PTHR ID Gene Family Description	Total Nodes	Annotated Nodes	Total Annotations	CC Annotations	MF Annotations	BP Annotations	NOT Annotations
PTHR10000 PHOSPHOSERINE PHOSPHATASE	208	45	124	28	69	27	0
PTHR10003 SUPEROXIDE DISMUTASE [CU-ZN]-RELATED	319	188	1117	395	532	190	0
PTHR10005 SKI ONCOGENE-RELATED	152	24	109	29	37	43	0
PTHR10006 MUCIN-1-RELATED	20	2	4	4	0	0	0
PTHR10009 PROTEIN YELLOW-RELATED	61	35	114	26	31	57	0
PTHR10012 SERINE/THREONINE-PROTEIN PHOSPHATASE 2A REGULATORY SUBUNIT B	142	76	525	214	215	96	0
PTHR10019 SNF5	97	52	329	52	1	276	0
PTHR10025 TETRAHYDROFOLATE DEHYDROGENASE/CYCLOHYDROLASE FAMILY MEMBER	326	91	451	119	249	83	89
PTHR10027 CALCIUM-ACTIVATED POTASSIUM CHANNEL ALPHA CHAIN	206	32	102	30	47	25	1
PTHR10032 ZINC FINGER PROTEIN WITH KRAB AND SCAN DOMAINS	697	365	782	334	372	76	2
PTHR10046 ATP DEPENDENT LON PROTEASE FAMILY MEMBER	283	70	577	101	268	208	0
PTHR10048 PHOSPHATIDYLINOSITOL KINASE	669	354	1090	504	582	4	1
PTHR10063 TUBERIN	203	26	113	38	18	57	0
PTHR10073 DNA MISMATCH REPAIR PROTEIN (MLH, PMS, MUTL)	410	77	465	186	171	108	0
PTHR10125 P2X PURINOCEPTOR	225	37	90	20	49	21	0
PTHR10130 PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR (PEX5)	134	34	142	64	34	44	2
PTHR10138 TRYPTOPHAN 2,3-DIOXYGENASE	70	21	64	1	42	21	0
PTHR10146 PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG PROTEIN	136	29	29	0	29	0	0
PTHR10150 DNA REPAIR ENDONUCLEASE XPF	109	20	114	16	32	66	0
PTHR10159 DUAL SPECIFICITY PROTEIN PHOSPHATASE	1460	316	973	178	287	508	36
PTHR10169 DNA TOPOISOMERASE/GYRASE	334	77	457	102	69	286	27
PTHR10170 HUNTINGTON DISEASE PROTEIN	69	8	16	8	4	4	0
PTHR10194 RAS GTPASE-ACTIVATING PROTEINS	489	65	281	114	55	112	0
PTHR10202 PRESENILIN	124	26	383	262	27	94	1
PTHR10218 GTP-BINDING PROTEIN ALPHA SUBUNIT	860	185	1251	342	631	278	4
PTHR10224 ES1 PROTEIN HOMOLOG, MITOCHONDRIAL	40	1	1	0	0	1	0
PTHR10233 TRANSLATION INITIATION FACTOR EIF-2B	480	116	458	136	142	180	122
PTHR10250 MICROSOMAL GLUTATHIONE S-TRANSFERASE	186	67	316	110	147	59	13
PTHR10290 DNA TOPOISOMERASE I	139	15	25	6	4	15	4
PTHR10322 DNA POLYMERASE CATALYTIC SUBUNIT	429	70	470	115	106	249	68
PTHR10371 NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 2, MITOCHONDRIAL	143	42	116	39	40	37	1
PTHR10373 T-CELL-SPECIFIC TRANSCRIPTION FACTOR	155	29	429	25	116	288	0
PTHR10394 40S RIBOSOMAL PROTEIN S8	146	29	103	24	26	53	0
PTHR10442 40S RIBOSOMAL PROTEIN S21	119	25	129	21	21	87	0
PTHR10459 DNA LIGASE	345	75	406	136	63	207	16
PTHR10496 40S RIBOSOMAL PROTEIN S24	158	30	94	45	2	47	0
PTHR10516 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	1136	214	848	240	383	225	2
PTHR10529 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED	782	39	222	25	45	152	5
PTHR10559 TRANSCOBALAMIN-1/GASTRIC INTRINSIC FACTOR	78	10	18	0	8	10	0
PTHR10569 GLYCOGEN DEBRANCHING ENZYME	108	11	40	15	16	9	0
PTHR10663 GUANYL-NUCLEOTIDE EXCHANGE FACTOR	923	140	488	191	121	176	96
PTHR10668 PHYTOENE DEHYDROGENASE	376	40	74	29	19	26	0
PTHR10682 POLY(A) POLYMERASE	175	95	311	107	91	113	1
PTHR10732 40S RIBOSOMAL PROTEIN S17	159	32	85	29	1	55	0
