

DHFR-PCA Network proteins, Molecular Function, Over-representation

GOMFID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0030515	2.62E-06	6.75	5.03	16	26	snoRNA binding
GO:0005515	3.75E-06	1.71	81.11	118	419	protein binding
GO:0016818	8.93E-06	1.89	49.56	78	256	hydrolase activity, acting on acid anhydrides, in phosphoru

DHFR-PCA Network proteins, Biological process, Over-representation

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0009987	1.74E-38	3.08	821.39	984	4243	cellular process
GO:0016043	4.83E-25	2.05	329.29	474	1701	cell organization and biogenesis
GO:0051179	2.09E-15	2.06	139.58	222	1012	localization
GO:0051649	8.32E-15	2.23	100.47	171	519	establishment of cellular localization
GO:0045045	9.31E-13	2.93	41.04	85	212	secretory pathway
GO:0044255	1.00E-11	2.76	42.59	85	220	cellular lipid metabolism
GO:0043487	9.92E-11	20.11	4.45	19	23	regulation of RNA stability
GO:0000288	4.28E-10	23.95	3.87	17	20	mRNA catabolism, deadenylation-dependent decay
GO:0006401	1.41E-09	4.84	12.39	34	64	RNA catabolism
GO:0006897	6.30E-09	4.05	14.71	37	76	endocytosis
GO:0008104	1.08E-08	2.15	56.33	96	291	protein localization
GO:0016197	1.58E-08	6.36	7.74	24	40	endosome transport
GO:0048193	1.88E-08	2.76	28.26	57	146	Golgi vesicle transport
GO:0030468	7.22E-08	3.09	20.33	44	105	establishment of cell polarity (sensu Fungi)
GO:0015031	8.43E-08	2.13	49.95	85	258	protein transport
GO:0009628	1.72E-07	1.98	60.01	97	310	response to abiotic stimulus
GO:0007163	1.93E-07	2.94	20.91	44	108	establishment and/or maintenance of cell polarity
GO:0009653	6.58E-07	2.09	45.11	76	233	morphogenesis
GO:0007034	6.90E-07	3.56	13.16	31	68	vacuolar transport
GO:0048308	8.69E-07	5.22	7.36	21	38	organelle inheritance
GO:0007114	9.35E-07	3.17	15.87	35	82	cell budding
GO:0006605	1.39E-06	2.05	45.11	75	233	protein targeting
GO:0042254	1.65E-06	2	47.62	78	246	ribosome biogenesis and assembly
GO:0008152	3.47E-06	1.35	579.02	647	2991	metabolism
GO:0006810	3.79E-06	1.63	101.44	142	953	transport
GO:0030036	3.94E-06	2.66	20.13	40	104	actin cytoskeleton organization and biogenesis
GO:0006694	4.39E-06	4.69	7.36	20	38	steroid biosynthesis
GO:0006999	5.28E-06	6.13	5.23	16	27	nuclear pore organization and biogenesis
GO:0006665	6.20E-06	5.52	5.81	17	30	sphingolipid metabolism

GO:0006364	6.28E-06	2.2	31.36	55	162	rRNA processing
GO:0000910	7.25E-06	2.65	19.17	38	99	cytokinesis
GO:0016125	7.38E-06	4.45	7.55	20	39	sterol metabolism

DHFR-PCA Network proteins, Cellular Compartment, Over-representation

GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0005623	4.41E-28	3.58	951.87	1060	4917	cell
GO:0005622	9.36E-19	2.2	874.05	979	4515	intracellular
GO:0031090	2.31E-12	1.99	117.51	185	607	organelle membrane
GO:0012505	4.41E-12	2.52	54.79	103	283	endomembrane system
GO:0044425	1.35E-09	1.83	114.8	172	593	membrane part
GO:0005838	1.62E-09	15.22	4.45	18	23	proteasome regulatory particle (sensu Eukaryota)
GO:0005730	3.80E-08	2.29	43.17	77	223	nucleolus
GO:0005938	4.11E-08	3.23	19.36	43	100	cell cortex
GO:0015629	4.47E-08	3.47	16.84	39	87	actin cytoskeleton
GO:0005737	6.03E-08	1.44	634	713	3275	cytoplasm
GO:0005798	7.91E-08	4.12	12.2	31	63	Golgi-associated vesicle
GO:0005794	3.58E-07	2.36	33.3	61	172	Golgi apparatus
GO:0030863	3.63E-07	4.24	10.45	27	54	cortical cytoskeleton
GO:0030479	5.31E-07	5.17	7.74	22	40	actin cortical patch
GO:0031988	5.65E-07	2.92	19.55	41	101	membrane-bound vesicle
GO:0031410	5.65E-07	2.92	19.55	41	101	cytoplasmic vesicle
GO:0005783	8.15E-07	1.87	65.05	101	336	endoplasmic reticulum
GO:0005732	5.40E-06	3.55	11.03	26	57	small nucleolar ribonucleoprotein complex
GO:0044422	8.74E-06	1.35	393.37	456	2032	organelle part

DHFR-PCA Network proteins, Molecular Function, Under-representation

GOMFID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0003735	1.95E-21	0	42.01	0	217	structural constituent of ribosome
GO:0005554	1.05E-14	0.58	409.24	300	2114	molecular function unknown

DHFR-PCA Network proteins, Biological Process, Under-representation

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000004	5.27E-43	0.28	281.67	115	1455	biological process unknown
GO:0043037	2.28E-12	0.26	63.3	20	327	translation
GO:0009059	2.96E-08	0.49	106.67	61	551	macromolecule biosynthesis

DHFR-PCA Network proteins, Cellular Compartment, Under-representation

GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0008372	5.65E-28	0.28	169.39	62	875	cellular component unknown

GO:0005761	2.36E-08	0	15.68	0	81 mitochondrial ribosome
GO:0005840	8.07E-07	0.28	33.49	11	269 ribosome
GO:0015935	2.12E-06	0.13	18.58	3	96 small ribosomal subunit
GO:0005842	3.41E-06	0.1	16.07	2	83 cytosolic large ribosomal subunit (sensu Eukaryota)

is-containing anhydrides



