**Table S1.** Complete list of Groups I and II genes classified under major functional categories. Their expression levels are indicated by quartiles, i.e., L0 = lowly or unexpressed Group II genes, L1 to L4 = Group I genes with expression levels in the parasite oocysts at bottom to top quartiles. Genes with expression at L0 and L4 levels are highlighted by green and pink colors for easy identification.

Major Group	Subgroup	GeneID	Description	L0	L1	L2	L3	L4	Total	Signal Mean
Cell cycle	CDC related	cgd1 2180	CDC48 like AAA ATPase			1			1	4.136
con cycle	ODO TOIGICO	cgd2_1540	cell growth-regulating nucleolar protein, metal binding domain at				1		1	12.836
		oguz_1010	N-terminus				·			12.000
		cgd5_2510	Cdc2-like CDK2/CDC28 like protein kinase	1					1	0.598
		cgd6_1420	cdc2-related protein kinase, putative			1			1	2.612
		cgd6_1830	HT-1080/Cdc123p - like protein			1			1	3.440
		cgd6_2060	cdc39p protein-like; C-terminal Not1, CCR4-Not complex					1	1	41.270
		13.12	component; Not1							
		cgd7_1930	CDC68 like aminopeptidase family chromatinic protein (possible	1					1	0.382
			inactive enzyme)							
		cgd7_280	cell division control protein 28, putative		1				1	1.657
		cgd7_4470	CDC14 phosphatase				1		1	21.845
		cgd8_2380	CDC45 like protein, possible horizontal transfer	1					1	0.389
		cgd8_4460	cell differentiation protein rcd1, putative			1			1	2.494
	CDC related Total			3	1	4	2	1	11	8.333
	Cyclin related	cgd1_2320	cyclin B, saccharomyces Clb4p like				1		1	7.617
		cgd1_3150	cyclin'cyclin'	1					1	0.397
		cgd1_3310	cyclin domain protein, possible cyclin H	1					1	0.311
		cgd1_60	cyclin dependent kinase A, putative	1					1	0.359
		cgd2_2290	cyclin 6 pcl7			1			1	3.743
		cgd3_4050	cyclin	1					1	0.393
		cgd5_3540	cyclin domain protein					1	1	66.359
		cgd6_1840	cyclin M2-like membrane-associated protein with 4	1					1	0.568
		_	transmembrane domains and 2 CBS domains							
		cgd7_1200	cyclin		1				1	1.367
		cgd7_2490	cyclin'cyclin'	1					1	0.517
		cgd7_3780	cyclin					1	1	318.539
		cgd7_430	cyclin-dependent kinase-related kinase, putative				1		1	8.899
		cgd7_520	cyclin'cyclophilin like peptidyl-prolyl cis-trans isomerase fused to	1					1	0.521
			WD40 repeats at the N-terminus'							
		cgd7_660	cyclin; possible cyclin A	1					1	0.366
		cgd8_2510	Cyclin dependent kinase regulatory subunit, putative			1			1	5.273
	Cyclin related Total			8	1	2	2	2	15	27.682
Cell cycle Total				11	2	6	4	3	26	19.496
Chaperone	DNAj	cgd1_2280	DNAJ	1					1	0.442
		cgd1_2970	DNAJ like chaperone, 4 or more transmembrane domains			1			1	4.067
		cgd2_1330	DNAJ protein					1	1	26.709
		cgd2_2260	zuotin related factor-1 like protein with a DNAJ domain at the N-				1		1	21.815
			terminus and 2 SANT domains							
		cgd2_3230	heat shock protein DnaJ Pfj2, putative			1			1	3.822
		cgd3_930	DnaJ domain, possible zf-CSL following				1		1	14.780
		cgd4_2780	DNAj domain protein having a signal peptide	1					1	0.344
		cgd5_2950	DNAj domain protein				1		1	9.330
		cgd5_3520	chaperone'DNAj domain protein chaperone'			1			1	3.142
		cgd5_3530	DNAj domain protein	1					1	0.411
		cgd6_1190	DNAJ protein-like, putative	1					1	0.348
		cgd6_2650	heat shock protein, putative		1				1	2.095
		cgd7_3880	DNAJ domain protein sec63 ortholog, 4 transmembrane	1					1	0.298
			domains							
		cgd8_2820	membrane associated DNAJ with 6 transmembrane domain,	1					1	0.350
		40 0000	signal peptide						_	5 5 5 7
		cgd8_2860	DNAJ protein			1			1 .	5.557
		cgd8_3270	DNAJ'DNAJ protein'				1		1 .	22.075
		cgd8_3770	DNAJ like chaperone					1	1	183.367
		cgd8_450	DNAj-like protein			1			1	3.296
	DMATT	cgd8_4930	DNAJ protein	1	L .	<u> </u>	<u> </u>		1	0.352
	DNAj Total	1		7	1	5	4	2	19	
	HSP	cgd2_1800	heat shock 40 kDa protein, putative	1					1	0.434
		cgd2_20	heat shock 70 (HSP70) protein					1	1	417.813
		cgd3_3770	Hsp90					1	1	1,229.346
		cgd4_3270	heat shock 105kD; heat shock 105kD alpha; heat shock 105kD		1				1	1.673
			beta; heat shock 105kDa protein 1		١.					
		cgd6_1630	p23; HSP20-like chaperones fold		1				1	1.698
		cgd6_4970	Hsp60; GroEL-like chaperone (ATpase), predicted mitochondrial	1					1	0.439
		cad7 2400	chaperonin 10 Kd subunit, putative		4				4	1.244
		cgd7_2400	heat shock protein, Hsp70		'			- 4		I I
		cgd7_360						- 1		65.777
		cgd7_3670	heat shock protein 90 (Hsp90), signal peptide plus ER retention		1				1	1.640
		cad8 1610	motif sacsin like HSP90 chaperone domain, likely plant origin	1					1	0.335
	HSP Total	cgd8_1610	odosii iike 1101 30 onaperone domain, iikely plant ongin	3	4			3	10	
	Other	cad2 1950	etrass_induced protein sti1 like protein putative	3	4	4		3	10	3.400
	Culei	cgd2_1850	stress-induced protein sti1-like protein, putative [Tetratricopeptide repeat domain]			'			1	3.400
		cgd3 3440	heat shock protein HSP70, mitochondrial			1			1	3.006
		cgd5_3510	co-chaperone GrpE, putative			1			1	3.351
I	I	1-3-3-0010	I	ı	I	i '	I		'	1 0.001

		cgd8_2340	cold shock RNA binding domain of the OB fold					1	1	58.377
	Other Total					3		1	4	17.033
	TCP1	cgd2_600	TCP1_alpha; TCP-1 (CTT or eukaryotic type II) chaperonin	1					1	0.483
			family, alpha subunit.							
		cgd2_900	TCP1_theta; TCP-1 (CTT or eukaryotic type II) chaperonin			1			1	3.751
		14 0050	family, theta subunit.							4.04
		cgd4_3850	TCP1_gamma; TCP-1 (CTT or eukaryotic type II) chaperonin		1				1	1.847
		cgd6_5080	family, gamma subunit.  TCP1 beta; TCP-1 (CTT or eukaryotic type II) chaperonin			4			1	5.510
		cguo_5080	family, beta subunit.			'			'	5.510
		cgd7_3180	TCP1 epsilon; TCP-1 (CTT or eukaryotic type II) chaperonin		1				1	1.456
		cgu/_0100	family, epsilon subunit.							1.400
	TCP1 Total		in the state of th	1	2	2			5	2.609
Chaperone Total	1			11	7	10	4	6	38	55.373
Chromatin	Chromatin protein	cgd1 1640	chromatin protein with an AT hook and a PHD finger domain at			1			1	2.881
om omatin	Ornomatin protein	cgu 1_10+0	the C-terminus						'1	2.001
		cgd3 2540	histone H3					1	1	33.649
		cgd4 3220	histone H3			1		-	1	5.149
		cgd4_720	putative nucleosome assembly protein 19075338; besthit Py				1		1	8.005
		cgu+_/20	23481872						'1	0.000
		cgd5_2130	chromatin associated proein with a chromodomain at the C-			1			1	3.175
		0940_2 .00	terminus							0
		cgd5_3170	histone H2B			1			1	3.830
		cgd5_940	histone H2A					1	1	58.102
		cgd6_4510	telomeric DNA binding protein; SANT DNA-binding domain				1		1	5.823
		cgd7_1700	histone H2B					1	1	75.694
		cgd7_1700 cgd8_2170	histone H2A			4		'	1	3.817
				4		'			- 1	
		cgd8_2730	multidomain chromatinic protein with the following architecture: 3x PHD-bromo-3xPHD-SET domain and associated cysteine	1					1	0.474
			cluster at the C-terminus							
		cgd8_3970	NAP, nucleosome assembly protein			1			1	2.736
		cqd8 5230	histone H4			•	1		1	10.420
	Chromatin protoin Tota	, -	Inistone 114	1		6	3	3	13	16.442
	Chromatin protein Tota		OMI/ONE related matrix associated active description	- 1		0	3	) 3		
	Chromatin remodeling	cga1_1330	SWI/SNF-related, matrix associated, actin-dependent regulator			1			1	3.424
		oad2 2100	of chromatin subfamily A containing DEAD/H box 1			4			1	4 705
		cgd3_3190	GCN5 like acetylase + bromodomain	- 4		- 1			- 1	4.705
		cgd4_1340	bromo domain containing protein	1					1	0.321
		cgd6_1380	histone deacetylase HDA2/Rpd3p				1		1	18.823
		cgd6_2590	histone acetyltransferase (MYST family); chromo domain +					1	1	72.812
		10.00	C2H2 domain							0.044
		cgd6_80	RPD3/HD1 histone deacetylase				1		1	6.611
		cgd7_2030	bacterial-like Sir2 family protein (HDAC Class III)	1					1	0.386
		cgd7_3600	Hs17p, histone methylase	1					1	0.410
		cgd7_3630	TRF4/5 nucletotidyl transferase		1				1	1.951
		cgd7_5210	bromodomain protein					1	1	24.589
		cgd7_60	Hat1-like acetyltransferase (histone acetyltransferase-like)	1					1	0.381
		cgd8_480	histone deactylase of possible bacterial origin with ankyrin	1					1	0.368
			repeats at the N-terminus							
	Chromatin remodeling	Total		5	1	2	2	2	12	11.232
Chromatin Total				6	1	8	5	5	25	13.941
DNA metabolism	DNA repair	cgd1_2840	contains a UVDDB domain that is present in CPSF_A and			1			1	2.397
			damage specific DNA binding protein 1							
		cgd1_310	AP endonuclease of the TIM barrel fold, possible bacterial		1				1	1.803
			horizontal transfer							
		cgd2_700	PMS1'MutL family ATpase'		1				1	2.247
		cgd4_140	Swi2/Snf2 ATpase,Rad16 ortholog				1		1	17.634
		cgd4_2960	ERCC4/XP-G-type excision repair nuclease	1					1	0.408
		cgd4_2970	RAD1, NH2 terminal ERCC4-like helicase domain	1					1	0.370
			XPA binding protein 1				1		1	7.154
		cgd5 1900		1		ı I			1	1.710
					1					0.401
		cgd5_2190	Nuc1p like endonuclease G	1	1				1	
		cgd5_2190 cgd5_410	Nuc1p like endonuclease G Rad51	1	1	1			1	
		cgd5_2190 cgd5_410 cgd5_4290	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26	1	1	1			1	5.193
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p	1	1	1			1	5.193 1.856
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain	1	1 1 1	1			1 1 2	5.193 1.856 1.064
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase	1	1 1 1	1			1 1 2 1	5.193 1.856 1.064 1.976
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd6_2770	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative	1 1	1 1 1	1			1 1 2 1	5.193 1.856 1.064 1.976 0.484
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase	1 1	1 1 1	1	1		1 1 2 1	5.193 1.856 1.064 1.976 0.484 10.664
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd6_2770	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative	1 1 1	1 1 1	1	1		1 1 2 1	5.193 1.856 1.064 1.976
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd6_2770 cgd7_2090	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein	1 1 1	1 1 1 1 1 1	1	1		1 1 2 1 1	5.193 1.856 1.064 1.976 0.484 10.664
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd6_2770 cgd7_2090 cgd7_2660 cgd7_3350	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I	1 1 1	1 1 1 1	1	1		1 1 2 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein	1	1 1 1 1 1 1	1	1		1 1 2 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase	1	1 1 1 1	1	1		1 1 2 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase RAD3'DEXDc+HELICc protein'	1	1 1 1 1	1	1		1 1 2 1 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571 1.255
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80 cgd7_820 cgd7_820 cgd8_1940	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase RAD3'DEXDc+HELICc protein' RAD25, helicase involved in DNA repair	1	1 1 1 1	1	1		1 1 2 1 1 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571 1.255 0.389
		cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase RAD3'DEXDc+HELICc protein' RAD25, helicase involved in DNA repair UvrD like super family I helicase involved in nucleotide excision	1	1 1 1 1	1	1		1 1 2 1 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571 1.255 0.389
	DNA renair Total	cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80 cgd7_820 cgd7_820 cgd8_1940	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase RAD3'DEXDc+HELICc protein' RAD25, helicase involved in DNA repair	1 1 1 1 1 1	1 1 1 1	1	1 1		1 1 2 1 1 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571 1.255 0.389 0.308
	DNA repair Total	cgd5_2190 cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80 cgd7_820 cgd8_1940 cgd8_3210	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase RAD3'DEXDc+HELICc protein' RAD25, helicase involved in DNA repair UvrD like super family I helicase involved in nucleotide excision repair, possible bacterial horizontal transfer	1 1 1 1 1 1 9	1 1 1 1 1 1	2	1 1 1		1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571 1.255 0.389 0.308 0.510
	DNA repair Total DNA replication	cgd5_2190 cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80 cgd7_820 cgd8_1940 cgd8_3210	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase RAD3'DEXDc+HELICc protein' RAD25, helicase involved in DNA repair UvrD like super family I helicase involved in nucleotide excision repair, possible bacterial horizontal transfer  DNA replication complex GINS protein PSF2, putative	1 1 1 1 1 1	1 1 1 1 1	1	1 1 1		1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571 1.255 0.389 0.308 0.510
	<u> </u>	cgd5_2190 cgd5_2190 cgd5_410 cgd5_4290 cgd6_1530 cgd6_2610 cgd6_2660 cgd7_2090 cgd7_2660 cgd7_3350 cgd7_4730 cgd7_80 cgd7_820 cgd8_1940 cgd8_3210	Nuc1p like endonuclease G Rad51 Swi/SNf2 RAD26 DNA repair protein Rad4p ERCC1 excision repair 1; C-terminal HhH domain DNA repair helicase uvb-resistance protein uvr8, putative Ruv DNA-helicase-related protein RAD24/Rf-C activator 1 AAA+ ATpase eukaryotic DNA topoisomerase I RAD23p, UB+UBA domains protein XPA1 binding protein-like GTpase RAD3'DEXDc+HELICc protein' RAD25, helicase involved in DNA repair UvrD like super family I helicase involved in nucleotide excision repair, possible bacterial horizontal transfer	1 1 1 1 1 1 9	1 1 1 1 1 1 1 8	1	1 1		1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5.193 1.856 1.064 1.976 0.484 10.664 14.760 1.872 0.571 1.255 0.389 0.308 0.510

		cgd2_2500	DNA polymerase epsilon subunit	1					1	0.332
		cgd2_2730 cgd2_3180	Po1 beta superfamily nucleotidyltransferase replication factor C subunit 5, putative	1	1	1			1 2	2.854 0.854
		cgd2_4080	RP-A, OB fold single strand binding protein	1					1	0.403
		cgd3_1450	replication factor C like AAA+ ATpase	1				1	1	0.503
		cgd3_2210	replication protein A1 large subunit	1				i l	1	0.386
		cgd3_2720	putative topoisomerase VIA	1				i l	1	0.432
		cgd3_3170 cgd3_3820	replication factor RFC3 AAA+ ATpase DNA LIGASE I	1				i l	1	0.344 0.324
		cgd3_390	RecQ SF II RNA helicase, DEXDc+HELICc	'			1	i l	1	5.986
		cgd3 4290	DNA polymerase alpha catalytic subunit	1			'	i l	1	0.527
		cgd4_3920	DinB/family X-type DNA polymerase	1				i l	1	0.429
		cgd4_780	DNA topoisomerase II	1				i l	1	0.430
		cgd4_970	DNA replication licensing factor MCM7 like AAA+ ATpase	1				i l	1	0.347
		cgd5_1180	DNA topoisomerase III, putative	1	4			i l	1	0.529
		cgd6_2390 cgd6_240	DNA topoisomerase III beta-1, putative DNA replication licensing factor MCM6-like AAA ATpase	1	'			i l		1.911 0.422
		cgd6_4410	DNA polymerase delta catalytic subunit. DNAQ-like 3'-5' exonuclease; RNAseH fold	1					1	0.421
		cgd6_4420	RecQ bloom helicase (RNA helicase+hrdc)		1			i l	1	1.573
		cgd7_1690	meiotic recombination protein DMC1-like protein	1				1	1	0.398
		cgd7_4690	RF-C paralog (Ctf18p) AAA+ ATpase	1	1			i l	2	0.900
		cgd8_1240	DNA polymerase epsilon catalytic subunit	1				i	1	0.362
		cgd8_1350 cgd8_1410	topoisomerase VIA/SpoII nuclease subunit, toprim domain DNA primase large subunit	1					1	0.392 0.430
		cgd8_1620	DNA polymerase delta2, inactive calcineurin like phosphatase subunit	1					1	0.430
		cgd8_2940	replication factor C like AAA ATpase	1					1	0.416
		cgd8_4950	RecQ4 SF II RNA helicase	1				i l	1	0.458
		cgd8_610	DNA replication repC1, AAA+ ATpase with a BRCT domain at the N-terminus	1					1	0.561
		cgd8_870	DNA dependent DNA polymerase alpha subunit, inactive calcineurin like phosphatase subunit	1					1	0.396
	DNA replication Total Other	cgd1_2680	HUSSY-3 like methyltransferase	29	4	1	1	1	35 1	0.770 174.010
	Other	cgd1_3420	conserved possible MUS81 endonuclease	1				'	1	0.329
		cgd1_3530 cgd2_2120	Gbp1/Gbp2p-like, putative single stranded G-strand telomeric DNA-binding protein high mobility group small protein		1				1	60.981 1.762
		cgd2_3070	high mobility group (HMG)-box					1	1	425.649
		cgd2_4190	DEXDc+HELICc, mus308/POLQ like SFII DNA helicase, no polymerase domain	1					1	0.383
		cgd2_4280 cgd5_3460	holiday junction resolvase, S1x1p, URI domain nuclease nucleotidase (5'-nucleotidase/2'-cyclic phosphodiesterase) of	1					1	0.463 0.650
		cgu5_5400	the calcineurin superfamily					1	'	0.000
		cgd6_1580	exonuclease i/din7p-like; xeroderma pigmentosum G N-region plus xeroderma pigmentosum G I-region plus HhH2 domain	1					1	0.390
		cgd7_1720	endonuclease III, putative	1				1	1	0.395
		cgd7_2140	flap endonuclease 1	1				i l	1	0.321
	Other Total	cgd8_340	exoribonuclease PH, putative	1		l				0.359
NA metabolism To		1			1		$\vdash$	2	12	55.47/
	otal			8	1 13	3	5	3	12	
nzyme	AA synthesis	cgd3_80	S-adenosylhomocysteinase EC 3.3.1.1		1 13	3	5	3		10.982
inzyme		cgd3_80 cgd5_4540	S-adenosylhomocysteinase EC 3.3.1.1 asparagine synthetase A (AsnA) like protein	8	13	3	5		12	10.982 0.657
inzyme		cgd5_4540 cgd5_4560	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin	8	13	3	5		12 70 1 1	10.982 0.657 2.114 0.433
inzyme		cgd5_4540 cgd5_4560 cgd6_3720	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase	8	1 13	3	5		12	10.982 0.657 2.114 0.437 4.051
inzyme		cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6	8 46 1	13	3	5		12 70 1 1	10.982 0.657 2.114 0.437 4.057 8.223
inzyme		cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein	8 46 1	1 13	3	1 1		12 70 1 1	10.982 0.657 2.114 0.437 4.057 8.223 0.567
inzyme		cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase	8 46 1	1 13	3	1 1		12 70 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465
inzyme	AA synthesis	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein	8 46 1	1 13	3	1 1 2		12 70 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465
inzyme		cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 13	3	1 1 1 2 2 1		12 70 1 1 1 2 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567
inzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 13	1	1 1 1		12 70 1 1 1 2 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646
inzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase  glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase tyrosyl-tRNA synthetase (tyrosyl-tRNA ligase; TyrRS). class-l	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1	1 1	1 1 2 1		12 70 1 1 1 2 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646 4.640 2.270
Enzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_3840	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase  glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase (tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1	1 1 1	5 1 1 1 2 2 1		12 70 1 1 1 2 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646 2.270 2.173
inzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_3840 cgd6_2970 cgd6_4400 cgd6_560	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase (tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding domain plus tRNA synthetase) alanyl-tRNA synthetase (with HxxxH domain)	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1	1 1 1	5 1 1 1 2 2 1		12 70 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646 4.640 2.270 2.173 0.311
Enzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_3840 cgd6_2970 cgd6_4400	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase (tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding domain plus tRNA synthetase)	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 13 1 1 1 1	1 1	5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		12 70 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646 4.640 2.270 2.173 0.311 1.651 45.100
inzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_33840 cgd6_2970 cgd6_4400 cgd6_560 cgd6_960	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase tyrosyl-tRNA synthetase (tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding domain plus tRNA synthetase) alanyl-tRNA synthetase (with HxxxH domain) cysteinyl-tRNA synthetase	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1	1 1 1	22 1		12 70 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.982 0.657 2.114 0.433 4.057 8.225 0.5667 0.466 0.567 2.347 24.644 4.644 2.270 2.173 0.311 1.655 45.100 5.735
inzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_3840 cgd6_2970 cgd6_4400 cgd6_560 cgd6_960 cgd7_1490	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase  glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase tyrosyl-tRNA synthetase (tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding domain plus tRNA synthetase) alanyl-tRNA synthetase (with HxxxH domain) cysteinyl-tRNA synthetase tryptophanyl-tRNA synthetase	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1	1 1 1	5 1 1 1 1 1 1 1 1		12 70 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.982 0.657 2.114 0.431 4.054 8.223 0.567 0.465 0.567 2.347 24.646 4.640 2.270 2.173 0.311 1.651 45.100 5.739 102.610
Enzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_3840 cgd6_2970 cgd6_4400 cgd6_560 cgd7_1490 cgd7_1540 cgd7_1710 cgd8_3100	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase  glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding domain plus tRNA synthetase) alanyl-tRNA synthetase (with HxxxH domain) cysteinyl-tRNA synthetase tryptophanyl-tRNA synthetase aspartate—tRNA ligase threonyl-tRNA synthetase (RNA binding domain TGS+HxxxH+tRNA synthetase) valyl-tRNA synthetase	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 13 1 1 1	1 1 1	2 1		12 70 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646 4.640 2.270 2.173 0.311 1.651 45.100 5.739 102.610 0.565
inzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_3840 cgd6_2970 cgd6_4400 cgd6_560 cgd7_1490 cgd7_1540 cgd7_1710 cgd8_3100 cgd8_3320	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase (tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding domain plus tRNA synthetase) alanyl-tRNA synthetase (with HxxxH domain) cysteinyl-tRNA synthetase tryptophanyl-tRNA synthetase aspartatetRNA ligase threonyl-tRNA synthetase (RNA binding domain TGS+HxxXH+tRNA synthetase) valyl-tRNA synthetase phenylalanyl-tRNA synthetase beta chain	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 13 1 1 1	1 1 1	2 1		12 70 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	55.474 10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646 4.640 2.270 2.173 0.311 1.651 45.100 5.739 102.610 0.565
inzyme	AA synthesis  AA synthesis Total	cgd5_4540 cgd5_4560 cgd6_3720 cgd7_2650 cgd7_4940 cgd8_2580 cgd8_2610 cgd1_2130 cgd3_3320 cgd3_3840 cgd6_2970 cgd6_4400 cgd6_560 cgd7_1490 cgd7_1540 cgd7_1710 cgd8_3100	asparagine synthetase A (AsnA) like protein tryptophan synthase trpB of possible bacterial origin pyrroline-5-carboxylate reductase s-adenosylmethionine synthetase (SAM) EC 2.5.1.6 gamma-glutamyl phosphate reductase family protein mitochondrial serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase cytosolic serine hydroxymethyl transferase  glutaminyl-tRNA synthetase, of predicted bacterial origin putative phenylalanyl-tRNA synthetase isoleucine-tRNA synthetase tyrosyl-tRNA ligase; TyrRS). class-laaRS proline-tRNA synthetase; class II aaRS (ybak RNA binding domain plus tRNA synthetase) alanyl-tRNA synthetase (with HxxxH domain) cysteinyl-tRNA synthetase tryptophanyl-tRNA synthetase aspartate—tRNA ligase threonyl-tRNA synthetase (RNA binding domain TGS+HxxxH+tRNA synthetase) valyl-tRNA synthetase	8 46 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 13 1 1 1	1 1 1	2 1		12 70 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.982 0.657 2.114 0.431 4.051 8.223 0.567 0.465 0.567 2.347 24.646 4.640 2.270 2.173 0.311 1.651 45.100 5.739 102.610 0.565

	cgd8_4720 cgd8_790	seryl-tRNA synthetase, cytoplasmic glutamatetRNA ligase	1		1			1	3.620 0.357
AA-tRNA synthesis To	otal		5	3	4	3	2	17	12.440
Energy	cgd1_1710	phosphoglycerate mutase	1					1	0.320
	cgd1_2040	pyruvate kinase			1			1	4.077
	cgd1_3020	fructose-1,6-bisphosphate aldolase				1		1	16.932
	cgd1_3040	triosephosphate isomerase			1			1	2.966
	cgd2_210	glycerol-3-phosphate dehydrogenase		1				1	1.886
	cgd2_2130	pyrophosphate-dependent phosphofructokinase			1			1	3.315
	cgd2_2340	R1 like alpha-glucan water dikinase			1			1	5.585
	cgd2_3260	phosphoglucomutase, tandemly duplicated gene					1	1	35.506
	cgd2 3270	phosphoglucomutase, tandemly duplicated gene					1	1	38.373
	cgd3_1400	pyrophosphate-dependent 6-phosphofructokinase	1					1	0.583
	cgd3_1580	alpha glucosidase-like faimly 31 glycosyl hydrolases			1			1	2.422
	cgd4_690	pyruvate:ferredoxin oxidoreductase/NADPH-cytochrome P450		1				1	1.539
	-9	reductase PNO						· I	
	cgd5_1960	enolase (2-phosphoglycerate dehydratase)					1	1	323.176
	cgd5_2910	alpha amylase	1	1				2	1.076
	cgd5_70	phosphoenolpyruvate carboxylase		1				1	1.637
	cgd5_750	Mdh; malate dehydrogenase (oxaloacetate-				1		1	9.706
	-9	decarboxylating)(NADP+)						· I	
	cgd6_2450	glycogen phosphorylase				1		1	12.787
	cgd6_3280	glycogen branching enzyme (1,4-alpha-glucan branching		1				1	1.291
	-3	enzyme)						· I	
	cgd6_3790	glyceraldehyde 3-phosphate dehydrogenase					1	1	143.725
	cgd6_3800	hexokinase			1			1	3.319
	cgd6_4330	phosphoglycerate mutase family	1					1	0.427
	cgd6_4900	acylphosphatase, putative					1	1	65.07
	cgd6_880	Gdb1p; glycogen debranching enzyme			1		•	1	2.503
	1					1			
	cgd7_3120	pyruvate decarboxylase							13.325
	cgd7_4270	glycolytic phosphoglycerate mutase				1		1	15.288
	cgd7_470	malate dehydrogenase, adjacent gene encodes predicted				1		1	10.334
		lactate dehydrogenase					4	اد	0.004.000
	cgd7_480	lactate dehydrogenase, adjacent gene encodes predicted					1	1	3,064.620
	oad9 1720	malate dehydrogenase acetaldehyde reductase plus alcohol dehydrogenase (AdhE) of				1		1	6.279
	cgd8_1720	possible bacterial origin				'		'	0.278
Energy Total		possible bacterial origin	4	5	7	7	6	29	130.660
General	cgd1 1080	alpha beta hydrolase	-	1		-	_	1	1.296
Conordi	cgd1_1100	alpha beta hydrolase with 5 transmembrane domains	1					1	0.547
		1 '	'		1			1	
	cgd1_1730	haloacid dehalogenase family-like horizontal transfer into			- 1			'	4.116
	cgd1_2750	apicomplexans, signal peptide AAA superfamily ATpase	1					1	0.384
	cgd1_2730	short chain dehydrogenase/reductase of the rossmann fold,		4					2.273
	Cgu1_200	signal peptide		'				'	2.27
	cgd1_3390	katanin p60/fidgetin family AAA ATpase		1				1	2.028
	cgd1_3610	secreted protein of the alpha beta hydrolase superfamily, signal				1		1	8.260
	C901_5010	peptide				'		'	0.200
	cgd1 3730	glucosamine-fructose-6-phosphate aminotransferase	1					1	0.462
	cgd1_990	pyridine nucleotide/ NAD(P) transhydrogenase alpha plus beta	1					1	0.432
	ogu	subunits, duplicated gene, 12 transmembrane domain	·						002
	cgd2_1120	putative molybdopterin synthase sulphurylase				1		1	10.116
	cgd2_1190	methylase		1				1	2.094
	cgd2_1130	Ynr053p-like, Yjeg GTpase		, i		1		1	23.79
			1					1	0.439
	cgd2_380	COG0237: dephospho-CoA kinase						4	
	cgd2_3880	possible AAA domain containing protein	1					1	0.33
	cgd3_1360	methylase	1					1	0.510
	cgd3_2050	putative prolyl 4-hydroxylase alpha subunit homolog, 2-	1					1	0.300
	10.0000	oxoglutarate-dependent dioxygenase							47.44
	cgd3_2290	possible domain AAA, ATpase family				1		1	17.443
	cgd3_330	scully CG7113-PA, putative					1	1	356.414
	cgd3_3910	prolyl 4-hydroxylase alpha subunit				1		1	14.869
	cgd3_990	CG6144-like AlkB	1					1	0.303
	cgd4_1130	PhnP like hydrolase of the metallobetalactamase fold	1					1	0.29
	cgd4_1940	putative nucleoside-diphosphate kinase				1		1	16.18
	cgd4_1960	ThiF/moeB family			1			1	2.540
		putative phosphopantothenoylcysteine synthetase	1					1	0.434
	cad4 2250	I First Francisco Joseph Syntholic Control of the C			1			1	4.520
	cgd4_2250	oxidoreductase, short-chain dehydrogenase family, nutative							
	cgd4_2270	oxidoreductase, short-chain dehydrogenase family, putative		4				4	1 / [
	cgd4_2270 cgd4_2550	putative farnesyl pyrophosphate synthase		1				1	
	cgd4_2270 cgd4_2550 cgd4_430	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase		1 1				1	1.14
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase	1	1				1 1 1	1.14 0.36
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320 cgd5_1170	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase CPSF metallobeta-lactamase	1	1				1 1 1	1.14 0.366 0.342
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase	1	1			1	1 1 1 1	1.147 0.366 0.342
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320 cgd5_1170	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase CPSF metallobeta-lactamase	1 1	1			1	1 1 1 1 1	1.147 0.366 0.342 54.188
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320 cgd5_1170 cgd5_2010	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase CPSF metallobeta-lactamase nuclear VCP like protein with 2 AAA ATpase domains conserved possible esterase of the beta-lactamase family, of possible plant or bacterial origin, possible transmembrane		1			1	1 1 1 1 1	1.14 0.366 0.342 54.186
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320 cgd5_1170 cgd5_2010 cgd5_2410	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase CPSF metallobeta-lactamase nuclear VCP like protein with 2 AAA ATpase domains conserved possible esterase of the beta-lactamase family, of possible plant or bacterial origin, possible transmembrane domain within N terminal region	1	1			1	1	1.14 0.366 0.342 54.186 0.40
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320 cgd5_1170 cgd5_2010	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase CPSF metallobeta-lactamase nuclear VCP like protein with 2 AAA ATpase domains conserved possible esterase of the beta-lactamase family, of possible plant or bacterial origin, possible transmembrane domain within N terminal region predicted mannitol dehydrogenase; zinc dependent alcohol		1			1	1 1 1 1 1 1	1.14 0.366 0.342 54.186 0.40
	cgd4_2270 cgd4_2550 cgd4_430 cgd4_4320 cgd5_1170 cgd5_2010 cgd5_2410	putative farnesyl pyrophosphate synthase ORC5 like AAA+ ATpase ORC/CDC6 like AAA+ ATpase CPSF metallobeta-lactamase nuclear VCP like protein with 2 AAA ATpase domains conserved possible esterase of the beta-lactamase family, of possible plant or bacterial origin, possible transmembrane domain within N terminal region	1	1			1	1	1.750 1.147 0.366 0.342 54.188 0.407 0.404

		1						. 1	
	cgd5_3090	N-acetyltransferase subunit ARD1	1					1	0.350
	cgd5_310	putative polyphosphate synthetase VTC4, 3 transmembrane domains at C-terminus				1		1	7.600
	cgd5_3110	MDN1, midasin	1					1	0.302
	cgd5_3110	secreted protein of the alpha beta hydrolase superfamily					1	1	29.019
	cgd5_4330	conserved methylase				1	'	1	14.596
	cgd5_460	possible alpha beta hydrolase	1					<u>'</u>	0.364
	1	MRP like MinD family ATpase		4				<u>'</u>	1.579
	cgd5_900	acetyltransferase, GNAT family	1	' I					0.338
	cgd6_1800		- 1	4					1.446
	cgd6_2820	2 SAM dependent methyltransferase; S-adenosyl-L-methionine- dependent methyltransferases + spermidine synthase (SAM						'	1.440
		dependent methyltranferase)							
	cgd6_4020	phosphdiesterase, putative	1					1	0.329
	cgd6_4270	MinD type ATpase				1		1	8.560
	cgd6_4380	phosphatase subunit gene g4-1; of possible animal origin; EF-	1			-		1	0.390
	oguo_1000	hand, calcium binding domains							0.000
	cgd6_550	Pch2p like AAA ATpase	1					1	0.267
	cgd7_1410	AAA domain containing protein				1		1	9.647
	cgd7_160	putative methyltransferase-related					1	1	44.371
	cgd7_1640	SRP54. signal recognition 54. GTpase.				1		1	19.559
	cgd7_2310	ORC/CDC6 like AAA ATpase	1					1	0.307
	cgd7_2970	possible acyltransferase	1					1	0.438
	cgd7_3390	secreted alpha beta hydrolyse, signal peptide, secreted patatin				1		1	13.972
	ogucccc	like esterase (ralstonia best hits)				·		-	
	cgd7_3730	long chain fatty acyl diphosphate synthase [Trans-Isoprenyl	1					1	0.346
		Diphosphate Synthase]							
	cgd7_4590	Mth1. SpoU superfamily - SPOUT methylase				1		1	15.971
	cgd7_5250	methyltransfer with N-terminal ankyrin repeats				1		1	10.963
	cgd8_1700	NAD dependent dehydrogenase of possible bacterial origin	1					1	0.442
	cgd8_1970	NAD kinase involved in polyphosphate metabolism	1					1	0.541
	cgd8_2330	pyridine nucleotide/ NAD(P) transhydrogenase alpha plus beta				1		1	6.516
		subunits, duplicated gene, possible signal peptide plus 12							
		transmembrane regions							
	cgd8_2410	Sey1p like P-loop GTpase of the RHD3 subfamily with a	1					1	0.373
	cgd8_2670	transmembrane domain near C-terminus secreted glucose methanol choline like oxidoreductase of the			1			1	3.668
	cgu6_2670	FAD dependent oxidoreductase like fold, signal peptide						'	3.000
	cgd8_2700	phenol 2-monooxygenase like FAD dependent oxidoreductase	1					1	0.349
	ogus	of plant origin in apicomplexans	·					-	0.0.0
	cgd8_3140	MRP like MinD family ATpase of the SIMIBI class of P-loop		1				1	1.958
		GTpases							
	cgd8_3290	secreted bacterial type DHHB/UbiG like methyltransferase		1				1	1.762
		involved in ubiquinone/menaquinone biosynthesis, signal							
	200	peptide				4		4	7 001
	cgd8_380	possible oxidase or dehydrogenase	4						7.001
	cgd8_3880	secreted alpha beta hydrolase family protein, signal peptide, duplicated adjacent gene	1					'	0.452
	cgd8_4130	secreted hydrolase superfamily, signal peptide	1					1	0.365
	cgd8_4230	FAD/NAD(P)-binding rossman fold oxidoreductase fused to a	1					1	0.529
	cguo_4200	glucose-methanol-choline (GMC) oxidoreductase domain	'					- 1	0.023
	cgd8 5260	Srp101p GTpase. signal recognition particle receptor alpha	1					1	0.361
	" -	subunit							
	cgd8_590	alpha/beta hydrolase superfamily protein	1					1	0.469
	cgd8_600	secrted alpha/beta hydrolase superfamiy protein					1	1	114.509
General Total			34	10	4	17	5	70	12.214
Glycosylation	cgd1_230	ALG-2 like alpha-1,3 mannosyltransferase	1					1	0.356
	cgd2_1650	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	1					1	0.440
		beta subunit (Wbp1p)							0.000
	cgd3_3590	dolichyl-phosphate-mannose-glycolipid alpha-	1					1	0.290
	cgd4_2990	mannosyltransferase involved in GPI anchor biosynthesis glycosyl transferase				1		1	10.754
	cgd4_23120	ALG6-like dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-	1					<u>'</u>	0.389
	09u0120	alucosyltransferase						'	0.508
	cgd5_2040	dolichol phosphate mannose synthase, putative		1				1	1.321
	cgd5_2240	DPAGT1 like N-acetylglucosamine-1-phosphate transferase				1		1	11.320
	cgd5_2590	Alg5 like dolichyl-phosphate beta-glucosyltransferase	1					1	0.487
	cgd5_3140	LPS glycosyltransferase of possible cyanobacterial origin			1			1	4.376
	cgd5_3260	secreted lipopolysaccharide sugar transferase like family 8	1		-			1	0.332
	-9	glycosyltransferase							
	cgd5_690	extracellular protein with a ricin domain and a family 2		1				1	1.863
		glycosyltransferase domain							
	cgd6_1450	secreted protein with signal peptide, fringe-like			1			1	2.714
		glycosyltransferase domain and a WcaK like glycosyltransferase							
	cade 2040	domain oligosaccharyl transferase STT3 protein				4		1	20.029
	cgd6_2040		1			- 1		1	20.928
	cgd6_5070	ribophorin I -like, putative dolichyl-diphosphooligosaccharide- protein glycosyltransferase 67kDa subunit precursor, signal						- 1	0.375
		peptide plus transmembrane domain at C-terminus							
	cgd7_1810	ALG1 like beta-1,4 mannosyltransferase with possible signal	1					1	0.455
		peptide							
	cgd7_4440	family 2 glycosyl transferase, possible fragment	1					1	0.354
	cgd7_4930	secreted glycosyltransferase, possible transmembrane domain			1			1	3.535
		near C-terminus							