PTHR10769 40S RIBOSOMAL PROTEIN S28	128	26	73	22	26	25	0
PTHR10795 PROPROTEIN CONVERTASE SUBTILISIN/KEXIN	1227	281	449	135	236	78	1
PTHR10845 REGULATOR OF G PROTEIN SIGNALING	871	150	551	290	148	113	0
PTHR10856 CORONIN	324	52	179	73	37	69	13
PTHR10871 30S RIBOSOMAL PROTEIN S13/40S RIBOSOMAL PROTEIN S18	212	65	256	104	51	101	9
PTHR10877 POLYCYSTIN-RELATED	604	398	1185	379	417	389	70
PTHR10878 SEGMENT POLARITY PROTEIN DISHEVELLED	168	34	209	53	22	134	3
PTHR10890 CYSTEINYL-TRNA SYNTHETASE	226	46	140	58	41	41	0
PTHR10927 RIBOSOME MATURATION PROTEIN SBDS	121	25	111	42	24	45	0
TOTAL	17761	4412	17488	5616	6204	5668	587

			Total Unique	% of Unique	1				
PTHR ID	Gene Family Description	Total Nodes	Annotation Sets	Annotation Sets	At Least 1 Shared Annotation		No Shared Annotations		
	PHOSPHOSERINE PHOSPHATASE	208	7	3.365384615	Pairs of Nodes			Average Distance	Difference
	SUPEROXIDE DISMUTASE [CU-ZN]-RELATED	319	35	10.97178683	956	4.571638075	20572	4.219736875	0.3519012
	SKI ONCOGENE-RELATED	152	16	10.52631579	17327	3.370855659	33394	2.742057495	0.62879816
	MUCIN-1-RELATED	20	3	15	268	3.003406716	11208	2.875069593	0.12833712
	PROTEIN YELLOW-RELATED	61	11	18.03278689	1	1.124	189	1.24921164	-0.1252116
	SERINE/THREONINE-PROTEIN PHOSPHATASE 2A REGULATORY SUBUNIT B	142	11	7.746478873	537	3.629810056	1293	3.158932715	0.47087734
PTHR10012		97	16	16.49484536	2846	2.889373858	7165	2.23755492	0.65181894
	TETRAHYDROFOLATE DEHYDROGENASE/CYCLOHYDROLASE FAMILY MEMBER	326	19	5.828220859	1288	2.889373858	3368	2.434377078	0.52471454
	CALCIUM-ACTIVATED POTASSIUM CHANNEL ALPHA CHAIN	206	11	5.828220859	3974	2.937868898	49001	2.942764637	-0.0048957
	ZINC FINGER PROTEIN WITH KRAB AND SCAN DOMAINS	697	31	4.447632712	447	3.561548098	20668	3.554066189	0.00748191
	ATP DEPENDENT LON PROTEASE FAMILY MEMBER	283	21	7.4204947	61896	8.642831411	180660	8.131445206	0.5113862
	PHOSPHATIDYLINOSITOL KINASE	669	28	4.185351271	2226	3.759056155	37677	3.35030711	0.40874905
PTHR10063		203	17	8.374384236	62436	5.216610385	161010	4.406688963	0.80992142
	DNA MISMATCH REPAIR PROTEIN (MLH, PMS, MUTL)	410	25	6.097560976	319	5.308705329	20184	4.92280871	0.38589662
	P2X PURINOCEPTOR	225	13	5.77777778	2854	5.188041345	80991	4.80274654	0.38529481
	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR (PEX5)	134	5	3.731343284	649	3.062964561	24551	2.632734634	0.43022993
	TRYPTOPHAN 2,3-DIOXYGENASE	70	3	4.285714286	528	2.753632576	8383	2.682073721	0.07155886
	PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG PROTEIN	136	3	2.205882353	210	1.461028571	2205	1.410672562	0.05035601
PTHR10150	DNA REPAIR ENDONUCLEASE XPF	109	10	9.174311927	406	2.730453202	8774	2.246188056	0.48426515
PTHR10159	DUAL SPECIFICITY PROTEIN PHOSPHATASE	1460	87	5.95890411	184	3.647673913	5702	3.144271133	0.50340278
PTHR10169	DNA TOPOISOMERASE/GYRASE	334	21	6.28742515	38059	5.192499383	1027011	4.993835216	0.19866417
PTHR10170	HUNTINGTON DISEASE PROTEIN	69	9	13.04347826	2744	3.746473761	52867	3.768275181	-0.0218014
PTHR10194	RAS GTPASE-ACTIVATING PROTEINS	489	16	3.27198364	19	1.596947368	2327	3.03136141	-1.434414
