

Regulator of chromosome condensation  
Regulatory protein SIR3  
Polycomb complex protein BMI-1  
Ubiquitin-conjugating enzyme E2 D3  
E3 ubiquitin-protein ligase RING2  
Ubiquitin carboxyl-terminal hydrolase 8  
Transcription and mRNA export factor SUS1  
SAGA-associated factor 11  
Polyubiquitin-B  
SAGA-associated factor 73  
55 kDa immediate-early protein 1  
Protein ORF73  
Guanine nucleotide exchange factor SRM1  
N-lysine methyltransferase KMT5A  
TP53-binding protein 1  
Gag polyprotein  
Chromo domain-containing protein 1  
Transcription regulatory protein SNF2  
Maltose/maltodextrin-binding periplasmic protein  
Centromere protein N  
RuvB-like 1  
RuvB-like 2  
Chromatin-remodeling ATPase INO80  
Actin-related protein 5  
INO80 complex subunit B  
RuvB-like helicase  
RuvB-like helicase (another gene? 37% identity)

3 Uncharacterized proteins from *Chaetomium thermophilum* (CTHT\_0004910, CTHT\_0032670, CTHT\_0032660)

SELENOMETHIONINE  
2-[[ (2R)-2-amino-2-carboxyethyl] sulfanyl]-N,N,N-trimethylethanaminium  
(2R)-2-amino-3-(2-dimethylaminoethylsulfanyl)propanoic acid  
2-[(2R)-oxiran-2-ylmethyl]-1H-benzo[de]isoquinoline-1,3(2H)-dione  
1-methyl-4-(1-methylethyl)benzene  
1,3,5-triaza-7-phosphatricyclo[3.3.1.1~3,7~]decane  
Cisplatin  
(ethane-1,2-diamine-kappa~2~N,N')[(1,2,3,4,5,6-eta)-1-methyl-4-(propan-2-yl)cyclohexane-1,2,3,4,5,6-hexayl]ruthenium  
N-ACETYLALANINE  
ACETYL GROUP  
[(1,2,3,4,5,6-eta)-1-methyl-4-(propan-2-yl)benzene]ruthenium  
N(6)-ACETYLLYSINE  
(6-4)photoproduct  
N-6-crotonyl-L-lysine  
CIS-SYN CYCLOBUTANE THYMINE DIMER  
5-METHYL-2'-DEOXY-CYTIDINE-5'-MONOPHOSPHATE  
(ethane-6-5,8,9,10-tetrahydroanthracene)Ru(II)(ethylene-diamine)Cl  
dichloro[(1,2,3,4,5,6-eta)-6-methylbenzene]1,3,5-triaza-7-lambda~5~-phosphatricyclo[3.3.1.1~3,7~]dec-7-ylruthenium  
triethylphosphanuidylgold(1+)  
AMINO GROUP  
1',2'-DIDEOXYRIBOFURANOSE-5'-PHOSPHATE  
ADENOSINE-5'-DIPHOSPHATE  
BERYLLIUM TRIFLUORIDE ION  
N2-ETHANETHIOL-2'-DEOXY-GUANOSINE-5'-MONOPHOSPHATE  
(1R,2R)-1,2-diphenylethane-1,2-diamine  
[ethane-6-3-(p-tolyl)propanoic acid]Ru(1,3,5-triaza-7-phosphaadamantane)Cl2  
(1S,2S)-1,2-diphenylethane-1,2-diamine  
(1S,2R)-1,2-diphenylethane-1,2-diamine  
ADENOSINE-5'-TRIPHOSPHATE

