GO Information

FDR Set 1 -

Coc. 0051794 Process Coc. 0050906 Process Coc. 0050906 Process Coc. 0050906 Process Coc. 0050906 Process Coc. 0050907 Proc				globular not	Set 2 - mature
GC:00059896 P response to stimulus 0.0010000013 0.01			•		
GCI-0009975 P response to stress 0.0000933 CCI-0009967 P response to stress 0.000000000000000000000000000000000			· · · · · · · · · · · · · · · · · · ·		
GC:0009595 P response to stress 0.00001 CC:0009595 P response to bitch stimulus 0.000046 CC:0009595 P catabotic process 0.000013 CC:0009595 P catabotic process 0.00013 CC:0009595 P catabotic process 0.000013 CC:0009595 P secondary metabolic process 0.00002 CC:0009595 P secondary metabolic process 0.00005 CC:0009595 P response to external stimulus 0.00004 CC:0009595 P response to external stimulus 0.00005 CC:0009595 P CC:0009595			·		
CSC-0009567 Page			·		
CG:0009356 P catabolic process 0.000346 0.000306 CG:0009306 P catabolic process involved in reproduction 0.00013 0.00036 0.0			·		
GO:0009356 P developmental process involved in reproduction 0.00024 0.033			·		
GO:0019748 P secondary metabolic process 0.00026		Р	·		
GO:0009719 P response to endogenous stimulus 0.00048 0.017	GO:0003006	P	developmental process involved in reproduction	0.00024	0.033
CG:00096019 P					
GO:0022414 P reproductive process 0.00063 0.0013			•		
CG-00006810 P			·		
GO:0000003 P reproduction 0.00067 0.0013					
GC:0048869 Cellular developmental process 0.00069 CC:0051179 CC:0007154 P cell communication 0.00094 0.000072 CC:0007156 P coll communication 0.00094 0.000072 CC:0007165 P signal transduction 0.0011 0.000037 CC:0032502 P developmental process 0.0014 0.0018 0.005 CC:0032502 P developmental process 0.0014 0.0058 CC:0032502 P developmental process 0.0018 0.005 CC:0032502 P developmental process 0.0018 0.005 CC:0032502 P developmental process 0.003 0.002 0.003 0.0			·		
GO:0051234 P			·		
GO:0051179 F Cocalization 0.00011 0.000037 GO:000155 P signal transduction 0.0011 0.000037 GO:0032502 P developmental process 0.0014 0.0058 GO:003154 P cell differentiation 0.0022 0.034 GO:0032501 P coll differentiation 0.0022 0.034 GO:0032501 P multicellular organismal process 0.003 0.002 0.0086 GO:0008152 P biological regulation 0.0055 GO:00065007 P biological regulation 0.0018 0.0016 GO:0016049 P cell growth 0.016 GO:0016049 P growth 0.016 GO:0006629 P lipid metabolic process 0.003 0.002 GO:00005215 F transporter activity 0.00000082 GO:00005215 F transporter activity 0.00000082 GO:0003700 F transporter activity 0.00000082 GO:0003700 F transporter activity 0.00000082 GO:0003700 F transcription factor activity 0.00000082 GO:0003703 F caracellular region 0.00000082 GO:0005215 C caracellular region 0.0055 GO:0005215 C caracellular region 0.0055 GO:0005216 C caracellular region 0.0055 GO:0005216 C caracellular region 0.0055 GO:0005216 C plasma membrane 0.0055 GO:0005216 C plasma membrane 0.0005 GO:0005216 C caracellular region part 0.036 GO:00050789 P regulation of cellular process GO:00050789 P regulation of cellular process GO:00050789 P regulation of pene expression 0.0000000000000000000000000000000000					
GO:0007165 P signal transduction 0.0011 0.000032 0.0014 0.0058 0.0014 0.0058 0.0014 0.0058 0.0014 0.0058 0.0015 0.0016 0.0015 0.0016 0.0016 0.0016 0.0015 0.0016 0.001	GO:0007154	Р	cell communication	0.00094	0.000072
GO:0032502 P	GO:0051179	Р	localization	0.00094	
GO:0048856 P			<u> </u>		
GO:0033151 P					
GO:0032501 P			•		
GO:00065007 P biological regulation 0.005 0.000066 0.0015 0.0000066 0.0015 0.0000066 0.0015 0.0000066 0.0015 0.0000066 0.0015 0.0000066 0.0016 0.00000025 0.000000025 0.00000025 0.000000025 0.000000025 0.0000000000000000000000000000000000					
G0:0065007 P cell growth			·		
GO:0016049 P cell growth 0.016			•		
GO:0040007 P growth 0.018 CO:0006629 P lipid metabolic process 0.042 CO:0005215 F transporter activity 0.00000082 CO:0003824 F catalytic activity 0.00000082 CO:0003824 F catalytic activity 0.00000082 CO:0008289 F lipid binding 0.00013 0.0000042 CO:0008289 F lipid binding 0.00015 CO:00030234 F earyme regulator activity 0.0072 CO:00005576 C extracellular region 7.9E-21 CO:0005576 C ecli wall 0.000000000000000000000000000000000					
G0:0005215 F transporter activity			<u> </u>		
G0:0003824 F Catalytic activity G0:0003700 F transcription factor activity, sequence-specific DNA binding 0.00013 0.0000042 0.00013 0.0000042 0.00013 0.00003 0.0000042 0.00013 0.0000042 0.00013 0.0000042 0.0000000000000000000000000000000000	GO:0006629	Р	lipid metabolic process	0.042	
