork processing	6	2.48E-05	0.000340513
BP	GO:0006312	Mitotic recombination	5	2.61E-05	0.000353262
BP	GO:0042276	Error-prone translesion synthesis	5	2.61E-05	0.000353262
BP	GO:0051782	Negative regulation of cell division	5	2.61E-05	0.000353262
BP	GO:0006890	Retrograde vesicle-mediated transport, Golgi to ER	9	2.78E-05	0.000374642
BP	GO:0072413	Signal transduction involved in mitotic cell cycle checkpoint	8	2.88E-05	0.000381627
BP	GO:1902402	Signal transduction involved in mitotic DNA damage checkpoint	8	2.88E-05	0.000381627
BP	GO:1902403	Signal transduction involved in mitotic DNA integrity checkpoint	8	2.88E-05	0.000381627
BP	GO:0070987	Error-free translesion synthesis	5	3.48E-05	0.000459828
BP	GO:0051255	Spindle midzone assembly	4	3.52E-05	0.000459861
BP	GO:0051315	Attachment of mitotic spindle microtubules to kinetochore	4	3.52E-05	0.000459861
BP	GO:0031571	Mitotic G1 DNA damage checkpoint	8	4.67E-05	0.000605232
BP	GO:0044819	Mitotic G1/S transition checkpoint	8	4.67E-05	0.000605232
BP	GO:0051438	Regulation of ubiquitin-protein transferase activity	7	4.92E-05	0.00063455
BP	GO:0071158	Positive regulation of cell cycle arrest	9	5.13E-05	0.000658078
BP	GO:0044783	G1 DNA damage checkpoint	8	5.25E-05	0.000669731
BP	GO:0007100	Mitotic centrosome separation	4	5.44E-05	0.000684449
BP	GO:0016446	Somatic hypermutation of immunoglobulin genes	4	5.44E-05	0.000684449
BP	GO:0035404	Histone-serine phosphorylation	4	5.44E-05	0.000684449
BP	GO:0045840	Positive regulation of mitotic nuclear division	7	5.66E-05	0.000709562
BP	GO:0007063	Regulation of sister chromatid cohesion	5	5.89E-05	0.000734755
BP	GO:1902806	Regulation of cell cycle G1/S phase transition	14	6.14E-05	0.000761789
BP	GO:0007131	Reciprocal meiotic recombination	6	6.43E-05	0.000794696
BP	GO:2000573	Positive regulation of DNA biosynthetic process	8	6.57E-05	0.000807871
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	10	7.34E-05	0.000898824
BP	GO:0035825	Homologous recombination	6	7.63E-05	0.00092975
BP	GO:0002566	Somatic diversification of immune receptors via somatic mutation	4	8.02E-05	0.000960895
BP	GO:0051095	Regulation of helicase activity	4	8.02E-05	0.000960895

BP	GO:0051299	Centrosome separation	4	8.02E-05	0.000960895
BP	GO:0051988	Regulation of attachment of spindle microtubules to kinetochore	4	8.02E-05	0.000960895
BP	GO:2001020	Regulation of response to DNA damage stimulus	14	8.51E-05	0.001014378
BP	GO:0071156	Regulation of cell cycle arrest	10	8.60E-05	0.001021046
BP	GO:2000045	Regulation of G1/S transition of mitotic cell cycle	13	8.88E-05	0.001049547
BP	GO:0000729	DNA double-strand break processing	5	9.41E-05	0.001103197
BP	GO:0006297	Nucleotide-excision repair, DNA gap filling	5	9.41E-05	0.001103197
BP	GO:0007292	Female gamete generation	11	0.000100544	0.001173302
BP	GO:0032467	Positive regulation of cytokinesis	6	0.00010545	0.001214908
BP	GO:0032506	Cytokinetic process	6	0.00010545	0.001214908
BP	GO:0060236	Regulation of mitotic spindle organization	6	0.00010545	0.001214908
BP	GO:0009314	Response to radiation	22	0.000125311	0.001437636
BP	GO:0044766	Multi-organism transport	8	0.000135431	0.001540738
BP	GO:1902579	Multi-organism localization	8	0.000135431	0.001540738
BP	GO:0072425	Signal transduction involved in G2 DNA damage checkpoint	4	0.000156952	0.001778135
BP	GO:0019985	Translesion synthesis	6	0.000165188	0.001863674
BP	GO:0075733	Intracellular transport of virus	7	0.000173193	0.001945916
BP	GO:0022412	Cellular process involved in reproduction in multicellular organism	18	0.000176917	0.001979576
BP	GO:0010569	Regulation of double-strand break repair via homologous recombination	6	0.000190146	0.002112766
BP	GO:0019886	Antigen processing and presentation of exogenous peptide antigen via MHC class II	9	0.000190374	0.002112766
BP	GO:0006298	Mismatch repair	5	0.000210894	0.002321544
BP	GO:0009112	Nucleobase metabolic process	5	0.000210894	0.002321544
BP	GO:2001252	Positive regulation of chromosome organization	12	0.00022584	0.002476041
BP	GO:0046794	Transport of virus	7	0.000239839	0.002599128
BP	GO:0051785	Positive regulation of nuclear division	7	0.000239839	0.002599128
BP	GO:0002495	Antigen processing and presentation of peptide antigen via MHC class II	9	0.000239934	0.002599128
BP	GO:0031396	Regulation of protein ubiquitination	13	0.000245341	0.002647157
BP	GO:0010458	Exit from mitosis	5	0.00025239	0.002691167
BP	GO:0045737	Positive regulation of cyclin-dependent protein serine/threonine kinase activity	5	0.00025239	0.002691167
BP	GO:0051443	Positive regulation of ubiquitin-protein transferase activity	5	0.00025239	0.002691167

BP	GO:0002504	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	9	0.000258659	0.002747243
BP	GO:2000134	Negative regulation of G1/S transition of mitotic cell cycle	10	0.000270209	0.002858743
BP	GO:0007096	Regulation of exit from mitosis	4	0.000276102	0.00290977
BP	GO:0006998	Nuclear envelope organization	6	0.000321163	0.003371588
BP	GO:0051168	Nuclear export	12	0.000328144	0.003431628
BP	GO:2000278	Regulation of DNA biosynthetic process	9	0.000371407	0.003869183
BP	GO:1902807	Negative regulation of cell cycle G1/S phase transition	10	0.000395242	0.004101766
BP	GO:0045143	Homologous chromosome segregation	6	0.000408844	0.004210784
BP	GO:0072698	Protein localization to microtubule cytoskeleton	6	0.000408844	0.004210784
BP	GO:0007099	Centriole replication	5	0.000414553	0.004221613
BP	GO:0045910	Negative regulation of DNA recombination	5	0.000414553	0.004221613
BP	GO:1901976	Regulation of cell cycle checkpoint	5	0.000414553	0.004221613
BP	GO:1904031	Positive regulation of cyclin-dependent protein kinase activity	5	0.000483012	0.004900414
BP	GO:0031398	Positive regulation of protein ubiquitination	9	0.000488373	0.004936377
BP	GO:0007095	Mitotic G2 DNA damage checkpoint	4	0.00055965	0.00563588
BP	GO:0000731	DNA synthesis involved in DNA repair	6	0.00057418	0.005739689
BP	GO:0044380	Protein localization to cytoskeleton	6	0.00057418	0.005739689
BP	GO:0006611	Protein export from nucleus	11	0.000628248	0.006257161
BP	GO:0022411	Cellular component disassembly	22	0.000681486	0.006762626
BP	GO:0070734	Histone H3-K27 methylation	4	0.000688147	0.006803898
BP	GO:0051169	Nuclear transport	16	0.000698102	0.00687732
BP	GO:0051261	Protein depolymerization	8	0.000715893	0.007027125
BP	GO:0098534	Centriole assembly	5	0.000739843	0.007236093
BP	GO:0006997	Nucleus organization	9	0.000813379	0.007926801
BP	GO:0097711	Ciliary basal body-plasma membrane docking	8	0.000824314	0.00800468
BP	GO:2000104	Negative regulation of DNA-dependent DNA replication	4	0.000836203	0.008064031
BP	GO:1903320	Regulation of protein modification by small protein conjugation or removal	13	0.000836358	0.008064031
BP	GO:0008156	Negative regulation of DNA replication	5	0.000844671	0.008115405
BP	GO:0007018	Microtubule-based movement	13	0.000871572	0.008344382
BP	GO:0006296	Nucleotide-excision repair, DNA incision, 5'-to lesion	5	0.000960174	0.009160397
BP	GO:0009263	Deoxyribonucleotide biosynthetic process	3	0.000963935	0.009164128
BP	GO:0006405	RNA export from nucleus	9	0.001032029	0.009777304

BP	GO:0002478	Antigen processing and presentation of exogenous peptide antigen	11	0.001076478	0.010162998
BP	GO:0006284	Base-excision repair	5	0.001087012	0.010226936
BP	GO:0071900	Regulation of protein serine/threonine kinase activity	21	0.001148257	0.010765903
BP	GO:0016579	Protein deubiquitination	14	0.001156547	0.010806357
BP	GO:0019884	Antigen processing and presentation of exogenous antigen	11	0.001181098	0.010997964
BP	GO:0033683	Nucleotide-excision repair, DNA incision	5	0.001225853	0.011375747
BP	GO:0051642	Centrosome localization	4	0.001413278	0.013070421
BP	GO:1903322	Positive regulation of protein modification by small protein conjugation or removal	9	0.001447091	0.013337767
BP	GO:0001556	Oocyte maturation	4	0.001655117	0.015152403
BP	GO:0061842	Microtubule organizing center localization	4	0.001655117	0.015152403
BP	GO:0000722	Telomere maintenance via recombination	3	0.001713288	0.015580032
BP	GO:0046112	Nucleobase biosynthetic process	3	0.001713288	0.015580032
BP	GO:0006913	Nucleocytoplasmic transport	15	0.001744663	0.015812466
BP	GO:0070646	Protein modification by small protein removal	14	0.001829708	0.016528157
BP	GO:0051781	Positive regulation of cell division	7	0.001838135	0.016549298
BP	GO:0016569	Covalent chromatin modification	19	0.001926167	0.017284646
BP	GO:0048002	Antigen processing and presentation of peptide antigen	11	0.001999179	0.017880816
BP	GO:0007140	Male meiotic nuclear division	5	0.00212414	0.018936187
BP	GO:0001833	Inner cell mass cell proliferation	3	0.002193081	0.019423414
BP	GO:0062033	Positive regulation of mitotic sister chromatid segregation	3	0.002193081	0.019423414
BP	GO:0015949	Nucleobase-containing small molecule interconversion	4	0.002222243	0.019554298
BP	GO:0090169	Regulation of spindle assembly	4	0.002222243	0.019554298
BP	GO:0009411	Response to UV	9	0.002311451	0.020273658
BP	GO:0018209	Peptidyl-serine modification	13	0.002497947	0.021838962
BP	GO:0070979	Protein K11-linked ubiquitination	4	0.002550552	0.022227403
BP	GO:0002200	Somatic diversification of immune receptors	6	0.0026831	0.023307825
BP	GO:0046606	Negative regulation of centrosome cycle	3	0.002748389	0.023723399
BP	GO:0051307	Meiotic chromosome separation	3	0.002748389	0.023723399
BP	GO:0140056	Organelle localization by membrane tethering	9	0.002808153	0.024162553
BP	GO:0071426	Ribonucleoprotein complex export from nucleus	8	0.002958898	0.02537932
BP	GO:0031110	Regulation of microtubule polymerization or depolymerization	6	0.003113283	0.026592608
BP	GO:0071166	Ribonucleoprotein complex localization	8	0.003119912	0.026592608

BP	GO:0016570	Histone modification	18	0.003221815	0.027375359
BP	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	6	0.003346721	0.028301497
BP	GO:0001325	Formation of extrachromosomal circular DNA	3	0.003382856	0.028301497
BP	GO:0006144	Purine nucleobase metabolic process	3	0.003382856	0.028301497
BP	GO:0090656	T-circle formation	3	0.003382856	0.028301497
BP	GO:0090737	Telomere maintenance via telomere trimming	3	0.003382856	0.028301497
BP	GO:0018105	Peptidyl-serine phosphorylation	12	0.003411893	0.028456866
BP	GO:0030262	Apoptotic nuclear changes	4	0.003732129	0.031032599
BP	GO:0008340	Determination of adult lifespan	3	0.0040998	0.03388254
BP	GO:0033262	Regulation of nuclear cell cycle DNA replication	3	0.0040998	0.03388254
BP	GO:0006283	Transcription-coupled nucleotide-excision repair	6	0.004125427	0.033991021
BP	GO:0022406	Membrane docking	9	0.004234666	0.03478567
BP	GO:0006409	Trna export from nucleus	4	0.004697896	0.038130084
BP	GO:0006921	Cellular component disassembly involved in execution phase of apoptosis	4	0.004697896	0.038130084
BP	GO:0051031	Trna transport	4	0.004697896	0.038130084
BP	GO:0071431	Trna-containing ribonucleoprotein complex export from nucleus	4	0.004697896	0.038130084
BP	GO:0031100	Animal organ regeneration	6	0.0047141	0.038147734
BP	GO:0006266	DNA ligation	3	0.004902224	0.039435348
BP	GO:0006349	Regulation of gene expression by genetic imprinting	3	0.004902224	0.039435348
BP	GO:0016445	Somatic diversification of immunoglobulins	5	0.005650134	0.045317741
BP	GO:0018205	Peptidyl-lysine modification	16	0.005697353	0.045528226
BP	GO:0016925	Protein sumoylation	6	0.005709866	0.045528226
BP	GO:0071312	Cellular response to alkaloid	4	0.005818719	0.046260514
BP	GO:0010833	Telomere maintenance via telomere lengthening	6	0.006073548	0.048005746
BP	GO:2001021	Negative regulation of response to DNA damage stimulus	6	0.006073548	0.048005746
CC	GO:0098687	Chromosomal region	70	3.97E-50	1.42E-47
CC	GO:0000775	Chromosome, centromeric region	52	1.78E-44	3.16E-42
CC	GO:0000793	Condensed chromosome	53	5.78E-44	6.85E-42
CC	GO:0000776	Kinetochore	40	6.17E-36	5.49E-34
CC	GO:0000779	Condensed chromosome, centromeric region	36	1.17E-33	8.33E-32
CC	GO:0005819	Spindle	54	3.02E-33	1.79E-31
CC	GO:0000777	Condensed chromosome kinetochore	33	4.56E-31	2.32E-29
CC	GO:0005813	Centrosome	48	4.21E-20	1.87E-18

CC	GO:0000922	Spindle pole	29	5.11E-20	2.02E-18
CC	GO:0044454	Nuclear chromosome part	44	3.39E-17	1.21E-15
CC	GO:0005876	Spindle microtubule	17	2.42E-16	7.84E-15
CC	GO:0072686	Mitotic spindle	19	9.18E-14	2.72E-12
CC	GO:0030496	Midbody	24	1.17E-13	3.17E-12
CC	GO:0000940	Condensed chromosome outer kinetochore	9	1.25E-13	3.17E-12
CC	GO:0000785	Chromatin	38	4.07E-12	9.65E-11
CC	GO:0005874	Microtubule	31	1.50E-11	3.33E-10
CC	GO:0000794	Condensed nuclear chromosome	14	3.42E-10	7.17E-09
CC	GO:0000781	Chromosome, telomeric region	19	5.33E-10	1.05E-08
CC	GO:0005657	Replication fork	12	7.57E-10	1.42E-08
CC	GO:0000790	Nuclear chromatin	23	1.19E-07	2.12E-06
CC	GO:0000784	Nuclear chromosome, telomeric region	14	1.96E-07	3.33E-06
CC	GO:0005720	Nuclear heterochromatin	8	2.63E-07	4.25E-06
CC	GO:0045120	Pronucleus	6	3.11E-07	4.81E-06
CC	GO:0000792	Heterochromatin	11	3.62E-07	5.38E-06
CC	GO:0097431	Mitotic spindle pole	7	6.90E-07	9.83E-06
CC	GO:0000780	Condensed nuclear chromosome, centromeric region	6	7.42E-07	1.02E-05
CC	GO:0000152	Nuclear ubiquitin ligase complex	8	8.46E-07	1.12E-05
CC	GO:0051233	Spindle midzone	7	9.15E-07	1.16E-05
CC	GO:0005814	Centriole	13	1.67E-06	2.05E-05
CC	GO:0044450	Microtubule organizing center part	15	2.43E-06	2.88E-05
CC	GO:0010369	Chromocenter	5	6.15E-06	7.06E-05
CC	GO:0000803	Sex chromosome	6	2.84E-05	0.000315849
CC	GO:0005721	Pericentric heterochromatin	5	4.30E-05	0.000463972
CC	GO:0042555	MCM complex	4	5.18E-05	0.000542028
CC	GO:0090734	Site of DNA damage	8	5.38E-05	0.00054766
CC	GO:0005680	Anaphase-promoting complex	5	5.55E-05	0.00054884
CC	GO:0018995	Host	8	8.30E-05	0.000778045
CC	GO:0043657	Host cell	8	8.30E-05	0.000778045
CC	GO:0044215	Other organism	8	0.000150572	0.001307403
CC	GO:0044216	Other organism cell	8	0.000150572	0.001307403
CC	GO:0044217	Other organism part	8	0.000150572	0.001307403
CC	GO:0045171	Intercellular bridge	7	0.000199814	0.001693658
CC	GO:0035098	ESC/E(Z) complex	4	0.000263136	0.002178517