ID ▾	Term ▾	Frequency (p-value) ▾	
GO:0005634	nucleus	26 (0.02)	<div></div>
GO:0005694	chromosome	17 (0.01)	<div></div>
GO:0005737	cytoplasm	12 (0.04)	<div></div>
GO:0032991	protein-containing complex	9 (0.08)	<div></div>
GO:0033202	DNA helicase complex	9 (0.02)	<div></div>
GO:0031248	protein acetyltransferase complex	8 (0.07)	<div></div>
GO:0016020	membrane	5 (0.46)	<div></div>
GO:0043230	extracellular organelle	4 (0.04)	<div></div>
GO:0005575	cellular_component	4 (0.05)	<div></div>
GO:0031982	vesicle	4 (0.01)	<div></div>
GO:0035097	histone methyltransferase complex	3 (0.01)	<div></div>
GO:0005856	cytoskeleton	3 (0.01)	<div></div>
GO:0000776	kinetochore	3 (0.01)	<div></div>
GO:1990904	ribonucleoprotein complex	3 (0.03)	<div></div>
GO:0005730	nucleolus	3 (0.06)	<div></div>
GO:0005768	endosome	2 (0.03)	<div></div>
GO:0000151	ubiquitin ligase complex	2 (0.01)	<div></div>
GO:0031519	PcG protein complex	2 (0.05)	<div></div>
GO:0042597	periplasmic space	1 (0.00)	<div></div>
GO:0005783	endoplasmic reticulum	1 (0.00)	<div></div>
GO:0043005	neuron projection	1 (0.04)	<div></div>
GO:0005643	nuclear pore	1 (0.01)	<div></div>
GO:0005813	centrosome	1 (0.06)	<div></div>
GO:0019012	virion	1 (0.29)	<div></div>
GO:0005739	mitochondrion	1 (0.50)	<div></div>
GO:0043025	neuronal cell body	1 (0.04)	<div></div>
GO:0005576	extracellular region	1 (0.01)	<div></div>
GO:0017053	transcriptional repressor complex	1 (0.02)	<div></div>
GO:0043229	intracellular organelle	1 (0.01)	<div></div>
GO:0043232	intracellular non-membrane-bounded organelle	1 (0.03)	<div></div>
GO:0044464	cell part	1 (0.59)	<div></div>
	unclassified	0	
Total UniProtKB ACCs in this JOB = 30			

## PANTHER GO-Slim Cellular Component

Total # Genes: 19 Total # component hits: 17



Click to get gene list for a category:

[cell part \(GO:0044464\)](#)[macromolecular complex \(GO:0032991\)](#)[organelle \(GO:0043226\)](#)

Color picker powered by



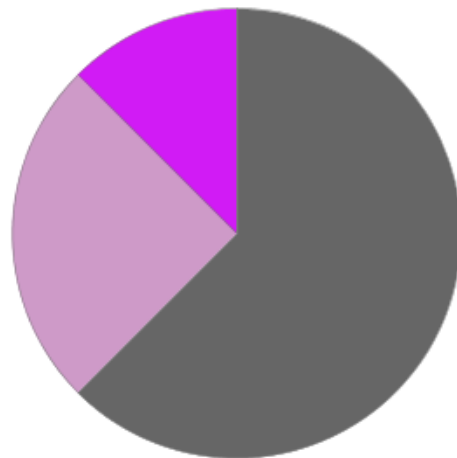
\*\*Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Component hits

ID ▾	Term ▾	Frequency ( <i>p</i> -value) ▾	
GO:0043167	ion binding	13 (0.00)	<div></div>
GO:0005515	protein binding	13 (0.03)	<div></div>
GO:0003676	nucleic acid binding	8 (0.00)	<div></div>
GO:0003682	chromatin binding	8 (0.02)	<div></div>
GO:0008144	drug binding	8 (0.00)	<div></div>
GO:0000166	nucleotide binding	8 (0.00)	<div></div>
GO:0004386	helicase activity	7 (0.01)	<div></div>
GO:0016787	hydrolase activity	4 (0.38)	<div></div>
GO:0003674	molecular_function	4 (0.00)	<div></div>
GO:0030234	enzyme regulator activity	2 (0.09)	<div></div>
GO:0005198	structural molecule activity	2 (0.07)	<div></div>
GO:0019787	ubiquitin-like protein transferase activity	2 (0.02)	<div></div>
GO:0005215	transporter activity	1 (0.62)	<div></div>
GO:0016740	transferase activity	1 (0.17)	<div></div>
GO:0008233	peptidase activity	1 (0.68)	<div></div>
	unclassified	7 (0.00)	<div></div>