Glycosylation Total		signal peptide	10	2	3	3		18	
Lipid	cgd1 1110	phosphatidylserine synthase I (serine-exchange enzyme I), 9x	10	1	3			10	
1	1-32/110	transmembrane domains							
	cgd1_320	oxysterol binding protein			1			1	
	cgd1 3290	carboxylesterase, putative				1		1	
	cgd1_3380	phosphatidylinositol-glycan-class c, pigC, 8x transmembrane	1						
	cgu 1_3300	domains	'					'	
	cgd1_3720	PIG-M mannosyltransferase,8 transmembrane domain	1					1	
	cgd2_1090	diacylglycerol acyltransferase 1	1						
	cgd2_1200	steroid reductase like intregral membrane protein with 4x	1						
	Cgu2_1200	transmembrane domains and an ubiquitin domain at its N-	'					'	
		terminus							
	cgd2_1340	possible phosphatidylinositol 3- and 4-kinase family protein		1				1	
	cgd2 2890	putative biotin-(acetyl-CoA carboxylase) ligase	1						
		phosphatidylinositol N-acetylglucosaminyltransferase subunit	'			1			
	cgd2_840	PIG-P, involved in GPI anchor biosynthesis,						'	
		multitransmembrane domain							
	cgd3_2030	putative choline kinase	1					1	
	cgd3_2100	l'				4			
		phosphatidylserine decarboxylase, putative		4					
	cgd3_2180	type I fatty acid synthase		1				1	
	cgd3_2370	steroid dehydrogenase kik-i, putative	1					1	
	cgd3_2630	diacylglycerol kinase	1					1	
	cgd3_2870	putative acyl-CoA synthetases	1					1	
	cgd3_2940	probable	1					1	
		phosphatidylserine/phosphatidylglycerophosphate/cardiolipin							
		synthase, 2x SMART_PLDc domains, possible bacterial origin							
	cgd3_320	N-myristoyltransferase	1					1	
	cgd3_640	acyl-CoA synthetase				1		1	
	cgd4_2100	PIG-A like N-acetylglucosaminyl-phosphatidylinositol	1					1	
	331_2100	biosynthetic protein	, i					'	
	cgd4_2560	phospholipase C, delta 1 ortholog with 2 EF hands plus				1		1	
	322000	phospholipase C domain plus C2 domain							
	cgd4 2580	oxysterol binding protein 1A-like pleckstrin homology (PH)	1					1	
	-5	domain containing protein						•	
	cgd4_2590	glycerophosphodiester phosphodiesterase-like protein	1					1	
	cgd4_2790	putative ethanolaminephosphotransferase (ETHPT) 9	1					1	
		transmembrane domain protein involved in lipid metabolism						·	
	cgd4_2900	polyketide synthase			1			1	
	cgd4_3400	putative long chain fatty acyl CoA synthetase having a signal					1	1	6
	cgu+_0+00	peptide						'	`
	cgd5_1850	GPI1/PIG-Q like N-acetylglucosaminyl-phosphatidylinositol				1		1	
	cgu3_1030	transferase involved in GIP anchor biosynthesis				·		'	
	cgd5 2300	DAD1/Ost2 like dolichyl-diphospho-oligosaccharide-protein				1		1	
	cguo_2000	glycosyltransferase, epsilon unit						'	
	cgd5_3070	acetylcholinesterase'secreted acetylcholinesterase of the	1					1	
	loguo_co/ c	alpha/beta hydrolase superfamily'	•						
	cgd5_320	carboxylesterase , lysophospholipase, signal peptide				1		1	
	cgd5_720	choline/ethanolamine kinase family protein		1					
		SCT1/Gpt2p-like glycerol-3-phosphate acyltransferase signal	4						
	cgd6_1270		1					'	
	ande 2200	peptide plus 3 transmembrane domain	4					ا ا	
	cgd6_2290	sphingomyelinase C precursor	1					1	
	cgd6_3240	Gpi16p/PIG-T/SPBC1604.15 family; glycosyl phosphatidyl	1					1	
		inositol 16 signal peptide and transmembrane domain or GPI							
	amslo 0000	anchor							
	cgd6_3390	membrane associated protein with 2 transmembrane domains	1					1	
		at the N-terminus and a phosphatidylinositol 4-kinase domain at							
	oad7 2050	the C-terminus	1					1	
	cgd7_2950	phospholipid cytidyltransferase HIGH family	1						
	cgd7_3480	cytidylyltransferase (HIGH family) exon-1			1			1	
	cgd7_450	putative cytidine diphosphate-diacylglycerol synthase; integral					1	1	2
		membrane protein with 7 or more transmembrane domains							
	cgd7_700	N-acetylglucosaminyl-phosphatidylinositolde-N-acetylase	1					1	
	cgd8_1150	choline-phosphate cytidylyltransferase					1	1	18
	cgd8_2260	phosphatidylinositol glycan class O, integral membrane protein	1					1	
		with signal peptide sequence and 12 or more transmembrane							
		domains							
	cgd8_2390	diacylglycerol kinase	1					1	
	cgd8_3280	phosphatidylinositol-4-phosphate 5-kinase, putative				1		1	
	cgd8_4500	phosphatidylinositol 4-kinase		1					
		i i i		- 1					
	cgd8_4630	7 pass integral membrane proteinwith FLHWFHH motif shared				1		1	
	and0 500	with fatty-acyl elongase							
	cgd8_560	CDP-diacylglycerolinositol 3-phosphatidyltransferase isoform	1					1	
Linid Total		1; phosphatidylinositol synthase; PtdIns synthase; PI synthase	25	E	0	10	2	46	
Lipid Total	and 4000	Funda like umail abanak - ikikf		5	3	10	3	46	
Nucleotide	cgd1_1900	Fur1p like uracil phosphoribosyltransferase	1					1	
	cgd1_3140	P-loop nucleotide (UMP) kinase					1	1	;
	cgd2_1270	membrane associated adenylyl cyclase with 6 transmembrane	1					1	
		regions and an adenylyl cyclase domain							
	cgd2_1630	cytidine and deoxycytidylate deaminase family, putative	1					1	
		***					1		
	cgd2_2780	dCMP deaminase, Dcd1p like	1					1	

	cgd4_1890	adenosine monophosphate deaminase 2			1			1	4.073
	cgd4_4460	dihydrofolate reductase-thymidylate synthase	1					1	0.369
	cgd5_1290	membrane associated adenyl cyclase with 2 transmembrane	1					1	0.555
		regions and an adenylyl cyclase domain							
	cgd5_1470	signal peptide containing protein having a NDK (nucleoside-					1	1	1,562.515
		diphosphate kinase) domain							
	cgd5_1710	CTP synthetase (UTP-ammonia lyase)					1	1	89.058
	cgd5_3360	adenylate kinase (AMP - ADP; dAMP - dADP)					1	1	149.775
	cgd5_3630	thymidylate kinase	1					1	0.419
	cgd5_4440	thymidine kinase of likely bacterial origin		1				1	1.411
	1	1 1		1					
	cgd5_4520	GMP synthase		1				1	2.203
	cgd6_1570	apyrase; calcium-activated nucleotidase SCAN-1-like protein;	1					1	0.414
		signal peptide							
	cgd6_1950	ribonucleotide-diphosphate reductase large chain; RIR1; c-		1				1	1.654
		terminal PFL-like glycyl radical enzymes-like fold							
	cgd6_20	inosine-5-monophosphate dehydrogenase					1	1	51.213
	cgd6_500	membrane associated HD superfamily cyclic nucleotide	1					1	0.413
		phosphodiesterase domain containing protein							
	cgd6_690	ribonucleotide reductase small subunit, duplicated adjacent	1					1	0.503
	1 -	gene							
	cgd6_700	ribonucleotide reductase small subunit			1			1	3.098
	cgd7_2190	putative guanylate kinase		1				1	2.072
	cgd7_5170	deoxyuridinetriphosphatase, possible bacterial origin					1	1	170.965
	1	adenosine kinase like ribokinase (Adenosine - AMP)		4				1	2.053
	cgd8_2370	1	,						
	cgd8_2810	uridine kinase like P-loop NTpase	1					1	0.368
Nucleotide Total			11	5	2	1	6	25	83.671
Peptidase	cgd1_1680	insulinase like protease, signal peptide	1					1	0.588
	cgd1_3690	aspartyl (acid) protease, putative		1				1	2.119
	cgd1_370	carboxypeptidase probably secreted, signal peptide	1					1	0.391
	cgd1_3840	insulinase-like peptidase, telomeric gene			1			1	3.519
	1				- '	4		1	
	cgd2_2480	methionine aminopeptidase, type II, putative , an1 domain				- 1		1	21.559
	cgd2_2760	peptidase'insulinase-like peptidase'	1					1	0.422
	cgd2_3320	secreted papain like protease, signal peptide	1					1	0.518
	cgd2_4270	secreted insulinase-like peptidase			1			1	2.496
	cgd2_710	predicted protease	1					1	0.508
	cgd2_920	peptidase'insulinase-like peptidase'	1					1	0.507
	1	peptidase'insulinase-like peptidase'	1					1	0.447
	cgd2_930	1, ,						- :1	
	cgd3_2160	SprT like metalloprotease	1					1	0.491
	cgd3_2390	proliferation-associated protein 2G4 metalloprotease,				1		1	8.596
		creatinase/aminopeptidase fold							
	cgd3_2920	possible peptidase family C54	1					1	0.314
	cgd3_3610	possible aspartyl aminopeptidase	1					1	0.342
	cgd3_4180	secreted insulinase like peptidase				1		1	11.207
	cgd3_4190	secreted insulinase like peptidase					1	1	99.822
	cgd3 4200	secreted insulinase like peptidase, signal peptide		1				1	2.078
	" -			4					
	cgd3_4210	secreted insulinase like peptidase, signal peptide		- 1				- !	1.548
	cgd3_4220	secreted insulinase like peptidase, signal peptide					1	1	32.433
	cgd3_4240	insulinase like peptidase			1			1	2.850
	cgd3_4250	secreted insulinase like peptidase, signal peptide				1		1	14.086
	cgd3 4260	peptidase'insulinase like peptidase'				1		1	25.027
	cgd3_4270	peptidase'insulinase like peptidase'				1		1	18.424
	cgd3_4280	secreted insulinase like peptidase, signal peptide			1			1	3.100
	1				4			,	
	cgd3_680	cathepsin like thiol protease possibly membrane associated,			T			Т	4.611
	and4 0440	putative			4				4.000
	cgd4_2110	preprocathepsin c precursor, putative			Т			1	4.293
	cgd4_2190	membrane associated aspartyl protease with a transmembrane	1					1	0.390
	and4 0040	domain at the C-terminus			4				0.050
	cgd4_2910	aminopeptidase			1			1	3.058
	cgd4_4120	metacaspase-like protein	1					1	0.586
	cgd4_4160	possible carboxypeptidase	1					1	0.322
	cgd4_4240	insulinase like peptidase			1			1	4.114
	cgd4_4430	OTU like cysteine protease				1		1	6.117
	cgd5_2810	ULP1 like chllamydin domain containing protease				1		1	6.714
	1					4		1	19.932
	cgd6_2750	cysteine protease, putative		4				,	
	cgd6_3550	endopeptidase, putative		1				1	1.348
	cgd6_3820	membrane bound aspartyl proteinase with a signal peptide plus		1				1	1.784
		transmembrane domain							
	cgd6_4880	cryptopain - cysteine proteinase secreted, possible	1					1	0.538
	10 1005	transmembrane domain near N-terminus							. =05
	cgd6_4990	predicted peptidase of the alpha/beta-hydrolase fold		1				1	1.502
	cgd6_5510	telomeric insulinase-like protease with signal peptide	1					1	0.260
	cgd6_5520	peptidase'insulinase like peptidase'	1					1	0.301
	cgd6_660	secreted pepsinogen like aspartyl protease having a signal	1					1	0.491
	5 - 2 - 2 - 2	peptide							2
	cgd6_900	SPAC25H1.04/CG16979-cterm -like; cysteine protease	1					1	0.304
	cgd7_140	SprT family metallopeptidase	, i		1			1	2.677
				4	,				
	cgd7_2850	cathepsin like thiol protease possibly membrane associated						1	1.401
	cgd7_2850 cgd7_3020	rhomboid family membrane associated protease, 7 transmembrane domain		·			1	1	169.568

	cgd8_2720 cgd8_3430	insulinase like metalloprotease zincin/aminopeptidase N like metalloprotease	- 1			1		1	0.3 9.0
Peptidase Total	<u> </u>		19	7	9	10	3	48	10.2
Protein folding	cgd1_800	protein disulfide isomerase, signal peptide plus possible ER	1					1	0.3
	cgd1_870	retention motif cyclophilin like peptidyl-prolyl cis-trans isomerase, signal					1	1	42.2
	sgar_ara	peptide						-	
	cgd2_1660	cyclophilin-like protein, putative	1					1	0.3
	cgd2_4120	20k cyclophilin, putative		1				1	1.4
	cgd6_120	disulfide-isomerase, signal peptide plus ER retention motif, putative ER protein		1				1	1.5
	cgd6_2690	macrophage infectivity potentiator (MIP);FKBP peptidyl-prolyl cis-trans isomerase-like fold, signal peptide + ER retention motif		1				1	1.5
	cgd6_3640	protein disulfide isomerase ; secreted protein with thioredoxin,	1					1	0.3
	cgd7_210	signal peptide plus ER retention motif fkbp					1	1	146.0
	cgd7_210 cgd7_5100	protein disulfide isomerase, signal peptide plus ER retention					1	1	31.4
		motif						-	
Dontoin folding Total	cgd8_2350	cyclophilin-RNA interacting protein, putative	2	1			0	1	1.6
Protein folding Total Protein kinase	cgd1 1220	S/T protein kinase	3	4			3	10	22.7
Totelli Killase	cgd1_1220	Ser/Thr protein kinase	1	'					0.4
	cgd1_2850	protein kinase domain		1				1	2.0
	cgd1 810	protein kinase	1	·				1	0.6
	cgd1_890	protein kinase domain				1		1	7.
	cgd2_1060	calcium/calmodulin dependent protein kinase with a kinas					1	1	32.
		domain and 4 calmodulin-like EF hands							02.
	cgd2_1300	calcium/calmodulin dependent protein kinase with a kinase		1				1	1.9
		domain and 4 calmodulin like EF hands							_
	cgd2_1880	protein kinase, putative		1				1	2.
	cgd2_1960	mitogen-activated protein kinase 1, serine/threonine protein			1			1	4.
	cgd2_3190	kinase, putative protein kinase, putative	1					1	0.
	cgd2_3340	Ser/Thr protein kinase	'	1				1	1.
	cgd2_3660	serine protease, subtilase family, signal peptide, putative	1					1	0.
	cgd2_3890	Ser/Thr protein kinase	1					1	0.
	cgd2_4340	mitogen-activated protein kinase 2, putative	'		1				3.
	cgd2_4340 cgd3_1810	casein kinase I			1				5. 5.
	cgd3_1850	putative casein kinase II regulatory subunit; besthit Pf 23508244					1	1	39.
	cgu3_1030	putative caselli kiliase il regulatory subullit, bestilit i i 25500244					'	'	55.
	cgd3_2900	protein Roco7, putative	1					1	0.
	cgd3_3030	MAPK, putative [Mitogen-activated protein kinase]	1					1	0.
	cgd3_3040	protein kinase, cAMP-dependent, catalytic chain					1	1	27.
	cgd3_3180	Ser/Thr protein kinase		1				1	1.
	cgd3_3230	Ser/Thr protein kinase				1		1	6.
	cgd3_3670	putative protein kinase CK2 regulatory subunit CK2B1				1		1	6.
	cgd3_40	casein kinase I	1					1	0.
	cgd3_920	calmodulin-domain protein kinase 1, putative					1	1	25.
	cgd4 290	putative protein phosphatase 2A regulatory B subunit				1		1	5.
	cgd4_3710	Ser/Thr protein kinase	1					1	0.
	cgd4 990	Ser/Thr protein kinase	1					1	0.
	cgd5_2270	maternal embryonic leucine zipper kinase					1	1	131.
	cgd5_250	serine/threonine kinase-1				1		1	12.
	cgd5_3180	Ser/Thr protein kinase	1					1	0.
	cgd5_4390	Ser/Thr protein kinase	1					1	0.
	cgd5_820	calcium/calmodulin dependent protein kinase with a kinase			1			1	4.
	5.1_520	domain and 4 calmodulin like EF hands							
	cgd6_3400	protein kinase			1			1	3.
	cgd6_4840	serine protease, subtilase family, signal peptide	1					1	0.
	cgd6_4960	serine/threonine-protein kinase, putative		1				1	1.
	cgd6_5060	Ser/Thr protein kinase			1			1	2.
	cgd6_520	Ser/Thr protein kinase			1			1	5.
	cgd6_5240	protein kinase	1					1	0.
	cgd6_620	casein kinase II, alpha subunit, putative					1	1	74.
	cgd7_1190	Ser/Thr protein kinase					1	1	33.
	cgd7_120	cAMP-dependent protein kinase regulatory subunit					1	1	50.
	cgd7_1260	calcium/calmodulin dependent protein kinase with an EF hand N terminal to the kinase domain and 4 calmodulin like EF hands at						1	0.
	cgd7_1320	the C-terminus casein kinase II, alpha subunit, putative			1			1	2.
	cgd7_1320 cgd7_1330	protein kinase iii, aipria suburiii, putative	1				1	2	22.
	cgu/_1330	terminus	'				1	2	22.
	cgd7_1840	calcium/calmodulin-dependent protein kinase with a kinase				1		1	7.
	3	domain and 4 calmodulin like EF hands							
	cgd7_2000	Bub1p related protein kinase	1					1	0.
	cgd7_2670	serine/threonine protein phosphatase, putative					1	1	173.
	cgd7_3050	protein kinase			1			1	3.
	cgd7_3430	protein kinase					1	1	49.
	cgd7_3890	calcium-dependent protein kinase 7 (CDPK)(CPK7)	1					1	0.

	cgd7_40	calcium/calmodulin-dependent protein kinase with a kinase	1					1	0.525
	oad7 440	domain and 2 calmodulin-like EF hands RIO-like kinase domain; N-terminal region conserved					1	1	126.665
	cgd7_440	· · · · · · · · · · · · · · · · · · ·	- 1				- 1	<u>'</u>	
	cgd7_590	Ser/Thr protein kinase	1						0.386
	cgd8_1230	proteine kinase protein kinase	- 1	4					0.354 2.308
	cgd8_1660	·	1	'				<u>'</u>	0.381
	cgd8_2430	Ser/Thr protein kinase with MORN repeats at the N-terminus and a sterile alpha motif (SAM domain						'	0.361
	cgd8_3070	serine/threonine protein kinase KKIALRE			1			1	3.836
	cgd8_5120	protein kinase NPK2	1					1	0.349
	cgd8_5320	Ser/Thr protein kinase				1		1	7.371
	cgd8_750	cyclic nucleotide (cGMP)-dependent protein kinase with 3 cNMP	1					1	0.389
	1311_11	binding domains and a Ser/Thr kinase domain							
Protein kinase Total			24	8	10	7	12	61	15.179
Protein modification	cgd1_1980	protein geranyl-geranyltransferase beta subunit			1			1	4.136
	cgd1_2660	n-terminal acetyltransferase complex ard1			1			1	3.864
	cgd1_730	glutamine cyclotransferase, predicted bacterial/plant origin	1					1	0.399
	cgd1_820	DHHC family palmitoyl transferases with 4 transmembrane	1					1	0.368
	10 4400	domains							0.070
	cgd2_1460	SUMO-1 activating enzyme subunit 2, putative	1					1	0.373
	cgd2_2190	DHHC family palmitoyl transferase fused to a KOW domain, signal peptide				1		1	6.329
	cgd2_30	cysteine desulfurase/selenocysteine lyase-like PLP dependent			1			1	4.312
	loguz_co	transferase superfamily protein						· I	1.012
	cgd3_2350	possible RAB geranylgeranyl transferase, b subunit1,			1			1	4.366
		pernyltransferase (prenyltransferase)							
	cgd3_4310	sexual stage-specific protein kinase		1				1	1.666
	cgd4_2080	DHHC family palmitoyl transferase with 4 transmembrane	1					1	0.439
		regions					4	ا،	04.054
	cgd5_3770	putative arginine N-methyltransferase	- 1				1	1	34.651
	cgd5_430	70 kDa peptidylprolyl isomerase, putative	1					1	0.555
	cgd6_2510	farnesyltransferase	1	,				1	0.352
	cgd7_1560	DHHC family palmitoyl transferase with a signal peptide and 4 transmembrane domains		1				1	1.961
	cgd8_1490	bacterial type serine/tyrosine phosphatase				1		1	13.749
	cgd8_2010	span like Riml family protein amino acetyltransferase		1				1	1.395
	cgd8_4730	DHHC family palmitoyl transferase with a signal peptide and 4		1				1	1.486
		transmembrane domains		·					
	cgd8_4760	arginine n-methyltransferase					1	1	29.544
Protein modification T	otal		6	4	4	2	2	18	6.108
Protein phosphatase	cgd1_2120	protein phosphatase regulator like heat repeats		1				1	1.665
	cgd1_2360	protein phosphatase 4 (formerly X), catalytic subunit; Protein					1	1	53.151
	14 0470	phosphatase 4, catalytic subunit							0.440
	cgd1_2470	phosphotyrosyl phosphatase activator protein-related	1				4	1	0.443
	cgd1_760	dual specificity phosphatase	- 4				1	1	86.436
	cgd2_1640	calcineurin like phosphatase with 3x Efhand domains at N-terminus						'	0.441
	cgd2_2960	phosphoprotein phosphatase related, putative			1			1	5.836
	cgd2 640	possible conserved acid phosphatase		1				1	1.981
	cgd3_1470	dual specificity phosphatase	1	·				1	0.423
	cgd3_1890	membrane bound phosphatase with 3 transmembrane domains	1					1	0.486
	oguoccc	and a dual specificity phosphatase	·						0.100
	cgd3_2020	PP2C like protein phosphatase	1					1	0.430
	cgd3_2150	protein phosphatase, signal peptide, 2-6 transmembrane	1					1	0.366
	10.055	domain protein							
	cgd3_250	protein serine/threonine phosphatase alpha	1					1	0.464
	cgd6_1010	PP2C like protein phosphatase	1					1	0.503
	cgd6_3570	myotubularin related protein 1, C-terminus protein	1					1	0.442
	cgd6_4200	tyrosine/serine phosphatase, catalytic domain protein phosphatase 2B catalytic subunit, calcineurin like		1				1	2.359
		phosphatse superfamily						'	2.009
	cgd6_440	PP2Cc like protein phosphatase	1					1	0.326
	cgd6_5000	phosphoprotein phosphatase 2A 65K regulatory chain-like with					1	1	56.488
		HEAT repeats							
	cgd7_3530	PP2C-like phosphatase	1					1	0.473
	cgd7_4150	PP2C phosphatase		1				1	2.050
	cgd7_4640	PP2C phosphatase					1	1	248.430
	cgd7_4790	Ptc7p phosphatase (PP2C family)					1	1	333.117
	cgd7_4970	protein phosphatase 2A regulatory subunit (contains a		1				1	1.630
	ogd7 040	conserved version of EF hands)						4	0.450
	cgd7_810	protein phosphatase PP2A, calcineurin like phosphoesterase superfamily	1					1	0.453
	cgd8_1430	PP2C like protein phosphatase			1			1	2.709
	cgd8_290	serine-threonine protein phosphatase	1					1	0.432
	cgd8_3180	protein phosphatase regulator like HEAT repeats containing			1			1	2.474
		protein that folds into a alpha-alpha superhelix							
Protein phosphatase	Total		13	5	3		5	26	30.923
Sugar & derivatives	cgd1_3060	oligosaccharide deacetylase domain	1					1	0.552
	cgd2_1770	mannose-1-phosphate guanylyltransferase	1					1	0.534
	cgd2_1900	dTDP-glucose 4-6-dehydratase-like protein, putative		1				1	1.749
	cgd4_2600	UDP-glucose 4-epimerase			1			1	2.593

		cgd4_810	UDP-N-acetylglucosamine pyrophosphorylase	1					1	0.395
		cgd4_960	phosphomannomutase	1					1	0.323
		cgd6_3750	1,4-alpha-glucan branching enzyme; alpha-amylase; glycogen brancing enzyme	1					1	0.537
		cgd7_1830	secreted UDP-N-acetylglucosamine pyrophosphorylase family	1					1	0.471
			protein, signal peptide							
		cgd7_2580	AMSJ/WSAK like polysaccharide polymerase	1					1	0.548
		cgd7_4120	(glycosyltransferase family) UDP-N-acetylgalactosamine: polypeptide N-	1					1	0.509
		Cgu7_4120	acetylgalactosaminyltransferase, signal peptide	'					'	0.503
		cgd8_4940	trehalose-6-phosphate synthase of likely plant origin	1					1	0.515
		cgd8_920	UDP-glucose 6-dehydrogenase	1					1	0.338
	Sugar & derivatives To		, ,	10	1	1			12	0.755
nzyme Total				170	60	50	62	47	389	25.786
Gene expression	RNA synthesis	cgd1_1620	RPB7 like OB fold RNA polymerase subunit	П		1			1	3.826
-		cgd1_1960	RPB7 subunit of the RNA polymerase III, OB fold	1				ı	1	0.379
		cgd1_2260	RNA polymerase II B8 subunit		1			ı	1	1.944
		cgd1_2710	RNA polymerase II B3 subunit			1		ı l	1	2.583
		cgd1_2770	RNA polymerase 1 beta subunit					1	1	114.168
		cgd2_2970	DNA-directed RNA polymerase II, putative				1		1	20.205
		cgd2_730	RNA polymerase III transcription factor (TF)IIIC subunit	1	1			ı	2	1.766
			tau/Tfc1p					ı		
		cgd2_980	putative DNA-directed RNA polymerase 2			1 1	1		1	21.906
		cgd2_990	queuine tRNA-guanine transglycosylase			1 1		1	1	36.009
		cgd3_1870	DNA-directed RNA polymerase 2 subunit		1	1 1			1	1.560
		cgd3_2620	putative DNA-directed RNA polymerase, possible RNA			1 1		1	1	28.707
			polymerase A/beta'/A" subunit, long PHYSPTS repeat at C-terminus			1 1				
		cgd4_3260	putative DNA-directed RNA polymerases I, II, and III 8.3 kda			1 1	1		1	17.908
		- Jan 7_0200	polypeptide				'	,	, 'I	17.300
		cgd5_730	DNA-directed RNA polymerase I, putative				1	,	1	5.562
		cgd6_3290	DNA-directed RNA polymerase III C1 subunit			1		,	1	4.484
		cgd6_4580	RNA polymerase III C34 subunit; rpc34p ortholog				1	,	1	16.501
		cgd7_3720	RNA polymerase beta subunit			1		ı	1	3.276
		cgd7_4250	RNA pol II carboxy terminal domain phosphatase of the HAD				1	ı	1	18.369
			superfamily with a BRCT domain at the C-terminus					ı		
		cgd7_4370	RNA polymerase II, putative		1	1 1		ı l	1	1.250
		cgd7_4390	NudC ortholog		1	1 1			1	1.897
		cgd7_4770	DNA-directed RNA polymerase subunit			1 1		1	1	72.834
		cgd7_510	RNA polymerase III subunit C11		1	1 1		ı l	1	1.950
		cgd8_170	DNA-directed RNA polymerase beta subunit			1			1	5.245
		cgd8_300	RNA polymerase III C5 subunit					1	1	82.368
		cgd8_3400	RNA polymerase II CTD/NL1 interacting protein like	1		1 1			1	0.469
		10 4040	phosphatase			1 1		ı l	ارا	0.040
		cgd8_4810	RNA pol II carboxy terminal domain phosphatase of the HAD superfamily with a BRCT domain at the C-terminus	1		1 1		ı l	1	0.348
	RNA synthesis Total		Superfamily with a BRCT domain at the C-terminus	4	6	5	6	5	26	17.972
	Transcription	cgd1 1560	domain KOG2577, transcription factor E2F/dimerization partner		H	Ť		1	1	81.378
	Trancomption	logu I_1000	(TDP)						· 'l	01.070
		cgd1_1570	transcription factor E2F					1	1	111.751
		cgd1_1700	GATA type DNA binding domain fused to an AT hook		1	1 1			1	2.221
			ELP3 like acetyltransferase involved in transcription							
		cgd1_2450	TELES like acetyltransierase involved in transcription		!	ļ		1	1	30.452
		cgd1_2450 cgd1_2600	transcription factor TAF5p, TBP associated protein involved in	1				1		
		cgd1_2600	transcription factor TAF5p, TBP associated protein involved in transcription	1				1	1	30.452 0.486
		cgd1_2600 cgd1_3620	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55	1		1		1	1 1	30.452 0.486 3.834
		cgd1_2600	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-	1		1 1		1	1	30.452 0.486
		cgd1_2600 cgd1_3620 cgd1_3780	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide	1		1 1		1	1 1 1 1	30.452 0.486 3.834 3.057
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative	1		1 1 1		1	1 1 1 1	30.452 0.486 3.834 3.057 3.512
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH	1	4	1 1 1 1		1	1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF	1	1	1 1 1 1 1		1	1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative	1	1	1 1 1 1		1	1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative	1	1	1 1 1 1	1	1	1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_1120	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains	1	1	1 1 1 1	1	1	1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_1120 cgd3_3110	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain	1	1	1 1 1 1	1 1	1	1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3250	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein	1	1	1 1 1 1 1	1 1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_1120 cgd3_3110	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-	1	1	1 1 1 1	1 1	1	1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_1120 cgd3_31110 cgd3_3250 cgd3_3750	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPC like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator	1	1	1 1 1 1 1 1	1 1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_31120 cgd3_3110 cgd3_3750 cgd3_4060	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative sNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein	1	1	1 1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3250 cgd3_3750 cgd3_4060 cgd3_4150	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative sNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative	1	1	1 1 1 1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_31120 cgd3_3110 cgd3_3750 cgd3_4060	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative HMG-like nuclear protein, Nhp2p, pelota RNA binding domain	1	1	1 1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3250 cgd3_3750 cgd3_4060 cgd3_4150	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative sNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative	1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3250 cgd3_3750 cgd3_4060 cgd3_4150 cgd3_760	transcription factor TAF5p, TBP associated protein involved in transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative HMG-like nuclear protein, Nhp2p, pelota RNA binding domain containing protein	1	1 1	1, 1 1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246 105.529 3.689
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_3420 cgd3_3110 cgd3_3250 cgd3_3750 cgd3_4060 cgd3_4150 cgd3_760 cgd4_1270	transcription factor TAF5p, TBP associated protein involved in transcription transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative programmed cell death 2, putative SNAPC like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative HMG-like nuclear protein, Nhp2p, pelota RNA binding domain containing protein factor TFIIIB, SANT domain chromodomain-helicase-DNA-binding'multidomain chromatin protein with the following architecture: chromo-bromo-chromo-	1	1 1	1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246 105.529
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3750 cgd3_4060 cgd3_4150 cgd3_760 cgd4_1270 cgd4_1590	transcription factor TAF5p, TBP associated protein involved in transcription transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative HMG-like nuclear protein, Nhp2p, pelota RNA binding domain containing protein factor TFIIIB, SANT domain transcription factor TFIIIB, SANT domain chromodomain-helicase-DNA-binding'multidomain chromatin protein with the following architecture: chromo-bromo-chromo-SNF2 ATpase'	1	1 1	1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246 105.529 3.689 1.472
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3250 cgd3_3750 cgd3_4060 cgd3_4150 cgd3_760 cgd4_1270 cgd4_1590 cgd4_1720	transcription factor TAF5p, TBP associated protein involved in transcription transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative HMG-like nuclear protein, Nhp2p, pelota RNA binding domain containing protein factor TFIIIB, SANT domain transcription factor TFIIIB, SANT domain chromodomain-helicase-DNA-binding'multidomain chromatin protein with the following architecture: chromo-bromo-chromo-SNF2 ATpase' CCAAT-box DNA binding protein subunit B	1	1 1 1	1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246 105.529 3.689 1.472
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3250 cgd3_3750 cgd3_4060 cgd3_4150 cgd4_1270 cgd4_1590 cgd4_1720 cgd4_310	transcription factor TAF5p, TBP associated protein involved in transcription transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative HMG-like nuclear protein, Nhp2p, pelota RNA binding domain containing protein transcription factor TFIIIB, SANT domain chromodomain-helicase-DNA-binding'multidomain chromatin protein with the following architecture: chromo-bromo-chromo-SNF2 ATpase' CCAAT-box DNA binding protein subunit B CCAAT-binding factor chain HAP5 like histone	1	1 1 1	1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246 105.529 3.689 1.472
		cgd1_2600 cgd1_3620 cgd1_3780 cgd2_1760 cgd2_2060 cgd2_220 cgd2_2820 cgd2_3420 cgd3_3110 cgd3_3250 cgd3_3750 cgd3_4060 cgd3_4150 cgd4_1270 cgd4_1590 cgd4_1720	transcription factor TAF5p, TBP associated protein involved in transcription transcription transcription factor TAF7p/TAFII55 domain KOG1015, transcription regulator XNP/ATRX, DEAD-box superfamily, signal peptide gata/ArfGAP, putative possible transcription factor TFIIH transcription factor TFIIF transcription factor, putative programmed cell death 2, putative SNAPc like transcription factor with 4 MYB/SANT domains transcription factor TFIIH with a vWA domain CCAAT-binding factor (CBF)/MAK21 family protein multiprotein bridging factor type 1 like transcriptional co-activator histone transcription regulator (HIR1)-like WD40 repeat protein cutinase negative acting protein, putative HMG-like nuclear protein, Nhp2p, pelota RNA binding domain containing protein factor TFIIIB, SANT domain transcription factor TFIIIB, SANT domain chromodomain-helicase-DNA-binding'multidomain chromatin protein with the following architecture: chromo-bromo-chromo-SNF2 ATpase' CCAAT-box DNA binding protein subunit B	1 1 1	1 1 1 1 1	1 1 1 1	1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30.452 0.486 3.834 3.057 3.512 3.906 2.172 2.405 9.343 6.242 0.454 11.631 2.464 1.489 315.246 105.529 3.689 1.472

	cgd4_880	ADA2 ortholog with a ZZ finger, SANT domain and a SWIRM domain					1	1	33.5
	cgd5_1280	tfc4p like TFIIIC subunit; TPR repeat containing basal transcription factor		1				1	1.6
	cgd5_1690	cactin-like protein		1				1	1.40
	cgd5_3290	transcription elongation factor TFIIS					1	1	69.36
	1	, ,				_ ,			
	cgd5_3790	SNF7 ortholog				1		1	12.6
	cgd5_4200	transcription initiation factor IIA	1					1	0.30
	cgd5_670	reptin52; reptin like TIP49 family AAA+ ATpase			1			1	4.95
	cgd6_1430	transcription factor E2F wHTH only					1	1	169.52
	1							- 1	
	cgd6_2430	BTF domain, basal transcription factor					1	1	94.67
	cgd6_2480	CCR4-NOT transcription complex, subunit 2; NOT2. C terminal Not2/Not3 domains			1			1	2.92
	cgd6_3860	SNF2 helicase, putative			1			1	3.44
	cgd6_4650	5kows transcription initiation protein SPT5			1			1	4.15
	cgd6_5250	transcription elongation factor, SPT6-like				1		1	10.88
	cgd7_3240	transcription activator, putative					1	1	34.50
			1		1				
	cgd7_3410	SNF5 like protein	- 1		1			2	1.98
	cgd7_3650	DP1 DNA binding protein					1	1	91.27
	cgd8_1850	E2F like domain containing transcription factor with the wHTH fold					1	1	63.69
	cad8 3030						4	1	77.68
	cgd8_2030	TATA-box factor binding protein					- 1	- 1	
	cgd8_210	transcription factor TFIID, TBP	L ∣		1		- 1	1	4.47
	cgd8_2420	transcription initiation factor IIF/ Rap30 like winged HTH	1				- 1	1	0.35
	cgd8_2770	SNF2L ortholog with a SWI/SNF2 like ATpase and a Myb				4	-	1	13.64
	C940_2110	Idomain				- '	- 1	'	13.04
	and0 4400						- 1	ار	^
	cgd8_4400	transcription elongation factor TFIIS			1		- 1	1	2.77
	cgd8_880	transcription initiation factor TFIIB Sua7p; ZnR+2cyclins			1			1	2.57
Transcription Total			7	8	15	7	13	50	28.34
Translation	cgd1_1860	GCN3p like EIF2B,translation initiation factor eIF-2B alpha			1	- 1		1	3.93
i anolalon	C94 1_ 1000	subunit			'		- 1	'	5.90
	cgd1 2420					-	4	1	100.76
		SUA5 like RNA binding domain containing protein							
	cgd1_880	eukaryotic initiation factor 4A (eIF4A) (eIF-4A)					1	1	889.38
	cgd2_110	Dbp6p, eIF4a-1 family RNA SFII helicase					1	1	28.75
	cgd2_1160	HSPC021/HSPC025 family protein			1			1	2.50
		7.			' '				
	cgd2_1500	possible translation initiation factor with possible PINT domain		1				1	1.71
	cgd2_2070	translation elongation factor EF-1, subunit alpha, putative				1		1	7.84
	cgd2_2430	ximpact ortholog conserved protein seen in bacteria and			1			1	2.76
		eukaryotes							
	cgd2_270	translation initiation factor eIF-3 subunit 7			1			1	4.99
	1					4		- 1	
	cgd2_360	prtip-like IF39 eukaryotic translation initiation factor 3				1		1	7.07
	cgd2_3920	elF4G eukaryotic initiation factor 4, Nic domain containing			1			1	2.63
		protein							
	cgd2_3930	deoxyhypusine synthase/spermidine:eIF5A-lysine 4- aminobutyltransferase				1		1	14.98
	2050			4				4	2.20
	cgd2_3950	putative translation elongation factor 1 beta 1		1				1	2.29
	cgd2_820	putative translation initiation factor 1 (eIF1), SUI1p					1	1	178.68
	cgd3_1650	eIF2G GTpase. eukaryotic translation initiation factor 2 gamma			1			1	3.53
		subunit (ZnR+GTpase)							
	cgd3_280	mRNA translation inhibitor SKI2 SFII helicase, DEXDc+HELICc	1					1	0.33
	cgd3_3020	possible guaning nucleotide exchange factor, eIF-2B				1		1	15.51
	cgd3 3340	SECIS binding protein. pelota RNA binding domain containing					1	1	85.73
	cgu3_3340	1					'	'	05.70
	222 2200	protein				4		4	16.07
	cgd3_3380	Dbp9p, eIF4A-1-family RNA SFII helicase, DEXDc+HELICc				1	- 1	1	16.37
	cgd3_4020	eIF-3 p25/subunit 11				1	- 1	1	9.58
	cgd4_1030	eukaryotic translation initiation factor			1		- 1	1	3.98
	cgd4_1840	Dbp7p, eIF4A-a-family RNA SFII helicase (DEXDc+HELICc)				4	- 1	1	14.21
	1					١,			
	cgd4_3130	putative eIF6, translation initiation factor 6					1	1	55.58
	cgd4_3180	Rrp3p, eIF4A-1-family RNA SFII helicase (DEXDc+HELICc)			1		- 1	1	5.39
	cgd5_1600	translation initiation factor if-2B beta; eIF-2			1		-	1	4.38
	cgd5_390	putative eukaryotic translation initiation factor 3			4		- 1	1	3.50
	cgd5_680	eukaryotic translation initiation factor 3 37.28 kDa subunit,			1			1	2.86
	5 1 - 1 - 1	putative					- 1	T.	
	cgd6 1020	translation initiation factor if-4E		4			- 1	1	1.43
				- 1			- 1	1	
	cgd6_1200	diphthine synthase; diphthamide biosynthesis methyltransferase				1	- 1	1	8.78
	l						- 1		
	cgd6_1590	eukaryotic translation initiation factor 4 gamma; Nic domain				1	- 1	1	13.96
		containing protein							
	cgd6_2180	Fun12p GTpase; translation initiation factor IF2					1	1	35.95
	cgd6_2230	diphthamide biosynthesis; OVCA1/DPH2 protein-like; AE group			1			1	4.02
	C940_2230				'		- 1	'	4.02
		(Note: old=diphtamide; Diphthamide is a modified histidine in eEF-2)					- 1		
	cgd6_2260	Hca4p helicase DBP4 (helicase CA4). EIF4A-1-family RNA SFII				1		1	8.12
		helicase							
		Rok1p, eIF4A-1-family RNA SFII helicase				1	- 1	1	18.83
	cgd6_3210				1		- 1	1	4.35
	1	Erf1 eukaryotic translation termination factor 1: N-terminal	ı l				1	.1	1.50
	cgd6_3210 cgd6_3380	Erf1 eukaryotic translation termination factor 1; N-terminal			I	I	,	Į.	
	cgd6_3380	RNAseH plus pelota domain containing protein	1					4	0.40
	cgd6_3380 cgd6_3420	RNAseH plus pelota domain containing protein translation initiation factor EIF-2B epsilon subunit	1					1	
	cgd6_3380 cgd6_3420 cgd6_3960	RNAseH plus pelota domain containing protein translation initiation factor EIF-2B epsilon subunit elongation factor-like protein	1			1		1	13.00
	cgd6_3380 cgd6_3420	RNAseH plus pelota domain containing protein translation initiation factor EIF-2B epsilon subunit	1			1	1	1	0.49 13.00 156.05
	cgd6_3380 cgd6_3420 cgd6_3960	RNAseH plus pelota domain containing protein translation initiation factor EIF-2B epsilon subunit elongation factor-like protein	1		4	1	1	1	13.00