CC	GO:0005881	Cytoplasmic microtubule	7	0.000273255	0.002210884
CC	GO:0000307	Cyclin-dependent protein kinase holoenzyme complex	5	0.00028293	0.00223829
CC	GO:0000235	Astral microtubule	3	0.00092922	0.006891718
CC	GO:0005818	Aster	3	0.00092922	0.006891718
CC	GO:0072687	Meiotic spindle	3	0.00092922	0.006891718
CC	GO:0031461	Cullin-RING ubiquitin ligase complex	9	0.001061784	0.007596264
CC	GO:0032153	Cell division site	6	0.001088229	0.007596264
CC	GO:0032155	Cell division site part	6	0.001088229	0.007596264
CC	GO:0005635	Nuclear envelope	19	0.001181418	0.008088167
CC	GO:1990023	Mitotic spindle midzone	3	0.001258266	0.008451746
CC	GO:0031519	Pcg protein complex	5	0.001628755	0.010737716
CC	GO:1990752	Microtubule end	4	0.001837626	0.011894449
CC	GO:0031965	Nuclear membrane	14	0.002132308	0.013555389
CC	GO:0044815	DNA packaging complex	8	0.002328189	0.014540969
CC	GO:0000151	Ubiquitin ligase complex	12	0.002401963	0.014702767
CC	GO:0090543	Flemming body	4	0.002436694	0.014702767
CC	GO:0000800	Lateral element	3	0.002651452	0.015731947
CC	GO:0035371	Microtubule plus-end	3	0.003956712	0.02309163
CC	GO:0015030	Cajal body	6	0.00443668	0.025475129
CC	GO:0034399	Nuclear periphery	8	0.004544908	0.025682337
CC	GO:0000795	Synaptonemal complex	4	0.005010451	0.027441857
CC	GO:0099086	Synaptonemal structure	4	0.005010451	0.027441857
CC	GO:0032154	Cleavage furrow	5	0.005360902	0.02891638
CC	GO:0016363	Nuclear matrix	7	0.006285255	0.033396278
CC	GO:0043073	Germ cell nucleus	3	0.006541372	0.034246008
CC	GO:0005643	Nuclear pore	5	0.007218772	0.037244678
MF	GO:0008094	DNA-dependent atpase activity	18	1.85E-14	7.50E-12
MF	GO:0043142	Single-stranded DNA-dependent atpase activity	8	2.69E-11	5.46E-09
MF	GO:0000217	DNA secondary structure binding	9	7.98E-10	9.76E-08
MF	GO:0016887	Atpase activity	26	9.61E-10	9.76E-08
MF	GO:0042623	Atpase activity, coupled	22	4.16E-09	3.38E-07
MF	GO:0003684	Damaged DNA binding	12	7.11E-09	4.81E-07
MF	GO:0000400	Four-way junction DNA binding	7	2.57E-08	1.49E-06
MF	GO:0140097	Catalytic activity, acting on DNA	17	5.47E-08	2.59E-06
MF	GO:0003682	Chromatin binding	30	5.75E-08	2.59E-06

MF	GO:0003697	Single-stranded DNA binding	13	1.00E-07	4.08E-06
MF	GO:0008017	Microtubule binding	17	1.99E-07	7.36E-06
MF	GO:0015631	Tubulin binding	21	2.58E-07	8.73E-06
MF	GO:0035173	Histone kinase activity	5	9.30E-06	0.000290359
MF	GO:0004386	Helicase activity	12	3.07E-05	0.000857198
MF	GO:0004518	Nuclease activity	14	3.17E-05	0.000857198
MF	GO:0003678	DNA helicase activity	7	3.67E-05	0.000930598
MF	GO:0000287	Magnesium ion binding	15	7.66E-05	0.001792576
MF	GO:0008022	Protein C-terminus binding	14	7.95E-05	0.001792576
MF	GO:0042393	Histone binding	13	0.000153081	0.003271092
MF	GO:0016893	Endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	6	0.000211675	0.004296995
MF	GO:0004536	Deoxyribonuclease activity	6	0.000280934	0.005431392
MF	GO:0004520	Endodeoxyribonuclease activity	5	0.000352528	0.006205616
MF	GO:0008409	5'-3' exonuclease activity	4	0.000363909	0.006205616
MF	GO:0003777	Microtubule motor activity	6	0.000366834	0.006205616
MF	GO:0003774	Motor activity	9	0.000507031	0.008234176
MF	GO:0004003	ATP-dependent DNA helicase activity	5	0.000576801	0.008779227
MF	GO:0004519	Endonuclease activity	9	0.00058384	0.008779227
MF	GO:0004523	RNA-DNA hybrid ribonuclease activity	3	0.001189271	0.016649793
MF	GO:0016888	Endodeoxyribonuclease activity, producing 5'-phosphomonoesters	3	0.001189271	0.016649793
MF	GO:1990939	ATP-dependent microtubule motor activity	3	0.002108851	0.028539777
MF	GO:0008536	Ran gtpase binding	4	0.003312179	0.043378855
MF	GO:0004527	Exonuclease activity	6	0.00383205	0.048619134

The co-expression genes of SKA3 with GO notes

Ontology	ID	Description	Count	P value	P adjust
BP	GO:0006260	DNA replication	94	1.24E-47	5.99E-44
BP	GO:0007059	Chromosome segregation	85	4.13E-37	9.96E-34
BP	GO:0006261	DNA-dependent DNA replication	57	1.41E-34	2.27E-31
BP	GO:0140014	Mitotic nuclear division	75	1.30E-33	1.57E-30
BP	GO:0000280	Nuclear division	90	1.32E-31	1.17E-28
BP	GO:0048285	Organelle fission	95	1.45E-31	1.17E-28
BP	GO:0000819	Sister chromatid segregation	59	2.78E-31	1.91E-28
BP	GO:0098813	Nuclear chromosome segregation	68	7.29E-30	4.39E-27
BP	GO:0000070	Mitotic sister chromatid segregation	52	7.00E-29	3.75E-26
BP	GO:1901990	Regulation of mitotic cell cycle phase transition	93	2.55E-27	1.23E-24
BP	GO:1901987	Regulation of cell cycle phase transition	96	1.88E-26	8.24E-24
BP	GO:0044839	Cell cycle G2/M phase transition	65	3.56E-23	1.43E-20
BP	GO:0000086	G2/M transition of mitotic cell cycle	62	6.86E-23	2.54E-20
BP	GO:0051983	Regulation of chromosome segregation	38	4.00E-22	1.38E-19
BP	GO:0044843	Cell cycle G1/S phase transition	67	1.13E-21	3.65E-19
BP	GO:0051052	Regulation of DNA metabolic process	81	1.31E-21	3.95E-19
BP	GO:0000082	G1/S transition of mitotic cell cycle	64	2.65E-21	7.50E-19
BP	GO:0000075	Cell cycle checkpoint	54	3.28E-21	8.79E-19
BP	GO:0007051	Spindle organization	46	7.78E-21	1.98E-18
BP	GO:1902749	Regulation of cell cycle G2/M phase transition	53	6.75E-20	1.63E-17
BP	GO:0000226	Microtubule cytoskeleton organization	84	1.41E-19	3.23E-17
BP	GO:0010389	Regulation of G2/M transition of mitotic cell cycle	50	1.92E-19	4.20E-17
BP	GO:0045930	Negative regulation of mitotic cell cycle	66	2.46E-19	5.17E-17
BP	GO:0044786	Cell cycle DNA replication	28	2.68E-19	5.39E-17
BP	GO:0007093	Mitotic cell cycle checkpoint	44	3.83E-19	7.38E-17
BP	GO:0010948	Negative regulation of cell cycle process	70	3.98E-19	7.38E-17
BP	GO:0007088	Regulation of mitotic nuclear division	43	5.94E-18	1.06E-15
BP	GO:0071103	DNA conformation change	60	9.16E-18	1.58E-15
BP	GO:0033260	Nuclear DNA replication	24	3.10E-17	5.15E-15
BP	GO:1901988	Negative regulation of cell cycle phase transition	56	3.54E-17	5.68E-15
BP	GO:0034502	Protein localization to chromosome	31	3.88E-17	6.04E-15

BP	GO:1901991	Negative regulation of mitotic cell cycle phase transition	53	8.94E-17	1.35E-14
BP	GO:0000723	Telomere maintenance	42	1.06E-16	1.55E-14
BP	GO:1902850	Microtubule cytoskeleton organization involved in mitosis	36	1.82E-16	2.57E-14
BP	GO:0006403	RNA localization	49	2.04E-16	2.81E-14
BP	GO:0006310	DNA recombination	53	4.92E-16	6.59E-14
BP	GO:0051054	Positive regulation of DNA metabolic process	50	7.13E-16	9.29E-14
BP	GO:0072331	Signal transduction by p53 class mediator	55	9.40E-16	1.19E-13
BP	GO:0051783	Regulation of nuclear division	43	1.46E-15	1.80E-13
BP	GO:0033045	Regulation of sister chromatid segregation	27	2.33E-15	2.81E-13
BP	GO:0032200	Telomere organization	42	2.49E-15	2.92E-13
BP	GO:0007091	Metaphase/anaphase transition of mitotic cell cycle	22	6.90E-15	7.74E-13
BP	GO:0010965	Regulation of mitotic sister chromatid separation	22	6.90E-15	7.74E-13
BP	GO:0031145	Anaphase-promoting complex-dependent catabolic process	28	1.88E-14	2.06E-12
BP	GO:0044784	Metaphase/anaphase transition of cell cycle	22	2.05E-14	2.15E-12
BP	GO:0051306	Mitotic sister chromatid separation	22	2.05E-14	2.15E-12
BP	GO:0007052	Mitotic spindle organization	30	3.53E-14	3.62E-12
BP	GO:0006275	Regulation of DNA replication	31	4.31E-14	4.33E-12
BP	GO:1905818	Regulation of chromosome separation	22	9.34E-14	9.19E-12
BP	GO:0006270	DNA replication initiation	17	1.38E-13	1.33E-11
BP	GO:0031570	DNA integrity checkpoint	36	1.50E-13	1.41E-11
BP	GO:0090329	Regulation of DNA-dependent DNA replication	21	1.52E-13	1.41E-11
BP	GO:0090068	Positive regulation of cell cycle process	53	3.02E-13	2.75E-11
BP	GO:0033044	Regulation of chromosome organization	56	3.51E-13	3.13E-11
BP	GO:0006302	Double-strand break repair	44	6.98E-13	6.12E-11
BP	GO:0045787	Positive regulation of cell cycle	62	7.67E-13	6.60E-11
BP	GO:0033047	Regulation of mitotic sister chromatid segregation	22	8.94E-13	7.56E-11
BP	GO:0006405	RNA export from nucleus	32	1.52E-12	1.27E-10
BP	GO:0000725	Recombinational repair	30	1.96E-12	1.61E-10
BP	GO:0030071	Regulation of mitotic metaphase/anaphase transition	19	2.94E-12	2.37E-10
BP	GO:0045839	Negative regulation of mitotic nuclear division	19	4.80E-12	3.80E-10
BP	GO:0051169	Nuclear transport	53	6.35E-12	4.94E-10
BP	GO:0051304	Chromosome separation	23	6.85E-12	5.24E-10
BP	GO:1902099	Regulation of metaphase/anaphase transition of cell cycle	19	7.71E-12	5.81E-10

BP	GO:0071897	DNA biosynthetic process	40	8.03E-12	5.95E-10
BP	GO:0050657	Nucleic acid transport	38	8.58E-12	6.17E-10
BP	GO:0050658	RNA transport	38	8.58E-12	6.17E-10
BP	GO:0000724	Double-strand break repair via homologous recombination	29	8.99E-12	6.37E-10
BP	GO:0071426	Ribonucleoprotein complex export from nucleus	30	1.12E-11	7.79E-10
BP	GO:0006323	DNA packaging	40	1.13E-11	7.79E-10
BP	GO:0071166	Ribonucleoprotein complex localization	30	1.42E-11	9.59E-10
BP	GO:0006913	Nucleocytoplasmic transport	52	1.44E-11	9.59E-10
BP	GO:0051236	Establishment of RNA localization	38	1.47E-11	9.59E-10
BP	GO:1901796	Regulation of signal transduction by p53 class mediator	38	1.47E-11	9.59E-10
BP	GO:0051225	Spindle assembly	26	1.75E-11	1.13E-09
BP	GO:0051310	Metaphase plate congression	20	3.53E-11	2.24E-09
BP	GO:0032392	DNA geometric change	25	3.68E-11	2.31E-09
BP	GO:0032508	DNA duplex unwinding	23	9.04E-11	5.59E-09
BP	GO:0000077	DNA damage checkpoint	31	9.19E-11	5.61E-09
BP	GO:0051784	Negative regulation of nuclear division	19	9.93E-11	5.99E-09
BP	GO:0032201	Telomere maintenance via semi-conservative replication	14	1.03E-10	6.11E-09
BP	GO:0034660	Ncrna metabolic process	67	1.13E-10	6.67E-09
BP	GO:1903405	Protein localization to nuclear body	9	1.20E-10	6.83E-09
BP	GO:1904851	Positive regulation of establishment of protein localization to telomere	9	1.20E-10	6.83E-09
BP	GO:1904867	Protein localization to Cajal body	9	1.20E-10	6.83E-09
BP	GO:0045841	Negative regulation of mitotic metaphase/anaphase transition	15	1.39E-10	7.73E-09
BP	GO:2000816	Negative regulation of mitotic sister chromatid separation	15	1.39E-10	7.73E-09
BP	GO:0033046	Negative regulation of sister chromatid segregation	16	1.52E-10	8.31E-09
BP	GO:0051168	Nuclear export	36	1.53E-10	8.31E-09
BP	GO:0070200	Establishment of protein localization to telomere	11	1.57E-10	8.40E-09
BP	GO:0050000	Chromosome localization	22	1.88E-10	9.85E-09
BP	GO:0051303	Establishment of chromosome localization	22	1.88E-10	9.85E-09
BP	GO:0051321	Meiotic cell cycle	39	1.91E-10	9.89E-09
BP	GO:2000573	Positive regulation of DNA biosynthetic process	21	2.08E-10	1.07E-08
BP	GO:1902100	Negative regulation of metaphase/anaphase transition of cell cycle	15	2.41E-10	1.21E-08

BP	GO:1905819	Negative regulation of chromosome separation	15	2.41E-10	1.21E-08
BP	GO:0051985	Negative regulation of chromosome segregation	16	2.48E-10	1.23E-08
BP	GO:0072401	Signal transduction involved in DNA integrity checkpoint	22	2.53E-10	1.23E-08
BP	GO:0072422	Signal transduction involved in DNA damage checkpoint	22	2.53E-10	1.23E-08
BP	GO:0072395	Signal transduction involved in cell cycle checkpoint	22	3.40E-10	1.64E-08
BP	GO:0000083	Regulation of transcription involved in G1/S transition of mitotic cell cycle	14	3.53E-10	1.67E-08
BP	GO:0008608	Attachment of spindle microtubules to kinetochore	14	3.53E-10	1.67E-08
BP	GO:0022613	Ribonucleoprotein complex biogenesis	57	4.53E-10	2.12E-08
BP	GO:0071459	Protein localization to chromosome, centromeric region	12	5.11E-10	2.37E-08
BP	GO:0031503	Protein-containing complex localization	42	6.10E-10	2.80E-08
BP	GO:0070203	Regulation of establishment of protein localization to telomere	9	6.26E-10	2.83E-08
BP	GO:1902750	Negative regulation of cell cycle G2/M phase transition	25	6.29E-10	2.83E-08
BP	GO:0044774	Mitotic DNA integrity checkpoint	24	6.48E-10	2.89E-08
BP	GO:0007098	Centrosome cycle	27	6.66E-10	2.94E-08
BP	GO:0033048	Negative regulation of mitotic sister chromatid segregation	15	6.71E-10	2.94E-08
BP	GO:0043044	ATP-dependent chromatin remodeling	22	7.92E-10	3.44E-08
BP	GO:0006611	Protein export from nucleus	33	1.17E-09	5.05E-08
BP	GO:0006336	DNA replication-independent nucleosome assembly	18	1.23E-09	5.21E-08
BP	GO:0034724	DNA replication-independent nucleosome organization	18	1.23E-09	5.21E-08
BP	GO:0042770	Signal transduction in response to DNA damage	29	1.35E-09	5.66E-08
BP	GO:0044773	Mitotic DNA damage checkpoint	23	1.38E-09	5.74E-08
BP	GO:0034508	Centromere complex assembly	18	1.74E-09	7.18E-08
BP	GO:1904874	Positive regulation of telomerase RNA localization to Cajal body	10	1.76E-09	7.21E-08
BP	GO:0070202	Regulation of establishment of protein localization to chromosome	9	2.37E-09	9.43E-08
BP	GO:1904816	Positive regulation of protein localization to chromosome, telomeric region	9	2.37E-09	9.43E-08
BP	GO:1990173	Protein localization to nucleoplasm	9	2.37E-09	9.43E-08
BP	GO:0043486	Histone exchange	18	2.44E-09	9.65E-08
BP	GO:0006409	Trna export from nucleus	14	2.95E-09	1.14E-07
BP	GO:0051031	Trna transport	14	2.95E-09	1.14E-07
BP	GO:0071431	Trna-containing ribonucleoprotein complex export from nucleus	14	2.95E-09	1.14E-07