Total UniProtKB ACCs in this JOB = 30

## PANTHER GO-Slim Molecular Function

Total # Genes: 19 Total # function hits: 8



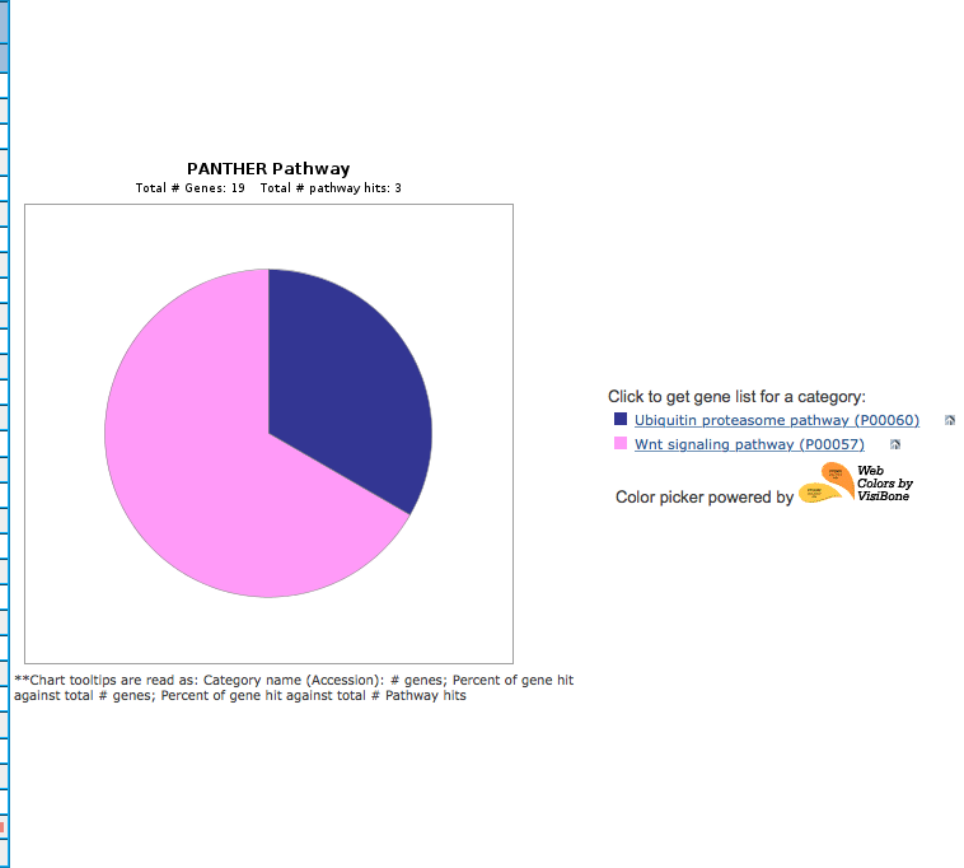
Click to get gene list for a category:

■ [binding \(GO:0005488\)](#) ■ [catalytic activity \(GO:0003824\)](#) ■ [structural molecule activity \(GO:0005198\)](#)