		cgd6_4860 cgd7_1080	nucleolar protein GU2. eIF4A-1-family. RNA SFII helicase eIF3-p47 with JAB/PAD domain			1		1	1	354.202 3.133
		cgd7_1000	translation initiation factor if-5A	i l		<u> </u>		1	1	1,056.848
		cgd7_2430	translation initiation factor eIF-5; Tif5p, ZnR+W2 domains	i l	ļ	.		1	1	1,025.727
		cgd7_3940	eIF4A-1; eukaryotic translation initiation factor 4A-1; RNA SFII	i l	4	.		'	1	1.640
		Jogur_J340	helicase	i l	- '				'	1.040
		cgd7_5180	eIF3 gamma/P40 with JAB/PAD domains; translation initiation factor IF-3 subunit 3				1		1	18.624
		cgd7_5270	Translation initiation factor 2, alpha subunit(eIF2-alpha); S1-like RNA binding domain			1			1	3.336
		cgd7_880	eIF-3A like translation initiation factor that has a WD40 repeat- containing beta propeller	1					1	0.415
		cgd8_2930	Eft2p GTpase; translation elongation factor 2 (EF-2)					1	1	35.996
		cgd8_3940	eIF-2B gamma, eukaryotic translation initiation factor 2B subunit 3 that has a nucleotide diphospho sugar transferase at the N-terminus and a UDP N-acetylglucosamine acyltransferase at the						1	0.379
		oad9 4430	C-terminus				4		1	20.970
		cgd8_4430 cgd8_4750	translation initiation factor if-2 betam beta subunit ZnR Dbp5p-like eIF4A-1-family RNA SFII helicase	i l		.	1			20.879 9.068
		cgd8_4750 cgd8_800	Prp5p C terminal KH. eIF4A-1-family RNA SFII helicase	1		.	'		1	0.342
	Translation Total		1 1909 O terminar (CI. CII 4/C 1 family (CV/CO) if ficiloase	5	4	16	15	12	52	82.085
Gene expression		-	+	16	18	36	28	30	128	48.070
General	General	cqd1 2980	14-3-3 protein	1					1	0.623
		cgd2_1700	2x Ef hands, calmodulin-like	1					1	0.511
		cgd2_810	calmodulin					1	1	53.413
		cgd3_1290	14-3-3 domain containing protein		1				1	1.619
		cgd6_730	14-3-3 domain containing protein	1					1	0.386
		cgd7_2470	14-3-3 domain containing protein	1					1	0.337
	_	cgd7_3950	2*FF domain protein (phosphopeptide binding)	1					1	0.310
	General Total			5	1			1	7	8.171
General Total	Mambassa	00014 4100	anain lika FNTH damair (-laba - laba - s. 1. 1. 2. 2. 1. 1. 1.	5	1			1	7	8.171
Membrane	Membrane traffic	cgd1_1120	epsin like ENTH domain (alpha-alpha superhelix)involved in vesicular transport VDP/USO1/YBL047C family vesicular transport factor	1	1				1	1.560 0.464
		cgd1_1340 cgd1_1770	putative Rab5-interacting protein			,	4		1	9.815
		cgd1_1770 cgd1_1830	TB2/DP1/HVA22 family integral membrane protein that may be			,	1	1		69.400
		Toga 1_1000	involved in membrane trafficking, 3x transmembrane domains	i l				'	'	00.700
		cgd1_1890	vesicle transport protein, putative	1					1	0.533
		cgd1_200	ADP-ribosylation factor-like protein 2 (ARL2), putative	1		,			1	0.413
		cgd1_2060	Rab2 GTPase, putative	1		,			1	0.478
		cgd1_2580	Arl1p/ARF like GTpase involved in vesicular transport	1					1	0.343
		cgd1_2830	syntaxin 5A ortholog, possible transmembrane domain or GPI at	1					1	0.370
		cgd1_2920	C-terminus golgi transport SNARE BOS1 secretory pathway protein, possible transmembrane or GPI anchor at C-terminus		1				1	1.551
		cgd1_580 cgd2_1140	dynamin-like protein syntaxin, putative, SMART syntaxin+tSNARE+transmembrane	1		1			1	2.707 0.376
			domain or GPI anchor at C-terminus		إ					
		cgd2_1570	putative vacuolar protein sorting/targeting protein 26	- 4	1				1	1.488
		cgd2_1940	RAB6 protein, putative	1					1	0.331
		cgd2_3010	N-ethylmaleimide-sensitive factor (NSF1)-like AAA ATpase involved in vesicular transport	1					- '	0.365
		cgd2_3400	dynamin-related protein, putative	1					1	0.485
		cgd2_3410	ARF1/2 like small GTpase, putative			,	1		1	20.351
		cgd3_1070	synaptobrevin like SNARE	1					1	0.515
		cgd3_180	domain KOG1666, V-SNARE (intracellular trafficking, secretion, and vesicular transport)			1			1	4.264
		cgd3_1820	putative Sec23			1			1	2.720
		cgd3_3150	Rab5 like small GTpase	1					1	0.401
		cgd4_2930 cgd4_3420	vacuolar sorting protein VPS52/suppressor of actin Sac2-family protein Vps53-N family protein involved invacuolar protein sorting	1					1	0.316 0.453
		cgd4_3420 cgd4_4300	beta adaptin	1		1				2.884
		cgd4_4300 cgd5_3850	adapter-protein complex 1 gamma subunit (gamma adaptin)	1		_ '			1	0.324
		cgd5_4180	vacuolar protein-sorting protein VPS45, putative	1					1	0.302
		cgd6_150	synaptobrevin'synaptobrevin, adjacent duplicated gene'				1		1	11.762
		cgd6_2070	adaptin AP complex subunit alpha; ARM repeats	1					1	0.346
		cgd6_3220	RAS small GTpases RIC1/ypt1		1				1	1.598
		cgd6_4930	beta-adaptin AP complex subunit-related; ARM/HEAT repeat protein	1					1	0.419
		cgd6_510	synaptobrevin/VAMP-like protein			,	1		1	5.863
		cgd7_1680	Rab7 GTPase, putative			1			1	3.055
		cgd7_1820	BET3 vesicular transport protein	1					1	0.313
		cgd7_1910	coatomer SEC21 gamma subunit like (beta adaptin)	1					1	0.486
		cgd7_2060	vacuolar protein sorting 29	1					1	0.388
		cgd7_2940	coatomer complex delta chain	1					1	0.347
		cgd7_3130 cgd7_4210	ER vesicle protein; Erv41p, transmembrane region near C terminus and possible N region transmembrane		1				1	2.014
		1000/ 1210	Sec61-gamma subunit of protein translocation complex, putative		1 1			- 1	11	1.396

disposphenic locus of 6 genes   signal peptide series proline rich, possible low mw mucin   disposphenic locus of 6 genes   signal peptide series proline rich, possible low mw mucin   disposphenic locus of 6 genes   signal peptide series proline rich, possible low mw mucin   disposphenic locus of 6 genes   cogd3_440   cogd3_3440   cogd6_34550   cogd6_51210   cogd6_5266   cogd6_5410   cogd6_5266   cogd6_5410   cogd6_											
OppT_5000   Control			cgd7_4380	Rablib [rab11b]	1					1	0.352
Copp. 1, 2000   Rab geranny/geranny/transferance uphas subunit   1   1   1   1   1   1   1   1   1			cgd7_4740	Rab GDP dissociation inhibitor	1					1	0.367
Content   Cont				coatomer complex beta	1	1				2	0.986
Copt					1					1	0.360
cgd8_1080   STXBPUNIC-18SEC1 syntain involved in golg transport   1   1   1   1   1   1   1   1   1			cgd7_5460	- ·		1				1	1.701
Code   1250					1					1	0.444
Vesicles				· · · · · · · · · · · · · · · · · ·	1					1	0.427
Cop8, 1270   Cop8, 1470   Cop			cgd8_1250		1					1	0.491
Cog88_1940   Qa88_1940   Qa8			cad9 1270	I and the second		4				1	1.801
page   1910   page   1910   page   1910   page   1910   page   1910   page   2910			1	1	1						0.352
Infections   Inf							1				5.178
Gag8, 1990   Gag			cguo_1910							'	3.170
cg68_2900 cg68_2910 cg68_2			cgd8_1990	1	1					1	0.420
cgd8_2900   ERIVAT like membrane associated protein involved in vesicular transport with a framsmerbrane region near the C-terminus (policy hypopolis protein involved in vesicular protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein associated protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein associated protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein associated protein sorting ages 390 / Aps 7ph/3r1 like deathran dasptor protein associated protein sorting ages 390 / Aps 7ph/3r1 like also associated protein involved in vesicular transport with a signal peptide and associated protein involved in vesicular protein sorting ages 391 / Aps 7ph/3r1 like was 291 / Aps 7ph/3r1 like also as 291 / Aps 7ph/3r1 like also as 291 / Aps 7ph/3r1 like was 291 / Aps 7ph/3r1 like also as 291 /			1	APG10/ Aut1p like like autophagocytosis protein involved in			1			1	3.449
transport with a transmembrane region near the C-terminus (py660 /py860 pilo lier protein involved in vacuolar protein sorting of the py860 py860 pilo lier protein involved in vacuolar protein sorting of the protein with a real protein pega 3, human vacuolar protein coatomer protein complex subunit pilan, putative vacuolar protein sorting 1-8 lier protein with a real pilonding domain at the C-cogd 950 capt 1, 1 and 1 apple domain.  Mucin (pgd 1, 3550) marchine to complex subunit pilan, putative vacuolar protein sorting 1-8 lier protein with a real pilanding of the complex of the protein with a real protein with a real protein with a real protein with a real protein with a signal peptide and an apple domain. signal peptide, serine stretches, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein erich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein erich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein erich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein erich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein erich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein erich, possible low mw mucin glycoprotein locus of 6 genes genes protein with a transmembrane domain and mucin-like inch regions serine protein erich, possible low mw mucin glycoprotein locus of 6 genes genes protein with a transmembrane domain and mucin-like inch regions series derived with a transmembrane domain and mucin-like inch regions series derived with a transmembrane domain and mucin-like inch regions series derived with a transmembrane domain and mucin-like inch regions and 12 kZAZA. repeats and a mucin-like inch regions with a signal peptide series mucin like glycoprotein with signal peptide and mucin-like inch regions and mucin-like inch regions with signal peptide series mucin like glycoprotein with signal peptide series mucin like glycop											
cg88_2910   cg98_2920   cg98			cgd8_2900			1				1	1.640
cg88_4040   cg88_8040   cg88_910   cg88_91			cad8 3030	1 '	1					1	0.390
Cg88_910   Costomer protein complex subunit alpha, putative   1   1   1   1   1   1   1   1   1											0.390
Autonomia				1				1			6.262
Membrane traffic Total   Mucin   cgd1_3550   mucin-like low complexity glycoprotein with a signal peptide and an apple domain.   signal peptide, serine stretches, possible low mw mucin glycoprotein locus of genes   signal peptide, serine stretches, possible low mw mucin glycoprotein locus of genes   signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of genes   signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of genes   signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of genes   signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of genes   signal peptide, serine proline rich, possible low mw mucin   1   1   1   1   1   1   1   1   1											6.480
Membrane traffic Total			3943_010					'		'	5.400
Membrane traffic Total   Mucin   Cgd1_3550				1 9 .							
Mucin cgd1_3550 mucin-like low complexity glycoprotein with a signal peptide and an anappe domain. signal peptide, serine stretches, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein focts, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein focts, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protine rich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of 6 genes capd3_440 children in the series of genes code and signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of 6 genes capd3_440 children in the series of genes capd3_440 children in the series capd5_4500 children in				clathrin coat assembly protein AP50						1	0.389
an apple domain.  cgd2_400  signal peptide, serine stretches, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine stretches, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine ropine rich, possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible low mw mucin glycoprotein locus of 6 genes  signal peptide, serine rich possible lo					34	10	7	6	1		3.173
cgd2_400   signal peptide, serine stretches, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine stretches, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protein rich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protien rich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protien fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protien fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protien fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protien fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide, serine protien fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide genes protein fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide genes protein fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide genes protein fich, possible low mw mucin glycoprotein locus of 6 genes signal peptide with a transmembrane domain and mucini-like thretorial respects with a signal peptide and 12 KAZAL repeats and a mucini-like stretch of threonines secreted protein with signal peptide and nucini-like threonine repeats of the protein with signal peptide and mucini-like threonine repeats of the protein with signal peptide and mucini-like threonine repeats of the protein with signal peptide and mucini-like threonine repeats of the protein with signal peptide plus thr stretch, cys rich, possible mucin cyplopsordial peptide plus threstretch, cys rich, possible mucin cyplopsordial mucin, large thr stretch, signal peptide sequence secreted protein with cysteme rich repeats and a mucini-like threonine repeats signal peptide sequence secreted protein with cysteme rich repeats and a mucini-like threonine rich repeats signal peptide, thr stretch signal peptide sequence secreted protein with cysteme rich repeats and a mucini-like threonine rich repeats signal		Mucin	cgd1_3550		1					1	0.402
glycoprotein locus of 6 genes   1   1   1   1   1   1   1   1   1			oad2 400	1 ''							70 000
cgd2_410   signal peptide, serine stretches, possible low mw mucin glycoprotein, locus of 6 genes   cgd2_430   cgd2_430   cgd2_430   cgd2_430   cgd2_430   cgd2_440   cgd2_440   cgd2_450   cgd2_440   cgd2_450   cgd3_440   cgd2_4556   cgd2_450   cgd2_45			cyu2_400						1	"	78.202
glycoprotein, locus of 6 genes   1   1   1   1   1   1   1   1   1			cgd2 410						1	1	48.299
glycoprotein locus of 6 genes   cgd2 430   cgd2 430   cgd2 430   cgd2 440   cgd2 450   cgd3 epitide, serine proline rich, possible low mw mucin glycoprotein locus of 6 genes   cgd3 440   cgd3 epitide, serine proline rich, possible low mw mucin glycoprotein locus of 6 genes   cgd3 440   cgd3 epitide, serine proline rich, possible own mw mucin glycoprotein locus of 6 genes   cgd3 440   cgd3 epitide, serine proline rich, possible mucin and mucin-like rich regions   cgd4 4560   cgd5 2000   cgd5 2000   cgd5 2000   cgd5 2000   cgd5 2000   cgd6 5400   cgd7 4020   cg											
Cgd2_430   Signal peptide, serine proline rich, possible low mw mucin glogd   1   1   1   1   1   1   1   1   1			cgd2_420						1	1	251.769
cqd2_440   cqd2_450   cqd2_43550   cqd4_33550   cqd4_33550   cqd4_33550   cqd4_3050   cqd2_5266   cqd2_450										ارا	4 700 540
cgd2_440   signal peptide, serine proline rich, possible low mw mucin group cyrotrein locus of 6 genes   cgd2_450   cgd2_450   cgd2_450   cgd3_440   cyropretine locus of 6 genes   cyropretine locus of 6			cga2_430						1	1	1,732.542
glycoprotein locus of 6 genes   cgd2,450   cgd3,440   cgd3,440   cgd3,440   cgd3,450   cgd6,2500   cgd6,2500   cgd6,2000   cgd6,2000   cgd6,2000   cgd6,2400   c			cad2 440					1		1	21.108
Cgd3_440   Cgd4_3550   Cgd4_3550   Cgd4_3550   Cgd4_3550   Cgd4_3550   Cgd4_3550   Cgd4_3550   Cgd4_3550   Cgd4_3560   Cgd4_3560   Cgd4_3560   Cgd4_3560   Cgd4_3560   Cgd4_360   Cgd4_36			ogu=_ : : o								200
Cayda   440			cgd2_450				1			1	2.636
and mucin-like rich regions   secreted protein with signal peptide and 12 KAZAL repeats and a mucin-like stretch of threonines   cgd5_2060   hypothetical protein with 1 hrs ristrethes, possible mucin   hypothetical protein with 1 hrs ristrethes, possible mucin   hypothetical protein with 1 hrs ristrethes, possible mucin   cgd6_5410   cgd6_5410   cgd6_5410   cgd6_5410   cgd7_4020   cryptopsoridial mucin, large thr stretch, charged repeats, likely mucin   cgd7_4020   cryptopsoridial mucin, large thr stretch, signal peptide sequence   cgd7_4660   cgd8_3520   cgd6_3520   cgd7_4660   cgd8_3520   cgd6_5410   cgd6_3420   cgd6_5410   cgd6_3420   cgd6_5410   cgd6_3420   cgd6_3											
Codd   3550   Secreted protein with signal peptide and 12 KAZAL repeats and a mucin-like stretch of throonines hypothetical protein with signal peptide and mucin-like threonine repeats   1			cgd3_440			1				1	1.791
a mucin-like stretch of threonines hypothetical protein with right and protein with signal peptide and mucin-like threonine repeats protein with signal peptide plus thr stretch, cys rich, possible mucin ogd6_5410   1 1 1   1   1   1   1   1   1   1			cad4 3550						1	1	495.075
Cgd5_2060			cgu+_5550							'	490.070
Cgd5_2060   hypothetical protein with signal peptide and mucin-like threonine repats   1   1   1   1   1   1   1   1   1			cgd5 1210					1		1	13.191
repeats   cgd6_5400   cgd6_5410   cgd7_4020   cgd6_5410   cgd7_4020   cgd7_4020   cgd7_4020   cgd7_4020   cgd7_4020   cgd7_4660   cgd8_3520   secreted mucin like glycoprotein, signal peptide sequence   1				I and the second					1	1	493.875
Cgd6_5410   Cgd7_4020   Cgd7_4020   Cgd7_4020   Cgd7_4020   Cgd7_4020   Cgd7_4020   Cgd7_4020   Cgd7_4020   Cgd7_4020   Cgd7_4060   Cgd7_4060   Cgd7_4060   Cgd7_4060   Secreted mucin like glycoprotein, signal peptide, thr stretch   1			-	1							
Cgd6_5410   cgd7_4020   signal peptide plus thr stretch, charged repeats, likely mucin cryptopsordial mucin, large thr stretch, signal peptide sequence cgd7_4660   cgd8_3520   secreted mucin like glycoprotein, signal peptide, thr stretch secreted protein with cysteine rich repeats and a mucin like threonine rich repeat, signal peptide   1 2 1 2 10 16			cgd6_5400						1	1	837.635
Cgd7_4020			and6 E410						4		1 210 260
Cgd7_4660   Secreted mucin like glycoprotein, signal peptide, thr stretch secreted protein with cysteine rich repeats and a mucin like threonine rich repeat, signal peptide   1									1	1 1	1,210.260
Mucin Total   TRAP   cgd1_3500   thrombospondin related adhesive protein   1   2   1   2   10   16   16   17   16   17   17   17   17			cgu7_4020	cryptopsondial mucin, large thi stretch, signal peptide sequence					- 1	'	40.935
Mucin Total   TRAP   cgd1_3500   thrombospondin related adhesive protein   1   2   1   2   10   16   16   17   16   17   16   17   17			cad7 4660	secreted mucin like glycoprotein, signal peptide, thr stretch		1				1	2.207
Mucin Total									1	1	864.971
TRAP				, , , , , , , , , , , , , , , , , , , ,							
TRAP Total   TRAP-C2 extracellular protein   TSP3 precursor   TRAP-C1   TRAP-C2 extracellular protein   TSP3 precursor					1	2	1	2	10	16	380.931
TRAP Total   TRAP-C2 extracellular protein   1		TRAP		i i			1			1	4.454
TRAP Total				- · · · · · · · · · · · · · · · · · · ·		1				1	1.937
Mitochondrial   Enzyme   cgd3_3120   AOX1,alternative oxidase, possible fungal or bacterial origin, 2 transmembrane regions   cgd4_3040   NifS-like protein; cysteine desulfurase   cgd5_3400   mitochondrial processing peptidase beta subunit   cgd6_1050   cgd7_1900   mitochondrial NADH dehydrogenase   mitochondrial processing peptidase, insulinase like   metalloprotease   cgd2_1360   ATP synthase beta chain, mitochondrial precursor, putative   cgd6_610   ATP synthase alpha chain   cgd3_3560   CorA family mitochondrial membrane protein with 2   cgd1   corA family mitochondrial membrane protein with 2   cgd1   corA family mitochondrial membrane protein with 2   cgd1   corA family mitochondrial membrane domains at C-terminus   cgd3_3560   corA family mitochondrial membrane protein with 2   cgd2_1360   cgd3_3560   corA family mitochondrial membrane protein with 2   cgd3_3560   corA family mitochondrial membrane protein with 2   cgd3_3560   corA family mitochondrial membrane protein with 2   cgd3_3560   cgd3_3560   corA family mitochondrial membrane protein with 2   cgd3_3560   cgd3_356			cgd5_3420	TRAP-C2 extracellular protein	-					1	0.425
Enzyme   cgd3_3120   AOX1,alternative oxidase, possible fungal or bacterial origin, 2 transmembrane regions   1		TRAP Total				1	1				2.272
transmembrane regions NifS-like protein; cysteine desulfurase cgd5_3400 mitochondrial processing peptidase beta subunit cgd6_1050 cgd7_1900 cgd7_2080 mitochondrial NADH dehydrogenase cgd7_2080 mitochondrial processing peptidase, insulinase like metalloprotease  Enzyme Total F-ATPase cgd2_1360 ATP synthase beta chain, mitochondrial precursor, putative cgd6_610 ATP synthase alpha chain  F-ATPase Total Membrane protein cgd3_3560 CorA family mitochondrial membrane protein with 2 transmembrane domains at C-terminus			16. 5		36	13	9	8	11	77	81.633
cgd4_3040 NifS-like protein; cysteine desulfurase cgd5_3400 mitochondrial processing peptidase beta subunit 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Mitochondrial	Enzyme	cgd3_3120		1					1	0.403
cgd5_3400 mitochondrial processing peptidase beta subunit cgd6_1050 lscU-like NifU protein, iron-sulfur protein cgd7_1900 mitochondrial NADH dehydrogenase cgd7_2080 mitochondrial processing peptidase, insulinase like metalloprotease  Enzyme Total F-ATPase cgd2_1360 atP synthase beta chain, mitochondrial precursor, putative cgd6_610 atP synthase alpha chain  F-ATPase Total Membrane protein cgd3_3560 cord family mitochondrial membrane protein with 2 transmembrane domains at C-terminus			cad4 3040					1		1	17.058
cgd6_1050   IscU-like NifU protein, iron-sulfur protein   1   1   1   1   1   1   1   1   1						1				1	1.844
cgd7_1900 mitochondrial NADH dehydrogenase mitochondrial processing peptidase, insulinase like mitochondrial processing pe									1	1	89.806
Cgd7_2080   mitochondrial processing peptidase, insulinase like   1   1   1   1     1     1     1     1     1     1     1     1     1     1     1     1     1     1     1     1     1   1     1								1		1	24.182
Enzyme Total				, ,		1				1	1.464
Enzyme Total  F-ATPase cgd2_1360 ATP synthase beta chain, mitochondrial precursor, putative cgd6_610 ATP synthase alpha chain  F-ATPase Total  Membrane protein cgd3_3560 CorA family mitochondrial membrane protein with 2 transmembrane domains at C-terminus  1 2 2 1 6 1 1 1 1 1 2 2 1 1 6 1 1 1 1 2 2 1 1 6											
cgd6_610   ATP synthase alpha chain   1   1   1   1   1   1   1   2					1	2		2	1	6	22.460
F-ATPase Total  Membrane protein cgd3_3560 CorA family mitochondrial membrane protein with 2 1 1 1 1 2 1 1 1 1 1 2 1 1 1 1 1 1 1		F-ATPase		The state of the s					1	1	351.081
Membrane protein cgd3_3560 CorA family mitochondrial membrane protein with 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			cgd6_610	ATP synthase alpha chain			1			1	4.079
transmembrane domains at C-terminus							1		1		177.580
		Membrane protein	cgd3_3560		1					1	0.393
		Mombrens protein T		transmembrane domains at C-terminus	- 4						0.000
		Membrane protein Tot		mitaghandrial carrier protein systems	1					1	0.393
Mito carrier protein cgd2_1030 mitochondrial carrier protein, putative		Iwillo carrier protein					1			1	3.194
cgd6_2350 mitochondrial carrier protein, 4 transmembrane domain 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				1	- 1			1		1	13.061 0.513
				· ·				4		1	0.513 9.244
cgd6_3880 mitochondrial carrier protein MRS2 with 2 transmembrane 1 1 1 domains				· ·							9.244
Mito carrier protein Total 1 2 4		Mito carrier protein To	tal		1		1	2		4	6.503

Interconordial Total		Translocase	cgd1_2560	Tom40p like translocase	1					1	0.335
Transocate total			cgd2_4140	mitochondrial import inner membrane translocase subunit tim17			1			1	2.460
Transduces Total				· · ·			1			1	
Problem degradation   Proteosorom   cgd1   2490   cgd2		Translocase Total	cga4_3170	putative mitochondrial inner membrane translocase	1	1	2			-	
Capt	Mitochondrial Total				4	3	4	4	2		
Cogd   3460   Producted proteosome regulatory complex component with a post   1	Protein degradation	Proteosome	-	1					1		
1911   100			-				۱ ،	1			
cgd2_1950   cgd2_1950   cgd2_1950   cgd2_1950   cgd2_1950   cgd2_1950   cgd2_1950   cgd2_1950   cgd2_1950   cgd2_2950   cgd2			cga1_3460				'			1	4.194
cgs2_1360   cgs2_1400   cgs2_1401   cgs2				, , , , , , , , , , , , , , , , , , , ,					1		
cpg2   2410     cpg2   2210   cpg2   cpg2   2210   cpg2			-	, , ,		4	1				
Georgia   10   1   1   1   6   645					1						
group   protessions regulatory subunit Rpn12 family   1   1   5.500								1		1	
Copt. 260			cad2 3370		1					1	0.520
hydrolase fold   cgd3_2170   cgd3_2200   PUP1-Introlessome subunit laipha 1   1   0.520   cgd4_2170   cgd4_220   cgd4_2				p	1					·	
Copd. 1707   Cop				hydrolase fold							
cpd4_250   cpd4_2540   cpd5_2450   cpd4_2540   cpd5_2450   cpd4_2540   cpd5_2450   cpd6_2470   cpd6_				l'	1		4				
cg44_250   proteasome subunit alpha type 4, NTN hydrolase fold   cg44_530   cg44_530   28S proteasome regulatory subunit 52 bik ex AAA Tipase   1   1   1   1   1   1   1   1   1				1 :	1		'			·	
Cog4				, , , , , , , , , , , , , , , , , , , ,	- 1			1		1	
two bibipution interacting motifs (UIM)   cgd5_200   27 like 265 proteasomal subunit with a PDZ domain   1			cgd4_2540					1			
Cogd 5,280   D27 like 258 proteasomal subunit with a PDZ domain   1			cgd4_530		1					1	0.385
cgd6_2300   Cut4/Act for IT/SG24 family protein; melotic check point regulator and 268 proteasome regulatory complex, PC-prepeats   1			cgd5_2360		1					1	0.464
and 28S proteasome regulatory complex; PC-rep repeats  cgd6_3270  cgd6_3950  cgd6_3950  cgd6_3950  cgd6_3950  cgd6_3950  cgd6_3950  cgd6_3950  cgd6_3950  cgd6_3950  cgd7_2900				1 1 1	-	1					
cgd6_3270   26S proteasome-associated Mov34MPN/FAD-1 family. JAB   1			cgd6_2300		1					1	0.265
Code				and 200 proteasome regulatory complex, 1 0-rep repeats							
Cgd6_3500   CSS proteasome regulatory subunit Rpn-6-liker, PINT domain containing protein   1			cgd6_3270		1					1	0.488
26s protease regulatory subunit 8, pulative			cgd6_3590	26S proteasome regulatory subunit Rpn6-like; PINT domain	1					1	0.393
Cogd7_29900   28S proteasome regulatory subunit, inactive JAB domain protein conteins protein capd8_3090   263 proteasome activator p28 /ki autoantigen   1			-		1					·	
cgd7_3660   cgd8_3090   cgd8_4060   cgd8_3090   cgd8_4060   cgd8_3090   cgd8_4060   cgd8_3090   cgd8_4060   cgd8_3030   cgd8_4060   26S proteasoma subunit 33; PINT domain containing protein   1				, , , , , , , , , , , , , , , , , , , ,	1		1			·	
NTIN hydrolase fold cpd8 3090   cpd8 4090   26S proteasome activator p28/ ki autoantigen   1   1   20.335   cpd8 4090   26S proteasomal subunit 83; PINT domain containing protein   1   1   20.335   cpd8 500   26S proteasomal subunit 83; PINT domain containing protein   1   1   7.003   cpd 40   26S proteasomal regulatory complex, subunit PSMD5   1   1   7.003   cpd 40   29S proteasomal regulatory subunit 12, PINT domain containing protein   1   1   1.335   cpd 40   29S proteasomal regulatory subunit 12, PINT domain containing protein containing protein   1   1   1.355   cpd 40   29S			-							•	
Codd   26S proteasomer sequilatory complex, subunit PSMD5   1   1   1   0.550			cgd7_3660						1	1	41.786
Proteosome Total			-	1:	4			1			
Protessome Total   Ubiquitin   Cgd1_1530   Cgd1_1530   Cgd1_1530   Cgd1_1600			-	1	1			1			
Rpn5 like 26S proteasomal regulatory subunit 12, PINT domain containing protein containing protein transducin / WD-40 repeat protein family		Proteosome Total	loguo_coc	200 protection regulatory complex, capanit r civilibe	14	2	4	6	3		
cgd1 1800   cgd1 290   Cgd1 290   Ub6p like ubiquitin at N-terminus and ubiquitin C terminal hydrolase at the C-terminus ubiquitin conjugating enzyme   1		Ubiquitin		1 · · · · · · · · · · · · · · · · · · ·		1					-
Cgd1_1800			cgd1_1530			1				1	1.535
hydrolase at the C-terminus   1			cgd1_1800		1					1	0.395
cgd1_410			cgd1_290		1					1	0.336
cgd1_860			cgd1 410		1					1	0.304
cgd3_2190							1			1	4.694
terminus cgd3_2410 ubiquitin-fusion degadation-2 (UFD2) family protein with a UBOX at the C-terminus cgd3_2460 UbiA prenythransferase family member (3I27), putative protein with UBC domain, ubiquitin conjugating enzyme E2 ubiquitin fusion degradation protein (UFD1); double Psi beta barrel fold Ubc1p like ubiquitin-conjugating enzyme E2 fused to a UBA domain (UBC+UBA) cgd4_2360 DSK2 like protein with a ubiquitin domain, 2 STI1 motifs and a UBA domain at its C-terminus cgd4_3150 cullin-like protein of probable plant origin cgd4_40 APG7-like ubiquitin activating enzyme E1 cgd5_2480 ubiquitin-conjugating enzyme ubiquitin domain at the C-terminus cgd6_2480 cgd6_1850 cgd6_1850 cgd6_1850 cgd6_2490 cgd6_4180 cgd6_4400 cgd6_4570 UBP_znfinger+UBA; UBPS like deubiquitinating enzyme with a UB hydrolase domain and two UBA domains at the C-terminus cgd7_2840 ubiquitin-conjugating enzyme 1 1 1 0.478 UB hydrolase domain and two UBA domains at the C-terminus cgd7_2840 ubiquitin-conjugating enzyme 1 1 1 0.478 UB hydrolase domain and two UBA domains at the C-terminus cgd7_2840 ubiquitin-conjugating enzyme 1 1 1 0.478 UB hydrolase domain and two UBA domains at the C-terminus cgd7_2840 ubiquitin-conjugating enzyme, putative 1 1 1.981 cgd7_2840 ubiquitin-conjugating enzyme, putative 1 1 1.981 cgd7_2840 ubiquitin-conjugating enzyme, putative 1 1 1.981					1			١.			
cgd3_2410			cgd3_2190					1		1	6.636
cgd3_2460			cgd3_2410	ubiquitin-fusion degadation-2 (UFD2) family protein with a	1					1	0.432
cgd4_1200 ubiquitin fusion degradation protein (UFD1); double Psi beta barrel fold cgd4_210 Ubc1p like ubiquitin-conjugating enzyme E2 fused to a UBA domain (UBC+UBA) cgd4_2360 DSK2 like protein with a ubiquitin domain, 2 STI1 motifs and a UBA domain at its C-terminus cullin-like protein of probable plant origin cgd4_40 APG7-like ubiquitin activating enzyme E1 1 1 2.419 cgd5_2480 ubiquitin-conjugating enzyme 1 1 1 1 0.374 cgd5_2500 ubiquitin C-terminal hydrolase of the cysteine proteinase fold cgd6_1850 cgd6_1850 cgd6_4040 cgd6_2490 cgd6_4040 cgd6_4040 cgd6_4180 ubiquitin-conjugating enzyme 2 1 1 1 1 0.478 ubiquitin-conjugating enzyme 2 1 1 1 1.981 ubiquitin-conjugating enzyme, putative 1 1 1 1.981 ubiquitin-conjugating enzyme, putative 1 1 1 1.981 ubiquitin-conjugating enzyme, putative 1 1 1.981			1 -	1		1				1	1.711
barrel fold   Ubc1p like ubiquitin-conjugating enzyme E2 fused to a UBA   domain (UBC+UBA)   DSK2 like protein with a ubiquitin domain, 2 STI1 motifs and a   UBA domain at its C-terminus   Cullin-like protein of probable plant origin   1   1   2.419   Cgd4_40   APG7-like ubiquitin activating enzyme E1   1   1   1   1.4735   1   1   1   1   1   1   1   1   1			-			1					
domain (UBC+UBA)   DSK2 like protein with a ubiquitin domain, 2 STI1 motifs and a UBA domain at its C-terminus   Cgd4_3150   UBA domain at its C-terminus   Cullin-like protein of probable plant origin   Cullin-conjugating enzyme				barrel fold	1		1				
UBA domain at its C-terminus cgd4_3150 cgd4_40 APG7-like ubiquitin activating enzyme E1 cgd4_570 ubiquitin-conjugating enzyme ubiquitin domain at the C-terminus cgd5_2480 cgd6_2490 cgd6_4404 cgd6_4404 cgd6_4180 cgd6_4550 UBP_znfinger+UBA; UBP5 like deubiquitive cgd7_2800 cgd7_2840 ubiquitin conjugating enzyme proved the C-terminus cgd7_2840 ubiquitin-conjugating enzyme proved the cysteine proteinase fold proved the cysteine proved the cysteine proteinase fold proved the cysteine proved the cysteine proteinase fold proved the cys				domain (UBC+UBA)	1	1					
cgd4_40         APG7-like ubiquitin activating enzyme E1         1         1         5.432           cgd4_570         ubiquitin-conjugating enzyme         1         1         10.077           cgd5_2480         ubiquitin domain at the C-terminus         1         1         1         0.374           cgd5_2500         ubiquitin C-terminal hydrolase of the cysteine proteinase fold         1         1         1         1.680           cgd6_1850         anaphase promoting complex subunit 10, putative         1         1         2         1.001           cgd6_2490         e3 ubiquitin-protein ligase, putative         1         1         3.439           cgd6_4040         cullin domain containing protein         1         1         0.429           cgd6_4180         ubiquitin-conjugating enzyme         1         1         1         10.291           cgd6_4550         UBP_znfinger+UBA; UBP5 like deubiquitinating enzyme with a UB hydrolase domain and two UBA domains at the C-terminus ubiquitin-conjugating enzyme E2, putative         1         1         1         1.981           cgd7_2800         ubiquitin-conjugating enzyme, putative         1         1         4.735				UBA domain at its C-terminus		'					
cgd4_570				_ · · · · · · · · · · · · · · · · · · ·			1				
cgd5_2480							1	1			
cgd5_2500 ubiquitin C-terminal hydrolase of the cysteine proteinase fold anaphase promoting complex subunit 10, putative 1 1 1 2 1.001					1			'			
cgd6_2490   c3 ubiquitin-protein ligase, putative   1   1   3.439   cgd6_4040   cullin domain containing protein   1   0.429   cgd6_4180   ubiquitin-conjugating enzyme   1   1   1   0.478   cgd6_4550   UBP_znfinger+UBA; UBP5 like deubiquitinating enzyme with a UB hydrolase domain and two UBA domains at the C-terminus   cgd7_2800   ubiquitin-conjugating enzyme E2, putative   1   1   1.981   cgd7_2840   ubiquitin conjugating enzyme, putative   1   1   4.735   1   4.735			cgd5_2500			1					
cgd6_4040 cgd6_4180 cgd6_4550 UBP_znfinger+UBA; UBP5 like deubiquitinating enzyme with a UB hydrolase domain and two UBA domains at the C-terminus cgd7_2800 cgd7_2840 ubiquitin-conjugating enzyme E2, putative 1 0.429 1 1 0.429 1 0.429 1 1 0.429 1 1 0.429 1 1 1 0.429 1 1 1 0.429 1 1 0.429 1 1 0.429 1 1 0.478 1 1 0.478					1	1	,				
cgd6_4180 ubiquitin-conjugating enzyme cgd6_4550 UBP_znfinger+UBA; UBP5 like deubiquitinating enzyme with a UB hydrolase domain and two UBA domains at the C-terminus ubiquitin-conjugating enzyme E2, putative 1 1 1 1.981 cgd7_2840 ubiquitin conjugating enzyme, putative 1 1 4.735			-		1		1			·	
cgd6_4550 UBP_znfinger+UBA; UBP5 like deubiquitinating enzyme with a UB hydrolase domain and two UBA domains at the C-terminus cgd7_2800 ubiquitin-conjugating enzyme E2, putative 1 1 1.981 cgd7_2840 ubiquitin conjugating enzyme, putative 1 1 4.735				j .	'			1		·	
cgd7_2800         ubiquitin-conjugating enzyme E2, putative         1         1         1.981           cgd7_2840         ubiquitin conjugating enzyme, putative         1         1         4.735				UBP_znfinger+UBA; UBP5 like deubiquitinating enzyme with a	1					1	
cgd7_2840 ubiquitin conjugating enzyme, putative 1 1 4.735			cad7 2800	1 *		1				1	1 981
						'	1				
			cgd7_4900			1				1	1.361