BP	GO:0034501	Protein localization to kinetochore	10	4.44E-09	1.70E-07
BP	GO:2000278	Regulation of DNA biosynthetic process	25	4.62E-09	1.76E-07
BP	GO:0051383	Kinetochore organization	11	4.79E-09	1.80E-07
BP	GO:0031023	Microtubule organizing center organization	27	5.00E-09	1.87E-07
BP	GO:1903311	Regulation of mrna metabolic process	44	5.66E-09	2.08E-07
BP	GO:0006406	Mrna export from nucleus	25	5.69E-09	2.08E-07
BP	GO:0071427	Mrna-containing ribonucleoprotein complex export from nucleus	25	5.69E-09	2.08E-07
BP	GO:0010972	Negative regulation of G2/M transition of mitotic cell cycle	22	6.12E-09	2.22E-07
BP	GO:0031055	Chromatin remodeling at centromere	16	6.91E-09	2.49E-07
BP	GO:0034404	Nucleobase-containing small molecule biosynthetic process	37	7.62E-09	2.72E-07
BP	GO:0007094	Mitotic spindle assembly checkpoint	13	7.98E-09	2.77E-07
BP	GO:0031577	Spindle checkpoint	13	7.98E-09	2.77E-07
BP	GO:0071173	Spindle assembly checkpoint	13	7.98E-09	2.77E-07
BP	GO:0071174	Mitotic spindle checkpoint	13	7.98E-09	2.77E-07
BP	GO:0015931	Nucleobase-containing compound transport	38	8.38E-09	2.89E-07
BP	GO:0071824	Protein-DNA complex subunit organization	40	8.56E-09	2.93E-07
BP	GO:0007080	Mitotic metaphase plate congression	15	9.22E-09	3.13E-07
BP	GO:1903046	Meiotic cell cycle process	30	1.05E-08	3.54E-07
BP	GO:0097064	Ncrna export from nucleus	14	1.15E-08	3.85E-07
BP	GO:0034080	CENP-A containing nucleosome assembly	15	1.35E-08	4.47E-07
BP	GO:0061641	CENP-A containing chromatin organization	15	1.35E-08	4.47E-07
BP	GO:0043487	Regulation of RNA stability	31	1.77E-08	5.79E-07
BP	GO:1904814	Regulation of protein localization to chromosome, telomeric region	9	1.92E-08	6.26E-07
BP	GO:1904872	Regulation of telomerase RNA localization to Cajal body	10	2.16E-08	7.01E-07
BP	GO:0065004	Protein-DNA complex assembly	36	2.23E-08	7.18E-07
BP	GO:0031571	Mitotic G1 DNA damage checkpoint	18	2.74E-08	8.68E-07
BP	GO:0044819	Mitotic G1/S transition checkpoint	18	2.74E-08	8.68E-07
BP	GO:0043488	Regulation of mrna stability	30	3.11E-08	9.80E-07
BP	GO:0072431	Signal transduction involved in mitotic G1 DNA damage checkpoint	17	3.28E-08	1.02E-06
BP	GO:1902400	Intracellular signal transduction involved in G1 DNA damage checkpoint	17	3.28E-08	1.02E-06
BP	GO:0070198	Protein localization to chromosome, telomeric region	12	3.53E-08	1.09E-06

BP	GO:0044783	G1 DNA damage checkpoint	18	3.59E-08	1.10E-06
BP	GO:2001251	Negative regulation of chromosome organization	26	3.73E-08	1.14E-06
BP	GO:0009124	Nucleoside monophosphate biosynthetic process	34	4.05E-08	1.23E-06
BP	GO:0061013	Regulation of mrna catabolic process	32	4.24E-08	1.27E-06
BP	GO:0090670	RNA localization to Cajal body	10	4.32E-08	1.27E-06
BP	GO:0090671	Telomerase RNA localization to Cajal body	10	4.32E-08	1.27E-06
BP	GO:0090672	Telomerase RNA localization	10	4.32E-08	1.27E-06
BP	GO:0090685	RNA localization to nucleus	10	4.32E-08	1.27E-06
BP	GO:0051984	Positive regulation of chromosome segregation	11	5.65E-08	1.64E-06
BP	GO:0070199	Establishment of protein localization to chromosome	11	5.65E-08	1.64E-06
BP	GO:0072413	Signal transduction involved in mitotic cell cycle checkpoint	17	5.79E-08	1.65E-06
BP	GO:1902402	Signal transduction involved in mitotic DNA damage checkpoint	17	5.79E-08	1.65E-06
BP	GO:1902403	Signal transduction involved in mitotic DNA integrity checkpoint	17	5.79E-08	1.65E-06
BP	GO:0043161	Proteasome-mediated ubiquitin-dependent protein catabolic process	47	5.98E-08	1.70E-06
BP	GO:0051028	Mrna transport	28	7.13E-08	2.01E-06
BP	GO:0045740	Positive regulation of DNA replication	13	7.35E-08	2.06E-06
BP	GO:0022616	DNA strand elongation	9	9.81E-08	2.73E-06
BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	48	9.94E-08	2.74E-06
BP	GO:0000398	Mrna splicing, via spliceosome	48	9.94E-08	2.74E-06
BP	GO:0000375	RNA splicing, via transesterification reactions	48	1.42E-07	3.89E-06
BP	GO:0140013	Meiotic nuclear division	27	1.46E-07	3.98E-06
BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	16	1.61E-07	4.37E-06
BP	GO:0010639	Negative regulation of organelle organization	48	2.01E-07	5.42E-06
BP	GO:0030261	Chromosome condensation	12	2.08E-07	5.57E-06
BP	GO:0045931	Positive regulation of mitotic cell cycle	28	2.30E-07	6.12E-06
BP	GO:0042254	Ribosome biogenesis	33	2.74E-07	7.27E-06
BP	GO:0070316	Regulation of G0 to G1 transition	14	2.99E-07	7.87E-06
BP	GO:0060249	Anatomical structure homeostasis	53	3.41E-07	8.94E-06
BP	GO:0010498	Proteasomal protein catabolic process	50	4.02E-07	1.05E-05
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	22	4.28E-07	1.11E-05
BP	GO:0032212	Positive regulation of telomere maintenance via telomerase	12	4.50E-07	1.16E-05

BP	GO:2001252	Positive regulation of chromosome organization	29	5.01E-07	1.29E-05
BP	GO:0031123	RNA 3'-end processing	22	5.08E-07	1.30E-05
BP	GO:0045023	G0 to G1 transition	14	5.44E-07	1.38E-05
BP	GO:1901293	Nucleoside phosphate biosynthetic process	48	5.96E-07	1.50E-05
BP	GO:0009163	Nucleoside biosynthetic process	13	6.20E-07	1.55E-05
BP	GO:0070317	Negative regulation of G0 to G1 transition	13	6.20E-07	1.55E-05
BP	GO:0016072	Rrna metabolic process	31	7.24E-07	1.80E-05
BP	GO:0006401	RNA catabolic process	48	7.57E-07	1.87E-05
BP	GO:0034470	Ncrna processing	41	7.83E-07	1.93E-05
BP	GO:1901659	Glycosyl compound biosynthetic process	13	8.47E-07	2.07E-05
BP	GO:0000076	DNA replication checkpoint	7	8.95E-07	2.17E-05
BP	GO:2000105	Positive regulation of DNA-dependent DNA replication	7	8.95E-07	2.17E-05
BP	GO:0007076	Mitotic chromosome condensation	8	9.03E-07	2.18E-05
BP	GO:0009165	Nucleotide biosynthetic process	47	9.60E-07	2.30E-05
BP	GO:0034728	Nucleosome organization	28	9.90E-07	2.36E-05
BP	GO:0006338	Chromatin remodeling	27	1.03E-06	2.45E-05
BP	GO:0097711	Ciliary basal body-plasma membrane docking	20	1.12E-06	2.65E-05
BP	GO:0007062	Sister chromatid cohesion	14	1.26E-06	2.93E-05
BP	GO:0036297	Interstrand cross-link repair	14	1.26E-06	2.93E-05
BP	GO:0075733	Intracellular transport of virus	15	1.26E-06	2.93E-05
BP	GO:1904358	Positive regulation of telomere maintenance via telomere lengthening	12	1.28E-06	2.96E-05
BP	GO:0006369	Termination of RNA polymerase II transcription	11	1.28E-06	2.96E-05
BP	GO:0006333	Chromatin assembly or disassembly	29	1.51E-06	3.47E-05
BP	GO:0009156	Ribonucleoside monophosphate biosynthetic process	30	1.57E-06	3.58E-05
BP	GO:0009116	Nucleoside metabolic process	22	1.58E-06	3.58E-05
BP	GO:1901989	Positive regulation of cell cycle phase transition	20	1.58E-06	3.59E-05
BP	GO:0044766	Multi-organism transport	17	1.62E-06	3.63E-05
BP	GO:1902579	Multi-organism localization	17	1.62E-06	3.63E-05
BP	GO:0032206	Positive regulation of telomere maintenance	14	1.63E-06	3.64E-05
BP	GO:1901657	Glycosyl compound metabolic process	24	1.65E-06	3.66E-05
BP	GO:0031124	Mrna 3'-end processing	19	1.65E-06	3.66E-05
BP	GO:0006284	Base-excision repair	12	1.76E-06	3.88E-05
BP	GO:0070507	Regulation of microtubule cytoskeleton organization	28	1.83E-06	4.01E-05
BP	GO:1900182	Positive regulation of protein localization to nucleus	17	1.98E-06	4.31E-05

BP	GO:0019882	Antigen processing and presentation	33	1.99E-06	4.31E-05
BP	GO:0061640	Cytoskeleton-dependent cytokinesis	18	2.02E-06	4.36E-05
BP	GO:0046112	Nucleobase biosynthetic process	7	2.03E-06	4.36E-05
BP	GO:0051988	Regulation of attachment of spindle microtubules to kinetochore	7	2.03E-06	4.36E-05
BP	GO:0090307	Mitotic spindle assembly	14	2.11E-06	4.50E-05
BP	GO:0051302	Regulation of cell division	27	2.20E-06	4.67E-05
BP	GO:0009123	Nucleoside monophosphate metabolic process	45	2.29E-06	4.84E-05
BP	GO:0031497	Chromatin assembly	26	2.32E-06	4.89E-05
BP	GO:0006334	Nucleosome assembly	24	2.49E-06	5.22E-05
BP	GO:0009112	Nucleobase metabolic process	10	2.50E-06	5.22E-05
BP	GO:0046794	Transport of virus	15	2.55E-06	5.29E-05
BP	GO:0006397	Mrna processing	58	2.56E-06	5.30E-05
BP	GO:0045005	DNA-dependent DNA replication maintenance of fidelity	11	2.62E-06	5.39E-05
BP	GO:0032210	Regulation of telomere maintenance via telomerase	14	2.70E-06	5.55E-05
BP	GO:0000018	Regulation of DNA recombination	18	2.92E-06	5.96E-05
BP	GO:1904666	Regulation of ubiquitin protein ligase activity	9	3.04E-06	6.18E-05
BP	GO:0000281	Mitotic cytokinesis	16	3.47E-06	7.02E-05
BP	GO:0006301	Postreplication repair	13	3.50E-06	7.05E-05
BP	GO:0000910	Cytokinesis	25	3.56E-06	7.16E-05
BP	GO:0140053	Mitochondrial gene expression	25	4.04E-06	8.09E-05
BP	GO:1902807	Negative regulation of cell cycle G1/S phase transition	23	4.36E-06	8.68E-05
BP	GO:0006282	Regulation of DNA repair	21	4.37E-06	8.68E-05
BP	GO:0006520	Cellular amino acid metabolic process	44	4.59E-06	9.08E-05
BP	GO:0006297	Nucleotide-excision repair, DNA gap filling	9	4.72E-06	9.29E-05
BP	GO:0009141	Nucleoside triphosphate metabolic process	43	5.01E-06	9.81E-05
BP	GO:0010833	Telomere maintenance via telomere lengthening	17	5.15E-06	0.000100555
BP	GO:0051782	Negative regulation of cell division	8	5.20E-06	0.000101031
BP	GO:0009262	Deoxyribonucleotide metabolic process	10	5.30E-06	0.00010215
BP	GO:0031297	Replication fork processing	10	5.30E-06	0.00010215
BP	GO:0006399	Trna metabolic process	26	5.45E-06	0.000104589
BP	GO:0140056	Organelle localization by membrane tethering	24	5.47E-06	0.000104589
BP	GO:2001020	Regulation of response to DNA damage stimulus	30	6.34E-06	0.000120797
BP	GO:2000134	Negative regulation of G1/S transition of mitotic cell cycle	22	6.68E-06	0.000126817

BP	GO:0006364	Rrna processing	25	8.35E-06	0.000157943
BP	GO:0046653	Tetrahydrofolate metabolic process	8	8.49E-06	0.000159897
BP	GO:0071158	Positive regulation of cell cycle arrest	17	8.76E-06	0.000162002
BP	GO:1901992	Positive regulation of mitotic cell cycle phase transition	17	8.76E-06	0.000162002
BP	GO:0002478	Antigen processing and presentation of exogenous peptide antigen	27	8.77E-06	0.000162002
BP	GO:0009127	Purine nucleoside monophosphate biosynthetic process	27	8.77E-06	0.000162002
BP	GO:0009168	Purine ribonucleoside monophosphate biosynthetic process	27	8.77E-06	0.000162002
BP	GO:1900180	Regulation of protein localization to nucleus	21	8.92E-06	0.000164186
BP	GO:0019884	Antigen processing and presentation of exogenous antigen	27	1.09E-05	0.000199372
BP	GO:0007004	Telomere maintenance via telomerase	15	1.10E-05	0.000201194
BP	GO:0042769	DNA damage response, detection of DNA damage	11	1.22E-05	0.000222403
BP	GO:0048002	Antigen processing and presentation of peptide antigen	28	1.33E-05	0.000240916
BP	GO:0000966	RNA 5'-end processing	8	1.34E-05	0.000241683
BP	GO:0046931	Pore complex assembly	7	1.40E-05	0.000251993
BP	GO:0036294	Cellular response to decreased oxygen levels	31	1.47E-05	0.000262802
BP	GO:0071456	Cellular response to hypoxia	30	1.53E-05	0.000272992
BP	GO:1904356	Regulation of telomere maintenance via telomere lengthening	14	1.59E-05	0.000283127
BP	GO:0006353	DNA-templated transcription, termination	15	1.61E-05	0.000284983
BP	GO:0022406	Membrane docking	24	1.62E-05	0.000285279
BP	GO:0051656	Establishment of organelle localization	51	1.81E-05	0.000319351
BP	GO:0016925	Protein sumoylation	16	1.84E-05	0.000322957
BP	GO:0034504	Protein localization to nucleus	31	1.93E-05	0.000336325
BP	GO:0006298	Mismatch repair	9	2.16E-05	0.00037226
BP	GO:0006760	Folic acid-containing compound metabolic process	9	2.16E-05	0.00037226
BP	GO:0015949	Nucleobase-containing small molecule interconversion	9	2.16E-05	0.00037226
BP	GO:1902751	Positive regulation of cell cycle G2/M phase transition	9	2.16E-05	0.00037226
BP	GO:0032204	Regulation of telomere maintenance	16	2.18E-05	0.000373882
BP	GO:0009260	Ribonucleotide biosynthetic process	36	2.26E-05	0.0003868
BP	GO:0008380	RNA splicing	50	2.29E-05	0.000390723
BP	GO:0051382	Kinetochore assembly	7	2.36E-05	0.000398781
BP	GO:0099116	Trna 5'-end processing	7	2.36E-05	0.000398781
BP	GO:0072522	Purine-containing compound biosynthetic process	37	2.43E-05	0.000409233