PTHR10202	PRESENILIN	124	14	11.29032258	2039	5.627784698	117277	5.45167865	0.17610605
PTHR10218	GTP-BINDING PROTEIN ALPHA SUBUNIT	860	82	9.534883721	300	2.160966667	7326	1.904738329	0.25622834
	ES1 PROTEIN HOMOLOG, MITOCHONDRIAL	40	2	5	16096	3.117376305	353274	2.952318263	0.16505804
	TRANSLATION INITIATION FACTOR EIF-2B	480	15	3.125	0	N/A	780	0.900638462	N/A
	MICROSOMAL GLUTATHIONE S-TRANSFERASE	186	23	12.3655914	4883	4.471405079	110077	4.266658584	0.2047465
	DNA TOPOISOMERASE I	139	2	1.438848921	2064	3.819453973	15141	3.447479757	0.37197422
	DNA POLYMERASE CATALYTIC SUBUNIT	429	26	6.060606061	0	N/A	9591	1.910268168	N/A
	NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 2, MITOCHONDRIAL	143	5	3.496503497	2293	4.512476232	89513	4.414259672	0.09821656
	T-CELL-SPECIFIC TRANSCRIPTION FACTOR	155	19	12.25806452	816	2.833448529	9337	1.875329763	0.95811877
	40S RIBOSOMAL PROTEIN S8	146	7	4.794520548	381	1.636732283	11554	2.01719344	-0.3804612
		119		7.56302521	401		10184		0.05017574
	40S RIBOSOMAL PROTEIN S21		9		294	1.348331671		1.298155931	
PTHR10459		345	21	6.086956522		1.442520408	6727	1.376968783	0.06555163
	40S RIBOSOMAL PROTEIN S24	158	12	7.594936709	2606	5.309938219	56734	4.322866235	0.98707198
	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	1136	33	2.904929577	373	1.475241287	12030	1.266154613	0.20908667
	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED	782	24	3.069053708	22258	7.268916524	622422	7.374198324	-0.1052818
	TRANSCOBALAMIN-1/GASTRIC INTRINSIC FACTOR	78	3	3.846153846	362	6.749651934	305009	9.74411538	-2.9944634
	GLYCOGEN DEBRANCHING ENZYME	108	6	5.55555556	45	2.689911111	2958	2.714791751	-0.0248806
	GUANYL-NUCLEOTIDE EXCHANGE FACTOR	923	35	3.791982665	49	1.603734694	5729	2.304497469	-0.7007628
	PHYTOENE DEHYDROGENASE	376	15	3.989361702	9477	5.896578242	416026	5.566500512	0.33007773
	POLY(A) POLYMERASE	175	11	6.285714286	585	5.588805128	69915	6.055902868	-0.4670977
PTHR10732	40S RIBOSOMAL PROTEIN S17	159	8	5.031446541	4458	2.771760655	10767	2.163001486	0.60875917
PTHR10769	40S RIBOSOMAL PROTEIN S28	128	4	3.125	431	1.248786543	12130	1.052334955	0.19645159
PTHR10795	PROPROTEIN CONVERTASE SUBTILISIN/KEXIN	1227	41	3.341483293	325	0.758495385	7803	0.666034602	0.09246078
PTHR10845	REGULATOR OF G PROTEIN SIGNALING	871	22	2.525832377	31785	8.115946988	720366	8.574990354	-0.4590434
PTHR10856	CORONIN	324	21	6.481481481	10597	5.425885439	368288	5.129542809	0.29634263
	30S RIBOSOMAL PROTEIN S13/40S RIBOSOMAL PROTEIN S18	212	17	8.018867925	1177	3.589627867	51149	3.561149309	0.02847856
	POLYCYSTIN-RELATED	604	21	3.476821192	1914	2.213934169	20452	2.163962449	0.04997172
	SEGMENT POLARITY PROTEIN DISHEVELLED	168	33	19.64285714	77841	11.03156934	104265	9.90374608	1.12782326
PTHR10890	CYSTEINYL-TRNA SYNTHETASE	226	7	3.097345133	517	2.855524178	13511	3.112988084	-0.2574639
PTHR10927	RIBOSOME MATURATION PROTEIN SBDS	121	8	6.611570248	1030	2.831790291	24395	2.524547571	0.30724272
	TOTAL	17761	964	5.427622319	1030	2.286290541	24333	2.1582803	0.12801024
	ITOTAL	1//01	JU4	3.42/022319	L	2.200230341	L	2.1302003	0.12001024