		cgd7_4990	ubiquitin ligase with a HECT domain at the C-terminus	1					1	0.458
		cgd7_5020 cgd8_1200	ubiqutin family protein E3A like HECT domain containing ubiquitin protein ligase	1	1				1	1.696 0.356
		cgd8_1200 cgd8_1530	ubiquitin carboxyl terminal hydrolase domain that is fused to a	'	1				1	1.628
			MATH domain							
		cgd8_160	ubiquitin activating enzyme E1	1					1	0.438
		cgd8_1730	Uba3p like ubiquitin activating enzyme E1	1		4			1	0.418
		cgd8_3850	Ubc6p like ubiquiting conjugating enzyme E2, possible transmembrane domain at C			'			'	3.408
		cgd8_4340	ubiquitin carboxyl-terminal hydrolase of the cysteine proteinase fold			1			1	4.183
		cgd8_580	ubiquitin-conjugating enzyme E2, putative			1			1	2.735
		cgd8_930	RBX1 ortholog, RING finger (Associated with E3 ubiquitin-	1					1	0.433
	Ubiquitin Total		protein ligase complex)	15	11	9	3		38	2.294
Protein degradation				29	13	13	9	3	67	6.565
	Ferredoxin/FdxR	cgd6_3000	ferredoxin-like protein Fd1, putative	1					1	0.595
		cgd8_2710	NADPH:ferredoxinNADP+ reductase with a rossman fold	1					1	0.368
	Ferredoxin/FdxR Total		nucleotide binding domain and a 2Fe-2S ferredoxin domain	2					2	0.481
	Glutaredoxin	cgd2_2540	glutaredoxin related protein					1	1	250.416
		cgd3_460	glutathione peroxidase				1		1	7.518
		cgd6_3970	glutaredoxin-like protein; 2 thioredoxin folds		1				1	1.456
	Glutaredoxin Total				1		1	1	3	86.463
	SOD	cgd5_3230	superoxide dismutase	1					1	0.489
	SOD Total	oad2 1700	DDI like thiorodoxin domain containing protein	1					1	0.489
	Thioredoxin	cgd2_1780 cgd2_4320	PDI like thioredoxin domain containing protein thioredoxin reductase 1	1				1	1	122.554
		cgd2_4520 cgd4_1650	possible thioredoxin H-type of possible fungal or plant origin,		1			'	1	1.427
		ogu	small protein						•	
		cgd4_740	thioredoxin peroxidase-like protein		1				1	1.488
		cgd5_2030	thioredoxin, putative	1					1	0.405
		cgd5_2230	membrane associated thioredoxin thioredoxin domain containing protein	1					1	0.445 0.486
		cgd5_660 cgd6_2470	thioredoxin (quiescin Q6 like) having signal peptide and 12		1				' 1	2.249
		oguo_zo	transmembrane domains		·				•	2.2.10
		cgd6_850	thioredoxin; protein disulfide isomerase A6, signal peptide,	1					1	0.330
		cgd7_3170	possible transmembrane domain in C-terminal region thioredoxin fold protein related to phosducin	1					1	0.433
		cgd7_3170	phosducin related thioredoxin fold protein	1					1	0.369
		cgd7_5330	thioredoxin/PDI, cyanobacterial type, signal peptide plus 4		1				1	1.675
			transmembrane domains							
		cgd8_3510	thioredoxin-like protein, fragment	1					1	0.477
	Thiorodovin Total			0	4			4	40	
Redox homeostasis	Thioredoxin Total			8	4		1	1	13 19	10.209
Redox homeostasis	Total	cad1 3130	conserved eukaryotic nuclear protein that shares a domain with	11	4 5		1	1 2	13 19	20.714
Redox homeostasis Ribosome biogenesi	Total	cgd1_3130	conserved eukaryotic nuclear protein that shares a domain with yeast Lcp5p, a component of the U3 small nucleolar		5		1		19	
	Total		yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein		5		1		19	20.714 42.968
	Total	cgd2_2420	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase		5	1	1	2	19 1	20.714 42.968 4.514
	Total	cgd2_2420 cgd2_3680	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative		5	1	1		19 1 1 1	20.714 42.968 4.514 53.157
	Total	cgd2_2420 cgd2_3680 cgd2_4090	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase		5	1	1	2	19 1 1 1 1	20.714 42.968 4.514 53.157 18.447
	Total	cgd2_2420 cgd2_3680	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative		5	1	1	2	19 1 1 1	20.714 42.968 4.514 53.157
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56		5	1	1	2	19 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S		5	1	1	2	19 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit		5	1	1	1 1 1 1 1 1	19 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase		5	1	1	2	19 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit		5	1	1	1 1 1 1 1 1	19 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal		5	1	1	1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd4_660	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis		5	1	1 1	1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein		5	1	1 1	1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_3320 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein		4 5	1	1 1 1 1 1	1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein		4 5	1	1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase		4 5	1	1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1520 cgd4_1520 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_1620 cgd7_4110 cgd7_4130	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Yn1022cp-like. SUN family methylase		4 5	1	1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_1620 cgd7_4110	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc		4 5	1	1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1520 cgd4_1520 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_1620 cgd7_4110 cgd7_4130	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexan-		4 5	1	1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1520 cgd4_1520 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_1620 cgd7_4110 cgd7_4130	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc		4 5	1	1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_1620 cgd7_4110 cgd7_4130 cgd8_1550	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Yn1022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexanspecific globular domain KRE33p like superfamily I ATPAse fused to an acetylase S. pombe SPAC1687.04 like conserved eukaryotic protein that		4 5	1 1 1	1 1 1 1 1	1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053 2.783
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_1620 cgd7_4110 cgd7_4130 cgd8_1550	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexanspecific globular domain KRE33p like superfamily I ATPAse fused to an acetylase S. pombe SPAC1687.04 like conserved eukaryotic protein that shares a domain with several MCM7, probably involved in DNA		4 5	1 1 1	1 1 1 1 1	1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053 2.783
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd5_1190 cgd5_11240 cgd6_3230 cgd7_1620 cgd7_4110 cgd7_4130 cgd8_1550 cgd8_2000 cgd8_3360	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexanspecific globular domain KRE33p like superfamily I ATPAse fused to an acetylase S. pombe SPAC1687.04 like conserved eukaryotic protein that shares a domain with several MCM7, probably involved in DNA replication		4 5	1 1 1	1 1 1 1 1	1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053 2.783
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_1620 cgd7_4110 cgd7_4130 cgd8_1550	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexanspecific globular domain KRE33p like superfamily I ATPAse fused to an acetylase S. pombe SPAC1687.04 like conserved eukaryotic protein that shares a domain with several MCM7, probably involved in DNA		4 5	1 1 1	1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053 2.783 54.173 2.357
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd6_3230 cgd7_4110 cgd7_4130 cgd8_1550 cgd8_2000 cgd8_3360 cgd8_3380	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexanspecific globular domain KRE33p like superfamily I ATPAse fused to an acetylase S. pombe SPAC1687.04 like conserved eukaryotic protein that shares a domain with several MCM7, probably involved in DNA replication Rrp12p like nucleolar protein ribosomal processing protein, putative Ydr449cp/Utp6p; small (ribosomal) subunit (SSU)		4 5	1 1 1	1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053 2.783 54.173 2.357
	Total Associated E/Pep	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd7_4110 cgd7_4130 cgd8_1550 cgd8_33360 cgd8_3380 cgd8_3380 cgd8_900	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexanspecific globular domain KRE33p like superfamily I ATPAse fused to an acetylase S. pombe SPAC1687.04 like conserved eukaryotic protein that shares a domain with several MCM7, probably involved in DNA replication Rrp12p like nucleolar protein, putative		4 5	1 1	1 1 1 1 1 1	2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053 2.783 54.173 2.357 42.952 16.800 26.978
	Total	cgd2_2420 cgd2_3680 cgd2_4090 cgd2_50 cgd3_1340 cgd4_1480 cgd4_1520 cgd4_1580 cgd4_3320 cgd4_4040 cgd4_660 cgd5_1190 cgd5_1240 cgd7_4110 cgd7_4130 cgd8_1550 cgd8_33360 cgd8_3380 cgd8_3380 cgd8_900	yeast Lcp5p, a component of the U3 small nucleolar ribonucleoprotein Yd1036cp-like RluD, S4+type 1 pseudouridine synthase eukaryotic ribosome biogenesis; Erb1p, putative YawG/Kre35p-like, Yjeq GTpase SIK1 nucleolar protein Nop56 NMD3p like protein involved in nonsense mediated decay BMS1 like GTpase involved in ribosome biogenesis Brx1p nucleolar protein required for biogenesis of the 60S ribosomal subunit Spb1p-like, FtsJ methylase Noc3 like protein involved in nuclear export of pre-ribosomes Yer006wp-like. Yjeq GTpase Nip7 like PUA domain containing protein involved in ribosomal biogenesis nucleolar protein NOP4; rrm domain containing protein Tsr1p GTpase, multitransmembrane region protein Nop2p family of SUN/fmu RNA methylase nop15p/nopp34; nucleolar protein with 1 RRM domain WD40 protein (part of U3 processesome) Ynl022cp-like. SUN family methylase S. cerevisiae YLR387c-like protein with 2x C2H2 like zinc fingers conserved across eukaryotes plus an apicomplexanspecific globular domain KRE33p like superfamily I ATPAse fused to an acetylase S. pombe SPAC1687.04 like conserved eukaryotic protein that shares a domain with several MCM7, probably involved in DNA replication Rrp12p like nucleolar protein ribosomal processing protein, putative Ydr449cp/Utp6p; small (ribosomal) subunit (SSU)		4 5	1 1 1	1 1 1 1 1 1 6	1 1 1 1 1 1 1 1 1 1	19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20.714 42.968 4.514 53.157 18.447 135.992 160.626 77.938 83.744 100.386 13.214 39.810 75.875 11.459 68.678 8.442 24.411 38.307 12.053 2.783 54.173 2.357

cgd1_2270	40S ribosomal protein S26			1		1	19.394
cgd1_300	40S ribosomal protein S21				1	1	91.571
cgd1_3000	60S ribosomal protein L27				1	1	91.898
cgd1_850	40S ribosomal protein S19 40S ribosomal protein S25				1	1	58.470 90.960
cgd2_1070	ribosomal protein L29				1		70.698
cgd2_120 cgd2_130	60S acidic ribosomal protein LP2			1 1	'	1	14.045
cgd2_170	40s ribosomal protein s24			1		1	13.318
cgd2_2200	60S ribosomal protein L37			'	1	1	35.157
cgd2_280	60S ribosomal protein L15				1	1	124.917
cgd2_2870	40S ribosomal protein S28, no good start Met				1	1	25.847
cgd2_2990	60S ribosomal protein L13, putative				1	1	33.295
cgd2_3000	40S ribosomal protein S16			1		1	17.480
cgd2_350	60S ribosomal protein L39				1	1	36.593
cgd2_4260	40S ribosomal protein S6				1	1	63.051
cgd3_1250	ribosomal protein L14				1	1	33.055
cgd3_1300	60S ribosomal protein L12				1	1	64.008
cgd3_2090	40S ribosomal protein SAe				1	1	41.474
cgd3_2250	60S ribosomal protein L37A				1	1	303.987
cgd3_2440	ribosomal protein S18A, rps18ap, HhH domain				1	1	33.305
cgd3_3790	60S ribosomal protein L19			1	1	1	12.318 27.176
cgd3_3890	60S ribosomal protein L30, pelota RNA binding domain containing protein				'	'1	27.170
cgd3 3930	60S ribosomal protein L27A or L27a				1	1	122.472
cgd3_4100	conserved protein, COG SSU ribosomal protein S8E				1	1	40.342
cgd3_830	60S ribosomal protein L35				1	1	72.728
cgd4_1230	60S ribosomal protein L28				1	1	27.811
cgd4_2260	ribosomal protein PO like protein of the L10 family				1	1	122.290
cgd4_2400	60S ribosomal protein L31				1	1	121.935
cgd4_3080	ribosomal protein S27a, ubiquitin plus zincribbon, UB13p				1	1	36.928
cgd4_3160	putative 40S ribosomal protein S3A				1	1	46.278
cgd4_4020	40S ribosomal protein S2/S5. DSRBD RNA binding domain				1	1	42.169
cgd4_470	60S ribosomal protein L18				1	1	134.102
cgd4_840	possible 60S ribosomal protein L24				1	1	45.215
cgd5_2110	protein with conserved N-terminal localized cysteine-rich domain; predicted archaeo-eukaryotic ribosomal protein					1	3.085
cgd5_2210	40S ribosomal protein S13				1	1	80.909
cgd5_2370	60S acidic ribosomal protein LP1 like protein of possible plant				1	1	25.728
1.3	origin						
cgd5_2630	60S ribosomal protein L7-B; Rp17bp; L30 RNA binding domain				1	1	33.575
cgd5_2780	40S ribosomal protein S10			1		1	8.092
cgd5_3040	40S ribosomal protein S7				1	1	99.993
cgd5_3720	40S ribosomal protein S17				1	1	201.603
cgd5_3740	40S ribosomal protein S12. pelota RNA binding domain containing protein				1	1	80.500
cgd5_970	60S ribosomal protein L13A				1	1	86.027
cgd6_1390	ribosomal protein S23				1	1	166.953
cgd6_2170	60S ribosomal protein L11				1	1	216.518
cgd6_2460	60s ribosomal protein L21				1	1	55.563
cgd6_3180	40S ribosomal protein S15			1		1	7.340
cgd6_3190	60S ribosomal protein-like, putative				1	1	85.370
cgd6_3340	60S ribosomal protein L32				1	1	27.353
cgd6_3710	40S ribosomal protein S30				1	1	28.469
cgd6_4190	60S ribosomal protein L10, alpha/beta hammerhead				1	1	85.290
cgd6_4320	40S ribosomal protein S5			1		1	15.540
cgd6_4620	60S ribosomal protein L26				1	1	31.469
cgd6_4630	40S ribosomal protein S8				1	1	146.828
cgd6_570	60S ribosomal protein L23				1	1	137.766
cgd7_1040	Imp3p-like 40S ribosomal protein S9. S4 RNA binding domain				1	1	50.011
cgd7_130	40S ribosomal protein S14				1	1	79.747
cgd7_1460	ribosomal protein S27				1	1	193.971
cgd7_1600 cgd7_1880	ribosomal protein of the PO/L10 family 60S ribosomal protein L44				1		101.283 90.826
cgd7_1000 cgd7_2110	60S ribosomal proteins L8/L2				1	1	122.703
cgd7_2110	40S ribosomal protein S3, KH domain				1	1	30.563
cgd7_2280	60S ribosomal protein L40				1	1	49.851
cgd7_2420	60S ribosomal protein L22			1		1	10.990
cgd7_2540	60S ribosomal protein L35A			Ι΄	1	1	164.629
cgd7_320	putative 60S ribosomal protein L18A				1	1	45.051
cgd7_4050	ribosomal protein L38				1	1	127.806
cgd7_4460	60S ribosomal protein L6				1	1	76.053
cgd7_4760	ribosomal protein S4, putative				1	1	88.747
cgd7_5060	putative 40S ribosomal protein S20			1		1	21.823
cgd7_5310	60S ribosomal protein L24				1	1	206.286
cgd8_1840	40S ribosomal subunit protein S9, putative				1	1	29.131
cgd8_2870	60S ribosomal protein L10A				1	1	27.680
cgd8_3450	60S ribosomal protein L17	l			1	1	33.615

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Image: comparison of the com			cgd8_3480	60S ribosomal protein L34					1	1	359.597
GSS (Research protects 1.73   1   1   47.125   1   1   47.125   1   1   47.125   1   1   47.125   1   1   47.125   1   1   47.125   1   1   47.125   1   1   1   47.125   1   1   1   47.125   1   1   1   47.125   1   1   1   1   1   1   1   1   1			-	· ·					1		
Comparison   Com				•					1		
Commonwealth   1   1   1   1   1   1   1   1   1				·					1	- 1	
Cogst   500   50				· ·					- 1		
Recommal protein Totals				1				'			
Ribosome protein Total				I '					1	1	
FRNA processing   cgd1_1360   cgd2_1360		D		60S ribosomai protein L23A			4	44	70		
Cogst   1.000				1 5 10 5 4 5			1	11			
Page		rRNA processing	1	1					1		
1				, , , , , , , , , , , , , , , , , , , ,	1					- 1	
WO-M opesate   Comparison   C				/					1	- 1	
293   2960   robosomal RNA assembly protein mis-Sidnible(RT)   K1 domain			cgd3_1090					1		1	11.642
Cagin   3850   Cagin   3850   Cagin   3850   Cagin   3850   Cagin   3850   Cagin   3870   Cagin   3870   Cagin   3870   Cagin   2770   Cagi			oad2 2050						1	4	E2 167
protein with a type I pseudouruline synthase comain (gdd. 3970)  right 1700 r			cgu3_2950	Inbosoniai Kiva assembly protein miss/unbble/kii ip. kii domain					'	'	55.107
protein with a type I pseudouruline synthase comain (gdd. 3970)  right 1700 r			cad3 3850	Cbf5p: centromere-binding factor 5 like PUA domain containing					1	1	236.852
protein   ggist_1700   Ggist_2741   ggist_1700   Ggist_2741   Ggist_			5 - 1 - 1 - 1								
Copd.   1700   Copd.   2780   Copd			cgd3_3970	Yer007c-ap/MCT-1 like PUA RNA binding domain containing			1			1	3.618
Capid				l'							
PAPP   Family protein with WD-40 repeats   1   1   239 24   220   230			-						1		
Cog4   3800   Cop4   3800   Cop4   3800   Cop4   3900   Cox16   ph. MOSE/AbU-Like. S. IN Tainly methylase   1			1	· ·					1	1	
Codd   Sept   Codd   Sept   Codd   Sept   Codd   Sept   Sept   Codd   Sept   Sept   Codd   Sept			cgd4_2750	PWP1 family protein with WD40 repeats					1	1	239.214
Copt7_2570   addnikise_FTSJ family RNA methylase   1   1   1   6.987			cgd4_3800	Rrp8p like methyltransferase involved in rRNA processing				1		1	8.222
Copf. 3590   Copf. 2006   Cop			cgd5_3560	CNcl1p/MJ0026/YebU-like. SUN family methylase			1			1	5.874
Copf. 3590   Copf. 2006   Cop			cgd7_2570	adrift-like. FTSJ family RNA methylase				1		1	6.987
Copt   2050   RAPPE   Rike protein involved in rRNA biogenesis with 7 S1 domains and 5 HAT repeats   242.943   242			cgd7_3590	I and the second				1		1	6.951
Code									1	1	146.228
MIP4 domain at its N-terminus and is involved in rRNA processing Total			-								
Processing			cgd8_3390						1	1	242.943
Ribosome biogenesis Total				I and the second							
RNA binding		rDNA processing Tota	1	processing	1		2	1	0	16	88 007
RNA binding	Dibasama biaganasi		1		1		6	21			
Cgd1_1580   RING finger domain at N-terminus, CCCH domain at C-terminus, involved in RNA metabolism, HC-23 protein ATP-dependent RNA helicase, putative cycle (CGH RNA helicase) (CGH			cad1 1290	domain KOC1676, K homology typo PNA hinding proteins		1	U	21	94	$\overline{}$	
terminus, involved in RNA metabolism, HC-23 protein	NNA IIIetabolisiii	INA billuling	1			<u>'</u>			1		
ATP-dependent RNA helicase, putative   1   1   1   5.533			Cgu1_1560						'	'	250.526
cgd1 _ 2780			cad1 250				1			1	5.533
Sinding domain TGS			-					1		- 1	
cgd1 2960   protein kinase CMGC group, Sky1p like ST protein kinase probably involved in RNA metabolism   sen1p/ NAM7 like superfamily I RNA helicase   1			ogu 1_2700								11.700
cgd1_830   sentp/NAM7 like superfamily I RNA helicase   1   1   34.575			cgd1_2960						1	1	55.879
cgd3_1590   Spb4p, elF4a-1/amily RNA SFII helicase, DEXDc+HELICC domains   cgd3_200   zfwd1 protein, CCCH like RNA binding domain fused to WD repeats   cgd3_2580   RNA binding protein   cgd3_2840   FmRP interacting protein like, contains 2 C2H2 zinc fingers   cgd3_3920   Cgd3_3920   Cgd3_3920   Cgd4_3000   Dgh1p, elF4a-1 family RNA SFII helicase, putative   cgd4_3000   Cgd4_3800   cgd3_3800   cgd5_13800   cgd4_42300   ATP-dependent RNA helicase, putative   cgd4_3800   cgd5_13800   cgd5_13800   cgd4_42300   ATP-dependent helicase, putative   cgd4_42300   ATP-dependent helicase, putative   cgd5_13800   cgd5_24600   cgd5_2			-	probably involved in RNA metabolism							
cgd3_200   cgwd1 protein, CCCH like RNA binding domain fused to WD repeats   cgd3_2840   FMRA binding protein   like, contains 2 C2H2 zinc fingers   linvived in RNA metabolism   DEAD/DEAH box ATP-dependent RNA helicase, putative   cgd4_3000   cgd4_3880   map RNA binding domain protein (N terminal low complexity region)   cgd4_1230   cgd5_1360   cdd4_1230   cdd5_1360   cdd4_1230   cdd5_1380   cdd5_1380   cdd4_1230   cdd4_			cgd1_830	sen1p/ NAM7 like superfamily I RNA helicase			1			1	2.655
Cgd3_200			cgd3_1590	Spb4p, eIF4a-1-family RNA SFII helicase, DEXDc+HELICc					1	1	34.575
repeats											
cgd3_2840			cgd3_200						1	1	168.129
Cgd3_2840			oad2 2500					4		4	0.012
Involved in RNA metabolism			-							- 1	
Cgd3_3920   DEAD/DEAH box ATP-dependent RNA helicase, putative   Dbp1p, elF4a-1 family RNA SFII helicase (DEXDCHELICC)   1			cga3_2840					1		1	10.285
cgd4_3800   Dbp1p, elF4a-1 family RNA SFII helicase (DEXDC+HELICc)   1   1   1   1   18.046			cad3 3920						1	1	92 761
cgd4_3880   emap RNA binding domain protein (N terminal low complexity region)   cgd4_4230   ATP-dependent helicase, putative   1   1   72.883   cgd5_1380   cCCH RNA binding domain involved in RNA metabolism   cgd5_1830   cf1M21.28-like protein having 3 CCCH RNA binding domains; involved in RNA metabolism   cgd5_2470   cgd5_2460   cgd5_2470   cgd5_2460   cgd5_2470   cgd5_2460   cgd5_2470   cgd5_2460   cgd5_2870   cgd5_2870   cgd5_2870   cgd5_3870   cgd5_3870   cgd5_3870   cgd6_3010   cgd6_30								1		'	
region   ATP-dependent helicase, putative   1 1 72.883   Cgd5_1370   CCCH RNA binding domain involved in RNA metabolism   1 1 2.353   Cgd5_1380   F11M21.28-like protein having 3 CCCH RNA binding domains; involved in RNA metabolism   1 1 1.705   Cgd5_1830   Cgd5_2870   SPAC694_02. SNI family SFII helicase   1 1 1 1.2.737   Cgd5_2460   Cgd5											
Cgd4_4230			Cgu4_3660					'		'	0.720
CCCH RNA binding domain involved in RNA metabolism cgd5_1380   F11M21_28-like protein having 3 CCCH RNA binding domains; involved in RNA metabolism cgd5_2870   F11M21_28-like 3 CCCH RNA binding domain protein involved in RNA metabolism cgd5_2270   SPAC694_02_SK1 family SFII helicase cgd5_2870   RNA binding RGG repeats plus RRM domain containing protein cgd5_2870   F11M21_28-like; 3 CCH RNA binding domain protein involved in RNA metabolism cgd5_3870   Cgd6_3870   Cgd6_3870   Cgd6_3910   Cgd6_4910   F11M21_28-like; protein with 3 CCCH RNA binding domains, involved in RNA metabolism cgd7_2560   RNA metabolism cgd7_2560   Cgd7_3510   Cgd8_1820   Cgd8_1820   Cgd8_2520   Cgd8_2520   Cgd8_2520   Cgd8_3220   Cgd8_2520   Cgd8_3220   Cgd8_3220   Cgd8_3220   Cgd8_3220   Cgd8_3220   RNA binding Total   RNA binding Total   RNA binding Total   RNA binding Total   RNA degradation   Cgd2_2090   mitotic control protein dis3, putative cgd3_3270   possible nucleotide kinase related to CMP and AMP kinases   1			cgd4 4230						1	1	72.883
cgd5_1380			1				1			1	
Involved in RNA metabolism			1	<u>-</u>		1				1	
cgd5_1830			39.5_1000			,				'	1.700
in RNA metabolism			cgd5_1830		1					1	0.546
Cgd5_2460   RNA binding RGG repeats plus RRM domain containing protein cgd5_2870   F11M21.28-like; 3 CCH RNA binding domain protein involved in RNA metabolism cgd5_3870   yprA. Lhrt/Ski2 family RNA SFII helicase   1   0.366   cgd6_3010   poly(a)-binding protein fabm, putative   1   1   482.085   cgd6_4910   F11M21.28-like protein with 3 CCCH RNA binding domains, involved in RNA metabolism   Cgd7_2560   Sgd1p; NIC plus MI domains containing protein involved in RNA metabolism   cgd7_3510   helicase, putative   1   1   1.845   cgd8_1820   ATP-dependent RNA helicase, putative   1   1   1.5.336   cgd8_2520   Mt4p like SKI family SFII helicase   1   1   3.2.047   cgd8_3220   cgd8_3220   La domain fused to two RRMs (as in the La autoantigen) which is further fused to a C-terminal domain present in the plant DCL protein and the C-terminus of the alpha subunit of the plant RNA polymeras   RNA binding Total   RNA degradation   cgd2_2090   mitotic control protein dis3, putative   1   1   2.745   RNA degradation   cgd2_2090   mitotic control protein dis3, putative   1   1   2.745   1   1   7.351			-	in RNA metabolism							
Cgd5_2870			-	SPAC694.02. SKI family SFII helicase				1		1	12.737
RNA metabolism   yprA. Lhr1/Ski2 family RNA SFII helicase   1   1   0.366			cgd5_2460	RNA binding RGG repeats plus RRM domain containing protein			1			1	4.249
cgd5_3870   cgd6_3010   cgd6_3010   cgd6_3010   cgd6_4910   cgd6_4910   F11M21.28-like protein with 3 CCCH RNA binding domains, involved in RNA metabolism   cgd7_2560   Sgd1p; NIC plus MI domains containing protein involved in RNA metabolism   cgd7_3510   helicase, putative   cgd8_1820   cgd8_1820   cgd8_2520   cgd8_2520   cgd8_3220   La domain fused to two RRMs (as in the La autoantigen) which is further fused to a C-terminal domain present in the plant DCL protein and the C-terminus of the alpha subunit of the plant RNA polymeras   cgd2_2090   mitotic control protein dis3, putative   cgd3_3270   mitotic control protein dis3, putative   cgd8_added   control protein disd, putative   cgd3_3270   cgd3_3270   cgd3_3270   cgd3_3270   cgd1   control protein dis3, putative   cgd2_200   cgd3_3270   cgd3_3270   cgd2_2090   cgd3_3270   cgd3_3270   cgd2_2090   cgd3_3270   cgd2_2090   cgd3_3270   cgd3_			cgd5_2870		1					1	0.346
cgd6_3010   cgd6_4910   F11M21.28-like protein fabm, putative   F11M21.28-like protein with 3 CCCH RNA binding domains, involved in RNA metabolism   cgd7_2560   Sgd1p; NIC plus MI domains containing protein involved in RNA metabolism   cgd7_3510   helicase, putative   cgd8_1820   ATP-dependent RNA helicase, putative   1   1   1   1   1   1   1   1   1											0.000
Cgd6_4910			-	157	1					1	
involved in RNA metabolism			1						1	1	
Cgd7_2560   Sgd1p; NIC plus MI domains containing protein involved in RNA metabolism   1   1   1   1   1   1   1   1   1			cgd6_4910						1	1	482.085
metabolism			cad7 2560			4				1	1 0/F
Cgd7_3510   helicase, putative   1   1.453			cgu7_2560			1				'	1.040
ATP-dependent RNA helicase, putative   1   1   5.336			cad7 3510			1				1	1 453
cgd8_2520 Mtr4p like SKI family SFII helicase La domain fused to two RRMs (as in the La autoantigen) which is further fused to a C-terminal domain present in the plant DCL protein and the C-terminus of the alpha subunit of the plant RNA polymeras  RNA binding Total RNA degradation cgd2_2090 mitotic control protein dis3, putative cgd3_3270 possible nucleotide kinase related to CMP and AMP kinases    1			1				1			1	
cgd8_3220 La domain fused to two RRMs (as in the La autoantigen) which is further fused to a C-terminal domain present in the plant DCL protein and the C-terminus of the alpha subunit of the plant RNA polymeras  RNA binding Total RNA degradation cgd2_2090 mitotic control protein dis3, putative cgd3_3270 possible nucleotide kinase related to CMP and AMP kinases  La domain fused to two RRMs (as in the La autoantigen) which is further fused to a C-terminal domain present in the plant DCL protein and the plant RNA polymeras  3 4 5 6 10 28 65.921  1 1 73.442			1						1	1	
is further fused to a C-terminal domain present in the plant DCL protein and the C-terminus of the alpha subunit of the plant RNA polymeras  RNA binding Total  RNA degradation cgd2_2090 mitotic control protein dis3, putative cgd3_3270 possible nucleotide kinase related to CMP and AMP kinases  is further fused to a C-terminal domain present in the plant DCL protein the plant RNA plant RNA polymeras  3 4 5 6 10 28 65.921  1 1 7.351									1	- 1	
protein and the C-terminus of the alpha subunit of the plant RNA polymeras  RNA binding Total  RNA degradation cgd2_2090 mitotic control protein dis3, putative 1 2.745 cgd3_3270 possible nucleotide kinase related to CMP and AMP kinases 1 1 7.351			3943_0220							'	70.772
RNA binding Total   3 4 5 6 10 28 65.921   RNA degradation   cgd2_2090   mitotic control protein dis3, putative   1   1   2.745     cgd3_3270   possible nucleotide kinase related to CMP and AMP kinases   1   1   7.351				protein and the C-terminus of the alpha subunit of the plant RNA							
RNA degradation cgd2_2090 mitotic control protein dis3, putative 1 2.745 cgd3_3270 possible nucleotide kinase related to CMP and AMP kinases 1 1 7.351				polymeras							
cgd3_3270 possible nucleotide kinase related to CMP and AMP kinases 1 7.351			10		3	4	5	6	10	28	
		RNA degradation					1			1	
			1	l'				1		- 1	
			Jogus_330	1 opzp-like 3.3 exonuclease, OOR4-NOT transcription complex						- 1	12.238

	cgd3 800	POP4 like ribonuclease P protein subunit			1		ı	1	3.0
	cgd3_000 cgd4_1950	RPR46-like RNAse PH domain			1				2.3
	cgd4_1930	archeo-eukaryotic exosomal RNAse			'	1			5.7
	1	1		4		'		1	
	cgd6_2080	Kem1p-like 5'-3' exonuclease		1				1	1.8
	cgd7_230	RPR45-like archaeo-eukaryotic exosomal RNAse PH			1			1	3.7
	cgd7_2380	RRP45-like archaeo-eukaryotic exosomal rnase, PH domain			1			1	3.6
	cgd8_2250	Rat1 Kar1/Rat1 like 5'-3' exonuclease				1		1	8.6
	cgd8_3310	S. cerevisiae Ylr022cp like protein that has a C2H2 zinc finger		1				1	1.8
		and is a component of the exosome							
	cgd8_5150	ssd1p/F48E8.6-like RNAseII			1			1	2.7
RNA degradation Tota	ıİ			2	6	4		12	4.6
RNA modification	cgd1_1310	cleavage stimulation factor subunit 2 that has a CSF1 like RRM				1		1	8.3
		domain							
	cgd1_1720	tRNA (Gm18) ribose methylase; trm3p; SpoU superfamily -	1					1	0.4
	J -	SPOUT methylase							
	cgd1_3440	Dus1p, tRNA dihydrouridine synthase		1				1	1.9
	cgd2_2710	TrmA RNA methylase			1			1	4.8
	cgd2_3570	YjbN-like Dus1p tRNA dihydouriding synthase Tim barrel				1		1	10.3
		Maf protein like, involved in RNA metabolism			4	'		1	5.3
	cgd2_4300	1 .						l I	
	cgd2_570	tRNA/rRNA methyltransferase-like protein, putative			1			1	2.4
	cgd3_2040	Cca1p, tRNA adenylyltransferase	1					1	0.3
	cgd3_3500	Nop12p nucleolar protein, RRM domain			1			1	2.3
	cgd3_4330	Dbr1p-like RNA lariat debranching enzyme	1					1	0.3
	cgd3_450	Ctl1p-like mRNA capping enzyme beta subunit (polynucleotide	1					1	0.
	0900_100	5'-triphosphatase)						i i	0.
	cgd4 2830	Mra1/NEP1 like protein, involved in pre-rRNA processing,					1	1	73.
	2000	adjacent genes putative paralogs						'	73.
	cgd4 2840	Mra1/NEP1 like protein, involved in pre-rRNA processing,					1	1	40.
	cgu+_20+0	adjacent genes putative paralogs					'	'I	40.
	cgd4 3250	Trm1p. N2,N2-dimethylguanosine tRNA methyltransferase			1			1	5.4
		Ydr140wp-like HemK family methylase. archaeal-like. RNA	1						0.1
	cgd4_3740		'					'	0
	cgd4_930	methylase pap1p; poly A polymerase (eukaryotic type)			4			1	2.
	1							1	
	cgd5_1730	nclip/MJ0026/YebU-like; SUN family methylase				1		1	7.
	cgd5_2390	GCD10p. RNA methylase				1		1	5.
	cgd5_2470	GCD14 RNA methylase			1			1	3.
	cgd5_2880	C1p1p GTpase. Pre-mRNA cleavage complex protein	1					1	0.
	cgd5_4420	MJ0710-like (thump + methylase domains). RNA methylase			1			1	4.
	cgd5_520	MJ1157-like thiouridine synthase (Pploop atpase) plus Zn	1					1	0.
	0900_020	ribbon. involved in RNA metabolism.	'					'	0.
	cgd6_1230	GTpase Grc3p-like Pre-mRNA cleavage complex			1			1	3.
				1					1.
	cgd6_1520	2-methylthioadenine synthetase; MiaB						1	
	cgd6_2010	YbiN-like RNA methylase (NPPY variety; HemK family)	1					1	0.
	cgd6_2380	mRNA capping enzyme; RNA guanylyltransferase Ceg1p		1				1	2.
	cgd6_2540	tRNA delta(2)-isopentenylpyrophosphate transferase, putative			1			1	4.
	cgd6_3560	MJ0041-family pseudouridylate synthase; Zn finger +thump +				1		1	11.
		Psusyn							
	cgd6_400	Pre-mRNA polyadenylation factor			1			1	3.
	cgd6 410	Sgn1p-like RRM domain containing protein			1			1	2.
	cgd6 5130	Trm5 RNA methyltransferase				1		1	11.
	-	The state of the s						الاا	
	cgd6_930	Dim1p-like ERMB/KSGA methylase (dimethyladenosine				1		1	6.
	17 4500	transferase)						ا ا	0.4
	cgd7_1530	ART-4 protein; PIN+Zn ribbon domains. involved in RNA				1		1	24.
		metabolism							-
	cgd7_1630	Ncl1p/MJ0026/YebU-like. SUN family RNA methylase	1					1	0.
	cgd7_2810	ortholog of kin17 (RNA metabolism proteins): a family of highly	1					1	0.
		conserved zinc binding C-rich proteins with KOW domains							
	cgd7_830	queunine tRNA-ribosyltransferase				1		1	7.
	cgd8_1100	NRAP like nucleolar RNA associated protein		1				1	1.
	cgd8_1120	HBS1 eRFS. GTpase. (RNA metabolism; translation)			1			1	4.
	cgd8_1460	Sex-lethal interacting like				1		1	9.
		Ţ			4	'		1	
	cgd8_1580	saccharomyces Yor006cp like protein conserved across euks						1	3.
	and0 1050	and archaea					4	1	76.
	cgd8_1650	partner of Nob1; Pno1p; Yor145cp like KH domain containing					'	'	70.
	2240 2660	protein				4		4	0
	cgd8_3660	RNA 3'-Terminal Phosphate Cyclase-like protein				1		1	8.
	cgd8_4150	RRM+RGG RNA binding repeats			1			1	5.
		fibrillarin. RNA methylase					1	1	106.
	cgd8_4330	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1					1	0.
		Icleavage and polyagenylation specifity factor protein. CPSF							
	cgd8_4330 cgd8_460	cleavage and polyadenylation specifity factor protein, CPSF metallobeta-lactamase	·						
	cgd8_460	metallobeta-lactamase			1			1	3
	cgd8_460 cgd8_510	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA		1	1			1	
DNA modification Total	cgd8_460 cgd8_510 cgd8_5280	metallobeta-lactamase		1	1	44	1	1	2.
	cgd8_460 cgd8_510 cgd8_5280	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA	11	1 5	16	11	4	1 47	2. 10.
	cgd8_460 cgd8_510 cgd8_5280 at cgd1_2250	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA small nucealr riboprotein SMD3, SM domain	11	1 5 1	16	11	4	1 47 1	2. 10. 2.
	cgd8_460 cgd8_510 cgd8_5280	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA small nucealr riboprotein SMD3, SM domain Ro ribonucleoprotein-binding protein 1, RNA binding protein with	11	1 5 1	16	11	4	1 47	2. 10. 2.
	cgd8_460 cgd8_510 cgd8_5280 al cgd1_2250 cgd1_2730	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA  small nucealr riboprotein SMD3, SM domain Ro ribonucleoprotein-binding protein 1, RNA binding protein with 3x RRM domains	11	1 5 1	16	11	1	1 47 1	2. 10. 2. 29.
	cgd8_460 cgd8_510 cgd8_5280 at cgd1_2250	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA  small nucealr riboprotein SMD3, SM domain Ro ribonucleoprotein-binding protein 1, RNA binding protein with XRM domains splicing factor U2AF like SnRNP auxilary factor large subunit,	11	1 5 1	16	11	1	1 47 1	2. 10. 2. 29.
RNA modification Tota RNA splicing	cgd8_460 cgd8_510 cgd8_5280 al cgd1_2250 cgd1_2730 cgd1_3080	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA  small nucealr riboprotein SMD3, SM domain Ro ribonucleoprotein-binding protein 1, RNA binding protein with 3x RRM domains	11	1 5 1	16	11	1	1 47 1 1	3. 2.7 10.3 2.2 29.0
	cgd8_460 cgd8_510 cgd8_5280 al cgd1_2250 cgd1_2730	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA  small nucealr riboprotein SMD3, SM domain Ro ribonucleoprotein-binding protein 1, RNA binding protein with XRM domains splicing factor U2AF like SnRNP auxilary factor large subunit,	11	1 5 1	16	11	1	1 47 1 1	2.7 10.3 2.2 29.0
	cgd8_460 cgd8_510 cgd8_5280 al cgd1_2250 cgd1_2730 cgd1_3080	metallobeta-lactamase Pus1p-like type II pseudousynthas TruA Deg1p-like type II pseudouridylate synthase TruA  small nucealr riboprotein SMD3, SM domain Ro ribonucleoprotein-binding protein 1, RNA binding protein with 3x RRM domains splicing factor U2AF like SnRNP auxilary factor large subunit, RRM domain	11	1 5 1	16	11	1	1 47 1 1	2.7 10.3 2.2 29.0