G0:0003700 F transcription factor activity, sequence-specific DNA binding 0.00013 0.0000042	GO:0005215	F	transporter activity	0.00000082	
G0:0008289 F			· · · · · · · · · · · · · · · · · · ·		
G0:0016787 F					
G0:0030234 F			·		
GO:0005576 C extracellular region GO:0030312 C external encapsulating structure 3.6E-10 GO:0005618 C cell wall C cextracellular region part C cextracellular matrix C cextracellular matrix C cextracellular matrix C cextracellular matrix C cextracellular process C cellular process C cellula					
GO:0030312 C external encapsulating structure 3.6E-10					
GO:0005618 C cell wall			_		
GO:0016020 C membrane 0.036	GO:0005618	С			
GO:0044421 C extracellular region part 0.036 CO:0031012 C extracellular matrix 0.036 CO:0050794 P regulation of cellular process CO:0050789 P regulation of biological process CO:0050789 P regulation of biological process CO:0060255 P regulation of macromolecule metabolic process CO:00060255 P regulation of gene expression CO:00060255 P regulation of macromolecule metabolic process CO:00060259 P regulation of metabolic process CO:00060259 P regulation of metabolic process CO:000000000000000000000000000000000000	GO:0005886	С	plasma membrane	1.6E-09	
GO:0031012 C extracellular matrix 0.036					
GO:0050794 P regulation of cellular process 0.0000002 GO:0050789 P regulation of biological process 0.00000034 GO:0060255 P regulation of macromolecule metabolic process 0.0000001 GO:0010468 P regulation of gene expression 0.0000038 GO:0019222 P regulation of metabolic process 0.0000043 GO:0009908 P flower development 0.00001 GO:0006259 P DNA metabolic process 0.0001 GO:0007049 P cell cycle 0.0016 GO:0007275 P multicellular organism development 0.0071 GO:0009653 P anatomical structure morphogenesis 0.0083 GO:0044260 P cellular macromolecule metabolic process 0.0098 GO:0048608 P reproductive structure development 0.014 GO:004377 F DNA binding 0.033			- · ·		
GO:0050789 P regulation of biological process GO:0060255 P regulation of macromolecule metabolic process GO:0010468 P regulation of gene expression GO:0006139 P nucleobase-containing compound metabolic process GO:0019222 P regulation of metabolic process GO:0006259 P flower development GO:0006259 P DNA metabolic process GO:0007049 P cell cycle GO:0007275 P multicellular organism development GO:0009653 P anatomical structure morphogenesis GO:0004260 P cellular macromolecule metabolic process GO:0044260 P cellular macromolecule metabolic process GO:0044260 P cellular macromolecule metabolic process GO:0003077 F DNA binding GO:0003677 F DNA binding GO:0005488 F binding GO:0005488 F binding GO:0005486 F carbohydrate binding GO:00030246 F carbohydrate binding GO:0003676 F nucleic acid binding GO:0003676 F oxygen binding GO:0003676 F oxygen binding GO:0003685 F oxygen binding GO:0003686 F oxygen binding				0.036	
G0:0060255 P regulation of macromolecule metabolic process 0.000001 G0:0010468 P regulation of gene expression 0.0000038 G0:0006139 P nucleobase-containing compound metabolic process 0.0000038 G0:0019222 P regulation of metabolic process 0.000004 G0:0009908 P flower development 0.0001 G0:0006259 P DNA metabolic process 0.00019 G0:0007049 P cell cycle 0.0016 G0:0007275 P multicellular organism development 0.0071 G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009979 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0086 G0:00448608 P reproductive structure development 0.014 G0:0043170 P macromolecule metabolic process <t< td=""><td></td><td></td><td></td><td></td><td></td></t<>					
G0:0010468 P regulation of gene expression 0.0000038 G0:0006139 P nucleobase-containing compound metabolic process 0.0000038 G0:0019222 P regulation of metabolic process 0.0000043 G0:00090908 P flower development 0.0001 G0:0006259 P DNA metabolic process 0.0001 G0:0007275 P multicellular organism development 0.0016 G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0086 G0:0048608 P reproductive structure development 0.014 G0:0048608 P reproductive structure development 0.033 G0:00033170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process <td></td> <td></td> <td></td> <td></td> <td></td>					
G0:0006139 P nucleobase-containing compound metabolic process 0.0000038 G0:0019222 P regulation of metabolic process 0.00001 G0:0009908 P flower development 0.0001 G0:0007049 P cell cycle 0.0016 G0:0007275 P multicellular organism development 0.0071 G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0091 G0:0048608 P reproductive structure development 0.014 G0:0043170 P macromolecule metabolic process 0.033 G0:000987 P cellular process 0.033 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0			j ,		