BP	GO:0010212	Response to ionizing radiation	23	2.48E-05	0.000416289
BP	GO:0032543	Mitochondrial translation	21	2.54E-05	0.000425494
BP	GO:0071453	Cellular response to oxygen levels	32	2.58E-05	0.000429876
BP	GO:1902806	Regulation of cell cycle G1/S phase transition	28	2.64E-05	0.000439359
BP	GO:0051653	Spindle localization	11	2.70E-05	0.000448094
BP	GO:0006402	Mrna catabolic process	41	2.78E-05	0.000458383
BP	GO:1901292	Nucleoside phosphate catabolic process	26	2.79E-05	0.000458989
BP	GO:0022411	Cellular component disassembly	54	2.90E-05	0.000475896
BP	GO:0040001	Establishment of mitotic spindle localization	9	3.01E-05	0.000492263
BP	GO:0046390	Ribose phosphate biosynthetic process	36	3.32E-05	0.000541061
BP	GO:2000045	Regulation of G1/S transition of mitotic cell cycle	26	3.41E-05	0.000553103
BP	GO:0018205	Peptidyl-lysine modification	44	3.47E-05	0.00056111
BP	GO:0006999	Nuclear pore organization	6	3.68E-05	0.000592794
BP	GO:0009161	Ribonucleoside monophosphate metabolic process	40	3.77E-05	0.000606313
BP	GO:0032886	Regulation of microtubule-based process	28	3.84E-05	0.00061518
BP	GO:0006732	Coenzyme metabolic process	43	3.86E-05	0.000615633
BP	GO:0006278	RNA-dependent DNA biosynthetic process	15	3.87E-05	0.000615633
BP	GO:0031398	Positive regulation of protein ubiquitination	19	4.10E-05	0.000650612
BP	GO:0046134	Pyrimidine nucleoside biosynthetic process	9	4.13E-05	0.000652014
BP	GO:0032465	Regulation of cytokinesis	16	4.14E-05	0.000652014
BP	GO:0009166	Nucleotide catabolic process	25	4.25E-05	0.000667598
BP	GO:0051973	Positive regulation of telomerase activity	10	4.52E-05	0.000707583
BP	GO:0051298	Centrosome duplication	13	5.03E-05	0.000785333
BP	GO:0007143	Female meiotic nuclear division	9	5.58E-05	0.000867355
BP	GO:0034471	Ncrna 5'-end processing	7	5.88E-05	0.000908198
BP	GO:0042276	Error-prone translesion synthesis	7	5.88E-05	0.000908198
BP	GO:0008334	Histone mrna metabolic process	8	6.26E-05	0.000960794
BP	GO:0010971	Positive regulation of G2/M transition of mitotic cell cycle	8	6.26E-05	0.000960794
BP	GO:0061418	Regulation of transcription from RNA polymerase II promoter in response to hypoxia	15	6.29E-05	0.000962375
BP	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	14	6.88E-05	0.001049638
BP	GO:0031396	Regulation of protein ubiquitination	27	7.59E-05	0.001155229
BP	GO:0009142	Nucleoside triphosphate biosynthetic process	25	7.62E-05	0.001156074
BP	GO:0006457	Protein folding	25	8.38E-05	0.001266074

BP	GO:1900034	Regulation of cellular response to heat	15	8.56E-05	0.001289273
BP	GO:0046605	Regulation of centrosome cycle	12	8.92E-05	0.001339483
BP	GO:0071156	Regulation of cell cycle arrest	18	0.000104694	0.001567813
BP	GO:0051438	Regulation of ubiquitin-protein transferase activity	11	0.000105931	0.001581424
BP	GO:0006575	Cellular modified amino acid metabolic process	25	0.000110443	0.001643698
BP	GO:2000779	Regulation of double-strand break repair	14	0.000111806	0.001658853
BP	GO:0009308	Amine metabolic process	20	0.000112207	0.0016597
BP	GO:0043618	Regulation of transcription from RNA polymerase II promoter in response to stress	18	0.000118285	0.001744258
BP	GO:0090305	Nucleic acid phosphodiester bond hydrolysis	33	0.000122312	0.00179813
BP	GO:0006165	Nucleoside diphosphate phosphorylation	20	0.000125227	0.0018354
BP	GO:0042455	Ribonucleoside biosynthetic process	9	0.000127065	0.001845497
BP	GO:0042558	Pteridine-containing compound metabolic process	9	0.000127065	0.001845497
BP	GO:0043094	Cellular metabolic compound salvage	9	0.000127065	0.001845497
BP	GO:0006164	Purine nucleotide biosynthetic process	34	0.000127797	0.001850555
BP	GO:0051972	Regulation of telomerase activity	11	0.000129831	0.001874388
BP	GO:0061982	Meiosis I cell cycle process	16	0.000130881	0.001883906
BP	GO:0009167	Purine ribonucleoside monophosphate metabolic process	37	0.000149392	0.00214396
BP	GO:0000079	Regulation of cyclin-dependent protein serine/threonine kinase activity	15	0.000153134	0.002191135
BP	GO:0046939	Nucleotide phosphorylation	20	0.000155327	0.00221594
BP	GO:0007568	Aging	37	0.000159267	0.002258784
BP	GO:0009126	Purine nucleoside monophosphate metabolic process	37	0.000159267	0.002258784
BP	GO:0009394	2'-deoxyribonucleotide metabolic process	8	0.000159944	0.002261733
BP	GO:0006289	Nucleotide-excision repair	17	0.000161351	0.002274952
BP	GO:0006144	Purine nucleobase metabolic process	6	0.000169482	0.002375707
BP	GO:0009200	Deoxyribonucleoside triphosphate metabolic process	6	0.000169482	0.002375707
BP	GO:0006188	IMP biosynthetic process	5	0.000173243	0.00239363
BP	GO:0046040	IMP metabolic process	5	0.000173243	0.00239363
BP	GO:0051231	Spindle elongation	5	0.000173243	0.00239363
BP	GO:0051255	Spindle midzone assembly	5	0.000173243	0.00239363
BP	GO:0051315	Attachment of mitotic spindle microtubules to kinetochore	5	0.000173243	0.00239363
BP	GO:2000104	Negative regulation of DNA-dependent DNA replication	7	0.000182253	0.002510921
BP	GO:0006418	Trna aminoacylation for protein translation	10	0.000186441	0.002561308
BP	GO:0009144	Purine nucleoside triphosphate metabolic process	37	0.000192513	0.002637214

BP	GO:0031109	Microtubule polymerization or depolymerization	16	0.000193741	0.00264651
BP	GO:0002200	Somatic diversification of immune receptors	13	0.000199192	0.002713284
BP	GO:0006220	Pyrimidine nucleotide metabolic process	12	0.000218697	0.002970578
BP	GO:0070125	Mitochondrial translational elongation	15	0.000230508	0.003122219
BP	GO:0009152	Purine ribonucleotide biosynthetic process	32	0.000236317	0.003191939
BP	GO:0043620	Regulation of DNA-templated transcription in response to stress	18	0.000237279	0.003195969
BP	GO:0043174	Nucleoside salvage	6	0.00025703	0.003448971
BP	GO:0002562	Somatic diversification of immune receptors via germline recombination within a single locus	12	0.000258208	0.003448971
BP	GO:0016444	Somatic cell DNA recombination	12	0.000258208	0.003448971
BP	GO:0009314	Response to radiation	46	0.000261454	0.003472955
BP	GO:0008156	Negative regulation of DNA replication	9	0.000262289	0.003472955
BP	GO:0051293	Establishment of spindle localization	9	0.000262289	0.003472955
BP	GO:1904029	Regulation of cyclin-dependent protein kinase activity	15	0.000262884	0.003472955
BP	GO:0072528	Pyrimidine-containing compound biosynthetic process	11	0.000276579	0.00363769
BP	GO:0019692	Deoxyribose phosphate metabolic process	8	0.000276863	0.00363769
BP	GO:1903320	Regulation of protein modification by small protein conjugation or removal	28	0.000280482	0.003670627
BP	GO:0042398	Cellular modified amino acid biosynthetic process	10	0.000280892	0.003670627
BP	GO:0009411	Response to UV	20	0.000287152	0.003742292
BP	GO:0034605	Cellular response to heat	18	0.000295384	0.003839198
BP	GO:0007127	Meiosis I	15	0.000299106	0.003877123
BP	GO:0001682	Trna 5'-leader removal	5	0.000301449	0.003884775
BP	GO:0016446	Somatic hypermutation of immunoglobulin genes	5	0.000301449	0.003884775
BP	GO:0046434	Organophosphate catabolic process	28	0.000302113	0.003884775
BP	GO:0006521	Regulation of cellular amino acid metabolic process	12	0.000303622	0.003893786
BP	GO:1903322	Positive regulation of protein modification by small protein conjugation or removal	19	0.000325045	0.004157473
BP	GO:0001666	Response to hypoxia	39	0.000332687	0.004243965
BP	GO:0043039	Trna aminoacylation	10	0.000341383	0.004343397
BP	GO:0000729	DNA double-strand break processing	7	0.00034457	0.004372408
BP	GO:0009199	Ribonucleoside triphosphate metabolic process	36	0.000351606	0.004449986
BP	GO:0033238	Regulation of cellular amine metabolic process	14	0.000355865	0.00448626
BP	GO:0050821	Protein stabilization	23	0.00035676	0.00448626
BP	GO:0031572	G2 DNA damage checkpoint	8	0.000357263	0.00448626
BP	GO:0009264	Deoxyribonucleotide catabolic process	6	0.000376538	0.004716013

BP	GO:0031099	Regeneration	25	0.000392455	0.004902635
BP	GO:0006096	Glycolytic process	17	0.000407591	0.005065472
BP	GO:1903578	Regulation of ATP metabolic process	17	0.000407591	0.005065472
BP	GO:0043038	Amino acid activation	10	0.000412354	0.005111492
BP	GO:0032984	Protein-containing complex disassembly	34	0.000414933	0.005130279
BP	GO:1902036	Regulation of hematopoietic stem cell differentiation	13	0.000417972	0.005146847
BP	GO:0051188	Cofactor biosynthetic process	35	0.000418408	0.005146847
BP	GO:0043624	Cellular protein complex disassembly	25	0.000424379	0.00520701
BP	GO:0044106	Cellular amine metabolic process	18	0.000449573	0.005478489
BP	GO:0046031	ADP metabolic process	18	0.000449573	0.005478489
BP	GO:0070498	Interleukin-1-mediated signaling pathway	16	0.000449913	0.005478489
BP	GO:0006757	ATP generation from ADP	17	0.000454142	0.005516052
BP	GO:0007099	Centriole replication	8	0.000455689	0.005520934
BP	GO:0016445	Somatic diversification of immunoglobulins	11	0.000462241	0.005586276
BP	GO:0009132	Nucleoside diphosphate metabolic process	21	0.000481044	0.005798982
BP	GO:0000212	Meiotic spindle organization	5	0.000490514	0.005852239
BP	GO:0002566	Somatic diversification of immune receptors via somatic mutation	5	0.000490514	0.005852239
BP	GO:0007077	Mitotic nuclear envelope disassembly	5	0.000490514	0.005852239
BP	GO:1904668	Positive regulation of ubiquitin protein ligase activity	5	0.000490514	0.005852239
BP	GO:0009201	Ribonucleoside triphosphate biosynthetic process	22	0.000492397	0.005852239
BP	GO:0002204	Somatic recombination of immunoglobulin genes involved in immune response	10	0.000495171	0.005852239
BP	GO:0002208	Somatic diversification of immunoglobulins involved in immune response	10	0.000495171	0.005852239
BP	GO:0045190	Isotype switching	10	0.000495171	0.005852239
BP	GO:0007050	Cell cycle arrest	28	0.000499512	0.005889111
BP	GO:0060218	Hematopoietic stem cell differentiation	14	0.000525186	0.006164474
BP	GO:0022618	Ribonucleoprotein complex assembly	26	0.000525425	0.006164474
BP	GO:0006312	Mitotic recombination	6	0.000535425	0.006251377
BP	GO:0042772	DNA damage response, signal transduction resulting in transcription	6	0.000535425	0.006251377
BP	GO:0071826	Ribonucleoprotein complex subunit organization	27	0.000551555	0.006424145
BP	GO:0006414	Translational elongation	18	0.000606896	0.007048549
BP	GO:0036293	Response to decreased oxygen levels	39	0.000609275	0.007048549
BP	GO:0019985	Translesion synthesis	9	0.000609549	0.007048549
BP	GO:0042866	Pyruvate biosynthetic process	17	0.000622285	0.007178609

BP	GO:0002479	Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	13	0.000628556	0.007216418
BP	GO:0031100	Animal organ regeneration	13	0.000628556	0.007216418
BP	GO:0072527	Pyrimidine-containing compound metabolic process	15	0.000694659	0.007956405
BP	GO:0016447	Somatic recombination of immunoglobulin gene segments	10	0.000702375	0.008025722
BP	GO:0016579	Protein deubiquitination	30	0.000734091	0.008338123
BP	GO:0010569	Regulation of double-strand break repair via homologous recombination	9	0.000738715	0.008338123
BP	GO:0002244	Hematopoietic progenitor cell differentiation	21	0.000739572	0.008338123
BP	GO:0046386	Deoxyribose phosphate catabolic process	6	0.000741887	0.008338123
BP	GO:0046655	Folic acid metabolic process	6	0.000741887	0.008338123
BP	GO:0070987	Error-free translesion synthesis	6	0.000741887	0.008338123
BP	GO:0045132	Meiotic chromosome segregation	12	0.000742738	0.008338123
BP	GO:0031647	Regulation of protein stability	31	0.000743549	0.008338123
BP	GO:0001833	Inner cell mass cell proliferation	5	0.000756654	0.008445799
BP	GO:0042559	Pteridine-containing compound biosynthetic process	5	0.000756654	0.008445799
BP	GO:0006733	Oxidoreduction coenzyme metabolic process	24	0.000789529	0.008783009
BP	GO:0070646	Protein modification by small protein removal	31	0.000790507	0.008783009
BP	GO:0000731	DNA synthesis involved in DNA repair	10	0.000830073	0.009201402
BP	GO:0000959	Mitochondrial RNA metabolic process	8	0.000889102	0.009810641
BP	GO:0007019	Microtubule depolymerization	8	0.000889102	0.009810641
BP	GO:0042590	Antigen processing and presentation of exogenous peptide antigen via MHC class I	13	0.000922283	0.010153539
BP	GO:0006997	Nucleus organization	17	0.000927454	0.010187202
BP	GO:0000209	Protein polyubiquitination	32	0.000949195	0.010402314
BP	GO:0070126	Mitochondrial translational termination	14	0.000958544	0.010480953
BP	GO:0006213	Pyrimidine nucleoside metabolic process	10	0.000976237	0.010650261
BP	GO:0035690	Cellular response to drug	38	0.000991174	0.010788801
BP	GO:0072524	Pyridine-containing compound metabolic process	23	0.001004872	0.01091327
BP	GO:0009205	Purine ribonucleoside triphosphate metabolic process	34	0.001052239	0.011402017
BP	GO:0046394	Carboxylic acid biosynthetic process	43	0.00106053	0.011466092
BP	GO:0009119	Ribonucleoside metabolic process	14	0.001074091	0.011585737
BP	GO:0001824	Blastocyst development	15	0.001076402	0.011585737
BP	GO:0007339	Binding of sperm to zona pellucida	8	0.001090905	0.011663738
BP	GO:0098534	Centriole assembly	8	0.001090905	0.011663738
BP	GO:1901998	Toxin transport	8	0.001090905	0.011663738

BP	GO:0051053	Negative regulation of DNA metabolic process	19	0.001095984	0.011692113
BP	GO:0070482	Response to oxygen levels	40	0.00110018	0.011710964
BP	GO:0016053	Organic acid biosynthetic process	43	0.001110945	0.011764531
BP	GO:0000963	Mitochondrial RNA processing	5	0.001117411	0.011764531
BP	GO:0090231	Regulation of spindle checkpoint	5	0.001117411	0.011764531
BP	GO:0090266	Regulation of mitotic cell cycle spindle assembly checkpoint	5	0.001117411	0.011764531
BP	GO:1903504	Regulation of mitotic spindle checkpoint	5	0.001117411	0.011764531
BP	GO:0006415	Translational termination	15	0.001195552	0.012559809
BP	GO:0009108	Coenzyme biosynthetic process	28	0.001255083	0.013156545
BP	GO:0051443	Positive regulation of ubiquitin-protein transferase activity	7	0.001268507	0.013239699
BP	GO:0071168	Protein localization to chromatin	7	0.001268507	0.013239699
BP	GO:0045739	Positive regulation of DNA repair	11	0.001322208	0.013770378
BP	GO:0007063	Regulation of sister chromatid cohesion	6	0.001333882	0.013862024
BP	GO:0009135	Purine nucleoside diphosphate metabolic process	18	0.001392067	0.01440461
BP	GO:0009179	Purine ribonucleoside diphosphate metabolic process	18	0.001392067	0.01440461
BP	GO:0072525	Pyridine-containing compound biosynthetic process	19	0.001532736	0.015826241
BP	GO:0043101	Purine-containing compound salvage	5	0.001591375	0.016362108
BP	GO:0019362	Pyridine nucleotide metabolic process	22	0.001594814	0.016362108
BP	GO:0046496	Nicotinamide nucleotide metabolic process	22	0.001594814	0.016362108
BP	GO:0006296	Nucleotide-excision repair, DNA incision, 5'-to lesion	8	0.001603479	0.016416087
BP	GO:0009185	Ribonucleoside diphosphate metabolic process	18	0.001652215	0.016879192
BP	GO:0042752	Regulation of circadian rhythm	16	0.001711872	0.017451682
BP	GO:0045943	Positive regulation of transcription by RNA polymerase I	6	0.001739168	0.017655302
BP	GO:1903429	Regulation of cell maturation	6	0.001739168	0.017655302
BP	GO:0051170	Import into nucleus	17	0.001768703	0.017917403
BP	GO:0048511	Rhythmic process	31	0.00177825	0.017972463
BP	GO:0002381	Immunoglobulin production involved in immunoglobulin mediated immune response	10	0.001786428	0.017972463
BP	GO:0009408	Response to heat	20	0.00178657	0.017972463
BP	GO:0098781	Ncrna transcription	15	0.001789046	0.017972463
BP	GO:0016572	Histone phosphorylation	8	0.001922751	0.019275476
BP	GO:0009206	Purine ribonucleoside triphosphate biosynthetic process	20	0.001927994	0.019287941
BP	GO:0009303	Rrna transcription	7	0.001957394	0.019541521

