

GO Information

FDR

GO Term	Onto	Description	Set 3A - coleoptilar not cotyledonary -		Set 4 - cotyledonary
			maize IDs		
GO:0019748	P	secondary metabolic process	0.0011	---	
GO:0005975	P	carbohydrate metabolic process	0.023		0.0000076
GO:0009987	P	cellular process	---		3.1E-77
GO:0044237	P	cellular metabolic process	---		6.2E-50
GO:0008152	P	metabolic process	---		2E-46
GO:0044238	P	primary metabolic process	---		2.9E-37
GO:0016043	P	cellular component organization	---		1.3E-30
GO:0050896	P	response to stimulus	---		5.1E-28
GO:0009628	P	response to abiotic stimulus	---		9.7E-28
GO:0006139	P	nucleobase-containing compound metabolic process	---		1.2E-27
GO:0050789	P	regulation of biological process	---		8.4E-27
GO:0032502	P	developmental process	---		1E-26
GO:0048856	P	anatomical structure development	---		2.9E-25
GO:0050794	P	regulation of cellular process	---		3.5E-23
GO:0007275	P	multicellular organism development	---		4.5E-23
GO:0032501	P	multicellular organismal process	---		5.9E-23
GO:0009791	P	post-embryonic development	---		1.6E-21
GO:0043412	P	macromolecule modification	---		2.9E-19
GO:0044260	P	cellular macromolecule metabolic process	---		5E-19
GO:0043170	P	macromolecule metabolic process	---		5.5E-19
GO:0051179	P	localization	---		2.6E-18
GO:0051234	P	establishment of localization	---		9.9E-18
GO:0048608	P	reproductive structure development	---		1.2E-17
GO:0006810	P	transport	---		1.6E-17
GO:0065007	P	biological regulation	---		4.3E-17
GO:0006464	P	cellular protein modification process	---		5.4E-17
GO:0000003	P	reproduction	---		1.7E-16
GO:0006807	P	nitrogen compound metabolic process	---		2E-16
GO:0022414	P	reproductive process	---		2.9E-16
GO:0003006	P	developmental process involved in reproduction	---		4.2E-15
GO:0019222	P	regulation of metabolic process	---		5.3E-12
GO:0006950	P	response to stress	---		2.6E-11
GO:0009719	P	response to endogenous stimulus	---		6.6E-11
GO:0044249	P	cellular biosynthetic process	---		6.6E-11
GO:0009058	P	biosynthetic process	---		1.7E-10
GO:0006259	P	DNA metabolic process	---		2.1E-10
GO:0009790	P	embryo development	---		8.3E-10
GO:0006091	P	generation of precursor metabolites and energy	---		8.3E-10
GO:0015979	P	photosynthesis	---		8.5E-10
GO:0007049	P	cell cycle	---		8.5E-10
GO:0060255	P	regulation of macromolecule metabolic process	---		4.3E-09
GO:0009908	P	flower development	---		5.8E-09
GO:0009653	P	anatomical structure morphogenesis	---		0.00000007
GO:0009056	P	catabolic process	---		0.00000014
GO:0007165	P	signal transduction	---		0.00000005
GO:0007154	P	cell communication	---		0.00000023
GO:0010468	P	regulation of gene expression	---		0.00000072
GO:0006629	P	lipid metabolic process	---		0.000001
GO:0019538	P	protein metabolic process	---		0.000088
GO:0040007	P	growth	---		0.000098
GO:0044267	P	cellular protein metabolic process	---		0.00027
GO:0048869	P	cellular developmental process	---		0.00031
GO:0042592	P	homeostatic process	---		0.00032
GO:0019725	P	cellular homeostasis	---		0.0013
GO:0030154	P	cell differentiation	---		0.019
GO:0008219	P	cell death	---		0.02
GO:0016049	P	cell growth	---		0.021
GO:0010467	P	gene expression	---		0.035
GO:0005515	F	protein binding	---		4.3E-57
GO:0005488	F	binding	---		7E-56
GO:0003824	F	catalytic activity	---		2E-55