		cgd2_2770	U5 small nuclear ribonucleoprotein 200kDA helicase, Pre-mRNA	. 1					1	0.397
			splicing helicase BRR2 2 (RNA helicase plus Sec63 domain)							
		cgd2_3510	Cus1p U2 snRNP protein		1				1	1.504
		cgd2_740	cut up CG6998-PA, putative			1			1	3.650
		cgd3_1060	U1 like C2H2 zinc finger	1					1	0.431
		cgd3_1230	SPAC14C4.06c-like PWI+4CCCH domains			1			1	4.723
		cgd3_1920	possible PRP38 pre-mRNA splicing factor family member	1					1	0.497
		cgd3_2110	nucleolar protein NOP5/NOP58-like pre-mRNA splicinig factor					1	1	111.170
		cgd3_2880	prp31 U2 small nuclear ribonucleoprotein A' like LRR repeats	1					4	0.569
		cgd3_2660 cgd3_3690	U5 snRNP 100 kD protein, putative			1			1	2.353
		cgd3_3880	Snu114p GTpase, U5 snRNP-specific protein, 116 kDa			'	1		1	15.924
		cgd4_150	pre-mRNA splicing protein; Prp31plike		1				1	2.225
		cgd4_270	30 kDa splicing factor, SPF 30, tudor domain containing protein				1		1	5.659
		cgd4_3190	small nuclear ribonucleoprotein			1			1	3.633
		cgd5_1330	SPAC25G10.01-like RRM domain containing protein					1	1	329.994
		cgd5_1740	conserved protein, possible U4/U6 associated RNA splicing	1					1	0.490
			factor					4	اد	24 224
		cgd5_1760	small nucleolar RNP protein , Gar1 protein RNA binding region		4			1	1	31.331
		cgd5_2220	small nuclear ribonucleoprotein D1. SM domain containing protein						'	2.190
		cgd5_2960	U5snrp Brr2 SFII RNA helicase (sec63 and the second part of			1			1	5.387
			the RNA							
		cgd5_3710	small nuclear ribonucleoprotein U6			1			1	2.410
		cgd5_4090	DHR1/Ecm16p/kurz. HrpA family SFII helicase			1			1	2.720
		cgd5_700	musashi. RRM domain containing protein, splicing related					1	1	52.477
		cgd5_920	Pre-mRNA splicing factor Pro1/Prp6. HAT repeat protein pre-mRNA splicing factor ATP-dependent RNA helicase.			4	1		1	5.868
		cgd6_1410	pre-minima splicing factor ATP-dependent RNA helicase, putative			'			'1	5.044
		cgd6_1680	splicing factor U2AF U2 snRNP auxiliary factor large subunit; 3	1					1	0.420
		-	RRM domains							
		cgd6_2150	U1 snrnp, putative				1		1	13.022
		cgd6_2830	splicing factor 3a 66kD; N-terminus C2H2 domain	1					1	0.531
		cgd6_3850	HOI-POLLOI protein; U4/U6.U5 snRNP component; Snu13p; pelota RNA binding domain containing protein					1	1	494.940
		cgd6_4490	U2 snRNP. Hsh49p, RRM domain containing protein	1					1	0.389
		cgd6_4670	Prp9p-like splicing factor 3a subunit 3 snRNP. C-terminal C2H2			1			1	4.092
		cgd6_4710	5x RRM. Mrd1p like, splicing related					1	1	48.769
		cgd6_4750	splicing factor 3B subunit1-like HEAT repeat containing protein	1		1			2	1.965
		cgd6_990	U1 snrp Snp1p. RRM domain containing protein				1		1	6.729
		cgd7_1070	snRNP core protein		1				1	1.994
		cgd7_1750	step II splicing factor SLU7, putative		1				1	2.254
		cgd7_2040	small nuclear ribonucleo protein					1	1	40.264
		cgd7_2160	Pre-mRNA splicing factor SF3a. 2xSWAP domain protein		1				1	1.790
		cgd7_3610	RPR domain protein (involved in RNA metabolism)		1				1	1.394
		cgd7_3960	pleiotropic regulator 1 (spliceosome/RNA splicing)			1			1	3.349
		cgd7_4580	U6 snRNA-associated Sm-like protein LSm5. SM domain			4		1	1	27.760
		cgd7_5220 cgd7_5230	splicing factor with 3 RRM domains possible D-Tyr-tRNatyr deacylase		4	1			1	2.318 1.549
		cgd7_5230 cgd7_5490	PRP18 (SFM+PRP18 domains)		'		4			21.072
		cgd7_5490 cgd7_640	Prp16p pre-mRNA splicing factor. HrpA family SFII helicase				1		<u>'</u>	13.492
		cgd7_690	small nuclear ribonucleoprotein			1			1	4.467
		cgd7_940	splicing factor RRM domain containing protein; T22E16.120					1	1	871.806
			SC35-like splicing factor					· i		0
		cgd8_1480	RPR domain containing protein, present in proteins involved in					1	1	33.306
		oad0 100	mRNA splicing				4		4	22.207
		cgd8_190	Mak5 pre-mRNA splicing RNA SFII helicase shares a domain with a conserved HREF motif with the CWF15		4		1		1	22.297 1.842
		cgd8_1950	protein that is involved in mRNA splicing						'	1.042
		cgd8_3340	PWI domain containing protein that is typically seen in				1		1	20.209
			spliceosomal proteins							
		cgd8_3370	splicing factor SRP40 like 2x RRM domains		1				1	1.666
		cgd8_3690	mitosis protein DIM1			1			1	4.316
		cgd8_4100	PRP43 involved in spliceosome disassembly mRNA splicing U2AG splicing factor U2AF U2snRNP auxilliary factor small	1		7			1	2.591
		cgd8_5240	subunit CCCh+RRM+CCCh-like						'	0.444
	RNA splicing Total			11	13	15	9	11	59	38.629
	Rnase	cgd1_980	RNase L inhibitor-like protein				1		1	12.043
		cgd5_100	RRPp/PMC2 like exosome 3'-5' exoribonuclease subunit with an				1		1	17.426
		oad6 1010	RNAseD domain and an HRDc domain				4		4	10.010
	Phase Total	cgd6_1040	RNAse P Rpr2/Rpp21 subunit domain				7		3	12.210 13.893
	Rnase Total tRNA synthesis	cgd8 4870	tRNA synthetase class II, putative				3	1	1	13.893
	tRNA synthesis Total		u u v v syriuretase ciass II, putative					1	1	117.491
RNA metabolism Tot				25	24	42	33	26	150	32.173
Structure	Cytoskeleton	cgd1_1540	dynein intermediate chain			1	- 50		1	3.460
	1	cgd1_2430	ARP3 actin related protein		1				1	1.667
		cgd1_2530	TRAFAC type P-loop GTpase that may be related to kinesin		1				1	1.835
		cgd1_2740	centromere/kinetochore protein		1				1	2.215

		cgd2_70 cgd2_80 cgd2_90 cgd3_410	ABC transporter, with 12 x transmembrane domains and 2x AAA domains ABC transporter family protein, 2x AAA domain ABC transporter with 9x transmembrande domains and 2xAAA putative ABC transporter, 12x transmembrane domains plus 2x AAA			1		1 1	1 1 1	39.530 2.792 38.365 89.437
			domains	ì		1		1	1	
			LADO terran enten with 40 orter enten enten de entine en d'Orr A A A							20 520
		cgd2_3870	putative ABC transporter with 2x AAA and 11+ transmembrane domains	1					1	0.357
Transporter	ABC	cgd1_1350 cgd1_700	ATM1-like ABC transporter with 6 transmembrane domains ATP-binding cassette protein	1			1		1	0.410 12.399
Structure Total	,	1		19	16	9	8	4	56	19.575
	Oocyst wall Total	cgd8_3350	oocyst wall protein 4	1	1	1	2		1 5	1.637 9.410
		cgd7_1800	rich repeats oocyst wall protein 2	1					1	0.390
		cgd6_2090	CpCOWP1, oocyst wall protein with type I and type II cysteine-				1		1	19.890
	Oocyst wall	cgd4_3090 cgd6_200	oocyst wall protein 6 oocyst wall protein 8			1	1		1	5.214 19.890
	Cytoskeleton Total			18	15	8	6	4	51	20.572
		cgd8_5030 cgd8_710	articulin family protein, Pfs77 protein-related myosin heavy chain	1		1			1	2.483 0.351
		cgd8_500	caltractin, centrin			1			1	3.538
		cgd8_4120	belongs to the TRAFAC class GTpase superfamily caltractin (centrin)-like, contains 3x EFh domains	- 1					, 1	0.404
		cgd8_2450 cgd8_3300	formin homology 2 domain (FH2) protein centromere associated Kip3p, kinesin like P-loop NTpase that		1		1		1	1.720 7.440
		cgd8_2200	BRG1/brm-associated factor 53A like actin		1				1	1.359
		cgd8_1280 cgd8_1980	centrin, caltractin actin-related protein Arp23 like WD 40 repeate protein	1					1	0.545 0.299
		cgd8_1070	actin	1					1	0.434
		cgd7_4350	myosin'unconventional myosin fused to an RCC1 domain (unique)'			1			1	2.722
		cgd7_4090	alpha superhelical protein, divergent TPR like repeats, possible microtubule associated protein		1				1	1.203
		cgd7_3790	eukaryotes unconventional myosin					1	1	293.367
		cgd7_3330	Ced12 family of proteins that are conserved throughout		1				1	1.839
		cgd7_2370 cgd7_3060	EB1 like microtubule binding protein gamma-tubulin complex associated protein	1	1				1 1	0.503 1.624
		cgd7_2210	kinesin-like protein				1		1	12.644
		cgd7_1980	(possible variant metal binding site at N-terminus) gamma tubulin	1					1	0.404
		cgd7_1660	STOP repeat protein involved in microtubule stabilization		1				1	1.572
		cgd6_4560 cgd6_4760	myosin'myosin' tubulin beta chain	1			1		1	10.295 0.407
		cgd6_4340	myosin-related protein, putative		1				1	2.314
		cgd6_4150 cgd6_4210	formin-related protein, putative kinesin-like boursin, putative		1		1		1	2.108 10.185
		cgd6_3410	tubulin, gamma tubulin complex protein 3	1				•	1	0.315
		cgd6_1920 cgd6_3370	putative kinesin heavy chain microtubule-associated protein	1				1	1 1	0.285 35.773
		cgd6_1900	kinesin heavy chain, putative				1		1	13.879
		cgd5_60 cgd5_640	centrin like protein with 4x EF hands articulin family protein	1		1			1 1	0.609 4.728
		cgd5_4080	articulin family protein	1					1	0.470
		cgd5_2800 cgd5_3160	actin depolymerizing factor actin					1 1	1	122.394 475.922
		cgd5_2330	actin-like	1					1	0.394
		cgd4_3300 cgd5_1320	articulin family protein, adjacent paralogous gene actin-like protein, putative		1	1			1	4.038 1.832
		cgd4_3290	articulin family protein, adjacent paralogous gene		1				1	1.613
		cgd3_3650 cgd4_2860	centrin like EF hand protein alpha tubulin	1		1			1	0.520 2.574
		cgd3_2590	kinesin-related protein K2	1					1	0.302
		cgd3_2120	myosin fused to 3 IQ motifs (that interact with calmodulin) and Rcc1 domain			1			1	2.251
		cgd3_140	b-tubulin specific chaparone	1	'				1	0.344
		cgd2_1430 cgd2_4150	dynactin subunit p62, putative articulin family protein	1	1				1	0.387 1.771
		cgd1_920	actin		1		,		1	1.558
		cgd1_3460 cgd1_3570	F-actin capping protein, beta subunit myosin regulatory light chain	1			1		1	0.363 7.894

	cgd6_5450 cgd7_2730	ABC transporter, AAA domain ABC transporter with ATpase domain plus 3 transmembrane		1 1				1	1.474 1.561
	cgd7_4510	regions ATP-binding cassette, sub-family C (CFTR/MRP), member 2; Canalicular multispecific organic anion transporter; multidrug					1	1	215.298
	cgd7_4520	resist ABC ATpase (2 ABC domains) with 10 transmembrane					1	1	59.214
	cgd7_4800	domains, adjacent duplicated gene ABC transporter, amino acid transporter 12 transmembrane				1		1	5.654
	cgd8_3250	spanning subunit ABC1 like protein kinase			1			1	3.306
ABC Total			5	3	2	2	6	18	28.056
lon	cgd1_2190 cgd1_2620	K+/H+ antiporter of possible bacterial origin, signal peptide calcium antiporter, Na/Ca exchange associated membrane	1				1	1	0.314 48.636
	cgd1_3050	protein with 11 transmembrane domains cation diffusion facilitator like membrane protein transporter, 6x	1					1	0.441
	cgd2_2680	transmembrane domains possible MgtA, cation transport ATpase, signal peptide, 12			1			1	3.968
	cgd3_2730	transmembrane domains protein with 10 transmembrane domains, possible calcium	1					1	0.343
	cgd3_3520	transporting ATpase or aminophospholipid transporter putative sodium/calcium cation exchanger having 12				1		1	25.496
	cgd4_1470	transmembrane domains and signal peptide vacuolar proton translocating ATpase with 7 transmembrane					1	1	33.580
	cgd6_130	regions near C-terminus possible Na+/H+ and K+/H+ antiporter with 12 transmembrane			1			1	4.089
	cgd6_140	domains, duplicated adjacent gene possible Na+/H+ and K+/H+ antiporter with 12 transmembrane domains, duplicated adjacent gene					1	1	99.176
	cgd7_4070	arsenical pump-driving ATPase	1					1	0.378
	cgd7_4190	cation-transporting P-type ATpase with 11 or more transmembrane domains				1		1	9.950
	cgd7_90	high affinity sulfate transporter-related			1			1	2.295
	cgd8_2090	cation-transporting ATpase 2 with 8 transmembrane domains				1		1	15.144
Ion Total MFS	and0 1450	major facilitator aumorfamily protein mutative 12	4		3	3	3	13	18.755
MF5	cgd2_1450	major facilitator superfamily protein, putative, 12 transmembrane domain	1					1	0.294
	cgd7_3450	major facilitator (MFS) superfamily transporter containing 12 transmembrane domains				1		1	7.739
MFS Total			1			1		2	4.016
Nuclear transport	cgd3_2360 cgd3_300	putative nucleoporin, FG-rich motifs within N-terminal region rasputin. nuclear transport factor 2 (NTF2) domain plus RRM domain	1	1				1	1.722 0.399
	cgd3_3060	putative exportin 1			1			1	2.438
	cgd5_3950	Ran-binding protein		1				1	2.101
	cgd6_4610	mRNA export protein, putative				1		1	7.614
	cgd7_1670	nuclear pore protein RBP16/17 (RAN binding protein 16/17)				1		1	8.334
	cgd7_1780	tRNA exportin type nuclear export protein					1	1	25.649
	cgd7_1970	nuclear pore associated protein (NLP4) with N-terminal ubiquitin domain	1					1	0.559
	cgd7_220	GTP-binding nuclear protein ran/tc4	4				1	1	59.764
	cgd7_3030	importin/karyopherin	- 1				1	1	0.527 32.072
	cgd7_3270 cgd8_2100	importin/karyopherin (Arm repeats) RAN binding domain				1	1		21.037
	cgd8_2100	RCC1 like beta propeller protein [The regulator of chromosome	1			·		1	0.353
		condensation (RCC1), interact with Ran GTPase]	·	1					
	cgd8_3260 cgd8_3440	importin alpha subunit importin beta like ARM repeat alpha superhelix		1	1			1	1.551 2.939
Nuclear transport Tota			4	3	2	3	3	15	11.137
Nutrient	cgd1_40	UDP-galactose transporter, predicted signal peptide and 9	1					1	0.448
		transmembrane domains				4			40.004
	cgd1_600	oxoglutarate/malate translocator protein				1 1		1	10.621
	cgd2_2400 cgd2_2660	ATPase, class II, type 9B, putative UDP N-acetylglucosamine transporter-like nucleotide sugar				'	1	1	18.081 153.274
	cgd2_2670	transporter with 10 transmembrane domains UDP N-acetylglucosamine transporter-like nucleotide sugar					1	1	53.888
	cgd2_310	transporter with 10 transmembrane domains nucleoside transporter, 10 transmembrane domain domain,					1	1	69.085
	cgd2_590	nucleoside binding domain nucleotide-sugar transporter, UDP N-acetylglucosamine-like,	1					1	0.363
	cgd3_1610	signal peptide, 9 or more transmembrane domains protein containing a possible START(Steroidogenic acute regulatory (STAR) related lipid transfer) domain				1		1	10.286
	cgd3_3100	12 transmembrane domain protein MFS family sugar transporter			1			1	5.019
	cgd3_4070	putative sugar transporter with 12 transmembrane domains					1	1	34.775
	cgd3_490	putative fucose translocator with 8 transmembrane domains, within locus of 3 paralogous genes		1				1	2.022
	cgd3_500	putative fucose translocator with 8 transmembrane domains, within locus of 3 paralogous genes					1	1	32.577
	cgd3_510	putative fucose translocatorw ith 8 transmembrane domains, within locus of 3 paralogous genes					1	1	398.701
	cgd4_2770	11 transmembrane domain protein, possible aa transporter					1	1	51.906

		cgd4_2870	putative sugar transporter, 12x transmembrane domain protein				1		1	14.544
		cgd4 80	Sac1p family protein				1		1	11.114
		cgd5_1140	cinnamyl-alcohol dehydrogenase-like nucleoside diphosphate	1					1	0.521
		C903_1140	, , , , , , , , , , , , , , , , , , , ,							0.521
		15 0440	sugar epimerase							0.004
		cgd5_3410	possible phosphate/phosphoenolpyruvate translocator with 9	1					1	0.324
			transmembrane domains							
		cgd6_2020	BT1 family protein (biopterin transporter 1)	1					1	0.611
		cgd8 1370	DP-fucose transporter with 9 transmembrane domains	1					1	0.358
		cgd8_1440	nucleotide sugar transporter like integral membrane protein with		1				1	1.327
			9 transmembrane domains							
		cgd8_1600	sugar phosphate permease with 11 transmembrane domains			1			1	3.082
		cgd8_3640	niemann-Pick type C1 disease protein/ patched like cholesterol		1				1	1.870
		cguo_50+0							· 'I	1.070
			transporter of the SecD family, 12 transmembrane domain							
		cgd8_3740	Yer119cp like amino acid transporter, 11 transmembrane					1	1	87.487
			domain							
		cgd8_80	10 transmembrane domain, possible aa transporter					1	1	27.209
	Nutrient Total	loguo_co	To danomornation domain, possible da danoperter	6	3	2	5	9	25	39.580
				0	3		3	9		
	P-type ATPase	cgd3_1110	P-type ATpase fused to two adenyl cyclase domains and 21	1					1	0.286
			predicted transmembrane regions							
		cgd3_4140	P-type ATpase3, 13 transmembrane regions				1 1		1	17.025
			**			4			1	
		cgd4_2720	P-type ATpase involved in cation transport			'J				3.238
		cgd7_1760	P-type ATpase (calcium/phospholipid-transporter), 9		1				1	1.619
			transmembrane domains							
	P-type ATPase Total			1	1	1	1		4	5.542
	Undefined	ond/ 2440	10 transmembrane domain protein, possible translocator	1	<u> </u>	$\vdash$	$\vdash$	$\vdash$	1	0.571
	Ondenned	cgd4_3110	' ''	, I					1	
		cgd4_4050	putative transporter with signal peptide and 12 transmembrane		1				1	2.012
			domains							
		cgd5_1570	YIP1 protein like transporter GTpase interacting factor having 5		1				1	1.932
		35.557.6	Itransmembrane domain		· '					1.002
		andE 0500								0.507
		cgd5_3580	putative transport protein				1		1	9.507
		cgd5_3590	putative transport protein			1			1	3.503
		cgd6_4890	transporter protein with conserved Zn ribbon C11C7CxxC				1		1	5.637
							[		1	
		cgd6_490	zinc ZIP transporter protein, putative				1		1	5.787
		cgd7_3290	cleft lip and palate family of eukaryotic membrane proteins			1			1	2.945
		-3	(potential transporters) with 9 transmembrane domains							
		cgd7_4290	membrane associated transporter, 10 transmembrane domain					1	1	53.911
		cgu7_4290	Internolatie associated transporter, 10 transmembrane domain		_		oxdot	- 1		
	Undefined Total			1	2	2	3	1	9	9.534
	V-ATPase	cgd1_520	vacuolar ATP synthetase subunit					1	1	88.252
		cgd1_540	vacuolar ATP synthase subunit, possible signal peptide					1	1	47.341
							ا. ا	'	· ·	
		cgd2_3960	vacuolar ATP synthase subunit 54kD				1		1	9.850
		cgd4_540	putative vacuolar ATP synthase subunit C				1		1	9.712
			1					1	1	
		cgd5_3340	putative vacuolar ATP synthase subunit d					1		60.151
		cgd5_530	vacuolar H-ATpase subunit D					1	1	33.137
		cgd5_850	vacuolar ATP synthase subunit F					1	1	67.741
			The state of the s				ارا	'		
		cgd7_5000	vacuolar ATP synthase subunit A				1		1	12.560
		cgd8_1670	vacuolar ATP synthase subunit B			1			1	3.837
		cgd8_360	putative vacuolar ATP synthase subunit E					1	1	61.054
			1				!	'	· ·	
		cgd8_4790	proteolipid subunit of the vacuolar ATpase				1		1	11.382
	V-ATPase Total					1	4	6	11	36.820
Transporter Total				22	12	13	22	28	97	25.014
•	Concernat	and4 4050	appeared by nothericalt-i	- 22	12	10		20		
Unknown	Conserved	cgd1_1050	conserved hypothetical protein			1	( )		1	3.063
	1	cgd1_1130	conserved hypothetical protein	1		1 /	1 1		1	0.313
	1	cgd1 1210	conserved hypothetical protein	1		1 /	1 1		1	0.526
	1		1	'		1 .	( '		· · · · · · · · · · · · · · · · · · ·	
	1	cgd1_140	conserved hypothetical protein	L		1	( '		1	5.432
	1	cgd1_1550	conserved hypothetical protein	1			( )		1	0.443
	1	cgd1_160	conserved hypothetical protein	1		1 /	1 1		1	0.335
	1		1	1		1	1 1		· ·	
	1	cgd1_2220	apicomplexan specific protein	L		1	1 1		1	4.609
	1	cgd1_2720	hypothetical protein with predicted apicomplexan-conserved	1		1	( '		1	0.436
	1	5 - 1	Idomain					( I	. 1	
	1	cgd1_2910	conserved hypothetical protein	1			( )		1	0.334
			portion roa hypothiculai protein	, i		1 /	1 1			
						1 '	, ,	1	1	27.886
		cgd1_3070	multidomain protein with a conserved eukaryotic domain also			1 1	1 1			
			multidomain protein with a conserved eukaryotic domain also present in the human DRIM protein at N- terminus and an							
			· · · · · · · · · · · · · · · · · · ·							
		cgd1_3070	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus				1		1	6 873
		cgd1_3070 cgd1_3340	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein				1		1	6.873
		cgd1_3070 cgd1_3340 cgd1_360	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein conserved hypothetical protein				1		1	17.909
		cgd1_3070 cgd1_3340	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein				1 1 1			
		cgd1_3070 cgd1_3340 cgd1_360 cgd1_3630	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein		1		1 1 1		1	17.909 10.329
		cgd1_3070 cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein		1		1 1 1		1 1 1	17.909 10.329 1.938
		cgd1_3070 cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700 cgd1_3750	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein	1	1		1 1 1		1 1 1 1	17.909 10.329 1.938 0.415
		cgd1_3070 cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein	1 1	1		1 1 1		1 1 1	17.909 10.329 1.938
		cgd1_3070 cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700 cgd1_3750 cgd1_380	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein		1		1 1 1	1	1 1 1 1	17.909 10.329 1.938 0.415 0.391
		cgd1_3070 cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700 cgd1_3750 cgd1_380 cgd1_3810	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein		1		1 1 1	1	1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576
		cgd1_3070 cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700 cgd1_3750 cgd1_380	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein		1	1	1 1 1	1	1 1 1 1	17.909 10.329 1.938 0.415 0.391
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein		1	1	1 1 1	1	1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved		1	1	1 1 1	1	1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein		1	1	1 1 1	1	1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved		1	1	1 1 1	1	1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3700 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840 cgd2_1010	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein		1	1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197 2.547
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840 cgd2_1010 cgd2_1210	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein		1	1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197 2.547 3.756
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840 cgd2_1010 cgd2_1210 cgd2_1220	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein		1	1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197 2.547 3.756 13.063
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840 cgd2_1010 cgd2_1210	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein		1	1 1 1	1 1 1 1	1	1 1 1 1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197 2.547 3.756
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840 cgd2_1010 cgd2_1210 cgd2_1220 cgd2_140	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein apicomplexan-tonserved protein hypothetical protein protein conserved hypothetical protein		1	1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197 2.547 3.756 13.063 836.204
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840 cgd2_1010 cgd2_1210 cgd2_1220 cgd2_140 cgd2_190	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein		1	1 1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197 2.547 3.756 13.063 836.204 4.060
		cgd1_3070  cgd1_3340 cgd1_360 cgd1_3630 cgd1_3750 cgd1_380 cgd1_3810 cgd1_720 cgd1_770 cgd1_840 cgd2_1010 cgd2_1210 cgd2_1220 cgd2_140	present in the human DRIM protein at N- terminus and an archaeal-bacterial domain at C-terminus conserved hypothetical protein apicomplexan-conserved protein hypothetical protein, possible apicomplexan-conserved conserved hypothetical protein apicomplexan-tonserved protein hypothetical protein protein conserved hypothetical protein		1	1 1 1 1	1 1 1	1	1 1 1 1 1 1 1 1 1 1 1	17.909 10.329 1.938 0.415 0.391 501.576 2.411 0.318 28.197 2.547 3.756 13.063 836.204

cgd2_2000	apicomplexan protein with signal peptide and 3 transmembrane		1	١	1		1	1.584
	domains					4		05.404
cgd2_2230	conserved hypothetical protein	1				1	1	25.464
cgd2_2320	conserved hypothetical protein	1				4	1	0.369
cgd2_250	conserved hypothetical protein	1				1	1	52.866
cgd2_2510	conserved hypothetical protein	1					1	0.509
cgd2_2610	conserved hypothetical protein	'	1				1	0.460
cgd2_2790	conserved hypothetical protein	1	<u> </u>				1	1.653
cgd2_2810	conserved hypothetical protein	1					1	0.444 0.463
cgd2_2920	conserved hypothetical protein					1	1	85.144
cgd2_2940	conserved hypothetical protein			1		- 1	1	
cgd2_320	conserved hypothetical protein		1	<u>'</u>			1	5.125
cgd2_3380	conserved hypothetical protein		<u> </u>		1		1	1.488
cgd2_3520	conserved hypothetical protein	1			'			14.974
cgd2_3600	conserved hypothetical protein	1			4		1	0.397
cgd2_3650	conserved hypothetical protein				1	4	1	12.884
cgd2_3730	conserved hypothetical protein			4		1	1	648.512
cgd2_3760	conserved hypothetical protein			1			1	2.971
cgd2_40	conserved hypothetical protein	1					1	0.519
cgd2_4170	conserved hypothetical protein		1				1	1.901
cgd3_10	conserved hypothetical protein				1		1	6.573
cgd3_1140	conserved hypothetical protein		1				1	1.859
cgd3_1150	conserved hypothetical protein		1				1	2.080
cgd3_1160	conserved hypothetical protein				1		1	15.224
cgd3_1170	conserved hypothetical protein		1				1	2.263
cgd3_1420	conserved small protein					1	1	30.229
cgd3_1560	apicomplexan specific region near N-terminus			1			1	5.696
cgd3_1620	conserved hypothetical protein		1				1	2.147
cgd3_1700	conserved hypothetical protein	1					1	0.472
cgd3_1710	conserved hypothetical protein		1				1	2.241
cgd3_1720	conserved hypothetical protein	1					1	0.396
cgd3_1730	conserved hypothetical protein		1				1	1.294
cgd3_1750	conserved hypothetical protein				1		1	16.963
cgd3_1760	conserved hypothetical protein				1		1	10.677
cgd3_1770	conserved hypothetical protein			1			1	2.984
cgd3_1780	conserved hypothetical protein	1					1	0.454
cgd3_1790	conserved hypothetical protein	1					1	0.518
cgd3_1940	conserved hypothetical protein					1	1	354.170
cgd3_2240	conserved hypothetical protein	1					1	0.464
cgd3_230	conserved hypothetical protein	1					1	0.307
cgd3_2520	conserved hypothetical protein	1					1	0.444
cgd3_2570	conserved protein	1					1	0.426
cgd3_2820	conserved hypothetical protein	1					1	0.538
cgd3_2970	conserved hypothetical protein	1					1	0.308
cgd3_2980	conserved COOH terminal-specific cysteine rich domain	1					1	0.462
cgd3_3090	conserved hypothetical protein	1					1	0.431
cgd3_3360	conserved hypothetical protein				1		1	5.916
cgd3_3390	conserved hypothetical protein	1					1	0.408
cgd3_3660	conserved hypothetical protein				1		1	8.462
cgd3_3810	conserved hypothetical protein	1					1	0.309
cgd3_3870	conserved hypothetical protein					1	1	94.766
cgd3_4010	conserved protein				1		1	7.066
cgd3_4160	conserved hypothetical protein					1	1	198.349
cgd3_4320	conserved hypothetical protein	1					1	0.550
cgd3_4360	conserved hypothetical protein	1					1	0.450
cgd3_50	conserved hypothetical protein		1				1	1.289
cgd3_670	conserved hypothetical protein					1	1	35.845
cgd3_730	conserved expressed protein			1			1	3.959
cgd3_950	hypothetical conserved protein	1					1	0.408
cgd4_1080	conserved hypothetical protein			1			1	3.738
cgd4_1090	conserved hypothetical protein				1		1	6.043
cgd4_1150	hypothetical conserved protein with possible signal peptide	1					1	0.360
cgd4_1190	hypothetical protein, possible apicomplexan conserved	1					1	0.398
cgd4_1220	conserved hypothetical protein					1	1	49.713
cgd4_1400	conserved hypothetical protein					1	1	40.717
cgd4_1440	apicomplexan specific protein		1				1	1.278
cgd4_1510	conserved hypothetical protein			1			1	2.308
cgd4_1530	conserved protein				1		1	21.579
cgd4_1550	conserved hypothetical protein			1			1	3.800
cgd4_1570	hypothetical protein, possible conserved				1		1	8.908
cgd4_1680	conserved hypothetical protein	1					1	0.396
cgd4_1910	conserved hypothetical protein		1				1	1.853
cgd4_2010	conserved hypothetical protein			1			1	5.265
cgd4_2020	conserved hypothetical protein				1		1	5.904
cgd4_2060	conserved hypothetical protein	1					1	0.385
cgd4_2210	conserved hypothetical protein	1					1	0.429
1 5 =			. '	'	'	'	'	ļ