BP	GO:0008033	Trna processing	15	0.00197075	0.01963421
BP	GO:0002474	Antigen processing and presentation of peptide antigen via MHC class I	14	0.002040218	0.020284393
BP	GO:0006110	Regulation of glycolytic process	12	0.00205514	0.020353554
BP	GO:0007569	Cell aging	16	0.002055616	0.020353554
BP	GO:1901532	Regulation of hematopoietic progenitor cell differentiation	13	0.002073484	0.020488405
BP	GO:0009145	Purine nucleoside triphosphate biosynthetic process	20	0.002078778	0.020498704
BP	GO:0007096	Regulation of exit from mitosis	5	0.002197896	0.021410614
BP	GO:0009219	Pyrimidine deoxyribonucleotide metabolic process	5	0.002197896	0.021410614
BP	GO:0030397	Membrane disassembly	5	0.002197896	0.021410614
BP	GO:0033262	Regulation of nuclear cell cycle DNA replication	5	0.002197896	0.021410614
BP	GO:0051081	Nuclear envelope disassembly	5	0.002197896	0.021410614
BP	GO:0051131	Chaperone-mediated protein complex assembly	5	0.002197896	0.021410614
BP	GO:0006458	'De novo' protein folding	6	0.002231379	0.021491976
BP	GO:0044818	Mitotic G2/M transition checkpoint	6	0.002231379	0.021491976
BP	GO:0060147	Regulation of posttranscriptional gene silencing	16	0.002247997	0.021491976
BP	GO:0060966	Regulation of gene silencing by RNA	16	0.002247997	0.021491976
BP	GO:0006264	Mitochondrial DNA replication	4	0.002254184	0.021491976
BP	GO:0009162	Deoxyribonucleoside monophosphate metabolic process	4	0.002254184	0.021491976
BP	GO:0009263	Deoxyribonucleotide biosynthetic process	4	0.002254184	0.021491976
BP	GO:0042023	DNA endoreduplication	4	0.002254184	0.021491976
BP	GO:0075522	IRES-dependent viral translational initiation	4	0.002254184	0.021491976
BP	GO:1901838	Positive regulation of transcription of nucleolar large rrna by RNA polymerase I	4	0.002254184	0.021491976
BP	GO:0097327	Response to antineoplastic agent	14	0.002255855	0.021491976
BP	GO:0009266	Response to temperature stimulus	25	0.002259733	0.021491976
BP	GO:0006754	ATP biosynthetic process	19	0.002278608	0.021628836
BP	GO:1900542	Regulation of purine nucleotide metabolic process	17	0.0022888	0.021652232
BP	GO:0033683	Nucleotide-excision repair, DNA incision	8	0.002290054	0.021652232
BP	GO:0060968	Regulation of gene silencing	18	0.002296908	0.021674539
BP	GO:1901976	Regulation of cell cycle checkpoint	7	0.002395392	0.022543623
BP	GO:0045840	Positive regulation of mitotic nuclear division	9	0.002398357	0.022543623
BP	GO:0019886	Antigen processing and presentation of exogenous peptide antigen via MHC class II	14	0.002489967	0.023359182
BP	GO:0042278	Purine nucleoside metabolic process	11	0.002522902	0.023622205

BP	GO:0030811	Regulation of nucleotide catabolic process	12	0.002581737	0.024126228
BP	GO:0010824	Regulation of centrosome duplication	8	0.00271018	0.025277538
BP	GO:0002377	Immunoglobulin production	14	0.002743724	0.025541003
BP	GO:1902369	Negative regulation of RNA catabolic process	9	0.002779953	0.025828389
BP	GO:0000132	Establishment of mitotic spindle orientation	6	0.002821609	0.026165001
BP	GO:0019359	Nicotinamide nucleotide biosynthetic process	18	0.002908494	0.026867355
BP	GO:0019363	Pyridine nucleotide biosynthetic process	18	0.002908494	0.026867355
BP	GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	5	0.002956795	0.027105829
BP	GO:0009148	Pyrimidine nucleoside triphosphate biosynthetic process	5	0.002956795	0.027105829
BP	GO:0034629	Cellular protein-containing complex localization	5	0.002956795	0.027105829
BP	GO:0097329	Response to antimetabolite	5	0.002956795	0.027105829
BP	GO:0043687	Post-translational protein modification	36	0.00303862	0.027803089
BP	GO:0006140	Regulation of nucleotide metabolic process	17	0.003175604	0.028951166
BP	GO:0002639	Positive regulation of immunoglobulin production	8	0.003188111	0.028951166
BP	GO:0043489	RNA stabilization	8	0.003188111	0.028951166
BP	GO:0090224	Regulation of spindle organization	8	0.003188111	0.028951166
BP	GO:0000387	Spliceosomal snrnp assembly	9	0.003207976	0.029076802
BP	GO:0007623	Circadian rhythm	23	0.003214619	0.029082351
BP	GO:0002495	Antigen processing and presentation of peptide antigen via MHC class II	14	0.003315076	0.029935008
BP	GO:0007100	Mitotic centrosome separation	4	0.003370033	0.030093143
BP	GO:0008655	Pyrimidine-containing compound salvage	4	0.003370033	0.030093143
BP	GO:0009143	Nucleoside triphosphate catabolic process	4	0.003370033	0.030093143
BP	GO:0035404	Histone-serine phosphorylation	4	0.003370033	0.030093143
BP	GO:0043097	Pyrimidine nucleoside salvage	4	0.003370033	0.030093143
BP	GO:0048875	Chemical homeostasis within a tissue	4	0.003370033	0.030093143
BP	GO:0043467	Regulation of generation of precursor metabolites and energy	18	0.003387236	0.030190853
BP	GO:0046034	ATP metabolic process	30	0.003414878	0.030381077
BP	GO:0051196	Regulation of coenzyme metabolic process	13	0.003471402	0.030827076
BP	GO:0006730	One-carbon metabolic process	6	0.003521277	0.031155226
BP	GO:0045830	Positive regulation of isotype switching	6	0.003521277	0.031155226
BP	GO:0002504	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	14	0.00363522	0.032104454
BP	GO:0006221	Pyrimidine nucleotide biosynthetic process	8	0.003728999	0.032872453

BP	GO:0006303	Double-strand break repair via nonhomologous end joining	12	0.00396387	0.034879164
BP	GO:0006690	Icosanoid metabolic process	14	0.003980112	0.034958286
BP	GO:0002312	B cell activation involved in immune response	11	0.004016101	0.035210257
BP	GO:0002223	Stimulatory C-type lectin receptor signaling pathway	15	0.004051672	0.035393408
BP	GO:0060964	Regulation of gene silencing by mirna	15	0.004051672	0.035393408
BP	GO:0006090	Pyruvate metabolic process	18	0.004226527	0.036854091
BP	GO:0009150	Purine ribonucleotide metabolic process	46	0.004533821	0.039462251
BP	GO:0072330	Monocarboxylic acid biosynthetic process	32	0.004561309	0.039558689
BP	GO:1903829	Positive regulation of cellular protein localization	32	0.004561309	0.039558689
BP	GO:0000722	Telomere maintenance via recombination	4	0.004809792	0.041489831
BP	GO:0051095	Regulation of helicase activity	4	0.004809792	0.041489831
BP	GO:0051299	Centrosome separation	4	0.004809792	0.041489831
BP	GO:0006283	Transcription-coupled nucleotide-excision repair	11	0.004989792	0.042924672
BP	GO:0001832	Blastocyst growth	5	0.005011736	0.042924672
BP	GO:0009147	Pyrimidine nucleoside triphosphate metabolic process	5	0.005011736	0.042924672
BP	GO:0032069	Regulation of nuclease activity	5	0.005011736	0.042924672
BP	GO:0001676	Long-chain fatty acid metabolic process	13	0.005071706	0.04336129
BP	GO:0071478	Cellular response to radiation	20	0.005132277	0.043801485
BP	GO:0002220	Innate immune response activating cell surface receptor signaling pathway	15	0.005190973	0.04414616
BP	GO:2000736	Regulation of stem cell differentiation	15	0.005190973	0.04414616
BP	GO:0042273	Ribosomal large subunit biogenesis	6	0.005295655	0.044957127
BP	GO:0006767	Water-soluble vitamin metabolic process	12	0.005347722	0.045239854
BP	GO:0043470	Regulation of carbohydrate catabolic process	12	0.005347722	0.045239854
BP	GO:0001738	Morphogenesis of a polarized epithelium	17	0.005404686	0.045561881
BP	GO:0051384	Response to glucocorticoid	17	0.005404686	0.045561881
BP	GO:0000380	Alternative mrna splicing, via spliceosome	9	0.005461655	0.045961784
BP	GO:0046128	Purine ribonucleoside metabolic process	10	0.005603726	0.0470752
BP	GO:0042551	Neuron maturation	8	0.005783094	0.048497527
BP	GO:0045911	Positive regulation of DNA recombination	7	0.005810332	0.048557051
BP	GO:0048255	Mrna stabilization	7	0.005810332	0.048557051
CC	GO:0098687	Chromosomal region	99	3.51E-41	2.03E-38
CC	GO:0000793	Condensed chromosome	69	5.44E-34	1.58E-31
CC	GO:0000775	Chromosome, centromeric region	65	1.79E-32	3.45E-30
CC	GO:0000776	Kinetochore	49	3.37E-26	4.88E-24

CC	GO:0005819	Spindle	76	1.14E-24	1.33E-22
CC	GO:0000779	Condensed chromosome, centromeric region	43	4.73E-24	4.57E-22
CC	GO:0000777	Condensed chromosome kinetochore	40	6.56E-23	5.42E-21
CC	GO:0044454	Nuclear chromosome part	81	1.42E-17	1.03E-15
CC	GO:0005813	Centrosome	77	2.68E-15	1.72E-13
CC	GO:0000922	Spindle pole	39	9.78E-15	5.66E-13
CC	GO:0005874	Microtubule	59	2.72E-12	1.43E-10
CC	GO:0000781	Chromosome, telomeric region	36	3.19E-12	1.54E-10
CC	GO:0042555	MCM complex	10	7.57E-12	3.37E-10
CC	GO:0072686	Mitotic spindle	27	1.60E-11	6.62E-10
CC	GO:0000794	Condensed nuclear chromosome	23	5.83E-11	2.25E-09
CC	GO:0005657	Replication fork	18	1.56E-09	5.65E-08
CC	GO:0000940	Condensed chromosome outer kinetochore	9	2.22E-09	7.57E-08
CC	GO:0000785	Chromatin	66	3.06E-09	9.84E-08
CC	GO:0030496	Midbody	33	3.55E-09	1.03E-07
CC	GO:0000784	Nuclear chromosome, telomeric region	27	3.57E-09	1.03E-07
CC	GO:0005876	Spindle microtubule	17	8.65E-09	2.38E-07
CC	GO:0005635	Nuclear envelope	56	3.43E-08	9.02E-07
CC	GO:0101031	Chaperone complex	10	4.04E-08	1.02E-06
CC	GO:0044215	Other organism	19	8.58E-08	1.91E-06
CC	GO:0044216	Other organism cell	19	8.58E-08	1.91E-06
CC	GO:0044217	Other organism part	19	8.58E-08	1.91E-06
CC	GO:0000790	Nuclear chromatin	43	4.12E-07	8.83E-06
CC	GO:0018995	Host	17	6.27E-07	1.25E-05
CC	GO:0043657	Host cell	17	6.27E-07	1.25E-05
CC	GO:0090734	Site of DNA damage	16	1.35E-06	2.61E-05
CC	GO:0031965	Nuclear membrane	39	1.51E-06	2.73E-05
CC	GO:0005681	Spliceosomal complex	27	1.51E-06	2.73E-05
CC	GO:0005643	Nuclear pore	15	1.86E-06	3.26E-05
CC	GO:0005759	Mitochondrial matrix	52	7.24E-06	0.000123339
CC	GO:0000792	Heterochromatin	16	9.99E-06	0.000165291
CC	GO:0000152	Nuclear ubiquitin ligase complex	11	1.14E-05	0.000183901
CC	GO:0045120	Pronucleus	7	1.34E-05	0.000209183
CC	GO:0005720	Nuclear heterochromatin	10	1.83E-05	0.000279492
CC	GO:0051233	Spindle midzone	9	2.04E-05	0.000303279

CC	GO:0034708	Methyltransferase complex	17	2.13E-05	0.000308851
CC	GO:0034399	Nuclear periphery	21	2.59E-05	0.00036641
CC	GO:0034709	Methylosome	6	3.53E-05	0.000486656
CC	GO:0042599	Lamellar body	7	3.62E-05	0.000487871
CC	GO:0044450	Microtubule organizing center part	25	4.19E-05	0.000551966
CC	GO:0000502	Proteasome complex	13	6.77E-05	0.000871358
CC	GO:1905369	Endopeptidase complex	13	8.09E-05	0.001018693
CC	GO:0000800	Lateral element	6	0.00010312	0.001226123
CC	GO:0010369	Chromocenter	6	0.00010312	0.001226123
CC	GO:1905368	Peptidase complex	14	0.000103765	0.001226123
CC	GO:0097431	Mitotic spindle pole	8	0.000113198	0.00131083
CC	GO:0005721	Pericentric heterochromatin	7	0.000122711	0.001366345
CC	GO:0030894	Replisome	7	0.000122711	0.001366345
CC	GO:0005680	Anaphase-promoting complex	7	0.000174357	0.001904771
CC	GO:0005814	Centriole	19	0.000195856	0.002061834
CC	GO:1904813	Ficolin-1-rich granule lumen	19	0.000195856	0.002061834
CC	GO:0035861	Site of double-strand break	11	0.000217034	0.002243972
CC	GO:0060205	Cytoplasmic vesicle lumen	38	0.00023005	0.002336827
CC	GO:0031983	Vesicle lumen	38	0.00024418	0.00243759
CC	GO:0000307	Cyclin-dependent protein kinase holoenzyme complex	8	0.000263765	0.002588469
CC	GO:0017101	Aminoacyl-trna synthetase multienzyme complex	5	0.000291538	0.002813341
CC	GO:0046540	U4/U6 x U5 tri-snrnp complex	9	0.000310991	0.002904257
CC	GO:0097526	Spliceosomal tri-snrnp complex	9	0.000310991	0.002904257
CC	GO:0022624	Proteasome accessory complex	7	0.000329897	0.00303191
CC	GO:0071007	U2-type catalytic step 2 spliceosome	8	0.000340494	0.003080404
CC	GO:0034774	Secretory granule lumen	36	0.000348101	0.003100779
CC	GO:0000780	Condensed nuclear chromosome, centromeric region	6	0.000362313	0.003121415
CC	GO:0034719	SMN-Sm protein complex	6	0.000362313	0.003121415
CC	GO:0044452	Nucleolar part	21	0.000366591	0.003121415
CC	GO:0031970	Organelle envelope lumen	14	0.000430884	0.003615678
CC	GO:0000313	Organellar ribosome	14	0.000554881	0.004525019
CC	GO:0005761	Mitochondrial ribosome	14	0.000554881	0.004525019
CC	GO:0042575	DNA polymerase complex	5	0.000732321	0.005889083
CC	GO:0005732	Small nucleolar ribonucleoprotein complex	7	0.00075285	0.005890541
CC	GO:1990752	Microtubule end	7	0.00075285	0.005890541