GO:0000166	F	nucleotide binding	---	3.8E-29
GO:0016787	F	hydrolase activity	---	1.3E-17
GO:0016740	F	transferase activity	---	3.5E-17
GO:0016817	F	hydrolase activity, acting on acid anhydrides	---	1.8E-11
GO:0016818	F	hydrolase activity, acting on acid anhydrides, in phosphorus-con	---	1.9E-11
GO:0016462	F	pyrophosphatase activity	---	2.4E-11
GO:0017111	F	nucleoside-triphosphatase activity	---	3.3E-10
GO:0016772	F	transferase activity, transferring phosphorus-containing groups	---	0.00000072
GO:0005215	F	transporter activity	---	0.0000004
GO:0005198	F	structural molecule activity	---	0.00000053
GO:0003677	F	DNA binding	---	0.000001
GO:0016788	F	hydrolase activity, acting on ester bonds	---	0.0000018
GO:0016301	F	kinase activity	---	0.0000032
GO:0004518	F	nuclease activity	---	0.00034
GO:0003676	F	nucleic acid binding	---	0.0021
GO:0003774	F	motor activity	---	0.013
GO:0008135	F	translation factor activity, RNA binding	---	0.017
GO:0060089	F	molecular transducer activity	---	0.019
GO:0004872	F	receptor activity	---	0.019
GO:0003682	F	chromatin binding	---	0.021
GO:0004871	F	signal transducer activity	---	0.036
GO:0005623	C	cell	---	4.3E-187
GO:0044464	C	cell part	---	5.1E-187
GO:0005622	C	intracellular	---	1.7E-144
GO:0044424	C	intracellular part	---	1.8E-143
GO:0044422	C	organelle part	---	1.4E-128
GO:0044446	C	intracellular organelle part	---	1.8E-128
GO:0005737	C	cytoplasm	---	5.5E-111
GO:0043226	C	organelle	---	6.7E-111
GO:0043229	C	intracellular organelle	---	7.4E-111
GO:0043227	C	membrane-bounded organelle	---	8.9E-101
GO:0043231	C	intracellular membrane-bounded organelle	---	1.4E-100
GO:0044444	C	cytoplasmic part	---	4.8E-96
GO:0009536	C	plastid	---	3.1E-59
GO:0032991	C	macromolecular complex	---	3E-48
GO:0005829	C	cytosol	---	4.8E-47
GO:0016020	C	membrane	---	4.6E-44
GO:0031975	C	envelope	---	2.8E-32
GO:0031967	C	organelle envelope	---	2.8E-32
GO:0012505	C	endomembrane system	---	3.4E-28
GO:0043232	C	intracellular non-membrane-bounded organelle	---	7.6E-28
GO:0043228	C	non-membrane-bounded organelle	---	7.6E-28
GO:0005773	C	vacuole	---	6.1E-27
GO:0031974	C	membrane-enclosed lumen	---	5.2E-25
GO:0043233	C	organelle lumen	---	5.2E-25
GO:0070013	C	intracellular organelle lumen	---	5.2E-25
GO:0044428	C	nuclear part	---	6.7E-25
GO:0005886	C	plasma membrane	---	2E-22
GO:0009579	C	thylakoid	---	2.5E-22
GO:0031981	C	nuclear lumen	---	1.1E-20
GO:0005634	C	nucleus	---	5.8E-19
GO:0005794	C	Golgi apparatus	---	1.7E-17
GO:0005783	C	endoplasmic reticulum	---	2.3E-13
GO:0005768	C	endosome	---	2.7E-11
GO:0005730	C	nucleolus	---	1.2E-10
GO:0030529	C	intracellular ribonucleoprotein complex	---	2.6E-10
GO:0005654	C	nucleoplasm	---	3.3E-09
GO:0005840	C	ribosome	---	0.00000049
GO:0005856	C	cytoskeleton	---	0.00000025
GO:0005777	C	peroxisome	---	0.00015
GO:0042579	C	microbody	---	0.00015
GO:0005635	C	nuclear envelope	---	0.00047
GO:0030312	C	external encapsulating structure	---	0.007
GO:0005618	C	cell wall	---	0.007