cgdd_2850         hypothetical protein, possible apicomplexan conserved typothetical protein conserved hypothetical protein conserved protein having 3 transmembrane domain apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein conserved protein having 3 transmembrane domain apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein conserved drypothetical protein conserved hypothetical protein conserved h	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4.047 0.441 3.333 2.245 10.942 32.062 38.743 8.784 44.812 21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334 0.469
cgd4_3570         conserved hypothetical protein         1           cgd4_3580         conserved hypothetical protein         1           cgd4_3630         conserved hypothetical protein         1           cgd4_4140         conserved hypothetical protein         1           cgd4_4280         conserved hypothetical protein         1           cgd4_700         conserved protein of possible plant or bacterial origin         1           small conserved protein with possible plant or bacterial origin         1           cgd5_130         apicomplexan conserved protein with 9 transmembrane domain         1           cgd5_1310         apicomplexan conserved protein with possible ER protein         1           cgd5_1310         conserved hypothetical protein         1           cgd5_1310	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3.333 2.245 10.942 32.062 38.743 8.784 44.812 21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_3580 conserved hypothetical protein hypothetical conserved protein, possible transmembrane domain near C-terminus conserved hypothetical protein conserved protein of possible plant or bacterial origin small conserved protein of possible plant or bacterial origin small conserved protein of possible plant or bacterial origin small conserved protein with 9 transmembrane domain all apicomplexan conserved protein with 9 transmembrane domain all possible ER retention motif, possible ER protein conserved protein with possible ER protein conserved protein with possible ER protein conserved protein with possible ER protein conserved hypothetical p	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2.245 10.942 32.062 38.743 8.784 44.812 21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_3590 conserved hypothetical protein cgd4_3630 conserved hypothetical protein apicomplexan conserved protein with 9 transmembrane domain and possible ER retention motif; possible ER protein conserved protein motif; possible ER protein conserved hypothetical protein possible apicomplexan-specific serine rich low complexity protein unchacterized apicomplexan specific, low complexity protein hypothetical protein possible apicomplexan-specific conserved hypothetical protein c	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.942 32.062 38.743 8.784 44.812 21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_3630 conserved hypothetical protein cgd4_3760 conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein domain near C-terminus conserved hypothetical protein conserved protein of possible plant or bacterial origin spill conserved protein of possible plant or bacterial origin spill conserved protein with 9 transmembrane domain apicomplexan conserved protein conserved protein having 3 transmembrane domains and possible ER retention motift, possible ER protein conserved protein with possible signal peptide and ER retention motift, possible ER protein conserved hypothetical protein conserv	1 1 1 1 1 1 1 1 1 1 1 1	32.062 38.743 8.784 44.812 21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_3650 conserved hypothetical protein cgd4_4110 hypothetical protein protein domain near C-terminus conserved hypothetical protein conserved protein of possible plant or bacterial origin small conserved protein depossible plant or bacterial origin conserved protein having 3 transmembrane domain apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein apicomplexan conserved hypothetical protein possible apicomplexan-specific conserved hypothetical protein con	1 1 1 1 1 1 1 1 1 1 1	38.743 8.784 44.812 21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_3770 cgd4_4710 hypothetical conserved protein, possible transmembrane domain near C-terminus cgd4_4280 conserved hypothetical protein cgd4_470 conserved hypothetical protein conserved protein of possible plant or bacterial origin small conserved protein with 9 transmembrane domain apicomplexan conserved protein cgd5_1030 apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein cgd5_1310 conserved protein having 3 transmembrane domains and possible ER retention motif; possible ER protein conserved protein with possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved hypothetical protein conserved protein conserved hypothetical protein possible apicomplexan-specific conserved hypothetical protein possible apicomplexan-specific conserved hypothetical protein	1 1 1 1 1 1 1 1 1 1	8.784 44.812 21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_4110 hypothetical conserved protein, possible transmembrane domain near C-terminus conserved hypothetical protein conserved protein of possible plant or bacterial origin spill apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein motif, possible ER protein conserved protein motif, possible ER protein conserved protein hypothetical protein conserved hypothetical protein possible apicomplexan specific conserved hypothetical protein conserved h	1 1 1 1 1 1 1 1 1	21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
domain near C-terminus cgd4_4140 cgd4_4280 cgd4_4490 cgd4_700 cgd4_700 cgd4_700 cgd4_700 cgd5_1020 cgd5_1020 cgd5_1020 cgd5_1030 cgd5_11270 conserved protein of possible plant or bacterial origin cgd5_1310 conserved protein with 9 transmembrane domain apicomplexan conserved protein with 9 sissible ER retention motif; possible ER protein cgd5_1310 cgd5_1310 conserved protein with possible ER protein cgd5_1310 conserved protein in with 9 transmembrane domain apicomplexan conserved protein with possible ER retention motif; possible ER protein cgd5_1310 conserved protein in with 9 sissible signal peptide and ER retention motif; possible ER protein cgd5_1310 conserved protein in exposible ER protein conserved hypothetical protein cgd5_1410 cgd5_1410 cgd5_1410 cgd5_1490 cgd5_1860 cgd5_1860 cgd5_2380 conserved hypothetical protein conserved protable heaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein cgd5_3360 cgd5_3450 cgd5_4530 conserved hypothetical protein conserved hypothetical pr	1 1 1 1 1 1 1 1	21.495 0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_4140 conserved hypothetical protein conserved protein of possible plant or bacterial origin small conserved protein with 9 transmembrane domain apicomplexan conserved protein with possible ER protein conserved protein with possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein conserved	1 1 1 1 1 1 1 1	0.324 0.377 11.116 1.442 0.360 0.427 5.334
cgd4_4280 conserved hypothetical protein cgd4_470 conserved hypothetical protein cgd4_70 conserved hypothetical protein cgd4_700 conserved protein of possible plant or bacterial origin cgd4_700 small conserved protein of possible plant or bacterial origin cgd5_1020 apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein cgd5_1030 apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein cgd5_1270 conserved protein having 3 transmembrane domains and possible ER retention motif, possible ER protein conserved protein with possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved hypothetical protein cgd5_1340 conserved hypothetical protein cgd5_1480 conserved hypothetical protein conserved hypothetical	1 1 1 1 1 1 1	0.377 11.116 1.442 0.360 0.427 5.334
cgd4_4490 cgd4_700 cgd4_700 cgd4_700 cgd4_790 cgd5_1020 small conserved protein of possible plant or bacterial origin cgd5_1020 small conserved protein of possible plant or bacterial origin cgd5_1020 cgd5_1030 cgd5_1030 cgd5_1270 conserved protein with 9 transmembrane domain cgd5_1270 conserved protein having 3 transmembrane domains and possible ER retention motif, possible ER protein conserved protein with possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved disponsible capacities capacities conserved protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved protein conserved protein conserved hypothetical protein co	1 1 1 1 1 1	11.116 1.442 0.360 0.427 5.334
cgd4_70 conserved hypothetical protein conserved protein of possible plant or bacterial origin small conserved protein of possible plant or bacterial origin small conserved protein of possible plant or bacterial origin small conserved protein with 9 transmembrane domain apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein with 9 transmembrane domain and possible ER retention motif; possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein possible apicomplexan-specific conserved hypothetical conserved protein conserved hypothetical protein conserved	1 1 1 1 1 1	11.116 1.442 0.360 0.427 5.334
cgd4_700 cgd4_790 small conserved protein of possible plant or bacterial origin cgd5_1020 apicomplexan conserved protein with 9 transmembrane domain cgd5_1270 cgd5_1270 conserved protein having 3 transmembrane domains and possible ER retention motif; possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein cgd5_1340 conserved hypothetical protein cgd5_1540 conserved hypothetical protein cgd5_1860 cgd5_1860 cgd5_1880 cgd5_280 unchacterized apicomplexan-specific serine rich low complexity protein cgd5_2520 cgd5_270 Unc45-like TPR repeat containing protein cgd5_2740 cgd5_2740 cgd5_3600 hypothetical protein cgd5_3890 cgd5_3940 cgd5_3940 cgd5_4060 cgd5_4960 cgd5_4860 conserved hypothetical protein cgd5_4530 conserved hypothetical protein cgd5_4530 conserved hypothetical protein cgd5_45400 conserved hypothetical protein conserved hypothetical protein cgd5_4890 conserved hypothetical protein conserved h	1 1 1 1 1 1	1.442 0.360 0.427 5.334
cgd4_790 small conserved protein cgd5_1020 apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein cogd5_1270 conserved protein having 3 transmembrane domains and possible ER retention motif; possible ER protein conserved protein with possible ER protein conserved protein with possible ER protein conserved hypothetical protein conserved	1 1 1 1 1	0.360 0.427 5.334
cgd5_1020 apicomplexan conserved protein with 9 transmembrane domain apicomplexan conserved protein conserved protein apicomplexan conserved protein conserved protein having 3 transmembrane domains and possible ER retention motif; possible ER protein conserved protein with possible ER protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved eukaryotic protein conserved hypothetical conserved protein conserved hypothetical protein conserve	1 1 1 1	0.427 5.334
cgd5_1030 apicomplexan conserved protein conserved protein having 3 transmembrane domains and possible ER retention motif; possible ER protein conserved protein with possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved ewaryotic protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical prote	1 1 1	5.334
cgd5_1370 conserved protein having 3 transmembrane domains and possible ER retention motif; possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein possible apicomplexan specific, low complexity protein conserved hypothetical protein conserved hyp	1 1 1	
possible ER retention motif; possible ER protein conserved protein with possible signal peptide and ER retention motif; possible ER protein cods_1340 conserved hypothetical protein cgd5_1410 conserved hypothetical protein cgd5_1540 conserved hypothetical protein cgd5_1790 conserved eukaryotic protein cgd5_1880 conserved hypothetical protein cgd5_2380 unchacterized apicomplexan-specific serine rich low complexity protein cgd5_270 cgd5_270 cgd5_270 cgd5_360 hypothetical protein cgd5_3890 possible apicomplexan specific, low complexity protein cgd5_3890 possible apicomplexan specific, low complexity protein cgd5_4300 conserved hypothetical protein cgd5_4470 cgd5_4530 conserved hypothetical protein cgd5_4530 conserved hypothetical protein cgd5_4530 conserved hypothetical protein cgd5_4500 conserved hypothetical protein cgd5_4600 conserved hypothetical protein cgd5_4500 conserved hypothetical protein cgd5_4000 conserved hypothetical protein cgd5_4500 conserved hypothetical protein cgd5_500 conserved hypothetical protein cgd5_600 conserved hypothetical protein cgd5_790 conserved protein having a signal peptide	1	0.469
cgd5_1310	1	
cgd5_1340 conserved hypothetical protein cgd5_1410 conserved protein conserved protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein cgd5_1860 conserved hypothetical protein cgd5_1880 conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein uncyd5_2860 hypothetical protein cgd5_2740 conserved hypothetical protein uncyd5_3860 hypothetical conserved protein uncyd5_3890 possible apicomplexan specific, low complexity protein uncyd5_3940 hypothetical protein uncyd5_4370 conserved hypothetical protein uncyd5_4370 conserved hypothetical protein uncyd5_4580 conserved hypothetical protein uncyd5_490 conserved hypothetical protein uncyd5_490 conserved hypothetical protein uncyd5_490 conserved hypothetical protein uncyd5_620 conserved hypothetical protein uncyd6_620 conserved hypothetical protein uncyd6_620 conserved hypothe		2.461
cgd5_1410 conserved protein conserved hypothetical protein conserved hypothetical protein conserved eukaryotic protein conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein unchacterized apicomplexan-specific serine rich low complexity protein unchacterized apicomplexan-specific serine rich low complexity protein unchacterized apicomplexan-specific serine rich low complexity protein unchacterized apicomplexan-specific conserved hypothetical protein unchacterized hypothetical protein unchacterized apicomplexan-specific conserved hypothetical conserved protein unchacterized hypothetical protein unchacterized		
cgd5_1540 conserved hypothetical protein conserved eukaryotic protein conserved eukaryotic protein conserved hypothetical protein conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein 1 c	1	11.264
cgd5_1790 conserved eukaryotic protein conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein possible apicomplexan specific, low complexity protein conserved hypothetical	- 1	0.339
cgd5_1860 conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein conserved hypothetical protein 1 cgd5_270 Unc45-like TPR repeat containing protein 1 cgd5_3660 conserved hypothetical protein 1 cgd5_3890 possible apicomplexan specific, low complexity protein 1 cgd5_3940 conserved hypothetical protein 1 cgd5_4060 conserved hypothetical protein 1 conserved	1	1.551
cgd5_1860 conserved hypothetical protein conserved probable chaperonin containing TCP-1 delta subunit unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein conserved hypothetical protein 1 cgd5_270 Unc45-like TPR repeat containing protein 1 cgd5_3660 conserved hypothetical protein 1 cgd5_3890 possible apicomplexan specific, low complexity protein 1 cgd5_3940 conserved hypothetical protein 1 cgd5_4060 conserved hypothetical protein 1 conserved	1	1.817
cgd5_2380 unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein dunctorized hypothetical conserved hypothetical protein dunctorized hypothetical prote	1	22.521
cgd5_2380 unchacterized apicomplexan-specific serine rich low complexity protein conserved hypothetical protein dunctorized hypothetical conserved hypothetical protein dunctorized hypothetical prote	1	1.432
cgd5_2520 conserved hypothetical protein cgd5_270 Unc45-like TPR repeat containing protein cgd5_2740 conserved hypothetical protein cgd5_3660 hypothetical conserved protein cgd5_3890 possible apicomplexan specific, low complexity protein cgd5_3940 hypothetical protein, possible apicomplexan-specific cgd5_4370 conserved hypothetical protein cgd5_4530 conserved hypothetical protein cgd5_4580 conserved hypothetical protein cgd5_4600 conserved hypothetical protein cgd5_500 conserved hypothetical protein cgd5_500 conserved hypothetical protein cgd5_620 conserved hypothetical protein cgd5_650 conserved hypothetical protein cgd5_790 conserved hypothetical protein cgd5_790 conserved hypothetical protein	1	1.593
cgd5_270 Unc45-like TPR repeat containing protein cgd5_2740 conserved hypothetical protein hypothetical conserved protein cgd5_3890 possible apicomplexan specific, low complexity protein lypothetical protein, possible apicomplexan-specific conserved hypothetical protein locd5_4370 conserved hypothetical protein locd5_4530 conserved hypothetical protein locd5_4580 conserved hypothetical protein locd5_4600 conserved hypothetical protein locd5_4600 conserved hypothetical protein locd5_490 conserved hypothetical protein locd5_500 conserved hypothetical protein locd5_620 conserved hypothetical protein locd5_620 conserved hypothetical protein locd5_620 conserved hypothetical protein locd5_650 conserved hypothetical protein locd5_790 conserved hypothetical protein locd5_7		
cgd5_2740 conserved hypothetical protein hypothetical conserved protein cgd5_3890 possible apicomplexan specific, low complexity protein cgd5_3940 hypothetical protein, possible apicomplexan-specific conserved hypothetical protein conserved hypothe	1	0.343
cgd5_3660 hypothetical conserved protein cgd5_3890 hypothetical protein, possible apicomplexan specific, low complexity protein thypothetical protein, possible apicomplexan-specific conserved hypothetical protein to conserved hypothetical prote	1	0.395
cgd5_3890 possible apicomplexan specific, low complexity protein thypothetical protein, possible apicomplexan-specific conserved hypothetical protein conse	1	2.064
cgd5_3940 hypothetical protein, possible apicomplexan-specific cod5_4060 conserved hypothetical protein 1 cod5_4370 conserved hypothetical protein 1 conserved hypoth	1	3.297
cgd5_4060       conserved hypothetical protein       1         cgd5_4370       conserved hypothetical protein       1         cgd5_4530       conserved hypothetical protein       1         cgd5_4580       conserved hypothetical protein       1         cgd5_4600       conserved hypothetical protein       1         cgd5_490       conserved hypothetical protein       1         cgd5_500       conserved protein       1         cgd5_620       conserved hypothetical protein       1         cgd5_650       conserved hypothetical protein       1         cgd5_790       conserved protein having a signal peptide       1	1	0.430
cgd5_4060       conserved hypothetical protein       1         cgd5_4370       conserved hypothetical protein       1         cgd5_4530       conserved hypothetical protein       1         cgd5_4580       conserved hypothetical protein       1         cgd5_4600       conserved hypothetical protein       1         cgd5_490       conserved hypothetical protein       1         cgd5_500       conserved protein       1         cgd5_620       conserved hypothetical protein       1         cgd5_650       conserved hypothetical protein       1         cgd5_790       conserved hypothetical protein       1         conserved hypothetical protein       1 <td>1</td> <td>8.912</td>	1	8.912
cgd5_4370       conserved hypothetical protein       1         cgd5_4530       conserved hypothetical protein       1         cgd5_4580       conserved hypothetical protein       1         cgd5_4600       conserved hypothetical protein       1         cgd5_490       conserved hypothetical protein       1         cgd5_500       conserved protein       1         cgd5_620       conserved hypothetical protein       1         cgd5_650       conserved hypothetical protein       1         cgd5_790       conserved hypothetical protein       1         cons	1	0.534
cgd5_4530     conserved hypothetical protein     1       cgd5_4580     conserved hypothetical protein     1       cgd5_4600     conserved hypothetical protein     1       cgd5_490     conserved hypothetical protein     1       cgd5_500     conserved protein     1       cgd5_620     conserved hypothetical protein     1       cgd5_650     conserved hypothetical protein     1       cgd5_790     conserved hypothetical protein     1	1	0.497
cgd5_4580     conserved hypothetical protein     1       cgd5_4600     conserved hypothetical protein     1       cgd5_490     conserved hypothetical protein     1       cgd5_500     conserved protein     1       cgd5_620     conserved hypothetical protein     1       cgd5_650     conserved hypothetical protein     1       cgd5_790     conserved hypothetical protein     1	1	5.858
cgd5_4600     conserved hypothetical protein     1       cgd5_490     conserved hypothetical protein     1       cgd5_500     conserved protein     1       cgd5_620     conserved hypothetical protein     1       cgd5_650     conserved hypothetical protein     1       cgd5_790     conserved hypothetical protein     1       conserved hypothetical protein     1       conserved hypothetical protein     1       conserved hypothetical protein     1       cgd5_790     conserve protein having a signal peptide     1	1	1.493
cgd5_490     conserved hypothetical protein     1       cgd5_500     conserved protein     1       cgd5_620     conserved hypothetical protein     1       cgd5_650     conserved hypothetical protein     1       cgd5_790     conserve protein having a signal peptide     1	1	2.389
cgd5_500 conserved protein 1 1 cgd5_620 conserved hypothetical protein 1 cgd5_650 conserved hypothetical protein 1 cgd5_790 conserve protein having a signal peptide 1	1	0.343
cgd5_620     conserved hypothetical protein     1       cgd5_650     conserved hypothetical protein     1       cgd5_790     conserve protein having a signal peptide     1	1	1.732
cgd5_650 conserved hypothetical protein cgd5_790 conserve protein having a signal peptide	1	3.964
cgd5_790 conserve protein having a signal peptide	1	1.747
	1	0.378
	- 1	
	1	0.359
cgd6_1080   conserved hypothetical protein	1	23.828
cgd6_1300   conserved hypothetical protein   1	1	0.464
cgd6_1310 hypothetical protein, possible conservation in apicomplexa	1	0.438
cgd6_1480   conserved hypothetical protein   1   1	1	1.974
cgd6_1550 uncharacterized conserved protein	1	0.416
cgd6_1640 conserved hypothetical protein	1	0.349
cgd6_1650   conserved hypothetical protein   1	1	0.370
cgd6_1660 conserved hypothetical protein	1	1.965
cgd6_1820 conserved hypothetical protein	1	47.127
cgd6_1910 conserved hypothetical protein	1	3.510
cgd6_230 conserved hypothetical protein 1	1	0.370
cgd6 2420   conserved hypothetical protein   1	1	11.272
cgd6_2550   conserved hypothetical protein   1	1	0.677
cgd6_30   conserved hypothetical protein   1	1	9.953
cgd6_3260 conserved hypothetical protein	1	0.350
cgd6_40 conserved hypothetical protein	1	878.258
cgd6_4080 conserved hypothetical protein	1	1.840
cgd6_4130   conserved hypothetical protein   1	1	8.262
cgd6_4660 possible apicomplexan-specific protein		106.625
lagara_recompression aprecompression process		0.457
	1	
	1	0.350
cgd6_5340 conserved hypothetical protein	1 1 1	0.422
cgd6_5380   conserved hypothetical protein   1	1 1 1 1	10.469
cgd6_5460 conserved hypothetical protein	1 1 1 1	
cgd6_5480   conserved hypothetical protein   1   1	1 1 1 1 1	
cgd6_5490 conserved hypothetical protein	1 1 1 1 1 1	0.448
cgd6_680 conserved protein with possible C2 domain	1 1 1 1 1 1 1	0.448 0.410
cgd6_70 conserved hypothetical protein	1 1 1 1 1 1 1 1 2	0.410 3.188
cgd6_830 conserved hypothetical protein	1 1 1 1 1 1 1	0.633 0.448 0.410 3.188 3.364 1.810

cgd6_870 cgd7_1060	possible apicomplexan conserved protein apicomplexan conserved protein with 2 or more transmembrane domains	1		1			1	0.438 2.333
cgd7_1150	uncharacterized conserved protein	1					1	0.262
cgd7_1160 cgd7_1160	conserved hypothetical protein	•	1				1	1.409
			' I	1				3.055
cgd7_1180	conserved hypothetical protein		1	۱'				
cgd7_1340	conserved hypothetical protein							1.616
cgd7_1380	conserved hypothetical protein			1			1	2.382
cgd7_1390	conserved hypothetical protein			1			1	2.436
cgd7_1500	conserved protein	1					1	0.405
cgd7_250	conserved protein				1		1	20.096
cgd7_2510	conserved hypothetical protein				1		1	9.015
cgd7_2520	conserved hypothetical protein				1		1	21.146
cgd7_2690	conserved hypothetical protein			1			1	2.914
		- 1		- 1			2	
cgd7_270	conserved hypothetical protein	1		1				2.618
cgd7_310	conserved hypothetical protein		1				1	2.18
cgd7_3100	conserved hypothetical protein				1		1	16.123
cgd7_3160	conserved hypothetical protein			1			1	3.784
cgd7_3220	conserved hypothetical protein			1			1	2.454
cgd7_3300	conserved hypothetical protein	1					1	0.503
cgd7_340	conserved hypothetical protein	1					1	0.588
		•				1		
cgd7_3490	conserved hypothetical protein					- 1		65.96
cgd7_350	conserved hypothetical protein	1					1	0.430
cgd7_3540	conserved hypothetical protein		1	I			1	2.220
cgd7_3550	conserved hypothetical protein			I	1		1	17.37
cgd7_3740	apicomplexan P36 family of proteins, appears to be a divergent	1		I			1	0.390
_	HAD family phosphatase			I				
cgd7_3810	conserved hypothetical protein				1		1	6.003
cgd7_3830	conserved hypothetical protein			1			1	3.059
cgd7_3840	conserved hypothetical protein			1			1	4.068
cgd7_3860	conserved hypothetical protein	1		١.			1	0.332
cgd7_3870	conserved hypothetical protein	1					1	0.31
cgd7_4410	conserved protein with YSHH motif. SOme fused to polo box.				1		1	8.532
cgd7_4710	conserved hypothetical protein					1	1	101.754
cgd7_4780	conserved hypothetical protein	1					1	0.357
cgd7_5080	conserved hypothetical protein	1					1	0.454
cgd7_5120	conserved hypothetical protein	1					1	0.55
cgd7_5400	conserved hypothetical protein	1					1	0.347
cgd7_5450	conserved hypothetical protein	1					1	0.496
cgd7_610	apicomplexan conserved protein		1				1	1.594
cgd7_650	conserved hypothetical protein			1			1	3.889
cgd8_1060	uncharacterized conserved protein				1		1	18.004
cgd8_130	conserved hypothetical protein	1					1	0.510
cgd8_1340	conserved hypothetical protein	1	1				2	0.976
cgd8_2080	conserved hypothetical protein		1				1	1.584
cgd8_2110	conserved hypothetical protein	1					1	0.44
cgd8_230	conserved hypothetical protein			1			1	2.33
cgd8_2320	hypothetical protein, potential AT hook	1					1	0.44
cgd8_2490	conserved hypothetical protein					1	1	160.860
cgd8_2540	apicomplexan specific coiled coil protein	1					1	0.445
cgd8_2550	apicomplexan specific membrane protein, 4+ transmembrane	1					1	0.387
0 _	domain							
cgd8_2640	conserved metal binding motif protein	1					1	0.337
cgd8_2650	conserved hypothetical protein	1					1	0.406
cgd8 270	conserved hypothetical protein	1					1	0.39
-								
cgd8_2780	conserved protein	1					1	0.56
cgd8_280	apcomplexan conserved protein			1			1	3.96
cgd8_2880	possible apicomplexan conserved motif		1				1	2.13
cgd8_2890	conserved hypothetical protein		1				1	1.43
cgd8_3150	hypothetical conserved protein			I	1		1	18.46
cgd8_3230	conserved hypothetical protein			I		1	1	507.63
	apicomplexan specific protein			I	1		1	12.14
					1		1	8.73
cgd8_3240							' ' '	
cgd8_3240 cgd8_3330	conserved hypothetical protein					- 1	اير	40 00
cgd8_3240 cgd8_3330 cgd8_3630	conserved hypothetical protein conserved hypothetical protein				1		1	
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein		1		1		1	1.24
cgd8_3240 cgd8_3330 cgd8_3630	conserved hypothetical protein conserved hypothetical protein	1	1		1		1 1	1.24
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein	1	1	1	1		1	1.24 0.46
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein	1	1	1	1	1	1 1	1.24 0.46 3.79
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein	1	1	1	1		1 1 1 1	1.24 0.46 3.79 320.23
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4260	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein	1	1	1	1	1 1	1 1 1 1	1.24 0.46 3.79 320.23 35.63
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4260 cgd8_4320	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein possible conserved domain (Zn finger?)	1	1	1	1	1 1	1 1 1 1 1	1.24 0.46 3.79 320.23 35.63 1,685.64
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4260 cgd8_4320 cgd8_4370	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein possible conserved domain (Zn finger?) conserved protein	1	1		1		1 1 1 1 1 1	1.24 0.46 3.79 320.23 35.63 1,685.64 73.34
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4260 cgd8_4320 cgd8_4370	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein possible conserved domain (Zn finger?) conserved protein apicomplexan specific Pf 23612804 and Py 23478322	1	1	1	1	1 1 1	1 1 1 1 1 1 1	1.24 0.46 3.79 320.23 35.63 1,685.64 73.34
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4260	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein possible conserved domain (Zn finger?) conserved protein	1	1		1	1 1	1 1 1 1 1 1	1.24 0.46 3.79 320.23 35.63 1,685.64 73.34 4.02
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4260 cgd8_4320 cgd8_4370 cgd8_4670	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein possible conserved domain (Zn finger?) conserved protein apicomplexan specific Pf 23612804 and Py 23478322	1	1		1	1 1 1	1 1 1 1 1 1 1	1.24 0.46 3.79 320.23 35.63 1,685.64 73.34 4.02 63.69
cgd8_3240 cgd8_3330 cgd8_3630 cgd8_4030 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4220 cgd8_4320 cgd8_4370 cgd8_4670 cgd8_4680 cgd8_4850	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein possible conserved domain (Zn finger?) conserved protein apicomplexan specific Pf 23612804 and Py 23478322 conserved protein; Py hit 23481194 conserved hypothetical protein				1	1 1 1	1 1 1 1 1 1 1 1 1 1 2	18.33 1.24 0.46 3.79 320.23 35.63 1,685.64 73.34 4.02 63.69 1.00 99.27
egd8_3240 cgd8_3330 cgd8_3630 cgd8_3730 cgd8_4030 cgd8_4170 cgd8_4220 cgd8_4220 cgd8_4320 cgd8_4320 cgd8_4370 cgd8_4670 cgd8_4680	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein apicomplexan specific coiled coil protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein possible conserved domain (Zn finger?) conserved protein apicomplexan specific Pf 23612804 and Py 23478322 conserved protein; Py hit 23481194				1	1 1 1	1 1 1 1 1 1 1 1	1.24 0.46 3.79 320.23 35.63 1,685.64 73.34 4.02 63.69

İ	cgd8 5350	conserved hypothetical protein				1		1	7.709
İ	cgd8_5360	conserved hypothetical protein					1	1	119.462
i	cgd8_5380	conserved hypothetical protein				1		1	16.047
	cgd8_5390	conserved hypothetical protein				1		1	10.551
	cgd8_5400	conserved hypothetical protein		1				1	1.761
		1					1		153.778
	cgd8_5420	conserved hypothetical protein	4						
	cgd8_690	conserved hypothetical protein	1					1	0.311
	cgd8_70	conserved hypothetical protein				1		1	8.491
	cgd8_940	conserved hypothetical protein					1	1	205.198
Conserved Total			97	41	40	49	34	261	39.608
Membrane	cgd1_10	predicted membrane associated protein with 11 transmembrane		1				1	1.697
		domains regions							
	cgd1_1470	hypothetical protein, possible transmembrane domain within N- terminus				1		1	6.311
	cgd1_1480	predicted membrane associated protein, 4 transmembrane domains and signal peptide			1			1	5.762
	cgd1_1820	predicted integral membrane protein, 4 transmembrane domains				1		1	15.664
	cgd1_20	predicted membrane associated protein with 11 transmembrane			1			1	3.252
	cgd1_2030	domains regions membrane associated protein with over 9 transmembrane			1			1	2.737
	cgd1_2080	domains, signal peptide hypothetical protein containing signal peptide and 3		1				1	1.910
	cgd1 2090	transmembrane domain regions hypothetical protein, C2C2 like finger		1				1	2.170
	-	1 5 5	4	'				- 1	
	cgd1_2510	hypothetical protein, transmembrane domain within N-terminus	1					1	0.438
	cgd1_2780	hypothetical protein, 4 transmembrane domains				1		1	16.287
	cgd1_2880	13 kda membrane protein subunit		1				1	2.242
	cgd1_30	predicted membrane protein with 12+xtransmembrane domain	1					1	0.579
	cgd1_3200	hypothetical protein with 2 transmembrane domains, possible apicomplexan conservation	1					1	0.380
	cgd1_3250	signal peptide, possible transmembrane domain near N-				1		1	12.450
	cgd1_3590	terminus, proline rich and His-stretch at C-terminus hypothetical protein, possible transmembrane domain	1					1	0.501
	cgd1_3680	extracellular membrane associated protein with 3 EGF domains	1					1	0.361
		and a transmembrane domain							
	cgd1_3820	hypothetical protein, transmembrane domain or GPI anchor near C-terminus					1	1	45.793
	cgd1_3850	signal peptide, possible 4-5x transmembrane domain, SKSR					1	1	172.377
	cgd1_780	family paralog, telomeric gene hypothetical protein, possible 2 transmembrane domains		1				1	1.471
	cgd1_950	hypothetical protein, membrane associated ankyrin repeats, 3X		1				1	1.907
	cgd2_1290	signal peptide plus transmembrane domain or GPI anchor hypothetical protein, signal peptide, transmembrane domain	1	4				2	0.909
	Cguz_1230	near C-terminus		'				-	0.303
	cgd2_1310	11 transmembrane domain protein				1		1	21.320
	cgd2_1590	extracellular protein with signal peptide, 5xEGF and apple domains		1				1	1.739
	cgd2_1710	hypothetical protein with signal peptide and one or more transmembrane domain regions	1					1	0.383
	cgd2_1990	hypothetical protein with possible transmembrane domain or	1					1	0.315
	cgd2 2250	GPI at C-terminus putative integral membrane protein			1			1	3.186
	-	,			'	4			
	cgd2_2390	hypothetical protein with 8 transmembrane domains							6.463
	cgd2_2490	hypothetical protein, possible transmembrane domain at C- terminus	1					1	0.388
	cgd2_2630	hypothetical protein, signal peptide plus 11 transmembrane domains		1				1	1.682
	cgd2_2650	hypothetical protein, signal peptide, transmembrane domain near C-terminus				1		1	5.900
	cgd2_2840	pleckstrin homology (PH) domain containing protein with N-		1				1	1.359
		terminal ankyrin repeats		4				اړ	0.00
	cgd2_3080	CpTSP10 protein		1				1	2.004
	cgd2_3100	hypothetical protein, 8 transmembrane domains			1			1	2.458
	cgd2_3120	possible transmembrane domain near N					1	1	24.537
	cgd2_3470	hypothetical protein with signal peptide and one or more transmembrane domains	1					1	0.230
	cgd2_3560	hypothetical protein with 8 transmembrane domains	1					1	0.290
	cgd2_3750	hypothetical protein, transmembrane domain near C-terminus		4					1.471
	1	hypothetical protein, transmembrane domain near C-terminus hypothetical protein with 12 transmembrane domains	1	'				1	0.360
	cgd2_4060	1 **	1	4				1	1.572
	cgd2_4350 cgd2_650	putative patched family protein with 12 transmembrane domain hypothetical protein with transmembrane domain within N-	1	- 1					0.352
	0942_000	terminus	'					'	0.002
	cgd2_790	CpCCp3, multidomain extracellular protein with a signal peptide			1			1	4.267
		and the following architecture: LH2+LCCL+2xSR+LCCL+pentraxin+2xLCCL							
			1					1	0.418
	cqd2 800	mypothetical protein with 10 transmembrane domains							
	cgd2_800 cad2_940	hypothetical protein with 10 transmembrane domains signal peptide plus transmembrane domain or GPI anchor					1	1	240 89
	cgd2_800 cgd2_940 cgd3_1010	signal peptide plus transmembrane domain or GPI anchor hypothetical protein with 3 transmembrane domains within C-	1				1	1 1	
	cgd2_940	signal peptide plus transmembrane domain or GPI anchor					1	- 1	240.895 0.538 0.312

l0 4500	lh			41	1	1	اد	0.040
cgd3_1520	hypothetical protein with transmembrane or GPI anchor sequence at carboxy terminus			1			1	2.618
cgd3_1600	hypothetical protein with 4 transmembrane domains	1					1	0.413
cgd3_1640	hypothetical protein with 7 transmembrane domains			1			1	4.519
cgd3_1740	hypothetical protein with signal peptide and 2 transmembrane domains				1		1	9.113
cgd3_1800	hypothetical protein with 12 transmembrane domains		1				1	1.303
cgd3_1860	extracellular protein with a signal peptide and 9 EGF domains	1					1	0.421
cgd3_1930	hypothetical protein with 4 transmembrane domains	1					1	0.391
cgd3_2080	large protein with 8 or more transmembrane domains within			1			1	4.105
cgd3_2300	NH2 region hypothetical protein with transmembrane domain within C- terminus				1		1	18.959
cgd3_2500	hypothetical protein with transmembrane region near N- terminus	1					1	0.444
cgd3_2780	hypothetical protein with transmembrane domain at carboxy terminus	1					1	0.468
cgd3_2990	hypothetical protein with signal peptide and 7 transmembrane domains		1				1	2.094
cgd3_340	hypothetical protein with signal peptide and 5 transmembrane domains				1		1	15.006
cgd3_3420	protein with 2x EF hands and 4 transmembrane regions	1					1	0.386
cgd3_3430	extracellular protein with a signal peptide sequence, MAM		1				1	1.291
-	domain and a Cu amine oxidase domain							
cgd3_3940	predicted membrane associated protein					1	1	189.171
cgd3_4030	hypothetical protein with 7 transmembrane domain domain					1	1	83.491
cgd3_4300	possible t-snare domain, possible transmembrane domain or				1		1	8.767
cgd3_470	GPI anchor signal at C-terminus hypothetical protein with 10 transmembrane domains					1	1	72.023
cgd3_470	protein with 12 transmembrane domains					1	1	95.706
cgd3_540	protein with 12 transmembrane domains					1	1	172.497
cgd3_590	hypothetical protein with 4 transmembrane domains, possible		1			•	1	1.585
	unusual phyletic distribution							
cgd3_610	hypothetical protein with possible 4 transmembrane domains					1	1	166.828
cgd3_740	hypothetical protein with 7 transmembrane domains			1			1	4.818
cgd3_970	hypothetical protein, possible 2 transmembrane domains	1					1	0.367
cgd4_1120	WD40 repeat containing protein that has a transmembrane region at the C-terminus	1					1	0.319
cgd4_1160	conserved protein with transmembrane region at C-terminus					1	1	36.075
cgd4_1310	hypothetical protein with transmembrane domain			1			1	2.641
cgd4_160	hypothetical protein, possible transmembrane domain within N-				1		1	9.120
cgd4_1670	terminus hypothetical protein with signal peptide and 3 to 6		1				1	1.856
cqd4 1760	transmembrane domains hypothetical protein with 2 transmembrane domains	1					1	0.382
cgd4_1700	hypothetical protein with 10 transmembrane domains		1				1	1.436
cgd4_1970	protein with central transmembrane domain followed by gly-met-		·	1			1	4.711
cgd4 2180	pro repeat hypothetical protein with 12+ transmembrane domains	1					1	0.376
cgd4_2420	extracelllular membrane associated protein with a signal	•	1				1	1.438
0941_2120	peptide, 5 ankyrin repeats, SUSHI domain and a transmembrane region		·					1.100
cgd4_2430	hypothetical protein containing a signal peptide and 2 transmembrane domains				1		1	11.650
cgd4_2530	possible transmembrane domain near C					1	1	27.238
cgd4_3340	pleckstrin homology (PH) domain containing protein					1	1	68.746
cgd4_3470	hypothetical protein with signal peptide and transmembrane domain near C, within large locus of signal peptide containing		1				1	1.483
cgd4_3480	proteins hypothetical protein with signal peptide plus possible GPI					1	1	95.528
cgu+_0+00	anchor or transmembrane domain near C-terminus, within large locus of signal peptide containing proteins						1	33.320
cgd4_350	hypothetical protein with 7 transmembrane domains	1					1	0.440
cgd4_3520	hypothetical protein with signal peptide and repeats, within large	1					1	0.450
0940020	locus of signal peptide containing proteins	·					1	000
cgd4_360	hypothetical protein with 5 transmembrane domains	1					1	0.457
cgd4_380	protein with signal peptide plus 12 transmembrane domain					1	1	55.249
cgd4_3970	domain protein, possible tranporter signal peptide plus transmembrane domain or GPI anchor,			1			1	3.008
094007 0	proline rich, acidic stretches			i i				0.000
cgd4_3990	hypothetical protein with possible transmembrane domain near N-terminus	1					1	0.354
cgd4_420	signal peptide + 4 transmembrane domain protein					1	1	132.630
cgd4_4210	hypothetical protein with signal peptide plus transmembrane domain		1				1	2.085
cgd4 4470	putative secreted, membrane-associated protein		1				1	2.226
cgd4_4480	putative secreted, membrane-associated protein	1					1	0.344
cgd4_60	extracellular membrane associated protein with a signal peptide,						1	0.370
	an EGF domain followed by 10 transmembrane domains							
cgd4_640	extracellular protein with a signal peptide, FN3 domain and a predicted transmembrane region	1					1	0.526
cgd4_750	extracellular protein with a signal peptide and 8 kazal repeats	1					1	0.438
			'	1	'	'	1	ı

cgd4_800 cgd4_980	Yip1p like integral membrane protein hypothetical protein with 7 transmembrane domains, possible	1	1				1	0.367 1.580
cgd5 1250	signal peptide hypothetical protein with transmembrane domain near N-	1					1	0.432
-	terminus	·	4				1	
cgd5_130	ferlin like type II membrane associated protein with 5 C2 domains and a transmembrane domain or GPI anchor sequence at the C-terminus		1				1	1.531
cgd5_1560	hypothetical protein, 2 transmembrane domains near C-terminus				1		1	11.530
cgd5_1630	protein with signal peptide, and 11 transmembrane domains			1			1	4.479
cgd5_1920 cgd5_1950	pleckstrin homology (PH) domain containing protein hypothetical protein with 5 transmembrane domains	1		1			1	2.352 0.400
cgd5_2020	extracellular protein	·		1			1	2.756
cgd5_2150	protein with signal peptide and 8 transmembrane domains;					1	1	87.906
cgd5_2490	possible ZIP zinc transporter family member hypothetical protein with 5 transmembrane domains within C terminus	1					1	0.395
cgd5_2530	protein with 12 transmembrane domains, possible apicomplexan-specific protein	1					1	0.413
cgd5_2580	hypothetical protein with signal peptide, possible transmembrane domain near C-terminus and predicted SMART			1			1	3.155
cgd5 290	Znf_C2H2 domain hypothetical protein, 6 transmembrane domains	1					1	0.302
cgd5_2990	hypothetical protein with transmembrane domain within C-terminal region				1		1	20.209
cgd5_3130	large hypothetical protein with 8 or more transmembrane domains	1					1	0.531
cgd5_3330	hypothetical protein with 5 transmembrane domains			1			1	2.482
cgd5_3500 cgd5_360	hypothetical protein having 10 transmembrane domains conserved protein with 2 transmembrane domain	1				1	1	245.766 0.331
cgd5_3690	protein with 8 transmembrane domains	'		1			1	4.705
cgd5_3970	protein with 3 transmembrane domains, ring domain, and possible signal peptide		1				1	2.199
cgd5_3980	hypothetical protein with possible transmembrane domain near N-terminus		1				1	1.511
cgd5_3990	protein with 4 transmembrane domains, signal peptide and a RING domain			1			1	3.176
cgd5_4050	hypothetical protein with 4 transmembrane domains	1					1	0.399
cgd5_4140	hypothetical protein with 4 transmembrane domains within C-terminus	1					1	0.417
cgd5_4220	membrane associated protein with a signal peptide, EGF domain and 7 transmembrane domains at the C-terminus	1					1	0.502
cgd5_4270	hypothetical protein with signal peptide and transmembrane region at C-terminus, possible N-terminal region transmembrane domain	1					1	0.355
cgd5_4280	hypothetical protein with signal peptide and possible transmembrane region at C-terminus	1					1	0.494
cgd5_4310	hypothetical protein with 7 transmembrane domains	1					1	0.367
cgd5_4450	hypothetical protein with 8 transmembrane domains	1					1	0.366
cgd5_4470	CpTSP7; extracellular membrane associated protein with a signal peptide followed by 2 TSP1 repeats, an EGF domain and a transmembrane region	1					1	0.332
cgd5_570	hypothetical protein, 5 transmembrane domains near N-terminus	1					1	0.303
cgd5_580	hypothetical protein with 5 transmembrane domains near N-terminus	1					1	0.463
cgd5_590	hypothetical protein with possible transmembrane domain within C	1					1	0.479
cgd6_110	conserved protein with signal peptide and transmembrane domain or GPI anchor signal near C-terminus	1					1	0.415
cgd6_1320	hypothetical protein, possible transmembrane domain near N-terminus			1			1	4.625
cgd6_1350	hypothetical protein with possible transmembrane domain within C-terminus	1					1	0.350
cgd6_1490	dbj				1		1	8.143
cgd6_1510 cgd6_2030	hypothetical protein with 6 transmembrane domains transmembrane protein with 6 transmembrane domains		1	1			1	1.398 3.869
cgd6_2120	hypothetical protein, conserved cysteine residues, possible			1			1	2.494
cgd6_2130	transmembrane domain or GPI anchor at C-terminus hypothetical protein with a C-terminus transmembrane domain		1	ı '			1	1.513
cgd6_2210	membrane-associated protein with 6 transmembrane domains possible apicomplexan conserved, duplicated adjacent gene			1			1	4.047
cgd6_2220	possible apicomplexan conserved, duplicated adjacent gene membrane-associated protein with 6 transmembrane domains possible apicomplexan conserved, duplicated adjacent gene			1			1	3.262
cgd6_2280	hypothetical protein with signal peptide and 12 or more transmembrane domains				1		1	6.014
cgd6_2340	hypothetical protein with signal peptide and 12 or more transmembrane domains				1		1	6.891
cgd6_2440	hypothetical protein having 6 transmembrane domains					1	1	29.134
cgd6_260	hypothetical protein with 4 transmembrane domains	1					1	0.331
cgd6_2620	vesicle-associated membrane protein,MSP (major sperm protein) domain, transmembrane domain or GPI at C					1	1	63.320
ı	hypothetical protein with 12 transmembrane domains	1	1				1	0.314