CC	GO:0043596	Nuclear replication fork	7	0.000963057	0.007434797
CC	GO:0030677	Ribonuclease P complex	5	0.001081877	0.008242197
CC	GO:0035578	Azurophil granule lumen	14	0.001253457	0.009425349
CC	GO:0071013	Catalytic step 2 spliceosome	13	0.001393812	0.010346374
CC	GO:0005741	Mitochondrial outer membrane	21	0.001496227	0.010771774
CC	GO:0031968	Organelle outer membrane	23	0.001517675	0.010771774
CC	GO:1990391	DNA repair complex	7	0.001520062	0.010771774
CC	GO:0005758	Mitochondrial intermembrane space	12	0.001525536	0.010771774
CC	GO:0000315	Organellar large ribosomal subunit	10	0.001694617	0.01168075
CC	GO:0005762	Mitochondrial large ribosomal subunit	10	0.001694617	0.01168075
CC	GO:0019867	Outer membrane	23	0.001742424	0.011868985
CC	GO:0035097	Histone methyltransferase complex	11	0.001859328	0.012505475
CC	GO:0000803	Sex chromosome	7	0.001879061	0.012505475
CC	GO:0035098	ESC/E(Z) complex	5	0.002129572	0.013667894
CC	GO:0035371	Microtubule plus-end	5	0.002129572	0.013667894
CC	GO:0005684	U2-type spliceosomal complex	12	0.002174463	0.013667894
CC	GO:0005838	Proteasome regulatory particle	4	0.002195361	0.013667894
CC	GO:0030681	Multimeric ribonuclease P complex	4	0.002195361	0.013667894
CC	GO:0031080	Nuclear pore outer ring	4	0.002195361	0.013667894
CC	GO:0098798	Mitochondrial protein complex	26	0.002333987	0.014376365
CC	GO:0000178	Exosome (rnase complex)	6	0.002722174	0.016248855
CC	GO:0005689	U12-type spliceosomal complex	6	0.002722174	0.016248855
CC	GO:1905354	Exoribonuclease complex	6	0.002722174	0.016248855
CC	GO:0005652	Nuclear lamina	4	0.00328326	0.019010076
CC	GO:0005687	U4 snrnp	4	0.00328326	0.019010076
CC	GO:1990023	Mitotic spindle midzone	4	0.00328326	0.019010076
CC	GO:0009295	Nucleoid	8	0.003570373	0.020070351
CC	GO:0031519	Pcg protein complex	8	0.003570373	0.020070351
CC	GO:0042645	Mitochondrial nucleoid	8	0.003570373	0.020070351
CC	GO:0000930	Gamma-tubulin complex	5	0.003769982	0.020592638
CC	GO:0043601	Nuclear replisome	5	0.003769982	0.020592638
CC	GO:0046930	Pore complex	5	0.003769982	0.020592638
CC	GO:0000795	Synaptonemal complex	7	0.004008337	0.021489142
CC	GO:0099086	Synaptonemal structure	7	0.004008337	0.021489142
CC	GO:0005637	Nuclear inner membrane	8	0.004155185	0.021937147

CC	GO:0005775	Vacuolar lumen	20	0.004167679	0.021937147
CC	GO:0035145	Exon-exon junction complex	5	0.004861261	0.025130985
CC	GO:0043073	Germ cell nucleus	5	0.004861261	0.025130985
CC	GO:0016363	Nuclear matrix	14	0.005300325	0.027158304
CC	GO:0120114	Sm-like protein family complex	13	0.00572595	0.0290818
CC	GO:0015030	Cajal body	11	0.005829302	0.029349271
CC	GO:0001650	Fibrillar center	16	0.006480256	0.032345417
CC	GO:0032153	Cell division site	9	0.007491147	0.03675741
CC	GO:0032155	Cell division site part	9	0.007491147	0.03675741
CC	GO:0061695	Transferase complex, transferring phosphorus-containing groups	20	0.007805365	0.037977363
CC	GO:0071005	U2-type precatalytic spliceosome	8	0.008254201	0.039497376
CC	GO:0071011	Precatalytic spliceosome	8	0.008254201	0.039497376
CC	GO:0005667	Transcription factor complex	27	0.00860447	0.040835967
CC	GO:0101002	Ficolin-1-rich granule	20	0.009842749	0.04633294
MF	GO:0008094	DNA-dependent atpase activity	25	1.34E-12	5.65E-10
MF	GO:0016887	Atpase activity	53	1.46E-12	5.65E-10
MF	GO:0140097	Catalytic activity, acting on DNA	36	7.62E-12	1.64E-09
MF	GO:0003684	Damaged DNA binding	22	8.46E-12	1.64E-09
MF	GO:0003697	Single-stranded DNA binding	25	3.27E-10	5.07E-08
MF	GO:0004386	Helicase activity	29	2.49E-09	3.22E-07
MF	GO:0043142	Single-stranded DNA-dependent atpase activity	9	3.75E-09	4.16E-07
MF	GO:0042623	Atpase activity, coupled	39	7.06E-09	6.85E-07
MF	GO:0000217	DNA secondary structure binding	11	5.55E-08	4.79E-06
MF	GO:0003678	DNA helicase activity	13	1.52E-06	0.000111003
MF	GO:0016874	Ligase activity	25	1.57E-06	0.000111003
MF	GO:0003682	Chromatin binding	55	1.93E-06	0.000124744
MF	GO:0015631	Tubulin binding	36	7.18E-06	0.000428551
MF	GO:0004003	ATP-dependent DNA helicase activity	10	1.65E-05	0.000916765
MF	GO:0008026	ATP-dependent helicase activity	13	2.06E-05	0.000999358
MF	GO:0070035	Purine NTP-dependent helicase activity	13	2.06E-05	0.000999358
MF	GO:0000400	Four-way junction DNA binding	7	3.31E-05	0.001510109
MF	GO:0051082	Unfolded protein binding	16	7.70E-05	0.003320167
MF	GO:0000287	Magnesium ion binding	29	9.22E-05	0.003763603
MF	GO:0140098	Catalytic activity, acting on RNA	34	0.000146159	0.00543444

MF	GO:0016893	Endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	10	0.000147066	0.00543444
MF	GO:0042393	Histone binding	25	0.000157391	0.005551602
MF	GO:0016879	Ligase activity, forming carbon-nitrogen bonds	10	0.000184757	0.006200471
MF	GO:0008017	Microtubule binding	24	0.000191767	0.006200471
MF	GO:0030983	Mismatched DNA binding	5	0.00022183	0.006885618
MF	GO:0008187	Poly-pyrimidine tract binding	7	0.00034897	0.010415406
MF	GO:0003727	Single-stranded RNA binding	13	0.000385599	0.011082413
MF	GO:0140142	Nucleocytoplasmic carrier activity	7	0.000473646	0.013126747
MF	GO:0070182	DNA polymerase binding	6	0.000498951	0.013351246
MF	GO:0016891	Endoribonuclease activity, producing 5'-phosphomonoesters	8	0.000645705	0.016702245
MF	GO:0000049	Trna binding	10	0.000744871	0.018645802
MF	GO:0016646	Oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	5	0.000960619	0.022589094
MF	GO:0019104	DNA N-glycosylase activity	5	0.000960619	0.022589094
MF	GO:0044389	Ubiquitin-like protein ligase binding	33	0.00100103	0.022759495
MF	GO:0008022	Protein C-terminus binding	24	0.001032436	0.022759495
MF	GO:0004540	Ribonuclease activity	15	0.001055853	0.022759495
MF	GO:0008266	Poly(U) RNA binding	6	0.001319994	0.026955673
MF	GO:0030515	Snorna binding	6	0.001319994	0.026955673
MF	GO:0017056	Structural constituent of nuclear pore	5	0.001414615	0.027443535
MF	GO:0035173	Histone kinase activity	5	0.001414615	0.027443535
MF	GO:0043021	Ribonucleoprotein complex binding	16	0.001488658	0.028034711
MF	GO:0031625	Ubiquitin protein ligase binding	31	0.001517343	0.028034711
MF	GO:0004521	Endoribonuclease activity	10	0.001693373	0.02947427
MF	GO:0004518	Nuclease activity	22	0.00170115	0.02947427
MF	GO:0008536	Ran gtpase binding	7	0.001718246	0.02947427
MF	GO:0070717	Poly-purine tract binding	6	0.001747186	0.02947427
MF	GO:0140101	Catalytic activity, acting on a trna	15	0.001805978	0.029817849
MF	GO:0016853	Isomerase activity	17	0.002350737	0.03800358
MF	GO:0004523	RNA-DNA hybrid ribonuclease activity	4	0.002733501	0.041592096
MF	GO:0033204	Ribonuclease P RNA binding	4	0.002733501	0.041592096
MF	GO:0097617	Annealing activity	4	0.002733501	0.041592096
MF	GO:0048037	Cofactor binding	44	0.002791545	0.041658439
MF	GO:0016741	Transferase activity, transferring one-carbon groups	24	0.002958887	0.043322575

The intersection co-expression genes among with SKA1/2/3 with GO notes

Ontology	ID	Description	Count	P value	P adjust
BP	GO:0006260	DNA replication	62	2.99E-53	7.18E-50
BP	GO:0007059	Chromosome segregation	63	6.04E-53	7.25E-50
BP	GO:0000280	Nuclear division	69	9.68E-53	7.74E-50
BP	GO:0048285	Organelle fission	70	8.25E-51	4.95E-48
BP	GO:0140014	Mitotic nuclear division	57	4.06E-49	1.95E-46
BP	GO:0000819	Sister chromatid segregation	47	2.07E-45	8.29E-43
BP	GO:0098813	Nuclear chromosome segregation	52	2.38E-44	8.16E-42
BP	GO:0000070	Mitotic sister chromatid segregation	43	2.26E-43	6.78E-41
BP	GO:0006261	DNA-dependent DNA replication	36	1.62E-33	4.32E-31
BP	GO:1901987	Regulation of cell cycle phase transition	57	2.97E-32	7.13E-30
BP	GO:1901990	Regulation of mitotic cell cycle phase transition	55	3.87E-32	8.44E-30
BP	GO:0051983	Regulation of chromosome segregation	31	8.26E-32	1.65E-29
BP	GO:0007088	Regulation of mitotic nuclear division	35	9.07E-30	1.68E-27
BP	GO:0000226	Microtubule cytoskeleton organization	53	1.37E-28	2.36E-26
BP	GO:0071103	DNA conformation change	43	1.81E-28	2.90E-26
BP	GO:0044839	Cell cycle G2/M phase transition	41	8.90E-28	1.34E-25
BP	GO:0051783	Regulation of nuclear division	35	1.42E-27	2.00E-25
BP	GO:0033045	Regulation of sister chromatid segregation	25	1.01E-26	1.34E-24
BP	GO:0000086	G2/M transition of mitotic cell cycle	38	8.34E-26	1.05E-23
BP	GO:0000075	Cell cycle checkpoint	35	1.86E-25	2.23E-23
BP	GO:0007091	Metaphase/anaphase transition of mitotic cell cycle	21	3.98E-25	4.34E-23
BP	GO:0010965	Regulation of mitotic sister chromatid separation	21	3.98E-25	4.34E-23
BP	GO:0007051	Spindle organization	31	5.02E-25	5.24E-23
BP	GO:0044784	Metaphase/anaphase transition of cell cycle	21	1.20E-24	1.15E-22
BP	GO:0051306	Mitotic sister chromatid separation	21	1.20E-24	1.15E-22
BP	GO:1905818	Regulation of chromosome separation	21	5.63E-24	5.20E-22
BP	GO:0044843	Cell cycle G1/S phase transition	39	9.72E-24	8.64E-22
BP	GO:0010948	Negative regulation of cell cycle process	42	1.02E-23	8.78E-22
BP	GO:1902850	Microtubule cytoskeleton organization involved in mitosis	27	3.77E-23	3.12E-21
BP	GO:0090068	Positive regulation of cell cycle process	38	5.15E-23	4.12E-21
BP	GO:0033047	Regulation of mitotic sister chromatid segregation	21	5.79E-23	4.48E-21
BP	GO:0000082	G1/S transition of mitotic cell cycle	37	8.42E-23	6.31E-21

BP	GO:0051321	Meiotic cell cycle	33	8.96E-23	6.52E-21
BP	GO:0007093	Mitotic cell cycle checkpoint	29	1.33E-22	9.41E-21
BP	GO:0051304	Chromosome separation	22	1.50E-22	1.03E-20
BP	GO:0045787	Positive regulation of cell cycle	42	2.46E-22	1.64E-20
BP	GO:0006323	DNA packaging	31	3.20E-21	2.07E-19
BP	GO:0030071	Regulation of mitotic metaphase/anaphase transition	18	7.66E-21	4.84E-19
BP	GO:1902749	Regulation of cell cycle G2/M phase transition	31	1.10E-20	6.77E-19
BP	GO:1902099	Regulation of metaphase/anaphase transition of cell cycle	18	2.03E-20	1.22E-18
BP	GO:0051052	Regulation of DNA metabolic process	41	3.65E-20	2.14E-18
BP	GO:0044786	Cell cycle DNA replication	19	6.40E-20	3.65E-18
BP	GO:0045930	Negative regulation of mitotic cell cycle	36	8.56E-20	4.78E-18
BP	GO:0007052	Mitotic spindle organization	22	5.07E-19	2.76E-17
BP	GO:1903046	Meiotic cell cycle process	26	8.22E-19	4.38E-17
BP	GO:0033044	Regulation of chromosome organization	35	9.81E-19	5.12E-17
BP	GO:0033260	Nuclear DNA replication	17	1.17E-18	6.00E-17
BP	GO:0010389	Regulation of G2/M transition of mitotic cell cycle	28	1.28E-18	6.41E-17
BP	GO:0006275	Regulation of DNA replication	22	2.64E-18	1.29E-16
BP	GO:1901988	Negative regulation of cell cycle phase transition	31	1.01E-17	4.86E-16
BP	GO:0033046	Negative regulation of sister chromatid segregation	15	1.69E-17	7.93E-16
BP	GO:0045839	Negative regulation of mitotic nuclear division	16	1.72E-17	7.93E-16
BP	GO:0034508	Centromere complex assembly	17	1.81E-17	8.20E-16
BP	GO:0051310	Metaphase plate congression	17	2.58E-17	1.15E-15
BP	GO:0051985	Negative regulation of chromosome segregation	15	2.75E-17	1.20E-15
BP	GO:0140013	Meiotic nuclear division	24	2.94E-17	1.26E-15
BP	GO:0045841	Negative regulation of mitotic metaphase/anaphase transition	14	5.49E-17	2.27E-15
BP	GO:2000816	Negative regulation of mitotic sister chromatid separation	14	5.49E-17	2.27E-15
BP	GO:1901991	Negative regulation of mitotic cell cycle phase transition	29	8.92E-17	3.63E-15
BP	GO:1902100	Negative regulation of metaphase/anaphase transition of cell cycle	14	9.39E-17	3.70E-15
BP	GO:1905819	Negative regulation of chromosome separation	14	9.39E-17	3.70E-15
BP	GO:0050000	Chromosome localization	18	1.99E-16	7.60E-15
BP	GO:0051303	Establishment of chromosome localization	18	1.99E-16	7.60E-15
BP	GO:0051784	Negative regulation of nuclear division	16	2.47E-16	9.14E-15

BP	GO:0006310	DNA recombination	29	2.47E-16	9.14E-15
BP	GO:0033048	Negative regulation of mitotic sister chromatid segregation	14	2.58E-16	9.38E-15
BP	GO:0031055	Chromatin remodeling at centromere	15	8.03E-16	2.88E-14
BP	GO:0071824	Protein-DNA complex subunit organization	28	1.35E-15	4.75E-14
BP	GO:0090329	Regulation of DNA-dependent DNA replication	15	1.66E-15	5.78E-14
BP	GO:0065004	Protein-DNA complex assembly	26	3.43E-15	1.18E-13
BP	GO:0051383	Kinetochore organization	11	4.93E-15	1.67E-13
BP	GO:0034080	CENP-A containing nucleosome assembly	14	5.27E-15	1.73E-13
BP	GO:0061641	CENP-A containing chromatin organization	14	5.27E-15	1.73E-13
BP	GO:0006336	DNA replication-independent nucleosome assembly	15	8.80E-15	2.81E-13
BP	GO:0034724	DNA replication-independent nucleosome organization	15	8.80E-15	2.81E-13
BP	GO:0071459	Protein localization to chromosome, centromeric region	11	1.02E-14	3.22E-13
BP	GO:0043044	ATP-dependent chromatin remodeling	17	1.32E-14	4.11E-13
BP	GO:0072331	Signal transduction by p53 class mediator	28	1.57E-14	4.82E-13
BP	GO:0043486	Histone exchange	15	1.62E-14	4.93E-13
BP	GO:0031145	Anaphase-promoting complex-dependent catabolic process	17	3.24E-14	9.73E-13
BP	GO:0006302	Double-strand break repair	25	3.32E-14	9.84E-13
BP	GO:0006270	DNA replication initiation	12	3.68E-14	1.03E-12
BP	GO:0007094	Mitotic spindle assembly checkpoint	12	3.68E-14	1.03E-12
BP	GO:0031577	Spindle checkpoint	12	3.68E-14	1.03E-12
BP	GO:0071173	Spindle assembly checkpoint	12	3.68E-14	1.03E-12
BP	GO:0071174	Mitotic spindle checkpoint	12	3.68E-14	1.03E-12
BP	GO:0034502	Protein localization to chromosome	17	4.03E-14	1.11E-12
BP	GO:0031570	DNA integrity checkpoint	21	4.10E-14	1.11E-12
BP	GO:2001251	Negative regulation of chromosome organization	20	4.12E-14	1.11E-12
BP	GO:0006333	Chromatin assembly or disassembly	23	5.60E-14	1.49E-12
BP	GO:0034728	Nucleosome organization	22	1.04E-13	2.75E-12
BP	GO:0007080	Mitotic metaphase plate congression	13	1.06E-13	2.78E-12
BP	GO:0006334	Nucleosome assembly	20	1.86E-13	4.81E-12
BP	GO:0051225	Spindle assembly	17	2.05E-13	5.24E-12
BP	GO:0031497	Chromatin assembly	21	2.15E-13	5.43E-12
BP	GO:0006338	Chromatin remodeling	21	3.18E-13	7.94E-12
BP	GO:1901989	Positive regulation of cell cycle phase transition	17	7.44E-13	1.84E-11

