

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	1.57e-02	8				
BP	methionine metabolic process	GO:0006555	42	4.04e-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-09			33	36	27
BP	reproduction of a single-celled organism	GO:0032505	203	9.67e-03			15		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 metabolic 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	86
BP	cellular component organization	GO:0016043	2045	4.56e-09					84
BP	single-organism process	GO:0046989	3755	2.03e-09		11	11	11	11
BP	cellular process	GO:0009987	4884	1.05e-05		12	13	12	13
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	40
BP	cellular response to DNA damage stimulus	GO:0006974	331	1.27e-11		23	24	34	33
BP	single-organism cellular process	GO:0044763	3397	9.14e-14		10	11	11	14
BP	cell division	GO:0051304	3357	1.92e-18		25	31	43	33
BP	cell budding	GO:0007111	60	6.18e-03					9
BP	cell cycle	GO:0007049	729	9.77e-34		43	60	57	68
BP	cell cycle process	GO:0022402	641	6.77e-33		35	50	57	64
BP	cell cycle phase transition	GO:0044770	140	3.93e-04			13	15	13
BP	cell cycle G2/M phase transition	GO:0044839	87	8.72e-04			8		
BP	cell cycle checkpoint	GO:0000075	35	3.78e-06				14	13
BP	meiotic cell cycle	GO:0051321	303	1.62e-04		21	23	20	23
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	39	45
BP	mitotic cell cycle process	GO:1903047	367	6.85e-29		26	36	44	56
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	14
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	43	39
BP	nuclear division	GO:0000280	341	3.34e-18		23	31	42	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	33
BP	meiosis I	GO:0007127	98	2.89e-06			11	12	13
BP	chromosome organization	GO:0051276	523	1.67e-17		27	32	47	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
BP	spindle pole body organization	GO:0051300	32	2.60e-04			8		7
BP	spindle pole body separation	GO:0000073	13	1.39e-04			6		6
BP	spindle organization	GO:0007051	40	2.21e-03				6	7
BP	mitotic spindle organization	GO:0007052	34	8.15e-03				7	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	41	34
BP	DNA strand elongation	GO:0022616	37	1.18e-03				8	8
BP	heteroduplex formation	GO:0030491	9	6.51e-04		4	4	5	4
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 DNA 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	24
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	4
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	32	32
BP	double-strand break repair	GO:0006284	18	3.77e-02				12	15
BP	double-strand break repair via homologous recombination	GO:0006302	109	1.70e-07			12	17	12
BP	recombinational repair	GO:0000725	67	1.91e-03				10	9
BP	double-strand break repair via homologous recombination	GO:0000724	59	5.35e-05				9	8
BP	telomere maintenance	GO:0000723	78	1.22e-05				11	13
BP	telomere maintenance via recombination	GO:0000722	34	8.15e-03				7	7
BP	gene silencing	GO:0016458	154	3.47e-02					13
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:0005427	255	3.94e-04			20	17	19
CC	cellular bud	GO:0005933	219	9.53e-07		18	22	18	19
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-1					