

source	term name	term ID	n. of term genes	corrected p-value	>	⊖	⊕	□	⊞
BP	DNA replication checkpoint	GO:0000076	10	4.90e-02			4	4	
BP	methionine metabolic process	GO:0060296	50	1.07e-02	8				
BP	methionine metabolic process	GO:0006555	42	4.54e-03					
BP	regulation of gene expression, epigenetic	GO:0040029	151	2.81e-02				13	
BP	anatomical structure homeostasis	GO:0060249	78	1.22e-05			11	13	
BP	response to stimulus	GO:0050896	1148	1.49e-04		45	51	53	
BP	response to stress	GO:0006950	730	1.92e-09		36	42	33	41
BP	reproduction	GO:0000003	486	8.31e-06			33	36	27
BP	reproduction of a single-celled organism	GO:0032505	203	9.67e-03			15	17	16
BP	asexual reproduction	GO:0019954	60	6.18e-03					9
BP	biological regulation	GO:0065007	1791	3.17e-06		61	70	72	
BP	regulation of biological quality	GO:0065008	477	1.35e-02			26	25	
BP	regulation of biological process	GO:0050789	1576	7.04e-04			55	59	61
BP	regulation of metabolic process	GO:0019222	1194	4.62e-02					46
BP	cellular component organization or biogenesis	GO:0071840	2397	5.45e-06			75	84	77
BP	cellular component organization	GO:0016043	2045	4.56e-09			73	82	72
BP	single-organism process	GO:0046989	3755	2.03e-09			114	116	115
BP	cellular process	GO:0009987	4884	1.05e-05			123	123	123
BP	cellular response to stimulus	GO:0051716	983	6.85e-06			41	49	49
BP	cellular response to stress	GO:0033554	631	7.47e-08			31	41	31
BP	cellular response to DNA damage stimulus	GO:0006974	331	1.27e-11			23	24	24
BP	single-organism cellular process	GO:0044763	3397	9.14e-14			105	111	114
BP	cell division	GO:0051304	350	1.92e-18			25	31	33
BP	cell budding	GO:0007111	65	6.18e-03					9
BP	cell cycle	GO:0007049	729	9.77e-34			43	60	57
BP	cell cycle process	GO:0022402	641	6.76e-33			35	50	57
BP	cell cycle phase transition	GO:0044770	140	3.93e-04			13	15	13
BP	cell cycle G2/M phase transition	GO:0044839	85	8.72e-04			8		
BP	cell cycle checkpoint	GO:0000075	37	3.78e-06				14	13
BP	meiotic cell cycle	GO:0051321	303	1.62e-04			21	23	20
BP	meiotic cell cycle process	GO:1903046	236	1.98e-04			18	19	20
BP	mitotic cell cycle	GO:0000278	379	3.17e-29			28	28	28
BP	mitotic cell cycle process	GO:1903047	367	6.85e-29			26	26	26
BP	regulation of transcription involved in G1/S transition of mi ...	GO:0000083	27	2.38e-02				6	6
BP	mitotic cell cycle phase transition	GO:0044772	137	2.95e-04				13	13
BP	G2/M transition of mitotic cell cycle	GO:0000086	36	6.96e-04				8	
BP	microtubule-based process	GO:0007017	122	1.31e-08			15	17	19
BP	chromosome segregation	GO:0007059	199	1.47e-15			17	31	30
BP	external encapsulating structure organization	GO:0045229	212	2.50e-02			16		
BP	cell wall organization	GO:0071555	212	2.50e-02			16		
BP	organelle organization	GO:0006996	1491	1.09e-12			59	72	61
BP	organelle fission	GO:0048285	351	1.21e-18			23	32	39
BP	nuclear division	GO:0000280	341	3.34e-18			23	31	39
BP	meiotic nuclear division	GO:0007126	170	4.56e-06			17	18	17
BP	single-organism organelle organization	GO:1902589	1007	9.55e-16			46	64	53
BP	mitotic nuclear division	GO:0007067	215	1.50e-16			18	22	32
BP	meiosis I	GO:0007127	98	2.89e-06			11	12	13
BP	chromosome organization	GO:0051276	523	1.67e-17			27	32	39
BP	DNA conformation change	GO:0071103	90	8.18e-06				11	14
BP	DNA packaging	GO:0006323	57	3.98e-03					9
BP	sister chromatid segregation	GO:0000819	112	1.24e-13			13	23	21
BP	mitotic sister chromatid segregation	GO:0000070	104	4.32e-12			12	21	21
BP	sister chromatid cohesion	GO:0007062	49	6.22e-11				15	13
BP	mitotic sister chromatid cohesion	GO:0007064	38	6.37e-10				12	10
BP	telomere organization	GO:0032200	79	1.38e-06				11	14
BP	cytoskeleton organization	GO:0007010	243	1.71e-09				20	25
BP	septin cytoskeleton organization	GO:0032185	29	3.69e-02					6
BP	septin ring organization	GO:0031106	28	2.98e-02					6
BP	microtubule cytoskeleton organization	GO:0002226	111	2.29e-09			15	17	16
BP	microtubule polymerization or depolymerization	GO:0031109	37	8.00e-05			8	9	9
BP	microtubule polymerization	GO:0046785	31	4.21e-03			6	7	7
BP	microtubule organizing center organization	GO:0031023	32	2.60e-04			8	7	8
BP	spindle pole body organization	GO:0051300	32	2.60e-04			8	7	8
BP	spindle pole body separation	GO:0000073	13	1.39e-04			6	6	6
BP	spindle organization	GO:0007051	40	2.21e-03					7
BP	mitotic spindle organization	GO:0007052	34	8.15e-03					7