BP	GO:0022616	DNA strand elongation	9	1.24E-12	3.00E-11
BP	GO:0034501	Protein localization to kinetochore	9	1.24E-12	3.00E-11
BP	GO:0000723	Telomere maintenance	20	2.34E-12	5.56E-11
BP	GO:0045931	Positive regulation of mitotic cell cycle	20	2.34E-12	5.56E-11
BP	GO:0000724	Double-strand break repair via homologous recombination	17	4.57E-12	1.08E-10
BP	GO:0000725	Recombinational repair	17	5.34E-12	1.24E-10
BP	GO:0007098	Centrosome cycle	17	8.39E-12	1.94E-10
BP	GO:0032200	Telomere organization	20	1.07E-11	2.45E-10
BP	GO:0032201	Telomere maintenance via semi-conservative replication	10	1.31E-11	2.97E-10
BP	GO:0070507	Regulation of microtubule cytoskeleton organization	20	1.49E-11	3.35E-10
BP	GO:0032392	DNA geometric change	15	1.84E-11	4.08E-10
BP	GO:0008608	Attachment of spindle microtubules to kinetochore	10	3.02E-11	6.66E-10
BP	GO:0031023	Microtubule organizing center organization	17	3.43E-11	7.48E-10
BP	GO:1901796	Regulation of signal transduction by p53 class mediator	20	3.87E-11	8.37E-10
BP	GO:0061982	Meiosis I cell cycle process	15	4.28E-11	9.17E-10
BP	GO:0070317	Negative regulation of G0 to G1 transition	11	6.72E-11	1.43E-09
BP	GO:0000910	Cytokinesis	18	8.14E-11	1.71E-09
BP	GO:0030261	Chromosome condensation	10	9.30E-11	1.94E-09
BP	GO:0010639	Negative regulation of organelle organization	27	9.90E-11	2.05E-09
BP	GO:0061640	Cytoskeleton-dependent cytokinesis	14	1.18E-10	2.40E-09
BP	GO:1901992	Positive regulation of mitotic cell cycle phase transition	14	1.18E-10	2.40E-09
BP	GO:0000281	Mitotic cytokinesis	13	1.51E-10	3.05E-09
BP	GO:0070316	Regulation of G0 to G1 transition	11	2.03E-10	4.06E-09
BP	GO:0032886	Regulation of microtubule-based process	20	2.65E-10	5.25E-09
BP	GO:0007127	Meiosis I	14	3.15E-10	6.19E-09
BP	GO:0045023	G0 to G1 transition	11	3.38E-10	6.59E-09
BP	GO:0032508	DNA duplex unwinding	13	5.37E-10	1.04E-08
BP	GO:0090307	Mitotic spindle assembly	11	1.09E-09	2.08E-08
BP	GO:1902750	Negative regulation of cell cycle G2/M phase transition	14	1.19E-09	2.27E-08
BP	GO:0000077	DNA damage checkpoint	16	1.21E-09	2.29E-08
BP	GO:0007143	Female meiotic nuclear division	9	1.25E-09	2.35E-08
BP	GO:0046605	Regulation of centrosome cycle	11	1.67E-09	3.10E-08
BP	GO:0051054	Positive regulation of DNA metabolic process	20	1.83E-09	3.39E-08

BP	GO:0072401	Signal transduction involved in DNA integrity checkpoint	12	4.03E-09	7.33E-08
BP	GO:0072422	Signal transduction involved in DNA damage checkpoint	12	4.03E-09	7.33E-08
BP	GO:0051984	Positive regulation of chromosome segregation	8	4.14E-09	7.48E-08
BP	GO:0051382	Kinetochore assembly	7	4.25E-09	7.62E-08
BP	GO:0072395	Signal transduction involved in cell cycle checkpoint	12	4.74E-09	8.42E-08
BP	GO:0045740	Positive regulation of DNA replication	9	5.73E-09	1.01E-07
BP	GO:0000076	DNA replication checkpoint	6	1.08E-08	1.89E-07
BP	GO:1902751	Positive regulation of cell cycle G2/M phase transition	8	1.20E-08	2.08E-07
BP	GO:0040001	Establishment of mitotic spindle localization	8	1.65E-08	2.85E-07
BP	GO:0045132	Meiotic chromosome segregation	11	1.83E-08	3.14E-07
BP	GO:0051656	Establishment of organelle localization	27	1.88E-08	3.20E-07
BP	GO:0000018	Regulation of DNA recombination	12	2.09E-08	3.53E-07
BP	GO:0000083	Regulation of transcription involved in G1/S transition of mitotic cell cycle	8	2.24E-08	3.76E-07
BP	GO:0051653	Spindle localization	9	2.60E-08	4.33E-07
BP	GO:0031572	G2 DNA damage checkpoint	8	3.01E-08	4.99E-07
BP	GO:0044774	Mitotic DNA integrity checkpoint	12	4.62E-08	7.60E-07
BP	GO:1904666	Regulation of ubiquitin protein ligase activity	7	5.80E-08	9.47E-07
BP	GO:0042770	Signal transduction in response to DNA damage	14	6.16E-08	9.99E-07
BP	GO:0043161	Proteasome-mediated ubiquitin-dependent protein catabolic process	22	6.41E-08	1.03E-06
BP	GO:0007076	Mitotic chromosome condensation	6	1.10E-07	1.76E-06
BP	GO:0010971	Positive regulation of G2/M transition of mitotic cell cycle	7	1.14E-07	1.82E-06
BP	GO:0051302	Regulation of cell division	15	1.41E-07	2.23E-06
BP	GO:0051293	Establishment of spindle localization	8	1.42E-07	2.23E-06
BP	GO:0007062	Sister chromatid cohesion	9	1.62E-07	2.51E-06
BP	GO:0036297	Interstrand cross-link repair	9	1.62E-07	2.51E-06
BP	GO:0000079	Regulation of cyclin-dependent protein serine/threonine kinase activity	11	1.80E-07	2.77E-06
BP	GO:0016572	Histone phosphorylation	8	2.23E-07	3.41E-06
BP	GO:0010498	Proteasomal protein catabolic process	23	2.25E-07	3.42E-06
BP	GO:0010972	Negative regulation of G2/M transition of mitotic cell cycle	11	2.31E-07	3.49E-06
BP	GO:0044773	Mitotic DNA damage checkpoint	11	2.61E-07	3.92E-06
BP	GO:1904029	Regulation of cyclin-dependent protein kinase activity	11	2.94E-07	4.39E-06

BP	GO:0051231	Spindle elongation	5	3.47E-07	5.14E-06
BP	GO:2000105	Positive regulation of DNA-dependent DNA replication	5	6.28E-07	9.24E-06
BP	GO:0051298	Centrosome duplication	9	7.10E-07	1.04E-05
BP	GO:0000212	Meiotic spindle organization	5	1.06E-06	1.52E-05
BP	GO:0007077	Mitotic nuclear envelope disassembly	5	1.06E-06	1.52E-05
BP	GO:1904668	Positive regulation of ubiquitin protein ligase activity	5	1.06E-06	1.52E-05
BP	GO:0071897	DNA biosynthetic process	15	1.27E-06	1.81E-05
BP	GO:0032465	Regulation of cytokinesis	10	1.61E-06	2.29E-05
BP	GO:0044818	Mitotic G2/M transition checkpoint	6	1.98E-06	2.79E-05
BP	GO:0090231	Regulation of spindle checkpoint	5	2.61E-06	3.61E-05
BP	GO:0090266	Regulation of mitotic cell cycle spindle assembly checkpoint	5	2.61E-06	3.61E-05
BP	GO:1903504	Regulation of mitotic spindle checkpoint	5	2.61E-06	3.61E-05
BP	GO:0007050	Cell cycle arrest	16	2.74E-06	3.78E-05
BP	GO:0070192	Chromosome organization involved in meiotic cell cycle	8	2.79E-06	3.82E-05
BP	GO:0006282	Regulation of DNA repair	11	3.76E-06	5.13E-05
BP	GO:2000779	Regulation of double-strand break repair	9	3.95E-06	5.36E-05
BP	GO:0090305	Nucleic acid phosphodiester bond hydrolysis	17	4.41E-06	5.94E-05
BP	GO:0010824	Regulation of centrosome duplication	7	4.86E-06	6.51E-05
BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	8	4.95E-06	6.61E-05
BP	GO:0030397	Membrane disassembly	5	5.53E-06	7.29E-05
BP	GO:0051081	Nuclear envelope disassembly	5	5.53E-06	7.29E-05
BP	GO:0072431	Signal transduction involved in mitotic G1 DNA damage checkpoint	8	5.68E-06	7.41E-05
BP	GO:1902400	Intracellular signal transduction involved in G1 DNA damage checkpoint	8	5.68E-06	7.41E-05
BP	GO:0071168	Protein localization to chromatin	6	6.87E-06	8.91E-05
BP	GO:0072413	Signal transduction involved in mitotic cell cycle checkpoint	8	7.40E-06	9.44E-05
BP	GO:1902402	Signal transduction involved in mitotic DNA damage checkpoint	8	7.40E-06	9.44E-05
BP	GO:1902403	Signal transduction involved in mitotic DNA integrity checkpoint	8	7.40E-06	9.44E-05
BP	GO:0010212	Response to ionizing radiation	12	7.63E-06	9.69E-05
BP	GO:0006312	Mitotic recombination	5	1.05E-05	0.000132394
BP	GO:0051782	Negative regulation of cell division	5	1.05E-05	0.000132394
BP	GO:0060249	Anatomical structure homeostasis	21	1.08E-05	0.000134728

BP	GO:2001020	Regulation of response to DNA damage stimulus	14	1.08E-05	0.000134728
BP	GO:0071158	Positive regulation of cell cycle arrest	9	1.17E-05	0.000144715
BP	GO:0031571	Mitotic G1 DNA damage checkpoint	8	1.22E-05	0.000148985
BP	GO:0044819	Mitotic G1/S transition checkpoint	8	1.22E-05	0.000148985
BP	GO:0044783	G1 DNA damage checkpoint	8	1.37E-05	0.000166895
BP	GO:0006301	Postreplication repair	7	1.48E-05	0.000178233
BP	GO:0051438	Regulation of ubiquitin-protein transferase activity	7	1.48E-05	0.000178233
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	10	1.49E-05	0.000178747
BP	GO:0022412	Cellular process involved in reproduction in multicellular organism	18	1.56E-05	0.000186474
BP	GO:0051255	Spindle midzone assembly	4	1.68E-05	0.000198645
BP	GO:0051315	Attachment of mitotic spindle microtubules to kinetochore	4	1.68E-05	0.000198645
BP	GO:0045840	Positive regulation of mitotic nuclear division	7	1.70E-05	0.000200569
BP	GO:0071156	Regulation of cell cycle arrest	10	1.76E-05	0.000205663
BP	GO:0007292	Female gamete generation	11	1.83E-05	0.000213126
BP	GO:0045005	DNA-dependent DNA replication maintenance of fidelity	6	1.88E-05	0.000217666
BP	GO:0007019	Microtubule depolymerization	6	2.25E-05	0.000259251
BP	GO:0009314	Response to radiation	21	2.35E-05	0.000269739
BP	GO:0007063	Regulation of sister chromatid cohesion	5	2.40E-05	0.000274081
BP	GO:0007100	Mitotic centrosome separation	4	2.60E-05	0.000293461
BP	GO:0016446	Somatic hypermutation of immunoglobulin genes	4	2.60E-05	0.000293461
BP	GO:0035404	Histone-serine phosphorylation	4	2.60E-05	0.000293461
BP	GO:0051053	Negative regulation of DNA metabolic process	11	3.39E-05	0.000380035
BP	GO:1902806	Regulation of cell cycle G1/S phase transition	13	3.54E-05	0.000395037
BP	GO:0044766	Multi-organism transport	8	3.64E-05	0.00040234
BP	GO:1902579	Multi-organism localization	8	3.64E-05	0.00040234
BP	GO:0032467	Positive regulation of cytokinesis	6	3.72E-05	0.000407518
BP	GO:0032506	Cytokinetic process	6	3.72E-05	0.000407518
BP	GO:0002566	Somatic diversification of immune receptors via somatic mutation	4	3.85E-05	0.000414881
BP	GO:0051299	Centrosome separation	4	3.85E-05	0.000414881
BP	GO:0051988	Regulation of attachment of spindle microtubules to kinetochore	4	3.85E-05	0.000414881
BP	GO:0000729	DNA double-strand break processing	5	3.85E-05	0.000414881
BP	GO:0042769	DNA damage response, detection of DNA damage	6	4.35E-05	0.000466321

BP	GO:0000132	Establishment of mitotic spindle orientation	5	4.80E-05	0.000512104
BP	GO:0006890	Retrograde vesicle-mediated transport, Golgi to ER	8	4.88E-05	0.000518217
BP	GO:0075733	Intracellular transport of virus	7	5.36E-05	0.000566868
BP	GO:2000045	Regulation of G1/S transition of mitotic cell cycle	12	6.00E-05	0.000631073
BP	GO:0010569	Regulation of double-strand break repair via homologous recombination	6	6.79E-05	0.00071135
BP	GO:0046794	Transport of virus	7	7.49E-05	0.000778595
BP	GO:0051785	Positive regulation of nuclear division	7	7.49E-05	0.000778595
BP	GO:0072425	Signal transduction involved in G2 DNA damage checkpoint	4	7.58E-05	0.000784451
BP	GO:0051493	Regulation of cytoskeleton organization	21	7.63E-05	0.000786199
BP	GO:0009112	Nucleobase metabolic process	5	8.74E-05	0.000896412
BP	GO:0010458	Exit from mitosis	5	0.000104907	0.00105789
BP	GO:0045737	Positive regulation of cyclin-dependent protein serine/threonine kinase activity	5	0.000104907	0.00105789
BP	GO:0051294	Establishment of spindle orientation	5	0.000104907	0.00105789
BP	GO:0051443	Positive regulation of ubiquitin-protein transferase activity	5	0.000104907	0.00105789
BP	GO:0006998	Nuclear envelope organization	6	0.000116042	0.001165273
BP	GO:0031297	Replication fork processing	5	0.000124985	0.001249854
BP	GO:0007096	Regulation of exit from mitosis	4	0.000134163	0.001336061
BP	GO:2000573	Positive regulation of DNA biosynthetic process	7	0.000138363	0.001372195
BP	GO:0045143	Homologous chromosome segregation	6	0.000148619	0.001461831
BP	GO:0072698	Protein localization to microtubule cytoskeleton	6	0.000148619	0.001461831
BP	GO:2001252	Positive regulation of chromosome organization	11	0.000173731	0.001682398
BP	GO:0007099	Centriole replication	5	0.000173848	0.001682398
BP	GO:0045910	Negative regulation of DNA recombination	5	0.000173848	0.001682398
BP	GO:1901976	Regulation of cell cycle checkpoint	5	0.000173848	0.001682398
BP	GO:0016569	Covalent chromatin modification	19	0.00019962	0.001924046
BP	GO:1904031	Positive regulation of cyclin-dependent protein kinase activity	5	0.000203156	0.001950295
BP	GO:0006997	Nucleus organization	9	0.000207794	0.001986874
BP	GO:0044380	Protein localization to cytoskeleton	6	0.000210621	0.002005912
BP	GO:0042276	Error-prone translesion synthesis	4	0.000219507	0.002082277
BP	GO:0031109	Microtubule polymerization or depolymerization	8	0.000220431	0.002082808
BP	GO:0097711	Ciliary basal body-plasma membrane docking	8	0.000237154	0.002232034
BP	GO:0051168	Nuclear export	11	0.000247445	0.002319801

BP	GO:0006405	RNA export from nucleus	9	0.000266976	0.00249316
BP	GO:0007131	Reciprocal meiotic recombination	5	0.000272911	0.002522136
BP	GO:0019886	Antigen processing and presentation of exogenous peptide antigen via MHC class II	8	0.000273723	0.002522136
BP	GO:0007095	Mitotic G2 DNA damage checkpoint	4	0.000274282	0.002522136
BP	GO:0070987	Error-free translesion synthesis	4	0.000274282	0.002522136
BP	GO:2000134	Negative regulation of G1/S transition of mitotic cell cycle	9	0.000301433	0.002761222
BP	GO:0035825	Homologous recombination	5	0.000313942	0.002854014
BP	GO:0098534	Centriole assembly	5	0.000313942	0.002854014
BP	GO:0002495	Antigen processing and presentation of peptide antigen via MHC class II	8	0.000337113	0.003051606
BP	GO:0070734	Histone H3-K27 methylation	4	0.00033822	0.003051606
BP	GO:0008156	Negative regulation of DNA replication	5	0.000359479	0.003230365
BP	GO:0002504	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	8	0.000360724	0.003230365
BP	GO:0016570	Histone modification	18	0.000388164	0.003463173
BP	GO:2000104	Negative regulation of DNA-dependent DNA replication	4	0.000412158	0.003663626
BP	GO:1902807	Negative regulation of cell cycle G1/S phase transition	9	0.000427553	0.003786447
BP	GO:2000278	Regulation of DNA biosynthetic process	8	0.000499856	0.004410493
BP	GO:0006611	Protein export from nucleus	10	0.000544085	0.004783163
BP	GO:0009263	Deoxyribonucleotide biosynthetic process	3	0.000557554	0.004883685
BP	GO:0019985	Translesion synthesis	5	0.000593106	0.005160469
BP	GO:0006297	Nucleotide-excision repair, DNA gap filling	4	0.000593454	0.005160469
BP	GO:0016579	Protein deubiquitination	13	0.000610919	0.005293158
BP	GO:0031396	Regulation of protein ubiquitination	11	0.000617181	0.005328179
BP	GO:0009411	Response to UV	9	0.000626563	0.005389789
BP	GO:0031398	Positive regulation of protein ubiquitination	8	0.000640026	0.005485934
BP	GO:0090224	Regulation of spindle organization	5	0.000666055	0.005688723
BP	GO:0006913	Nucleocytoplasmic transport	14	0.000802701	0.006831498
BP	GO:0001556	Oocyte maturation	4	0.00082509	0.006997231
BP	GO:0051169	Nuclear transport	14	0.000883146	0.007463209
BP	GO:0002478	Antigen processing and presentation of exogenous peptide antigen	10	0.000902186	0.007597359
BP	GO:0071426	Ribonucleoprotein complex export from nucleus	8	0.00090817	0.00762101
BP	GO:0007140	Male meiotic nuclear division	5	0.000925411	0.007738626
BP	GO:0070646	Protein modification by small protein removal	13	0.000958686	0.007976676