lande 0700	Investein with signal montide plus possible CDI signal or				l a	I I	اها	46 470
cgd6_2730	protein with signal peptide plus possible GPI signal or transmembrane domain at C-terminus				1		1	16.173
cgd6_3020	hypothetical protein with 8 transmembrane domains			1			1	3.109
cgd6_3350	hypothetical protein with transmembrane domain	1					1	0.306
cgd6_3530	hypothetical protein with possible 4 or more transmembrane		1				1	1.459
cad6 3590	domains				1		1	9.550
cgd6_3580 cgd6_3630	hypothetical protein with 3 or more transmembrane domains secreted protein with ankyrin repeats, signal peptide plus		1				1	1.767
cguo_5050	transmembrane domain or GPI anchor		'				'	1.707
cgd6_3730	large extracellular protein with a signal peptide, apple domain			1			1	2.950
	and a transmembrane region							
cgd6_3870	hypothetical integral membrane protein with 12 transmembrane	1					1	0.365
oad6 2010	domains				4		1	24.578
cgd6_3910 cgd6_4310	pleckstrin homology (PH) domain containing protein hypothetical low complexity	1					1	0.417
cgd6 4440	hypothetical protein with transmembrane region near N-	1					1	0.417
cguo_+++0	terminus						'	0.507
cgd6_4680	hypothetical protein with 12 transmembrane domains	1					1	0.376
cgd6_4730	hypothetical protein with 6 transmembrane domains		1				1	2.255
cgd6_4740	hypothetical protein with 6 transmembrane domains and signal					1	1	29.113
	peptide							
cgd6_4920	hypothetical protein with 4 transmembrane domains		1				1	2.107
cgd6_5140	ERGIC-53-like mannose binding lectin that is a type I			1			1	5.570
	membrane protein, transmembrane domain near C, signal peptide							
cgd6_5430	hypothetical protein, signal peptide plus transmembrane domain					1	1	79.165
" -	or GPI anchor							
cgd6_590	hypothetical protein with possible transmembrane domain or	1					1	0.367
	GPI anchor signal at C-terminus							0.070
cgd6_60	hypothetical protein with signal peptide and proline stretch at C-terminus	1					1	0.279
cgd6_670	extacellular protein with a signal peptide, clostripain like	1					1	0.248
	caspase/hemoglobinase domain, notch domain and 2 EGF	·					- 1	0.2.0
	domains							
cgd6_760	conserved protein with 6 transmembrane domain	1					1	0.413
cgd6_780	CpTSP8,predicted extracellular protein with 3 TSP1 repeats, an					1	1	849.606
	EGF domain and a C-terminal transmembrane domain. adjacent TSP domain containing gene.							
cgd6_800	CpTSP9, extracellular protein with 3 TSP1 domains and an EGF	1					1	0.513
loguo_coo	domain							0.010
cgd6_90	hypothetical protein with 5 transmembrane domains					1	1	68.318
cgd7_1310	extracellular protein with a signal peptide followed by a family 2	1					1	0.346
	glycosyltransferase and ricin domains							
cgd7_150	hypothetical protein with signal peptide and transmembrane domain near C-terminus	1					1	0.424
cgd7_1650	protein with signal peptide and 6 transmembrane domains		1				1	1.391
cgd7_1730	CpCCp1/Cpa135				1		1	6.106
cgd7_1860	P24 like gold domain protein, possible transmembrane region		1		·		1	1.688
-	near C-terminus, signal peptide							
cgd7_1960	membrane protein with multiple cysteines at the N-terminus.			1			1	4.872
cgd7_2150	transmembrane protein, putative	1					1	0.418
cgd7_2170	hypothetical membrane protein				1		1	5.912
cgd7_2590	integral membrane protein with 10 transmembrane domains		1				1	1.951
cgd7_300	CpCCP2; extracellular protein with a signal peptide, ricin,		1				1	1.654
	discoidin, NEC, LCCL, 2 levanase and an apicomplexan- specific cysteine-rich repeat (apicA repeat)							
cgd7_3040	membrane protein conserved in eukaryotes		1				1	1.729
cgd7_3070	hypothetical protein, signal peptide, transmembrane domain				1		1	19.438
ogur_co.c	near C-terminus				·		- 1	.000
cgd7_3250	membrane protein with no close homologs,					1	1	464.455
cgd7_3380	putative secreted cysteine rich protein, possible transmembrane			1			1	3.418
	domain near C, signal peptide							
cgd7_3560	hypothetical protein, signal peptide, possible 3 transmembrane domains	1					1	0.372
cgd7 3910	cysteine rich protein with two potential transmembrane domain	1					1	0.374
cgur_ooro	regions						'	0.074
cgd7_4160	extracellular protein with a signal peptide followed by family 2	1					1	0.533
	glycosyltransferase and ricin domains							
cgd7_4310	extracellular protein with a signal peptide and 4 SCP domains			1			1	3.296
cgd7_4540	CP15/60 sporozoite 60K protein			1			1	4.289
cgd7_4610	divergent membrane protein				1		1	5.624
cgd7_4810	CpFNPA, extracellular protein with a signal peptide, FN2 domain and an anthrax toxin-N-terminus like domain. starts at			1			1	5.244
	second Met with signal peptide following							
cgd7 4880	signal peptide plus GPI anchored membrane protein					1	1	36.784
cgd7_4910	conserved 3 transmembrane domain membrane associated				1		1	8.880
	RING finger domain (shared by plants and apicomplexans)							
cgd7_4920	membrane protein	1					1	0.326
cgd7_5140	A surface protein with 2 conserved cysteines		1				1	1.658
cgd7_5430	possible 2 transmembrane domains, low complexity protein	1					1	0.369
cgd7_5480	very large membrane protein				1		1	5.866
cgd7_550	hypothetical protein wtih 9 transmembrane domains, possible apicomplexan-specific protein				1		1	5.913
I	Japicompiesan-specific protein	I	ı		I		1	1

1	cgd7_70	integral membrane protein with 6 transmembrane domains and	1					1	0.365
	cgd7_720	possible ring domain PASILLA splice variant 3-like 2KH domains, transmembrane	1					1	0.530
	cgd7_900	domain at C-terminus hypothetical protein with 3 or more transmembrane domains	1					1	0.286
	cgd7_930	hypothetical transmembrane protein	1					1	0.366
	cgd8_1160	signal peptide plus His and thr repeats, signal peptide plus			1			1	5.490
	cgd8_150	transmembrane domain or GPI anchor, predicted mucin CpTSP4; extracellular protein with signal peptide and 2 repeats	1					1	0.280
	cgd8_1900	of an apple domain followed by a TSP1 domain predicted transmembrane domain, transmembrane domain	1					1	0.315
	cgd8_2280	within N-terminus uncharacterized protein with 5 transmembrane domain					1	1	40.631
	cgd8_240	hypothetical protein with 6 transmembrane domains	1					1	0.563
	cgd8_2470	hypothetical protein, signal peptide, 4 transmembrane domains					1	1	31.094
	cgd8_2480	signal peptide plus possible transmembrane domain paralogs				1		1	28.197
	cgd8_2500	hypothetical protein, signal peptide, membrane protein,				1		1	7.175
	1	transmembrane domain at C-terminus, paralogs							
	cgd8_2790	pleckstrin homology (PH domain) containing protein					1	1	27.645
	cgd8_2910	ferlin-like type II membrane associated protein with 5 C2	1					1	0.374
	cgd8_2950	domains, transmembrane domain or GPI anchor at C-terminus cervesiae Yh1017wp/PTM1 like protein; signal peptide plus 7		1				1	1.639
	cguo_2550	pass transmembrane regions							1.000
	cgd8_3000	SYG1/ ERD1 like integral membrane protein required for				1		1	15.278
		retention of ER lumen proteins, with 8-10 transmembrane domains							
	cgd8_3470	membrane associated protein with a RING finger,					1	1	215.651
	cgd8_3620	4xtransmembrane domain hypothetical protein with 6 transmembrane domains	1					1	0.528
	cgd8_3760	predicted membrane associated protein, signal peptide,	'		1			1	2.684
	cguo_0700	transmembrane domain near C			<u>'</u>				2.004
	cgd8_3890	membrane protein with signal peptide plus 12x transmembrane domains				1		1	13.850
	cgd8_3920	hypothetical protein, signal peptide, predicted membrane	1					1	0.387
	cgd8_4090	protein, transmembrane domain near C-terminus hypothetical protein, signal peptide + 5 transmembrane domains					1	1	28.561
	cgd8_4160	hypothetical protein, transmembrane domain			1			1	3.755
	cgd8_4410	hypothetical protein, possible transmembrane domain			'	1		1	16.317
	cgd8_4440	protein with 12x transmembrane regions	1					1	0.404
	cgd8_4880	3 transmembrane region protein					1	1	124.333
	cgd8_5090	hypothetical protein, possible transmembrane domain within N-	1					1	0.427
	1.3	terminus							
	cgd8_5140	possible coated vesicle proteins, emp24/gp25L/p24 family, signal peptide, possible transmembrane domain at C-terminus	1					1	0.340
	cgd8_5200	5 transmembrane domain proteiin					1	1	47.298
	cgd8_5220	signal peptide, 4+ transmembrane domains	1					1	0.367
	cgd8_5270	integral membrane protein predicted amino acid permease, 11x transmembrane domains	1					1	0.371
	cgd8_530	hypothetical protein with 4 transmembrane domains		1				1	1.952
	cgd8_540	CpTSP12; extracellular protein with 1 TSP1 domain	1					1	0.435
	cgd8_60	signal peptide, possible transmembrane domain near N					1	1	175.821
	cgd8_850	predicted membrane associated protein with 8 transmembrane	1					1	0.484
		domains					0.4		24.000
Membrane Total	14 400	lister also also also also and also	92	41	36	33	34	236	21.029
Unknown	cgd1_100	hypothetical protein	1					1	0.413
	cgd1_1000	hypothetical protein	1 1					1	0.377
	cgd1_1020 cgd1_1040	hypothetical protein hypothetical protein	1					1	0.422 0.386
	cgd1_1040 cgd1_1060	hypothetical protein	1					1	0.380
	cgd1_1000 cgd1_1070	RRM domain protein	'		1			1	3.300
	cgd1_1070	predicted secreted protein, signal peptide, paralogs			·	1		1	10.376
	cgd1_1150	hypothetical protein	1					1	0.360
	cgd1_1190	hypothetical protein	1					1	0.350
	cgd1_1100	hypothetical protein					1	1	220.734
	cgd1_1240	Sec14 domain containing protein	1					1	0.465
	cgd1_1250	predicted secreted protein, signal peptide	1					1	0.400
	cgd1_1260	hypothetical protein	1					1	0.348
	cgd1_1290	apicomplexa specific secreted protein Pf (23508265), signal				1		1	16.723
	-	peptide							
	cgd1_130	signal peptide, predicted secreted protein with a cysteine cluster at the C-terminus					1	1	51.078
	cgd1_1320	developmental protein, putative	1					1	0.426
	cgd1_1390	hypothetical protein	1					1	0.424
	cgd1_1400	hypothetical protein	1					1	0.418
	cgd1_1430	hypothetical protein	1					1	0.425
	cgd1_1440	hypothetical protein		1				1	1.758
	cgd1_1450	predicted secreted protein, signal peptide					1	1	42.773
	cgd1_1460	hypothetical protein	1					1	0.466
	cgd1_1490	NEK2 protein, putative	1					1	0.447
	cgd1_150	predicted secreted protein, signal peptide			1			1	3.693

cgd1_1500	hypothetical protein		1	1		1	1.336
cgd1_1510	predicted secreted protein, signal peptide		1			1	1.523
cgd1_1590	hypothetical protein				1	1	22.164
cgd1_1600	histidine triad (HIT) family zinc binding protein				1	1	123.796
cgd1_1630	hypothetical protein				1	1	8.652
cgd1_1650	hypothetical protein	1			•	1	0.438
cgd1_1690	PHD finger containing protein	1					0.450
		1					
cgd1_170	hypothetical protein					l I	0.478
cgd1_1740	hypothetical coiled coil protein	1				1	0.338
cgd1_1780	hypothetical protein		1			1	1.997
cgd1_1790	RING-H2 finger containing membrane associated protein, 8x	1				1	0.621
	transmembrane domain						
cgd1_1810	hypothetical protein	1				1	0.381
cgd1_1840	hypothetical protein				1	1	151.632
cgd1_1850	G-patch domain containing protein	1				1	0.407
cgd1_1880	hypothetical protein	1				1	0.305
cgd1_190	narf-like protein nuclear prelamin A recognition factor	1				1	0.482
cgd1_1920	large protein with a SPRY domain and HECT domain			1		1	2.524
cgd1_1940	possible RAN guanine nucleotide release factor			1		1	4.637
cgd1_1950	hypothetical protein				1	1	25.027
cgd1_1970	hypothetical protein			1		1	3.612
	1 21 1			-			
cgd1_1990	hypothetical protein			- '		1 1	3.460
cgd1_2000	predicted coiled coil protein				1	1	86.923
cgd1_2070	hypothetical protein	1				1	0.460
cgd1_2140	hypothetical protein	L_	1			1	1.803
cgd1_2150	hypothetical protein with GYF domain at the amino terminus	1				1	0.361
cgd1_2160	hypothetical protein with BTB/POZ domain and GYF domain	1				1	0.368
cgd1_2170	SET domain containing protein with a cysteine cluster at the C-				1	1	11.333
ogu o	terminus				1	'	
cgd1_2200	hypothetical protein	1				1	0.326
cgd1_2210	hypothetical protein		1			1	1.721
cgd1_2230	WD40 protein Ciao1	1				1	0.357
	1 .	1					
cgd1_2240	AT hook motif protein, putative	'				l I	0.684
cgd1_2290	predicted coiled coil protein		1			1	1.339
cgd1_2310	unnamed protein product		1			1	1.643
cgd1_2330	hypothetical protein with predicted SANT domain		1			1	1.250
cgd1_2340	hypothetical protein	1				1	0.309
cgd1_2350	hypothetical protein				1	1	16.095
cgd1_2390	hypothetical secreted/membrane associated protein signal		1			1	1.927
	peptide plus possible GPI signal						
cgd1_240	predicted secreted protein			1		1	5.573
cgd1_2400	signal peptide, secreted protein				1	1	226.789
cgd1 2440	eukaryotic orthologous group, signal peptide	1	1			2	1.052
cgd1_2460	hypothetical protein				1	1	47.223
cgd1_2480	hypothetical protein			1		1	3.837
cgd1_2500	signal recognition particle SPR68	1		- 1		1	0.467
	1					l I	
cgd1_2520	hypothetical protein	1				1	0.463
cgd1_2570	possible conserved eukaryotic alpha beta hydrolase			1		1	2.339
cgd1_2590	PGPD14 protein with at least one predicted RING finger,	1				1	0.340
	possible plant origin						
cgd1_260	predicted secreted protein, signal peptide	1				1	0.380
cgd1_2610	hypothetical protein	1				1	0.401
cgd1_2650	hypothetical protein	1	1			1	1.890
cgd1_2670	ankyrin-related protein, putative		1			1	1.765
cgd1_2790	hypothetical protein	1				1	0.308
cgd1_2810	S. pombe like (SPAC1805) eukaryotic protein with a possible	1				1 1	0.308
ogu 1_2010	metal binding domain at the N-terminus					'	0.000
cgd1_2860	hypothetical protein	1				1	0.386
cgd1_2870	N-terminal domain cerevisiae Yos9p-like that is involved in GPI-	1				1	0.609
cgu1_2070	anchored protein transport in the golgi, a cation independent	•				'	0.003
	mannose-6-po4 receptor like conserved Cys motif and a C-						
	terminal E. coli y						
cgd1 2900	hypothetical protein			1		1	2.824
cgd1_2930	hypothetical protein	1				1	0.395
cgd1_2940	hypothetical protein	1				1	0.335
	1 **			4		1	
cgd1_2950	hypothetical protein			1		l I	5.829
cgd1_3030	hypothetical protein containing WD40 repeats fused to a RING	1	1			2	0.842
oad1 2000	finger						0.000
cgd1_3090	very low complexity hypothetical protein, possible unreal ORF	1				1	0.239
cgd1_3100	hypothetical protein		1			1	1.628
cgd1_3110	hypothetical protein	1				1	0.295
cgd1_3120	peptide synthase like condensation domain	1				1	0.393
cgd1_3180	hypothetical protein	1				1	0.394
cgd1_3220	erythrocyte membrane-associated antigen	1				1	0.364
cgd1_3260	hypothetical protein				1	1	6.565
-343200	hypothetical protein				1	1	59.300
cad1 3270		i	ı <b>I</b>			ı 'I	JJ.JUU
	1 **			4	I	4	1 000
cgd1_3270 cgd1_3280 cgd1_3300	hypothetical protein ring domain protein			1		1 1	4.890 2.979

cgd1_3320	ring domain protein	1				1	0.346
cgd1_3330	hypothetical protein	1				1	0.323
cgd1 3350	hypothetical protein	1				1	0.279
cgd1_3360	predicted AFG1 ATpase family AAA ATpase	1				1 1	0.386
cgd1 3400	hypothetical protein		1			1 1	1.981
-	hypothetical protein	1	' '			1 1	0.414
cgd1_3430	1 3.	- 1				1 1	
cgd1_3450	hypothetical protein		1			1	1.340
cgd1_3520	hypothetical protein			1		1	2.558
cgd1_3540	TPR repeat proteini				1	1	13.434
cgd1_3560	hypothetical protein	1				1	0.345
cgd1_3580	hypothetical protein	1				1	0.511
cgd1_3640	hypothetical protein, signal peptide				1	1	87.129
cgd1_3650	1				1		34.068
0 -	hypothetical protein, signal peptide				'		
cgd1_3660	hypothetical protein	1				1	0.577
cgd1_3740	ankyrin repeat protein with over 9 transmembrane domains at C-	1				1	0.330
	terminus, signal peptide						
cgd1_3760	hypothetical coiled coil protein	1				] 1	0.293
cgd1_3770	hypothetical protein				1	1	79.010
cgd1_3790	hypothetical protein, signal peptide				1	1	6.004
cgd1_3830	hypothetical protein	1				1 1	0.495
cgd1_3860	hypothetical protein				1		98.631
1	1 2.			1	'		
cgd1_440	hypothetical protein					1 1	3.025
cgd1_450	hypothetical protein		1			1	1.937
cgd1_460	hypothetical protein	1				1	0.422
cgd1_470	predicted secreted protein, signal peptide, low complexity serine-			1		1	5.540
	threonine rich, possible mucin						
cgd1_490	hypothetical protein	1				1	0.474
cgd1 50	hypothetical protein with 2 TPR domains	1				1	0.366
cgd1_500	hypothetical protein	1				1	0.472
1	1 2.	1					0.406
cgd1_510	hypothetical protein	'			4	1 1	
cgd1_530	hypothetical protein				1	1	38.741
cgd1_560	hypothetical protein		1			1	1.484
cgd1_570	predicted secreted protein, signal peptide	1				1	0.373
cgd1_590	hypothetical protein, proline rich C-terminus, signal peptide, very	1	1			2	1.176
-	large protein						
cgd1_610	hypothetical protein				1	1	12.825
cgd1_620	hypothetical protein		1			1 1	1.485
cgd1_630	hypothetical protein			1		1	3.936
1	1 **			'	1	1	1,146.669
cgd1_640	signal peptide, large protein				!		
cgd1_650	predicted secreted protein, signal peptide	1				1	0.390
cgd1_660	predicted secreted protein, signal peptide	1				1	0.646
cgd1_670	predicted secreted protein, signal peptide		1			1	1.525
cgd1_680	hypothetical protein				1	1	26.652
cgd1_690	hypothetical protein		1			1	1.966
cgd1_70	hypothetical protein		1			1 1	1.461
	1 **		·		4	1 1	
cgd1_710	coiled coil protein				1	1 1	5.831
cgd1_740	hypothetical protein	1				1	0.475
cgd1_910	ZnF A20 and Znf AN1 domains, involved in signaling				1	1	249.040
cgd1_940	hypothetical protein	1				1	0.632
cgd1 960	RING finger containing protein			1		1	2.614
cgd1_970	RING finger containing protein			1		1	4.263
cgd2_10	hypothetical protein	1		-		1	0.349
1	1 **	1					
cgd2_1040	flavohemoprotein b5+b5R (DJ676J13.1) (flavohemoprotein b5+b5R cytochrome b-type NAD(P)H oxidoreductase), putative	'				'	0.363
cgd2 1050	signal peptide				1	1	65.673
" -							
cgd2_1080	hypothetical protein	L .	1			1 1	1.289
cgd2_1110	silencer-associated factor, putative	1				1	0.360
cgd2_1130	hypothetical protein	1				1	0.400
cgd2_1150	hypothetical protein				1	1	41.522
cgd2_1170	zinc finger protein				1	1	12.855
cgd2_1230	hypothetical protein			1		1	2.711
cgd2_1260	hypothetical protein	1				1 1	0.436
	1 2.	1				'	
cgd2_1280	hypothetical protein					1 1	0.405
cgd2_1370	hypothetical coiled coil protein			1		1	4.253
cgd2_1380	hypothetical protein	1				1	0.498
cgd2_1390	hypothetical protein			1		1	3.279
cgd2_1410	possible domain KOG3410, conserved alpha-helical protein				1	1	29.743
cgd2_1420	hypothetical protein				1	1	13.272
cgd2_1470	hypothetical protein	1					0.434
1	1 **	1				'	
cgd2_1490	hypothetical protein with signal peptide and 7 transmembrane domains	1				1	0.381
cad2 1520					1	1	93.538
cgd2_1520	hypothetical protein						
cgd2_1560	hypothetical protein		1			1 1	1.795
cgd2_1670	ING1 ike protein with an N-terminal globular domain and a PHD	1				1	0.296
	domain					1 .1	2
cgd2_1680	hypothetical protein				1	1 1	6.113
cgd2_1720	hypothetical protein	1				1	0.350
					•	•	•

	L				1		. 1	
cgd2_1730	hypothetical protein	1					1	0.418
cgd2_1740	RSC8 ortholog with a swirm domain, ZZ finger and Myb		4	1			1	2.541
cgd2_1750	ring domain		1				1	1.608
cgd2_1790	hypothetical protein			1	4		1	4.008
cgd2_180	hypothetical protein				1	4	1	7.810
cgd2_1820	hypothetical protein	- 1	4			1	1	24.622
cgd2_1830	hypothetical protein	1	1			- 4	2	1.202
cgd2_1840	signal peptide					1	1	133.856
cgd2_1860	TBC domain containing protein			1			1	5.556
cgd2_1870	guanine nucleotide-binding protein, putative					1	1	66.422
cgd2_1890	hypothetical protein		1				1	1.504
cgd2_1920	hypothetical protein	1					1	0.324
cgd2_1950	SAP+PHD+MIZ domains containing protein	1					1	0.468
cgd2_1970	hypothetical protein	1					1	0.374
cgd2_1980	hypothetical protein		1				1	1.526
cgd2_2010	hypothetical protein	1					1	0.628
cgd2_2020	hypothetical protein	1					1	0.443
cgd2_2080	hypothetical protein		1				1	1.483
cgd2_2100	hypothetical protein, possible signal peptide			1			1	2.637
cgd2_2110	hypothetical protein, possible signal peptide			1			1	2.406
cgd2 2150	hypothetical protein			1			1	3.148
cgd2_2180	hypothetical protein		1				1	1.494
cgd2 2270	hypothetical protein, signal peptide		1				1	1.380
cgd2_2330	hypothetical protein	1					1	0.345
cgd2_2350	MA3 domain containing protein					1	1	34.524
cgd2_2360	Dop1p family protein	1					1	0.581
cgd2_2370	hypothetical protein	1					1	0.329
cgd2_2380	hypothetical protein	1					1	0.329
cgd2_2410	SSM4 like RING finger protein	'			1		1	10.936
	hypothetical protein					1	1	123.210
cgd2_2440	1					1	1	29.351
cgd2_2450	hypothetical protein		1			- '		
cgd2_2460	hypothetical protein		1				1	2.039
cgd2_2520	hypothetical protein				1		1	14.384
cgd2_2530	hypothetical protein, signal peptide			1			1	4.807
cgd2_2550	hypothetical protein, signal peptide	1	1				2	1.117
cgd2_2560	hypothetical protein, signal peptide					1	1	57.962
cgd2_2570	hypothetical protein, possible signal peptide					1	1	31.925
cgd2_2580	hypothetical protein			1			1	4.451
cgd2_2590	hypothetical protein	1					1	0.323
cgd2_260	hypothetical protein					1	1	94.265
cgd2_2600	hypothetical protein				1		1	6.383
cgd2_2620	hypothetical protein		1				1	2.236
cgd2_2640	hypothetical protein			1			1	3.430
cgd2_2690	hypothetical protein				1		1	20.841
cgd2_2700	Brf1p like coiled coil protein			1			1	5.475
cgd2_2720	ARM repeat protein			1			1	3.969
cgd2_2740	hypothetical protein				1		1	7.770
cgd2_2800	THUMP RNA binding domain containing protein, Yg1232wp-like			1			1	2.839
cgd2_2850	hypothetical protein, possible signal peptide	1					1	0.435
cgd2_290	hypothetical protein	1					1	0.432
cgd2_2910	large WD repeat protein			1			1	4.738
cgd2_2930	hypothetical protein		1				1	1.729
cgd2_2950	ring domain at very C-terminus of large protein		1				1	1.474
cgd2_2980	hypothetical protein			1			1	4.842
cgd2_300	kelch repeat-containing proteins that is fused to a HSP90-like	1					1	0.396
	ATpase							
				- 1			1	0.525
cgd2_3020	hypothetical protein	1		I			1	0.423
cgd2_3020 cgd2_3030		1				I		
	hypothetical protein		1				1	1.643
cgd2_3030	hypothetical protein hypothetical protein, signal peptide		1	1				1.643 3.288
cgd2_3030 cgd2_3050	hypothetical protein hypothetical protein, signal peptide hypothetical protein		1	1	1		1	
cgd2_3030 cgd2_3050 cgd2_3060	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein		1	1	1	1	1	3.288
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor		1	1	1	1	1 1 1	3.288 7.387
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain	1	1	1	1	1	1 1 1 1	3.288 7.387 147.737 0.507
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein	1 1 1	1	1	1	1	1 1 1 1 1	3.288 7.387 147.737 0.507
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3160	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein	1	1		1	1	1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein	1 1 1	1	1	1	1	1 1 1 1 1 1 1	3.288 7.387 147.737 0.507
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3160	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein	1 1 1	1		1	1	1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3160 cgd2_3210	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein hypothetical protein	1 1 1	1		1	1	1 1 1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338 2.672
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3160 cgd2_3210 cgd2_3220	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein hypothetical protein hypothetical protein Sc6p-like, SM domain	1 1 1 1	1		1	1	1 1 1 1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338 2.672 10.398
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3160 cgd2_3210 cgd2_3220 cgd2_3220	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein Sc6p-like, SM domain ARF GAP-like zinc finger-containing protein	1 1 1 1			1	1	1 1 1 1 1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338 2.672 10.398 0.597
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3210 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3280	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein hypothetical protein hypothetical protein Sc6p-like, SM domain ARF GAP-like zinc finger-containing protein 3x TPR domain-containing protein hypothetical protein	1 1 1 1			1	1	1 1 1 1 1 1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338 2.672 10.398 0.597 1.843 0.251
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3160 cgd2_3210 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3250	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein hypothetical protein Sc6p-like, SM domain ARF GAP-like zinc finger-containing protein 3x TPR domain-containing protein	1 1 1 1			1	1	1 1 1 1 1 1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338 2.672 10.398 0.597 1.843 0.251
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3210 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3280	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein hypothetical protein hypothetical protein Sc6p-like, SM domain ARF GAP-like zinc finger-containing protein 3x TPR domain-containing protein hypothetical protein hypothetical protein hypothetical protein with a signal peptide plus thr stretch,	1 1 1 1			1	1	1 1 1 1 1 1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338 2.672 10.398 0.597 1.843
cgd2_3030 cgd2_3050 cgd2_3060 cgd2_3090 cgd2_3110 cgd2_3130 cgd2_3140 cgd2_3210 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3220 cgd2_3230 cgd2_3290	hypothetical protein hypothetical protein, signal peptide hypothetical protein hypothetical protein hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein containing a signal peptide hypothetical protein with possible transcriptional repressor EZH1 domain hypothetical protein hypothetical protein hypothetical protein Sc6p-like, SM domain ARF GAP-like zinc finger-containing protein 3x TPR domain-containing protein hypothetical protein hypothetical protein with a signal peptide plus thr stretch, possible mucin	1 1 1 1			1	1	1 1 1 1 1 1 1 1 1 1 1	3.288 7.387 147.737 0.507 0.478 0.338 2.672 10.398 0.597 1.843 0.251 25.356

	hypothetical protein			1	- 1	- 1	1	2.668
cgd2_3360	hypothetical protein	1					1	0.383
cgd2_340	signal peptide, large protein				1		1	6.139
cgd2_3430	SDA1-like protein				1		1	24.345
cgd2_3460	C- terminal region conserved, zinc finger, myb DNA binding	1					1	0.386
cgd2_3490	domain protein with low complexity regions and an apicomplexan			1			1	3.475
cguz_5490	specific domain			'			'	3.473
cgd2_3530	possible RNA binding motif, signal peptide	1					1	0.316
cgd2_3610	2x WD domain containing protein	1					1	0.417
cgd2_3630	hypothetical protein	1					1	0.500
cgd2_3640	hypothetical protein with region conserved in apicomplexa					1	1	26.158
cgd2_3690	WD repeat protein			1			1	2.648
cgd2_3710	Pfa MAL6P1.309 like protein	1					1	0.418
cgd2_3720	hypothetical protein	1					1	0.435
cgd2_3740	hypothetical protein, signal peptide	1					1	0.482
cgd2_3780	uncharacterized protein rich in Thr and Ser residues		1				1	1.793
cgd2_3800	hypothetical protein	1					1	0.421
cgd2_3820	hypothetical protein	1					1	0.307
cgd2_3830	hypothetical protein	-		1			1	3.677
cgd2_3840	hypothetical protein		1	1			1	1.645
cgd2_3850	possible FH2 formin homology domain	1					1	0.299
cgd2_3860	BBOX Zn finger domain containing protein	•	1				1	2.050
cgd2_390	hypothetical protein		1				1	1.817
cgd2_3910	hypothetical protein			1			1	2.363
cgd2_3910 cgd2_3980	Myb domain containing protein			1			1	4.911
cgd2_3900 cgd2_4010	MAL7P1.13-like						1	4.138
	signal peptide			'	1		1	17.160
cgd2_4020	• ' '				'	4	1	
cgd2_4100	hypothetical protein	4				1		392.489
cgd2_4110	possible UBC domain containing protein	1				4	1	0.340
cgd2_4160	hypothetical protein having possible hemolytic activity					1	1	25.970
cgd2_4180	hypothetical protein			1			1	3.574
cgd2_4200	hypothetical protein		1				1	2.204
cgd2_4210	uncharacterized protein with several coiled coil regions	1					1	0.579
cgd2_4220	hypothetical protein		1				1	2.245
cgd2_4250	SPAC1486.03c-like tuftelin-interacting protein, G-patch domain	1					1	0.474
cgd2_4290	hypothetical protein				1		1	8.404
cgd2_4310	hypothetical protein					1	1	342.642
cgd2_4360	hypothetical protein					1	1	35.148
cgd2_4370	signal peptide					1	1	37.937
cgd2_4380	signal peptide, repeats, gene anchored to telomere				1		1	7.503
cgd2_470	very low complexity large protein, possible unreal ORF?				1		1	19.177
cgd2_480	hypothetical protein				1		1	6.723
cgd2_490	hypothetical protein with signal peptide				1		1	14.691
cgd2_500	hypothetical protein	1					1	0.365
cgd2_530	possible proteasome component	1					1	0.413
cgd2_560	large low complexity protein	1					1	0.434
cgd2 60	hypothetical protein			1			1	4.221
cgd2_680	hypothetical protein	1					1	0.347
cgd2_690	large low complexity protein with glycine-rich repeats			1			1	5.312
cgd2_720	hypothetical protein				1		1	5.633
cgd2_750	bub3'bub3-like protein with WD40 repeats'	1					1	0.486
cgd2_770	hypothetical protein					1	1	25.904
cgd2_780	hypothetical protein				1		1	17.990
cgd2_850	hypothetical protein, signal peptide		1				1	2.326
							1	12.682
	**				4			
cgd2_870	drosophila CG6013 like HMG domain containing protein with a				1		.1	
cgd2_870	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus	1			1			
cgd2_870 cgd2_910	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein	1			1		1	0.477
cgd2_870 cgd2_910 cgd2_950	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein	1	1		1		1	0.477 0.408
cgd2_870 cgd2_910 cgd2_950 cgd2_970	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1	1		1		1 1 1	0.477 0.408 1.472
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide		1		1		1 1 1	0.477 0.408 1.472 0.363
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein	1	1		1		1 1 1 1	0.477 0.408 1.472 0.363 9.711
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein	1 1	1		1		1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein	1 1 1 1	1		1		1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040 cgd3_1050	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein	1 1 1 1 1	1		1		1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040 cgd3_1050 cgd3_1080	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1	1		1		1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040 cgd3_1050 cgd3_1080 cgd3_1100	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1	1		1		1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040 cgd3_1050 cgd3_1080 cgd3_1100 cgd3_1130	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1 1 1	1		1		1 1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272 0.381
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040 cgd3_1050 cgd3_1100 cgd3_1130 cgd3_1130 cgd3_1120	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1	1		1		1 1 1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272 0.381 0.304
cgd2_870 cgd2_950 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040 cgd3_1050 cgd3_1100 cgd3_1130 cgd3_1130 cgd3_120 cgd3_120	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein possible prefoldin-related protein	1 1 1 1 1 1 1 1	1		1 1		1 1 1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272 0.381 0.304 0.431 6.512
cgd2_870 cgd2_910 cgd2_950 cgd2_970 cgd3_100 cgd3_1020 cgd3_1030 cgd3_1040 cgd3_1050 cgd3_1100 cgd3_1130 cgd3_1130 cgd3_1120	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein having a signal peptide, conserved region,	1 1 1 1 1 1 1 1 1	1		1		1 1 1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272 0.381 0.304 0.431 6.512
cgd2_870  cgd2_910  cgd2_950  cgd2_970  cgd3_100  cgd3_1020  cgd3_1030  cgd3_1050  cgd3_1080  cgd3_1130  cgd3_1130  cgd3_1130  cgd3_1200  cgd3_1210	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein possible prefoldin-related protein hypothetical protein hypothetical protein having a signal peptide, conserved region, and three or more transmembrane domains	1 1 1 1 1 1 1 1	1		1 1	4	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272 0.381 0.304 0.431 6.512 0.459
cgd2_870  cgd2_910  cgd2_950  cgd2_970  cgd3_100  cgd3_1020  cgd3_1050  cgd3_1080  cgd3_1130  cgd3_1120  cgd3_1200  cgd3_1210  cgd3_1210  cgd3_1220	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein having a signal peptide, conserved region, and three or more transmembrane domains hypothetical protein	1 1 1 1 1 1 1 1 1 1	1		1 1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272 0.381 0.304 0.431 6.512 0.459
cgd2_870  cgd2_910  cgd2_950  cgd2_970  cgd3_100  cgd3_1020  cgd3_1030  cgd3_1050  cgd3_1080  cgd3_1130  cgd3_1130  cgd3_1130  cgd3_1200  cgd3_1210	drosophila CG6013 like HMG domain containing protein with a coiled coil region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with signal peptide hypothetical protein uncharacterized low complexity protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein possible prefoldin-related protein hypothetical protein hypothetical protein having a signal peptide, conserved region, and three or more transmembrane domains	1 1 1 1 1 1 1 1	1	41	1 1 1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.477 0.408 1.472 0.363 9.711 0.456 0.282 0.439 0.272 0.381 0.304 0.431 6.512

cgd3_130	DRG like OBG family GTpase fused to an RNA binding domain	1					1	0.379
cgd3_1310	TGS domain, Fun11p hypothetical protein	1					1	0.432
cgd3_1310 cgd3_1330	hypothetical protein having a signal peptide	•	1				1	1.879
			1				1	
cgd3_1390	hypothetical protein		1			4		1.659
cgd3_1410	small hypothetical protein					1	1	44.129
cgd3_1460	GAF domain containing protein	1					1	0.455
cgd3_1490	hypothetical protein	1					1	0.363
cgd3_150	hypothetical protein	1					1	0.564
cgd3_1500	hypothetical protein				1		1	13.340
cgd3_1530	hypothetical protein				1		1	16.831
cgd3_1540	large protein with signal peptide, cysteine-rich, threonine-rich,	1					1	0.475
-3	possible mucin	-					1	
cgd3_1550	Sec14 domain containing protein			1			1	5.563
cgd3_1570	sporozoite antigen, putative					1	1	1,957.286
cgd3_160	hypothetical protein					1	1	36.880
cgd3_1630	hypothetical protein				1	- 1	1	5.622
cgd3_170	hypothetical protein				1		1	8.071
		- 1			'		1	
cgd3_1830	hypothetical protein having a signal peptide	1					- 1	0.476
cgd3_1840	large uncharacterized protein	1					1	0.438
cgd3_1880	protein with 2x rrm domains		1				1	2.163
cgd3_190	latent transforming growth factor beta binding protein like			1			1	4.444
	(3F865)							
cgd3_1910	hypothetical protein	1					1	0.421
cgd3_1970	hypothetical protein	1	- 1				1	0.495
cgd3_1980	hypothetical protein				1		1	10.129
cgd3_1990	hypothetical protein	1					1	0.456
cgd3_20	hypothetical protein containing a signal peptide	1	J				1	0.395
cgd3_2000	WD repeat protein	1	- 1				1	0.419
cgd3_2010	hypothetical protein		- 1				1	0.380
	1		1				1	1.443
cgd3_2060	ring domain protein		'					
cgd3_2070	hypothetical protein				1		1	30.385
cgd3_210	hypothetical protein	1					1	0.518
cgd3_2130	hypothetical protein with signal peptide		1				1	1.219
cgd3_2140	hypothetical protein		1				1	1.720
cgd3_220	hypothetical protein	1	1				2	1.201
cgd3_2230	hypothetical protein				1		1	10.783
cgd3_2260	hypothetical protein					1	1	28.261
cgd3_2270	WD repeat protein			- 1			1	3.945
cgd3_2310	hypothetical protein			- 1			1	5.446
				'		1	1	238.164
cgd3_2330	hypothetical protein					- 1	- 1	
cgd3_2340	hypothetical protein				1		1	14.584
cgd3_2380	hypothetical protein	1					1	0.595
cgd3_240	hypothetical protein	1					1	0.456
cgd3_2400	Yn1201cp-family protein		1				1	2.078
cgd3_2470	hypothetical protein					1	1	236.906
cgd3_2480	hypothetical protein	1					1	0.487
cgd3_2490	hypothetical protein	1					1	0.403
cgd3 2510	myb domain-containing protein	-	1				1	1.971
cgd3_2510	hypothetical protein with carboxy terminus motif shared with		'		4		1	11.483
cgu3_2330	DNA-directed RNA polymerase subunit and TFIIS				'		'	11.400
cgd3_260	hypothetical protein	1					1	0.430
	hypothetical protein with conserved domain					1	1	
cgd3_2640	1 21					- 1		35.087
cgd3_2660	hypothetical protein		- 1		1		1	11.451
cgd3_2700	Trafficking protein particle complex subunit 6B, putative	1	- 1				1	0.326
cgd3_2750	hypothetical protein		- 1	1			1	4.007
cgd3_2800	hypothetical protein		- 1		1		1	12.280
cgd3_2830	hypothetical protein		J		1		1	8.344
cgd3_2860	hypothetical protein	1	- 1				1	0.478
cgd3_2890	Prp8. JAB/PAD domain		- 1	1			1	3.159
cgd3_2090 cgd3_3000	TBC domain containing protein		J	- 1			1	4.058
			J	- 1			1	
cgd3_3010	hypothetical protein			1			- 1	5.372
cgd3_3050	hypothetical protein	1	- 1				1	0.422
cgd3_3070	WD-40 repeat protein, SMART LisH domain	1	J				1	0.362
cgd3_3080	hypothetical protein				1		1	8.899
cgd3_3130	hypothetical protein	1	- 1				1	0.418
cgd3_3140	hypothetical protein	1	J				1	0.449
cgd3_3200	hypothetical protein		- 1	1			1	2.48
cgd3_3210	PV1H14080 P	1		- 1			1	0.410
	_	1	J				1	0.464
cgd3_3240	hypothetical protein		- 1	ار			- 1	
cgd3_3260	hypothetical protein			1			1	4.404
cgd3_3290	hypothetical protein with possible signal peptide and one	1	- 1				1	0.389
10.05	transmembrane region		J					
cgd3_3330	hypothetical protein	1	- 1				1	0.570
cgd3_3350	hypothetical protein		- 1		1		1	12.080
oguo_oooo			- 1	- 1	a	- 1	اہ	
cgd3_3370	large hypothetical protein with signal peptide			- 1	- 11	- 1	1	18.710