Color picker powered by Web Colors by VisiBone

\*\*Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Function hits

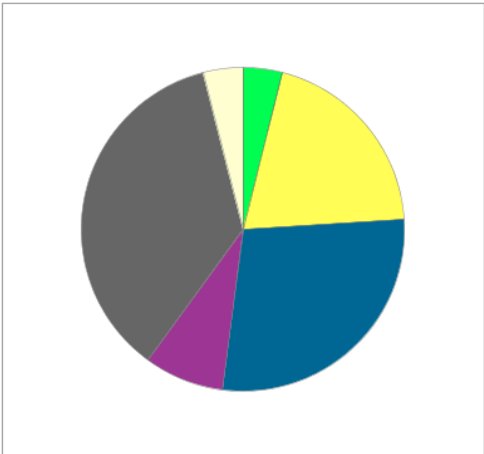
PATHWAY			
ID ▾	Term ▾	Frequency ( <i>p</i> -value) ▾	
(REACTOME) REACT_120956	Cellular responses to stress	4 (0.01)	<div></div>
(REACTOME) REACT_115566	Cell Cycle	4 (0.01)	<div></div>
(REACTOME) REACT_111102	Signal Transduction	3 (0.03)	<div></div>
(REACTOME) REACT_21300	Mitotic M-M/G1 phases	3 (0.03)	<div></div>
(REACTOME) REACT_116125	Disease	3 (0.06)	<div></div>
(REACTOME) REACT_216	DNA Repair	2 (0.03)	<div></div>
(REACTOME) REACT_71	Gene Expression	2 (0.01)	<div></div>
(REACTOME) REACT_6900	Immune System	2 (0.01)	<div></div>
(REACTOME) REACT_172623	Chromatin organization	2 (0.03)	<div></div>
(KEGG) ece02010	ABC transporters [PATH:ece02010]Z5632	1 (0.03)	<div></div>
(KEGG) hsa05012	Parkinson's disease [PATH:hsa05012]7314	1 (0.01)	<div></div>
(REACTOME) REACT_6782	TRAF6 Mediated Induction of proinflammatory cytokines	1 (0.01)	<div></div>
(KEGG) hsa04141	Protein processing in endoplasmic reticulum [PATH:hsa04141]7323	1 (0.02)	<div></div>
(REACTOME) REACT_15518	Transmembrane transport of small molecules	1 (0.01)	<div></div>
(REACTOME) REACT_11123	Membrane Trafficking	1 (0.08)	<div></div>
(REACTOME) REACT_111217	Metabolism	1 (0.01)	<div></div>
(KEGG) ecs02010	ABC transporters [PATH:ecs02010]ECs5017	1 (0.01)	<div></div>
(KEGG) hsa04120	Ubiquitin mediated proteolysis [PATH:hsa04120]7323	1 (0.01)	<div></div>
(REACTOME) REACT_8017	APC-Cdc20 mediated degradation of Nek2A	1 (0.01)	<div></div>
(REACTOME) REACT_578	Apoptosis	1 (0.01)	<div></div>
(REACTOME) REACT_21257	Metabolism of RNA	1 (0.04)	<div></div>
(REACTOME) REACT_24941	Circadian Clock	1 (0.08)	<div></div>
(KEGG) hsa00310	Lysine degradation [PATH:hsa00310]387893	1 (0.02)	<div></div>
(KEGG) ecs02030	Bacterial chemotaxis [PATH:ecs02030]ECs5017	1 (0.08)	<div></div>
(KEGG) ece02030	Bacterial chemotaxis [PATH:ece02030]Z5632	1 (0.01)	<div></div>
(REACTOME) REACT_383	DNA Replication	1 (0.07)	<div></div>
(REACTOME) REACT_6850	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	1 (0.01)	<div></div>
(REACTOME) REACT_2001	Receptor-ligand binding initiates the second proteolytic cleavage of Notch receptor	1 (0.07)	<div></div>
(KEGG) hsa04310	Wnt signaling pathway [PATH:hsa04310]8607	1 (0.01)	<div></div>
	unclassified	20 (0.02)	<div></div>
Total UniProtKB ACCs in this JOB = 30			