BP	GO:0071166	Ribonucleoprotein complex localization	8	0.000960525	0.007976676
BP	GO:0019884	Antigen processing and presentation of exogenous antigen	10	0.000984466	0.008147307
BP	GO:0000722	Telomere maintenance via recombination	3	0.000996315	0.008160938
BP	GO:0046112	Nucleobase biosynthetic process	3	0.000996315	0.008160938
BP	GO:0051095	Regulation of helicase activity	3	0.000996315	0.008160938
BP	GO:0002200	Somatic diversification of immune receptors	6	0.001035623	0.008454064
BP	GO:0006298	Mismatch repair	4	0.001114074	0.009033031
BP	GO:0015949	Nucleobase-containing small molecule interconversion	4	0.001114074	0.009033031
BP	GO:0001833	Inner cell mass cell proliferation	3	0.001278736	0.010292454
BP	GO:0062033	Positive regulation of mitotic sister chromatid segregation	3	0.001278736	0.010292454
BP	GO:0070979	Protein K11-linked ubiquitination	4	0.001282268	0.010292454
BP	GO:0046606	Negative regulation of centrosome cycle	3	0.001606802	0.012854412
BP	GO:0048002	Antigen processing and presentation of peptide antigen	10	0.001617159	0.012894289
BP	GO:0035690	Cellular response to drug	15	0.001630327	0.012956239
BP	GO:0000731	DNA synthesis involved in DNA repair	5	0.001659821	0.013147099
BP	GO:1903322	Positive regulation of protein modification by small protein conjugation or removal	8	0.001712007	0.013515843
BP	GO:1903320	Regulation of protein modification by small protein conjugation or removal	11	0.001757927	0.013832868
BP	GO:0007018	Microtubule-based movement	11	0.00182103	0.014282589
BP	GO:0031100	Animal organ regeneration	6	0.001863177	0.014565552
BP	GO:0001325	Formation of extrachromosomal circular DNA	3	0.001983001	0.015302901
BP	GO:0006144	Purine nucleobase metabolic process	3	0.001983001	0.015302901
BP	GO:0090656	T-circle formation	3	0.001983001	0.015302901
BP	GO:0090737	Telomere maintenance via telomere trimming	3	0.001983001	0.015302901
BP	GO:0016925	Protein sumoylation	6	0.002276776	0.01751366
BP	GO:0022411	Cellular component disassembly	18	0.002326848	0.017841647
BP	GO:0018205	Peptidyl-lysine modification	15	0.002350288	0.017963981
BP	GO:0006409	Trna export from nucleus	4	0.002395151	0.018129073
BP	GO:0051031	Trna transport	4	0.002395151	0.018129073
BP	GO:0071431	Trna-containing ribonucleoprotein complex export from nucleus	4	0.002395151	0.018129073
BP	GO:0008340	Determination of adult lifespan	3	0.002409656	0.018129073
BP	GO:0033262	Regulation of nuclear cell cycle DNA replication	3	0.002409656	0.018129073

BP	GO:2001021	Negative regulation of response to DNA damage stimulus	6	0.002428925	0.018216936
BP	GO:0016445	Somatic diversification of immunoglobulins	5	0.002541214	0.018909857
BP	GO:0006406	Mrna export from nucleus	7	0.002544952	0.018909857
BP	GO:0071427	Mrna-containing ribonucleoprotein complex export from nucleus	7	0.002544952	0.018909857
BP	GO:0006266	DNA ligation	3	0.002888925	0.021333597
BP	GO:0006349	Regulation of gene expression by genetic imprinting	3	0.002888925	0.021333597
BP	GO:0071312	Cellular response to alkaloid	4	0.002983171	0.021961997
BP	GO:0140056	Organelle localization by membrane tethering	8	0.003130146	0.022973546
BP	GO:0051781	Positive regulation of cell division	6	0.003307106	0.02415416
BP	GO:0097064	Ncrna export from nucleus	4	0.003311133	0.02415416
BP	GO:0050657	Nucleic acid transport	9	0.003549769	0.025738508
BP	GO:0050658	RNA transport	9	0.003549769	0.025738508
BP	GO:0006296	Nucleotide-excision repair, DNA incision, 5'-to lesion	4	0.003662805	0.026398594
BP	GO:0060236	Regulation of mitotic spindle organization	4	0.003662805	0.026398594
BP	GO:0002562	Somatic diversification of immune receptors via germline recombination within a single locus	5	0.003720776	0.026656303
BP	GO:0016444	Somatic cell DNA recombination	5	0.003720776	0.026656303
BP	GO:0051028	Mrna transport	8	0.00387073	0.027648075
BP	GO:0051236	Establishment of RNA localization	9	0.003967163	0.028252794
BP	GO:0001832	Blastocyst growth	3	0.004013157	0.028411729
BP	GO:0046599	Regulation of centriole replication	3	0.004013157	0.028411729
BP	GO:0006284	Base-excision repair	4	0.004038977	0.028510429
BP	GO:0031124	Mrna 3'-end processing	6	0.004402472	0.030985142
BP	GO:0033683	Nucleotide-excision repair, DNA incision	4	0.004440424	0.031160873
BP	GO:0022406	Membrane docking	8	0.004555163	0.031872861
BP	GO:0051101	Regulation of DNA binding	7	0.004807958	0.033543892
BP	GO:0007129	Synapsis	4	0.004867904	0.033863682
BP	GO:0019882	Antigen processing and presentation	10	0.005001113	0.034689801
BP	GO:0009163	Nucleoside biosynthetic process	4	0.005322158	0.036810317
BP	GO:0042451	Purine nucleoside biosynthetic process	3	0.005369928	0.036927871
BP	GO:0046129	Purine ribonucleoside biosynthetic process	3	0.005369928	0.036927871
BP	GO:0051261	Protein depolymerization	6	0.005455081	0.03740627
BP	GO:1901659	Glycosyl compound biosynthetic process	4	0.00580391	0.039684857
BP	GO:0043488	Regulation of mrna stability	8	0.006199477	0.042269161

BP	GO:0001701	In utero embryonic development	13	0.00666893	0.045341166
BP	GO:0048599	Oocyte development	4	0.006852711	0.046459059
BP	GO:0007064	Mitotic sister chromatid cohesion	3	0.006971229	0.046997053
BP	GO:0007141	Male meiosis I	3	0.006971229	0.046997053
BP	GO:0009124	Nucleoside monophosphate biosynthetic process	9	0.007106372	0.04777393
BP	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	5	0.007175077	0.048101073
BP	GO:0001824	Blastocyst development	6	0.007363676	0.049227919
BP	GO:0043487	Regulation of RNA stability	8	0.007434671	0.04956447
CC	GO:0098687	Chromosomal region	66	4.80E-51	1.58E-48
CC	GO:0000775	Chromosome, centromeric region	49	1.20E-44	1.97E-42
CC	GO:0000793	Condensed chromosome	50	2.66E-44	2.91E-42
CC	GO:0000776	Kinetochore	37	5.86E-35	4.80E-33
CC	GO:0000779	Condensed chromosome, centromeric region	33	3.10E-32	2.03E-30
CC	GO:0005819	Spindle	49	4.40E-32	2.41E-30
CC	GO:0000777	Condensed chromosome kinetochore	30	2.18E-29	1.02E-27
CC	GO:0000922	Spindle pole	27	5.44E-20	2.23E-18
CC	GO:0005813	Centrosome	43	2.04E-19	7.44E-18
CC	GO:0044454	Nuclear chromosome part	42	9.71E-19	3.19E-17
CC	GO:0030496	Midbody	22	1.73E-13	5.16E-12
CC	GO:0000785	Chromatin	36	2.86E-13	7.80E-12
CC	GO:0005876	Spindle microtubule	13	3.61E-12	9.11E-11
CC	GO:0072686	Mitotic spindle	16	7.82E-12	1.83E-10
CC	GO:0000794	Condensed nuclear chromosome	14	2.85E-11	6.23E-10
CC	GO:0000781	Chromosome, telomeric region	18	1.81E-10	3.71E-09
CC	GO:0000940	Condensed chromosome outer kinetochore	7	2.86E-10	5.52E-09
CC	GO:0005874	Microtubule	26	5.31E-10	9.67E-09
CC	GO:0000790	Nuclear chromatin	23	3.60E-09	6.22E-08
CC	GO:0005657	Replication fork	10	2.19E-08	3.59E-07
CC	GO:0000792	Heterochromatin	11	5.45E-08	8.51E-07
CC	GO:0005720	Nuclear heterochromatin	8	6.20E-08	9.24E-07
CC	GO:0045120	Pronucleus	6	1.02E-07	1.46E-06
CC	GO:0000784	Nuclear chromosome, telomeric region	13	1.49E-07	2.04E-06
CC	GO:0000152	Nuclear ubiquitin ligase complex	8	2.03E-07	2.66E-06
CC	GO:0000780	Condensed nuclear chromosome, centromeric region	6	2.46E-07	3.10E-06
CC	GO:0051233	Spindle midzone	7	2.57E-07	3.13E-06

CC	GO:0010369	Chromocenter	5	2.45E-06	2.87E-05
CC	GO:0044450	Microtubule organizing center part	13	7.18E-06	8.12E-05
CC	GO:0005814	Centriole	11	8.97E-06	9.81E-05
CC	GO:0000803	Sex chromosome	6	9.77E-06	0.000103408
CC	GO:0005721	Pericentric heterochromatin	5	1.74E-05	0.00017855
CC	GO:0018995	Host	8	2.19E-05	0.000211283
CC	GO:0043657	Host cell	8	2.19E-05	0.000211283
CC	GO:0005680	Anaphase-promoting complex	5	2.25E-05	0.000211283
CC	GO:0042555	MCM complex	4	2.48E-05	0.00022557
CC	GO:0044215	Other organism	8	4.05E-05	0.000340668
CC	GO:0044216	Other organism cell	8	4.05E-05	0.000340668
CC	GO:0044217	Other organism part	8	4.05E-05	0.000340668
CC	GO:0045171	Intercellular bridge	7	6.20E-05	0.000508357
CC	GO:0097431	Mitotic spindle pole	5	6.80E-05	0.0005437
CC	GO:0090734	Site of DNA damage	7	0.000115961	0.000897544
CC	GO:0000307	Cyclin-dependent protein kinase holoenzyme complex	5	0.000117666	0.000897544
CC	GO:0035098	ESC/E(Z) complex	4	0.000127644	0.000951527
CC	GO:0005635	Nuclear envelope	18	0.000334491	0.002438064
CC	GO:0031965	Nuclear membrane	14	0.00034779	0.002479891
CC	GO:0032153	Cell division site	6	0.000406208	0.002775755
CC	GO:0032155	Cell division site part	6	0.000406208	0.002775755
CC	GO:0072687	Meiotic spindle	3	0.000536815	0.003593375
CC	GO:0031519	Pcg protein complex	5	0.000703469	0.00461476
CC	GO:1990023	Mitotic spindle midzone	3	0.000728837	0.00468742
CC	GO:1990752	Microtubule end	4	0.000916807	0.005782939
CC	GO:0090543	Flemming body	4	0.001222481	0.007565543
CC	GO:0031461	Cullin-RING ubiquitin ligase complex	8	0.001289606	0.007833161
CC	GO:0034399	Nuclear periphery	8	0.001428937	0.008521663
CC	GO:0000800	Lateral element	3	0.001548046	0.009067124
CC	GO:0000151	Ubiquitin ligase complex	11	0.001648113	0.009483876
CC	GO:0016363	Nuclear matrix	7	0.002246087	0.012702006
CC	GO:0035371	Microtubule plus-end	3	0.002322297	0.012910396
CC	GO:0032154	Cleavage furrow	5	0.002403354	0.013138336
CC	GO:0000795	Synaptonemal complex	4	0.002555854	0.01352129
CC	GO:0099086	Synaptonemal structure	4	0.002555854	0.01352129

CC	GO:0044815	DNA packaging complex	7	0.003219405	0.016761347
CC	GO:0005643	Nuclear pore	5	0.003273233	0.016775317
CC	GO:0043073	Germ cell nucleus	3	0.003869543	0.01952631
CC	GO:0005881	Cytoplasmic microtubule	5	0.004059722	0.020175586
CC	GO:1902554	Serine/threonine protein kinase complex	5	0.004972732	0.02434412
CC	GO:1902911	Protein kinase complex	5	0.010092269	0.048680356
MF	GO:0008094	DNA-dependent atpase activity	17	9.94E-15	3.69E-12
MF	GO:0043142	Single-stranded DNA-dependent atpase activity	8	5.27E-12	9.77E-10
MF	GO:0016887	Atpase activity	25	6.53E-11	8.07E-09
MF	GO:0042623	Atpase activity, coupled	21	5.76E-10	5.35E-08
MF	GO:0003682	Chromatin binding	29	2.20E-09	1.63E-07
MF	GO:0000400	Four-way junction DNA binding	7	6.31E-09	3.90E-07
MF	GO:0140097	Catalytic activity, acting on DNA	16	1.91E-08	1.01E-06
MF	GO:0000217	DNA secondary structure binding	7	1.21E-07	5.61E-06
MF	GO:0015631	Tubulin binding	18	9.38E-07	3.87E-05
MF	GO:0003684	Damaged DNA binding	9	1.32E-06	4.89E-05
MF	GO:0008017	Microtubule binding	14	2.24E-06	7.57E-05
MF	GO:0035173	Histone kinase activity	5	3.45E-06	0.000106524
MF	GO:0003697	Single-stranded DNA binding	10	5.63E-06	0.000160757
MF	GO:0042393	Histone binding	13	1.92E-05	0.000509479
MF	GO:0004386	Helicase activity	11	2.31E-05	0.000571811
MF	GO:0016893	Endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	6	6.95E-05	0.001611662
MF	GO:0004518	Nuclease activity	12	7.38E-05	0.001611662
MF	GO:0004536	Deoxyribonuclease activity	6	9.29E-05	0.001915512
MF	GO:0003678	DNA helicase activity	6	0.000106777	0.002084955
MF	GO:0004520	Endodeoxyribonuclease activity	5	0.0001371	0.00254321
MF	GO:0008409	5'-3' exonuclease activity	4	0.000167147	0.002952932
MF	GO:0008022	Protein C-terminus binding	11	0.000638156	0.010114273
MF	GO:0004523	RNA-DNA hybrid ribonuclease activity	3	0.000658764	0.010114273
MF	GO:0016888	Endodeoxyribonuclease activity, producing 5'-phosphomonoesters	3	0.000658764	0.010114273
MF	GO:0004519	Endonuclease activity	8	0.000681555	0.010114273
MF	GO:0003777	Microtubule motor activity	5	0.001073699	0.015320854
MF	GO:1990939	ATP-dependent microtubule motor activity	3	0.001175389	0.01615072

MF	GO:0004527	Exonuclease activity	6	0.001387187	0.018380225
MF	GO:0008536	Ran gtpase binding	4	0.001582252	0.020020783
MF	GO:0000287	Magnesium ion binding	11	0.001646514	0.020020783
MF	GO:0004540	Ribonuclease activity	7	0.001672896	0.020020783
MF	GO:0031491	Nucleosome binding	5	0.001945756	0.022558614
MF	GO:0004003	ATP-dependent DNA helicase activity	4	0.00232928	0.024741835
MF	GO:0016891	Endoribonuclease activity, producing 5'-phosphomonoesters	4	0.00232928	0.024741835
MF	GO:0097472	Cyclin-dependent protein kinase activity	3	0.002334135	0.024741835
MF	GO:0004521	Endoribonuclease activity	5	0.002536688	0.026141981
MF	GO:0003774	Motor activity	7	0.002818811	0.028264291
MF	GO:0070182	DNA polymerase binding	3	0.003395373	0.033149568
MF	GO:0004674	Protein serine/threonine kinase activity	15	0.00353623	0.033639519
MF	GO:0051539	4 iron, 4 sulfur cluster binding	4	0.003660763	0.033953576