BP	microtubule nucleation	GO:0007020	18	1.76e-03			5	6	6
BP	regulation of cellular process	GO:0050794	1506	8.25e-04				57	52
BP	regulation of cell division	GO:0051302	127	2.31e-02					13
BP	regulation of nuclear division	GO:0051783	118	1.08e-02					12
BP	regulation of cell cycle	GO:0051726	214	3.84e-05			15	19	20
BP	regulation of cell cycle process	GO:0010564	154	7.15e-03				13	14
BP	regulation of spindle pole body separation	GO:0010695	9	2.48e-02			4		
BP	regulation of mitotic cell cycle	GO:0007346	121	3.83e-04				13	14
BP	negative regulation of biological process	GO:0048519	554	2.25e-05			27	33	34
BP	negative regulation of cellular process	GO:0048523	527	2.35e-05				32	32
BP	negative regulation of cell cycle	GO:0045786	97	1.81e-04				13	13
BP	negative regulation of mitotic cell cycle	GO:0045930	64	1.15e-05				12	11
BP	mitotic cell cycle checkpoint	GO:0007093	57	3.57e-05				11	10
BP	morphogenesis checkpoint	GO:0044879	4	2.59e-04			3	4	4
BP	negative regulation of metabolic process	GO:0009892	444	1.08e-03				26	27
BP	negative regulation of nitrogen compound metabolic process	GO:0051172	309	1.36e-02					20
BP	single-organism metabolic process	GO:0044710	2051	3.46e-03				71	71
BP	negative regulation of gene expression, epigenetic	GO:0045814	150	2.62e-02					13
BP	sulfate reduction	GO:0019419	3	1.25e-02			3		
BP	sulfate assimilation, macromoleculyl sulfate reduction by phosphoaden ...	GO:0019379	3	1.25e-02			3		
BP	negative regulation of macromolecule metabolic process	GO:0010605	399	1.70e-03				24	23
BP	regulation of cellular metabolic process	GO:0031323	1086	4.82e-02					43
BP	negative regulation of cellular metabolic process	GO:0031324	430	1.99e-03				25	26
BP	negative regulation of nucleobase-containing compound metabolic process	GO:0045934	304	1.07e-02					20
BP	DNA metabolic process	GO:0006259	542	1.12e-13			30	35	34
BP	DNA strand elongation	GO:0022616	37	1.18e-03				18	8
BP	heteroduplex formation	GO:0030491	9	6.51e-04			4	4	5
BP	regulation of DNA metabolic process	GO:0051052	107	5.82e-04				12	13
BP	negative regulation of DNA metabolic process	GO:0051053	41	2.70e-03				8	7
BP	DNA recombination	GO:0006310	203	3.62e-07			18	24	19
BP	reciprocal DNA recombination	GO:0035825	60	6.61e-04			9	10	10
BP	reciprocal meiotic recombination	GO:0007131	60	6.61e-04			9	10	10
BP	regulation of recombination	GO:0000018	27	6.15e-03				7	6
BP	mitotic recombination	GO:0006312	58	4.75e-04			8	10	10
BP	negative regulation of DNA recombination	GO:0045910	16	1.19e-02				5	2
BP	DNA replication	GO:0006260	211	4.11e-10			17	22	26
BP	DNA-dependent DNA replication	GO:0006261	122	1.25e-10			15	20	21
BP	DNA strand elongation involved in DNA replication	GO:0006271	34	5.84e-04				8	8
BP	lagging strand elongation	GO:0006273	18	1.76e-03				5	6
BP	DNA topological change	GO:0006265	10	4.90e-02				4	4
BP	DNA replication initiation	GO:0006270	53	2.00e-02				4	8
BP	maintenance of DNA repeat elements	GO:0043570	23	6.83e-07				7	9
BP	maintenance of DNA trinucleotide repeats	GO:0005753	8	1.40e-02				4	4
BP	base-excision repair	GO:0006281	284	6.43e-12			20	22	24
BP	double-strand break repair	GO:0006284	18	3.77e-02				5	5
BP	recombinational repair	GO:0006302	109	1.70e-07			12	17	12
BP	double-strand break repair via homologous recombination	GO:0000725	67	1.91e-03				10	9
BP	telomere maintenance	GO:0000724	59	5.35e-05				9	8
BP	telomere maintenance via recombination	GO:0000723	78	1.22e-05				11	13
BP	gene silencing	GO:0016458	154	3.47e-02				7	7
BP	chromatin silencing	GO:0006342	150	2.62e-02					13
BP	regulation of cell shape	GO:0008360	16	1.99e-02				5	

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CC	MBF transcription complex	GO:0030907	4	2.59e-04			4	4	
CC	extracellular region	GO:0005576	97	5.31e-16			24		
CC	site of polarized growth	GO:0030427	255	3.94e-04			20	17	19
CC	cellular bud	GO:0005933	219	9.53e-07			18	22	18
CC	cellular bud neck	GO:0005935	168	8.48e-05			17	16	17
CC	SBF transcription complex	GO:0033309	4	4.71e-02				3	3
CC	anchored component of membrane	GO:0031225	65	1.87e-03			10		
CC	cell periphery	GO:0071944	661	1.40e-04			37		
CC	external encapsulating structure	GO:0030312	106	1.01e-12			22		
CC	cell wall	GO:0005618	106	1.01e-12			22		
CC	fungal-type cell wall	GO:0009277	99	3.02e-12			21		
CC	mac								