GO SLIM >>			
ID ▾	Term ▾	Frequency (p-value) ▾	
GO:0050789	regulation of biological process	22 (0.01)	<div></div>
GO:0006351	transcription, DNA-templated	20 (0.02)	<div></div>
GO:0051276	chromosome organization	19 (0.04)	<div></div>
GO:0006464	cellular protein modification process	14 (0.02)	<div></div>
GO:0006281	DNA repair	12 (0.05)	<div></div>
GO:0050896	response to stimulus	10 (0.06)	<div></div>
GO:0007049	cell cycle	10 (0.02)	<div></div>
GO:0006508	proteolysis	9 (0.01)	<div></div>
GO:0065003	protein-containing complex assembly	9 (0.01)	<div></div>
GO:0051641	cellular localization	8 (0.01)	<div></div>
GO:0007154	cell communication	7 (0.02)	<div></div>
GO:0032502	developmental process	6 (0.05)	<div></div>
GO:0032501	multicellular organismal process	6 (0.07)	<div></div>
GO:0015031	protein transport	6 (0.01)	<div></div>
GO:0006259	DNA metabolic process	6 (0.05)	<div></div>
GO:0009057	macromolecule catabolic process	5 (0.05)	<div></div>
GO:0006509	regulation of molecular function	5 (0.01)	<div></div>
GO:0051301	cell division	5 (0.02)	<div></div>
GO:0006323	DNA packaging	4 (0.03)	<div></div>
GO:0002376	immune system process	4 (0.01)	<div></div>
GO:0043170	macromolecule metabolic process	4 (0.02)	<div></div>
GO:0016070	RNA metabolic process	3 (0.00)	<div></div>
GO:0015931	nucleobase-containing compound transport	3 (0.09)	<div></div>
GO:0051179	localization	3 (0.09)	<div></div>
GO:0007059	chromosome segregation	3 (0.06)	<div></div>
GO:0040007	growth	3 (0.01)	<div></div>
GO:0051640	organelle localization	3 (0.04)	<div></div>
GO:0000003	reproduction	3 (0.01)	<div></div>
GO:0022607	cellular component assembly	3 (0.02)	<div></div>
GO:0065008	regulation of biological quality	3 (0.00)	<div></div>
GO:0016032	viral process	3 (0.00)	<div></div>
GO:0006260	DNA replication	3 (0.02)	<div></div>
GO:0046794	transport of virus	2 (0.03)	<div></div>
GO:0006810	transport	2 (0.05)	<div></div>
GO:0051234	establishment of localization	2 (0.01)	<div></div>
GO:0042254	ribosome biogenesis	2 (0.00)	<div></div>
GO:0006354	DNA-templated transcription, elongation	2 (0.01)	<div></div>
GO:0051704	multi-organism process	2 (0.01)	<div></div>
GO:0007031	peroxisome organization	2 (0.03)	<div></div>
GO:0006396	RNA processing	2 (0.00)	<div></div>
GO:0005975	carbohydrate metabolic process	1 (0.63)	<div></div>
GO:0006457	protein folding	1 (0.00)	<div></div>
GO:0051606	detection of stimulus	1 (0.03)	<div></div>
GO:0019538	protein metabolic process	1 (0.00)	<div></div>
GO:0008283	cell proliferation	1 (0.02)	<div></div>
GO:0032989	cellular component morphogenesis	1 (0.01)	<div></div>
GO:0006996	organelle organization	1 (0.01)	<div></div>
GO:0007155	cell adhesion	1 (0.00)	<div></div>
GO:0061024	membrane organization	1 (0.02)	<div></div>
GO:0016458	gene silencing	1 (0.01)	<div></div>
GO:0009059	macromolecule biosynthetic process	1 (0.19)	<div></div>
GO:0040011	locomotion	1 (0.05)	<div></div>
GO:0008150	biological_process	1 (0.00)	<div></div>
GO:0006793	phosphorus metabolic process	1 (0.30)	<div></div>
GO:0006066	alcohol metabolic process	1 (0.00)	<div></div>
GO:0006928	movement of cell or subcellular component	1 (0.00)	<div></div>
GO:0016192	vesicle-mediated transport	1 (0.01)	<div></div>
GO:0000280	nuclear division	1 (0.09)	<div></div>
GO:0001775	cell activation	1 (0.01)	<div></div>
GO:0042710	biofilm formation	1 (0.06)	<div></div>
GO:0007005	mitochondrion organization	1 (0.01)	<div></div>
GO:0016049	cell growth	1 (0.07)	<div></div>
GO:0016043	cellular component organization	1 (0.02)	<div></div>
	unclassified	2 (0.04)	<div></div>
Total UniProtKB ACCs in this JOB = 30			

PANTHER GO-Slim Biological Process


Total # Genes: 19    Total # process hits: 25



\*\*Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Process hits

Click to get gene list for a category:

- [biological regulation \(GO:0065007\)](#) ⓘ
- [cellular component organization or biogenesis \(GO:0071840\)](#) ⓘ
- [cellular process \(GO:0009987\)](#) ⓘ
- [localization \(GO:0051179\)](#) ⓘ
- [metabolic process \(GO:0008152\)](#) ⓘ
- [response to stimulus \(GO:0050896\)](#) ⓘ

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