G0:0009908 P flower development 0.0001 G0:0006259 P DNA metabolic process 0.00019 G0:0007049 P cell cycle 0.0016 G0:0007275 P multicellular organism development 0.0071 G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.001 G0:0048608 P reproductive structure development 0.014 G0:00048710 P macromolecule metabolic process 0.033 G0:0003677 F DNA binding 0.033 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.048 G0:0019825 F oxygen binding 0.048					
G0:0006259 P DNA metabolic process 0.00019 G0:0007049 P cell cycle 0.0016 G0:0007275 P multicellular organism development 0.0071 G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0091 G0:0048608 P reproductive structure development 0.014 G0:0004970 P macromolecule metabolic process 0.033 G0:0003677 F DNA binding 0.033 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.048 G0:0019825 F oxygen binding 0.048	GO:0019222	Р	regulation of metabolic process		0.0000043
G0:0007049 P cell cycle 0.0016 G0:0007275 P multicellular organism development 0.0071 G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0091 G0:0048608 P reproductive structure development 0.014 G0:0043170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process 0.033 G0:0003677 F DNA binding 0.00000044 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.048 G0:0019825 F oxygen binding 0.048	GO:0009908	Р	flower development		0.0001
G0:0007275 P multicellular organism development 0.0071 G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0091 G0:0043170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process 0.033 G0:0003677 F DNA binding 0.00000044 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.048 G0:0019825 F oxygen binding 0.048			·		
G0:0009653 P anatomical structure morphogenesis 0.0083 G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0091 G0:0048608 P reproductive structure development 0.014 G0:0043170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process 0.033 G0:0003677 F DNA binding 0.000000044 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.048 G0:0019825 F oxygen binding 0.048			•		
G0:0009791 P post-embryonic development 0.0086 G0:0044260 P cellular macromolecule metabolic process 0.0091 G0:0048608 P reproductive structure development 0.014 G0:0043170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process 0.033 G0:0005488 F binding 0.00000044 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.043 G0:0019825 F oxygen binding 0.048			· · · · · · · · · · · · · · · · · · ·		
G0:0044260 P cellular macromolecule metabolic process 0.0091 G0:0048608 P reproductive structure development 0.014 G0:0043170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process 0.033 G0:0003677 F DNA binding 0.000000044 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.043 G0:0019825 F oxygen binding 0.048					
G0:0048608 P reproductive structure development 0.014 G0:0043170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process 0.033 G0:0003677 F DNA binding 0.000000044 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.043 G0:0019825 F oxygen binding 0.048			, ,		
G0:0043170 P macromolecule metabolic process 0.033 G0:0009987 P cellular process 0.033 G0:0003677 F DNA binding 0.000000044 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.043 G0:0019825 F oxygen binding 0.048			· ·		
G0:0003677 F DNA binding 0.000000044 G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.043 G0:0019825 F oxygen binding 0.048			·		
G0:0005488 F binding 0.035 G0:0016301 F kinase activity 0.035 G0:0016772 F transferase activity, transferring phosphorus-containing groups 0.035 G0:0030246 F carbohydrate binding 0.035 G0:0003676 F nucleic acid binding 0.043 G0:0019825 F oxygen binding 0.048	GO:0009987	Р	·		0.033
GO:0016301 F kinase activity 0.035 GO:0016772 F transferase activity, transferring phosphorus-containing groups GO:0030246 F carbohydrate binding 0.035 GO:0003676 F nucleic acid binding 0.043 GO:0019825 F oxygen binding 0.048			<u> </u>		
GO:0016772 F transferase activity, transferring phosphorus-containing groups GO:0030246 F carbohydrate binding GO:0003676 F nucleic acid binding GO:0019825 F oxygen binding 0.035 0.035 0.043 0.043					
GO:0030246 F carbohydrate binding 0.035 GO:0003676 F nucleic acid binding 0.043 GO:0019825 F oxygen binding 0.048			·		
GO:0003676 F nucleic acid binding 0.043 GO:0019825 F oxygen binding 0.048					
GO:0019825 F oxygen binding 0.048			· ·		
, 9			<u> </u>		
			, ,		