29d3_3460 hype 29d3_3510 hype 29d3_3580 hype 29d3_3780 hype 29d3_3780 hype 29d3_3780 hype 29d3_3780 hype 29d3_400 hype 29d3_4100 hype 29d3_70 hype 29d3_80 hype 29d3_90 hype 2	ypothetical protein ypothetical protein with cysteine rich regions roliferating cell nuclear antigen ypothetical protein ypothetical protein ypothetical protein RG-like OBG family GTpase fused to an RNA binding domain GS domain, Fun11p ypothetical protein ypothetical protein having a signal peptide IM domain and EF hand containing protein that also has a onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with signal peptide ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein, signal peptide	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1		1
29d3_3470   proiced   proi	roliferating cell nuclear antigen  large Sec7 domain containing protein  laypothetical protein  laypothetical protein  gypothetical protein  RG-like OBG family GTpase fused to an RNA binding domain  GS domain, Fun11p  laypothetical protein  laypothetical protein having a signal peptide  laypothetical protein having a signal peptide  laypothetical protein having a signal peptide  laypothetical protein  laypothetical  laypothetic	1 1 1 1 1 1 1 1 1 1 1 1 1	1	1 1 1 1 1 1 1 1 1	1		1 0.4 1 0.3 1 2.3 1 0.4 1 16.2 1 7.0 1 0.3 1 0.3 2 0.8 1 22.7 1 2.5 1 2.5 1 2.5 1 2.5 1 3.1
29d3_3480   large	arge Sec7 domain containing protein ypothetical protein ypothetical protein ypothetical protein RG-like OBG family GTpase fused to an RNA binding domain GS domain, Fun11p ypothetical protein ypothetical protein having a signal peptide IM domain and EF hand containing protein that also has a poserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with a signal peptide ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1	1		1 0.3 1 2.3 1 0.4 1 16.2 1 7.0 1 0.3 1 0.3 2 0.8 1 6.5 1 22.7 1 2.5 1 2.5 1 2.5 1 2.5 1 3.1
29d3_3510 hype 29d3_360 hype 29d3_420 hype 29d3_420 hype 29d3_480 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_70 hype 29d3_820 hype 29d3_80 hype 29d3_80 hype 29d3_80 hype 29d3_80 hype 29d3_90 hyp	ypothetical protein ypothetical protein RG-like OBG family GTpase fused to an RNA binding domain GS domain, Fun11p ypothetical protein having a signal peptide IM domain and EF hand containing protein that also has a posserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with a signal peptide ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1	1		1 2.5 1 0.4 1 16.2 1 7.0 1 0.3 2 0.8 1 22.7 1 2.5 1 2.5 1 2.5 1 2.5 1 2.5 1 3.1
gd3_3540 hyp gd3_360 hyp gd3_360 hyp gd3_360 hyp gd3_360 hyp gd3_360 hyp gd3_360 hyp gd3_3710 hyp gd3_3780 hyp gd3_380 hyp gd3_380 hyp gd3_380 hyp gd3_390 hyp gd3_400 hyp gd3_400 hyp gd3_4120 hyp gd3_420 hyp gd3_420 hyp gd3_430 hyp gd3_430 hyp gd3_430 hyp gd3_420 hyp gd3_420 hyp gd3_420 hyp gd3_430 hyp gd3_420 hyp gd3_420 hyp gd3_420 hyp gd3_420 hyp gd3_420 hyp gd3_420 hyp gd3_420 hyp gd3_480 hyp gd3_530 larg gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_70 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_90 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WC gd4_1210 Ms gd4_1210 Ms gd4_1220 hyp gd4_1250 hyp	ypothetical protein RG-like OBG family GTpase fused to an RNA binding domain GS domain, Fun11p ypothetical protein ypothetical protein having a signal peptide IM domain and EF hand containing protein that also has a onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1	1		1 0.4 1 16.2 1 7.0 1 0.3 1 0.3 2 0.8 1 22.7 1 2.5 1 2.5 1 2.5 1 2.5 1 3.1
gd3_360 hyp gd3_3640 UIIN gd3_3710 hyp gd3_3760 sma gd3_3780 hyp gd3_3780 hyp gd3_3880 coil gd3_3890 hyp gd3_400 hyp gd3_400 hyp gd3_400 hyp gd3_400 hyp gd3_400 hyp gd3_400 hyp gd3_4120 hyp gd3_420 hyp gd3_420 hyp gd3_450 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_60 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_70 hyp gd3_70 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 hyp	RG-like OBG family GTpase fused to an RNA binding domain GS domain, Fun11p ypothetical protein ypothetical protein having a signal peptide IM domain and EF hand containing protein that also has a conserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein with signal peptide ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1 1		1 1 1 1 1	1		1 16.2 1 7.0 1 0.3 1 10.0 1 0.3 2 0.8 1 22.7 1 2.0 1 2.5 1 2.8 1 2.8 1 3.1
TG:	GS domain, Fun11p ypothetical protein ypothetical protein having a signal peptide IM domain and EF hand containing protein that also has a onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1	1		1 7.0 1 0.3 1 10.0 2 0.8 1 6.5 1 22.7 1 2.0 1 2.5 1 2.8 1 2.8
egd3_360 hypegd3_3780 hypegd3_3800 hypegd3_420 hypegd3_420 hypegd3_420 hypegd3_420 hypegd3_420 hypegd3_420 hypegd3_660 hypegd3_660 hypegd3_660 hypegd3_660 hypegd3_70 hypegd3_80 hypegd3_80 hypegd3_80 hypegd3_80 hypegd3_80 hypegd3_90 hypegd4_100 hypegd4_1100 hypegd4_1100 hypegd4_1100 hypegd4_1100 hypegd4_120 hype	ypothetical protein ypothetical protein having a signal peptide IM domain and EF hand containing protein that also has a onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1			1 0.3 1 10.0 1 0.3 2 0.8 1 6.5 1 22.7 1 2.0 1 2.5 1 2.8 1 3.1
29d3_3640 hyp 29d3_3800 coil 29d3_3780 hyp 29d3_3780 hyp 29d3_3800 coil 29d3_3800 coil 29d3_3800 hyp 29d3_3900 hyp 29d3_4000 hyp 29d3_4120 hyp 29d3_4120 hyp 29d3_600 hyp 29d3_600 hyp 29d3_600 hyp 29d3_600 hyp 29d3_600 hyp 29d3_600 hyp 29d3_600 hyp 29d3_600 hyp 29d3_70 hyp 29d3_80 hyp 29d3_80 hyp 29d3_910 hyp 29d4_110 hyp 29d4_110 hyp 29d4_120 hy	ypothetical protein having a signal peptide  IM domain and EF hand containing protein that also has a onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with a signal peptide ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1			1 0.3 1 10.0 1 0.3 2 0.8 1 6.5 1 22.7 1 2.0 1 2.5 1 2.8 1 3.1
29d3_3680 UIM con 29d3_3710 hyp 29d3_3780 hyp 29d3_3880 coil 29d3_3890 hyp 29d3_400 hyp 29d3_4120 hyp 29d3_423 hyp 29d3_660 hyp 29d3_660 hyp 29d3_660 hyp 29d3_660 hyp 29d3_70 hyp 29d3_80 hyp 29d3_80 hyp 29d3_90 hyp 29d4_110 hyp 29d4_110 hyp 29d4_120 hyp	IM domain and EF hand containing protein that also has a onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1	1		1 10.0 1 0.3 2 0.8 1 6.5 1 22.7 1 2.0 1 2.5 1 2.8 1 3.1
con con con con con con con con con con	onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with a signal peptide ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1		1 1 1 1 1	1		1 0.3 2 0.8 1 6.5 1 22.7 1 2.0 1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
condaga 3710 hyp cadd 3,3780 hyp cadd 3,3880 hyp cadd 4,120 hyp cadd 3,600 hyp cadd 5,700 hyp cadd 3,780 hyp cadd 3,880 hyp cadd 3,880 hyp cadd 3,980 hyp ca	onserved domain between ypothetical protein mall protein with possible EF hand domains, calmodulin like ypothetical protein with a signal peptide ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1		1 1 1 1 1	1		2 0.8 1 6.5 1 22.7 1 2.0 1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
29d3_3760 smale special specia	mall protein with possible EF hand domains, calmodulin like ypothetical protein ypothetical protein poiled coil protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1 1		1 1 1 1 1	1		2 0.8 1 6.5 1 22.7 1 2.0 1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
29d3_3760 smale special specia	mall protein with possible EF hand domains, calmodulin like ypothetical protein ypothetical protein poiled coil protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with a signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein with signal peptide	1 1 1 1 1 1		1 1 1 1 1	1	:	1 6.5 1 22.7 1 2.5 1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
gd3_380 hyp gd3_380 hyp gd3_380 hyp gd3_390 hyp gd3_400 hyp gd3_400 hyp gd3_400 hyp gd3_4130 hyp gd3_420 hyp gd3_420 hyp gd3_430 hyp gd3_63 hyp gd3_63 hyp gd3_650 hyp gd3_660 hyp gd3_70 hyp gd3_710 larg gd3_720 ven gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_840 RSi gd3_850 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_910 hyp gd3_940 hyp gd3_940 hyp gd3_980 hyp gd3_980 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_1120 hyp gd4_1210 Mg2 gd4_1220 hyp	ypothetical protein ypothetical protein pieled coil protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide gree hypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide	1 1 1 1 1 1		1 1 1 1 1	1	:	1 6.5 1 22.7 1 2.5 1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
29d3_3830   nyp 29d3_3830   nyp 29d3_3830   nyp 29d3_3900   nyp 29d3_400   nyp 29d3_400   nyp 29d3_400   nyp 29d3_420   nyp 29d3_420   nyp 29d3_420   nyp 29d3_420   nyp 29d3_420   nyp 29d3_430   nyp 29d3_420   nyp 29d3_60   nyp 29d3_60   nyp 29d3_60   nyp 29d3_70   nyp 29d3_80   nyp 29d3_80   nyp 29d3_90   nyp 29d3_91   nyp 29d4_110   nyp 29d4_110   nyp 29d4_1210   nyp 29	ypothetical protein biled coil protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide ge hypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide	1 1 1 1 1	1	1 1 1 1 1	1		1 22.7 1 2.0 1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
29d3_3860 coil 29d3_3900 hyp 29d3_4000 hyp 29d3_4000 hyp 29d3_4000 hyp 29d3_4120 hyp 29d3_4200 hyp 29d3_4200 hyp 29d3_4200 hyp 29d3_4200 hyp 29d3_4200 hyp 29d3_600 hyp 29d3_600 hyp 29d3_70 hyp 29d3_90 hyp 29d4_100 hyp 29d4_110 hyp 29d4_110 hyp 29d4_120	biled coil protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide rge hypothetical protein with signal peptide ypothetical protein ypothetical protein ypothetical protein with signal peptide	1 1 1 1 1	1	1 1 1 1	1		1 2.0 1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
.gd3_3900 hyp .gd3_3990 hyp .gd3_4000 hyp .gd3_4000 hyp .gd3_4000 hyp .gd3_4120 hyp .gd3_4130 hyp .gd3_420 hyp .gd3_430 hyp .gd3_430 hyp .gd3_630 hyp .gd3_60 hyp .gd3_60 hyp .gd3_60 hyp .gd3_60 hyp .gd3_70 hyp .gd3_71 larg .gd3_72 ven .gd3_72 ven .gd3_780 hyp .gd3_780 hyp .gd3_780 hyp .gd3_880 hyp .gd3_880 hyp .gd3_880 hyp .gd3_880 hyp .gd3_800 hyp .gd3_90 hyp .gd4_100 hyp .gd4_100 hyp .gd4_100 hyp .gd4_110 hyp .gd4_120 Ms .gd4_120 Ms .gd4_120 hyp .gd4_1210 hyp .gd4_1250 hyp	ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide irge hypothetical protein with signal peptide ypothetical protein ypothetical protein ypothetical protein with signal peptide	1 1 1 1 1	1	1 1 1 1	1	:	1 2.5 1 0.3 1 2.8 2 1.5 1 3.1
29d3_3990   hyp 29d3_4000   hyp 29d3_4000   hyp 29d3_4000   hyp 29d3_4120   hyp 29d3_4120   hyp 29d3_423   hyp 29d3_530   larg 29d3_660   hyp 29d3_660   hyp 29d3_660   hyp 29d3_70   hyp 29d3_710   larg 29d3_720   ven 29d3_780   hyp 29d3_780   hyp 29d3_780   hyp 29d3_780   hyp 29d3_880   hyp 29d3_880   hyp 29d3_880   hyp 29d3_890   hyp 29d3_900   hyp 29d4_1000   hyp 29d4_1100   hyp 29d4_1100   hyp 29d4_1210   Ms 29d4_1210   Ms 29d4_1210   Ms 29d4_1250   hyp 29d8_1250    ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide rge hypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide	1 1 1 1 1		1 1 1 1	1	:	1 0.3 1 2.8 2 1.5 1 3.1	
1934         1909           1934         1900           1934 <td>ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide lurge hypothetical protein with signal peptide ypothetical protein ypothetical protein ypothetical protein ypothetical protein</td> <td>1 1 1 1 1</td> <td></td> <td>1 1 1</td> <td>1</td> <td></td> <td>1 2.8 2 1.5 1 3.1</td>	ypothetical protein ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide lurge hypothetical protein with signal peptide ypothetical protein ypothetical protein ypothetical protein ypothetical protein	1 1 1 1 1		1 1 1	1		1 2.8 2 1.5 1 3.1
gd3_4000 hyp gd3_4130 hyp gd3_4130 hyp gd3_420 hyp gd3_423 hyp gd3_420 hyp gd3_420 hyp gd3_630 hyp gd3_630 hyp gd3_660 hyp gd3_70 hyp gd3_80 hyp gd3_80 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_1210 hyp gd4_1210 hyp gd4_1210 hyp gd4_1210 hyp gd4_1210 hyp gd4_1220 hyp	ypothetical protein ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide urge hypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein ypothetical protein ypothetical protein	1 1 1		1 1 1	1		2 1.5 1 3.1
gd3_4040 hyp gd3_4130 hyp gd3_4230 hyp gd3_4230 hyp gd3_4230 hyp gd3_4230 hyp gd3_430 hyp gd3_630 hyp gd3_650 hyp gd3_650 hyp gd3_710 larg gd3_720 ven gd3_720 ven gd3_780 hyp gd3_780 hyp gd3_780 hyp gd3_880 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 myp gd4_120 Ms gd4_120 myp gd4_1210 Ms gd4_1210 Ms gd4_1210 Ms gd4_1210 hyp gd4_1210 Ms gd4_1210 hyp gd4_1210 hyp gd4_1210 Ms gd4_1210 myp	ypothetical protein with signal peptide, proline rich ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide lirge hypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein ypothetical protein ypothetical protein with signal peptide	1 1 1		1	1		1 3.1
1933         100         hyp           1934         1420         hyp           1934         150         hyp           1934         150         hyp           1934         150         hyp           1934         160         hyp           1934         160         hyp           1934         170         hyp           1934         170         hyp           1934         180         hyp           1934         190         hyp           1934         19	ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide urge hypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein ypothetical protein	1 1		1	1		
gd3_4120 hyp gd3_4230 hyp gd3_4230 hyp gd3_4230 hyp gd3_480 hyp gd3_530 larg gd3_630 hyp gd3_660 hyp gd3_660 hyp gd3_70 larg gd3_710 larg gd3_720 ven gd3_720 ven gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_820 hyp gd3_880 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_90 hyp gd3_80 hyp gd3_90 hyp gd3_900 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WD gd4_120 WD gd4_1210 Ms gd4_1210 Ms gd4_1210 Ms gd4_1220 Hyp gd4_1210 Ms gd4_1220 Hyp gd4_1210 Ms gd4_1220 Hyp gd4_1210 Ms gd4_1220 Hyp gd4_1210 Ms	ypothetical protein ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein with a signal peptide urge hypothetical protein with signal peptide ypothetical protein with signal peptide ypothetical protein ypothetical protein	1 1		1	1		
29d3_4130   hyp 29d3_420   hyp 29d3_4230   hyp 29d3_480   hyp 29d3_530   larg 29d3_60   hyp 29d3_660   hyp 29d3_710   larg 29d3_720   ven 29d3_720   hyp 29d3_720   hyp 29d3_720   hyp 29d3_720   hyp 29d3_780   hyp 29d3_820   hyp 29d3_880   hyp 29d3_880   hyp 29d3_880   hyp 29d3_880   hyp 29d3_890   hyp 29d3_900   hyp 29d4_100   hyp 29d4_100   hyp 29d4_110   hyp 29d4_110   hyp 29d4_110   hyp 29d4_120   hyp 29d4_120   hyp 29d4_120   hyp 29d4_120   hyp 29d4_1210   hyp 29d4_121	ypothetical protein ypothetical protein ypothetical protein, signal peptide ypothetical protein, signal peptide ypothetical protein with a signal peptide urge hypothetical protein with signal peptide ypothetical protein ypothetical protein	1 1			1		-1 7.1
gd3_420 hyp gd3_4230 hyp gd3_4230 hyp gd3_480 hyp gd3_630 hyp gd3_630 hyp gd3_650 hyp gd3_660 hyp gd3_710 larg gd3_720 veri gd3_780 hyp gd3_780 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_840 RSi gd3_840 RSi gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_80 hyp gd3_90 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 hyp gd4_120 hyp gd4_120 WD gd4_120 hyp gd4_1210 hyp gd4_1210 hyp gd4_1210 hyp	ypothetical protein ypothetical protein, signal peptide ypothetical protein, signal peptide ypothetical protein with a signal peptide urge hypothetical protein with signal peptide ypothetical protein ypothetical protein	1 1		1	1		1 0.3
gd3_4230   hyp gd3_480   hyp gd3_530   larg gd3_60   hyp gd3_660   hyp gd3_660   hyp gd3_710   larg gd3_720   ver ged3_730   hyp gd3_780   hyp gd3_780   hyp gd3_780   hyp gd3_820   hyp gd3_840   RSi gd3_850   hyp gd3_840   hyp gd3_80   hyp gd3_80   hyp gd3_90   hyp gd4_100   hyp gd4_100   hyp gd4_1100   hyp gd4_1100   hyp gd4_1100   hyp gd4_1100   hyp gd4_120   WD gd4_1210   Ms' gd4_1210   Ms' gd4_1210   Ms' gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp gd4_1220   hyp	ypothetical protein, signal peptide ypothetical protein with a signal peptide urge hypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide	1		1	1	1	
gd3_480 hyp gd3_630 hyp gd3_630 hyp gd3_630 hyp gd3_650 hyp gd3_660 hyp gd3_660 hyp gd3_70 hyp gd3_720 ven gd3_720 ven gd3_780 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_850 hyp gd3_860 hyp gd3_870 flav gd3_80 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WD gd4_120 Ms gd4_120 hyp	ypothetical protein with a signal peptide irge hypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide	1		1	1		1 0.3
gd3_530 hyp gd3_630 hyp gd3_630 hyp gd3_650 hyp gd3_650 hyp gd3_660 hyp gd3_70 hyp gd3_710 larg gd3_720 ven gd3_720 hyp gd3_780 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_840 RSi gd3_850 hyp gd3_870 flav gd3_870 hyp gd3_900 hyp gd3_900 hyp gd3_910 hyp gd3_940 hyp gd3_940 hyp gd3_940 hyp gd3_980 hyp gd3_980 hyp gd3_980 hyp gd3_980 hyp gd4_100 hyp gd4_1020 hyp gd4_1020 hyp gd4_1070 MY gd4_1070 MY gd4_1070 hyp gd4_1100 hyp gd4_1100 hyp gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_1210 Ms gd4_1210 Ms gd4_1250 hyp	rge hypothetical protein with signal peptide ypothetical protein ypothetical protein with signal peptide			1	1	1	1 0.4
gd3_60 hyp gd3_630 hyp gd3_650 hyp gd3_650 hyp gd3_660 hyp gd3_70 hyp gd3_710 larg gd3_720 ven gd3_720 ven gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_850 hyp gd3_850 hyp gd3_80 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WD gd4_1210 Ms gd4_1210 Ms gd4_1210 Ms gd4_1210 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp	ypothetical protein ypothetical protein with signal peptide			1			1 18.8
gd3_630 hyp gd3_660 hyp gd3_660 hyp gd3_70 hyp gd3_710 larg gd3_720 ven gd3_780 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_850 hyp gd3_850 hyp gd3_80 hyp gd3_80 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 hyp gd4_1250 hyp	ypothetical protein with signal peptide						1 3.4
gd3_630 hyp gd3_660 hyp gd3_660 hyp gd3_70 hyp gd3_710 larg gd3_720 ven gd3_780 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_850 hyp gd3_850 hyp gd3_80 hyp gd3_80 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 hyp gd4_1250 hyp	ypothetical protein with signal peptide			-			1 0.3
gd3_650 hyp gd3_660 hyp gd3_660 hyp gd3_70 hyp gd3_710 larg gd3_720 ver gd3_750 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_850 hyp gd3_870 flav gd3_80 hyp gd3_80 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_90 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WB gd4_120 WB gd4_120 hyp gd4_1210 Ms gd4_1210 Ms gd4_1250 hyp		,					1 0.4
gd3_660 hyp gd3_70 hyp gd3_710 larg gd3_720 ven gd3_720 ven gd3_720 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_850 hyp gd3_870 flav gd3_80 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_940 hyp gd3_940 hyp gd3_940 hyp gd3_940 hyp gd3_940 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WD gd4_120 Hyp gd4_1210 Hyp gd4_1210 Hyp gd4_1210 Hyp gd4_1220 Hyp				1		1	1 4.1
gd3_70 hyp gd3_710 larg gd3_710 larg gd3_710 larg gd3_720 ven ggd3_750 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_850 hyp gd3_80 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd3_900 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_120 WD gd4_120 WB gd4_120 WB gd4_120 WB gd4_1210 Ms gd4_1210 Ms gd4_1210 Ms gd4_1220 Hyp gd4_1210 Ms gd4_1220 Hyp gd4_1210 Ms	ypothetical protein, signal peptide	1		- 1			1 0.3
gd3_710 larg gd3_710 larg gd3_720 ven pep gd3_720 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_870 flav gd3_90 hyp gd3_90 hyp gd3_90 hyp gd3_910 hyp gd3_910 hyp gd3_90 hyp gd3_910 hyp gd3_960 hyp gd3_980 hyp gd3_980 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_1210 Ms gd4_1210 Ms gd4_1210 Ms gd4_1210 Ms gd4_1210 hyp gd4_1210 Ms							
gd3_720 ven pep pgd3_780 hyp pgd3_780 hyp pgd3_780 hyp pgd3_820 hyp pgd3_840 RS pgd3_850 hyp pgd3_870 flav pgd3_90 hyp pgd3_90 hyp pgd3_90 hyp pgd3_90 hyp pgd3_90 hyp pgd3_90 hyp pgd3_90 hyp pgd3_90 hyp pgd3_90 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_100 hyp pgd4_110 hyp pgd4_120 WD pgd4_120 WD pgd4_120 hyp	ypothetical protein						1 43.2
pep pegd3_750 hyp pgd3_780 hyp pgd3_780 hyp pgd3_820 hyp pgd3_840 hyp pgd3_870 flav pgd3_880 hyp pgd3_900 hyp pgd3_900 hyp pgd3_900 hyp pgd3_940 hyp pgd3_960 hyp pgd3_980 hyp pgd3_980 hyp pgd3_980 hyp pgd3_980 hyp pgd4_1000 hyp pgd4_1000 hyp pgd4_1000 hyp pgd4_1100 hyp pgd4_120 WD pgd4_120 WD pgd4_120 hyp pgd4_120 hyp	rge hypothetical protein with signal peptide		1			1	1 1.5
gd3_750 hyp gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_840 RSi gd3_850 hyp gd3_860 hyp gd3_900 hyp gd3_910 hyp gd3_940 hyp gd3_940 hyp gd3_960 hyp gd3_960 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_1100 hyp gd4_120 hyp gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD gd4_120 WD	ery large probable mucin, 11700 aa long protein with signal	1					1 0.3
gd3_780 hyp gd3_780 hyp gd3_820 hyp gd3_820 hyp gd3_840 RSi gd3_850 hyp gd3_870 flav gd3_870 hyp gd3_90 hyp gd3_910 hyp gd3_940 hyp gd3_940 hyp gd3_960 hyp gd3_960 hyp gd4_100 hyp gd4_100 hyp gd4_100 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_110 hyp gd4_120 WD gd4_120 WB gd4_120 WB gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp	eptide and pronounced Thr repeat (308 aa long)						
gd3_790 hyp gd3_820 hyp gd3_820 hyp gd3_820 hyp gd3_850 hyp gd3_870 flav gd3_880 hyp gd3_900 hyp gd3_940 hyp gd3_940 hyp gd3_960 hyp gd4_100 hyp gd4_100 hyp gd4_1070 MY gd4_110 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_120 WD gd4_120 WB gd4_120 WB gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp gd4_120 hyp	ypothetical protein						1 256.5
gd3_820 hyp gd3_840 RS6 gd3_850 hyp gd3_870 flav gd3_880 hyp gd3_900 hyp gd3_910 hyp gd3_940 hyp gd3_960 hyp gd3_960 hyp gd3_980 hyp gd4_100 hyp gd4_100 hyp gd4_1070 MY gd4_110 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1210 MS6 gd4_1240 hyp gd4_1250 hyp gd4_1250 hyp	ypothetical protein				1		1 6.3
29d3_820 hyp 29d3_840 RS6 29d3_850 hyp 29d3_870 flav 29d3_880 hyp 29d3_900 hyp 29d3_910 hyp 29d3_960 hyp 29d3_960 hyp 29d3_960 hyp 29d4_100 hyp 29d4_1070 MY 29d4_110 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1210 MS 29d4_1210 MS 29d4_1210 MS 29d4_1210 MS 29d4_1210 hyp 29d4	ypothetical protein	1					1 0.3
29d3_840 RSi 29d3_850 hyp 29d3_870 flav 29d3_880 hyp 29d3_90 hyp 29d3_90 hyp 29d3_910 hyp 29d3_960 hyp 29d3_960 hyp 29d3_960 hyp 29d4_100 hyp 29d4_1070 MY 29d4_110 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1100 hyp 29d4_1200 MSi 29d4_1200 MSi 29d4_1210 Msi 29d4_1210 hyp 29	ypothetical protein	1					1 0.6
gd3_850 hyp gd3_870 flav gd3_880 hyp gd3_90 hyp gd3_90 hyp gd3_910 hyp gd3_940 hyp gd3_980 hyp gd4_100 hyp gd4_1000 hyp gd4_100 hyp gd4_1100 hyp gd4_120 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1200 WD gd4_1210 Ms: gd4_1240 hyp gd4_1250 hyp	SC6/BAF60A ortholog with a SWIB domain				1	1	1 10.0
gdd_870 hyp gdd_980 hyp gdd_990 hyp gdd_990 hyp gdd_990 hyp gdd_990 hyp gdd_990 hyp gdd_990 hyp gdd_100 hyp gdd_100 hyp gdd_100 hyp gdd_100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_120 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1120 WD gdd_120 WD gdd_1210 Ms: gdd_1250 hyp	ypothetical protein			1	T.		1 4.5
gd3_880 hyp gd3_90 hyp gd3_90 hyp gd3_910 hyp gd3_940 hyp gd3_960 hyp gd3_980 hyp gd4_100 hyp gd4_1000 hyp gd4_1000 hyp gd4_10100 hyp	avoprotein, putative	1		- '[		1	1 0.4
gdd_90 hyp gdd_910 hyp gdd_910 hyp gdd_910 hyp gdd_980 hyp gdd_100 hyp gdd_1020 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1100 hyp gdd_1120 WD gdd_120 WD gdd_120 hyp gdd_1210 Ms gdd_1240 hyp gdd_1250 hyp		1					
gdd_900 hyp gdd_940 hyp gdd_1250 hyp gdd_1210 hyp gdd_1210 hyp gdd_1210 hyp gdd_1210 hyp gdd_1210 hyp gdd_1210 hyp gdd_1220 hyp gdd_1210 hyp gdd_1220 hyp gdd_1240 hyp gdd_1250 hyp gdd_1250 hyp gdd_1250 hyp gdd_1250 hyp	ypothetical protein						
gd3_910 hyp gd3_940 hyp gd3_960 hyp gd3_980 hyp gd4_100 hyp gd4_1020 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_120 WD gd4_120 WD gd4_1210 Ms gd4_1210 hyp gd4_1210 hyp gd4_1210 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp gd4_1220 hyp	ypothetical protein with signal peptide	1					1 0.3
gd3_940 hyp gd3_960 hyp gd3_980 hyp gd4_100 hyp gd4_1020 hyp gd4_1070 MY gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1210 Ms' gd4_1210 Ms' gd4_1240 hyp gd4_1250 hyp	ypothetical protein	1					1 0.4
gd3_960 hyp gd3_980 hyp gd4_100 hyp gd4_1020 hyp gd4_1070 MY gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_120 WD gd4_120 WB gd4_120 hyp gd4_1210 hyp gd4_1250 hyp	ypothetical protein	1					1 0.5
gd3_960 hyp gd3_980 hyp gd4_100 hyp gd4_1020 hyp gd4_1070 MY gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_120 WD gd4_120 WB gd4_1200 hyp gd4_1210 hyp gd4_1210 hyp gd4_1250 hyp	ypothetical protein	1					1 0.3
gd3_980 hyp gd4_100 hyp gd4_1020 hyp gd4_1070 MY gd4_1070 hyp gd4_110 hyp gd4_1100 hyp gd4_1100 hyp gd4_1120 wp gd4_1210 Ms gd4_1210 Ms gd4_1210 hyp gd4_1210 hyp	ypothetical protein			1			1 2.5
gd4_100 hyp gd4_1000 hyp gd4_1020 hyp gd4_1070 MY gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1180 hyp gd4_120 WD gd4_1210 Ms: gd4_1240 hyp gd4_1250 hyp	ypothetical protein					1	1 121.1
gd4_1000 hyp gd4_1020 hyp gd4_1070 MY gd4_1100 hyp gd4_1100 hyp gd4_1100 hyp gd4_1180 hyp gd4_120 WD gd4_1210 Ms: gd4_1240 hyp gd4_1250 hyp	ypothetical protein	1					1 0.3
gd4_1020 hyp gd4_1070 MY gd4_110 hyp gd4_110 hyp gd4_1100 hyp gd4_1180 hyp gd4_120 WD gd4_1210 Ms: gd4_1240 hyp gd4_1250 hyp		1					
gd4_1070 MY gd4_110 hyp gd4_1100 hyp gd4_1180 hyp gd4_120 WD gd4_1210 Ms: gd4_1240 hyp gd4_1240 hyp	ypothetical protein						
gd4_110 hyp gd4_1100 hyp gd4_1180 hyp gd4_120 WD gd4_1210 Ms gd4_1240 hyp gd4_1250 hyp	ypothetical protein	1			ار		1 0.3
2gd4_1100 hyp 2gd4_1180 hyp 2gd4_120 WD 2gd4_1210 Ms 2gd4_1240 hyp 2gd4_1250 hyp	IYND finger domain protein				1		1 21.1
gd4_1180 hyp gd4_120 WD gd4_1210 Ms gd4_1240 hyp gd4_1250 hyp	ypothetical protein		1				1 1.4
egd4_120 WD egd4_1210 Ms egd4_1240 hyp egd4_1250 hyp	ypothetical protein			1			1 2.3
egd4_120 WD egd4_1210 Ms egd4_1240 hyp egd4_1250 hyp		1					1 0.3
egd4_1210 Ms <sup>2</sup> egd4_1240 hyp egd4_1250 hyp	ypothetical protein	1				1	1 0.3
gd4_1240 hyp gd4_1250 hyp		,		1			1 5.2
gd4_1250 hyp	/D repeat protein			1			1 4.5
	/D repeat protein Is15p; KH + 2 Znknuckle (C2HC)	4		- '		1	
:qa4 1260  pos	D repeat protein ls15p; KH + 2 Znknuckle (C2HC) ypothetical protein	1					1 0.2
	/D repeat protein ls15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein	1					1 0.3
	/D repeat protein ls15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE	1					1 0.3
	D repeat protein ls15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH)	1					1 0.4
	/D repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible						.1
:gd4_1420 hyp	/D repeat protein /B15p; KH + 2 Znknuckle (C2HC) /pothetical protein /pothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible		1				1 1.9
gd4_1430 hyp	/D repeat protein /B 15p; KH + 2 Znknuckle (C2HC) /pothetical protein /pothetical protein ossible tRNA-INTRON ENDONUCLEASE /RM domain and KH domain protein (SPAC30D11.14-like KH) /pothetical protein secreted protein with thr rich regions, possible /pothetical protein					1	1 0.4
gd4_1460 hyp	/D repeat protein /B15p; KH + 2 Znknuckle (C2HC) /pothetical protein /pothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible	1					1 0.3
	/D repeat protein /B 15p; KH + 2 Znknuckle (C2HC) /pothetical protein /pothetical protein ossible tRNA-INTRON ENDONUCLEASE /RM domain and KH domain protein (SPAC30D11.14-like KH) /pothetical protein secreted protein with thr rich regions, possible /pothetical protein	1 1	1				1 1.3
	D repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein sssible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible lucin ypothetical protein ypothetical protein ypothetical protein		.1				1 47.3
	ID repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible nucin ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein		- 1				1 36.0
	ID repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) nucharacterized secreted protein with thr rich regions, possible nucin ypothetical protein			ار			
	ID repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible nucin ypothetical protein			1			1 3.7
gd4_1630 hyp	ID repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible fucin ypothetical protein	1					1 0.4
gd4_1640 hyp	ID repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible nucin ypothetical protein	1			- 1		1 0.4
gd4_170 hyp	ID repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible fucin ypothetical protein	1					1 10.5
gd4_1710 Lov	ID repeat protein Is15p; KH + 2 Znknuckle (C2HC) ypothetical protein ypothetical protein ossible tRNA-INTRON ENDONUCLEASE RM domain and KH domain protein (SPAC30D11.14-like KH) ncharacterized secreted protein with thr rich regions, possible lucin ypothetical protein	1			1		1 3.3

cgd4_1770	hypothetical protein			1			1	2.566
cgd4_180	hypothetical protein	1					1	0.456
cgd4_1810	hypothetical protein	1					1	0.410
cgd4_1870	hypothetical protein	1					1	0.433
cgd4_1880	hypothetical protein	1					1	0.488
cgd4_1900	hypothetical protein	1					1	0.323
cgd4 1930	possible origin recognition complex protein subunit 2, orc2	1					1	0.515
cgd4_1980	TBC domain containing protein		1				1	1.656
cgd4_1990	RRp1-like protein		1			1	1	40.954
cgd4_200	large low complexity coiled coil protien with large repeat region					1	1	24.512
		4				- 1		
cgd4_2040	SMART RPR domain at NH2 terminus, SMART AZnF_C2H2	1					1	0.388
cgd4_2120	PX domain containing protein	1					1	0.431
cgd4_2130	TBC domain containing protein				1		1	13.805
cgd4_2140	hypothetical protein		1				1	2.181
cgd4_2150	hypothetical protein					1	1	28.948
cgd4_2170	hypothetical protein	1					1	0.415
cgd4_2200	SMC2 protein	1					1	0.444
cgd4_2220	possible double-stranded DNA-binding domain, small conserved	1					1	0.425
cgd4_2230	protein uncharacterized protein	1					1	0.481
cgd4 2240	hypothetical protein	1					1	0.333
cgd4_2280	, ,				4		1	23.834
-	hypothetical protein				1		1	
cgd4_2290	hypothetical protein				1		1	10.438
cgd4_230	hypothetical protein containing a signal peptide	1					1	0.378
cgd4_2310	hypothetical protein	1					1	0.441
cgd4_2320	At3g18860/MCB22_3	1		l			1	0.394
cgd4_2350	multitransmembrane protein with signal peptide and GMGPP	1		l			1	0.492
	repeat at C-terminus							
cgd4_2380	possible SAND family protein	1					1	0.457
cgd4_2410	hypothetical protein		1				1	1.909
cgd4_2440	small hypothetical protein with signal peptide				1		1	8.578
cgd4_2460	hypothetical protein with a signal peptide, gene within locus of					1	1	160.198
cgd4_2470	signal-peptide containing hypothetical proteins hypothetical protein with a signal peptide, gene within locus of			1			1	2.909
cgd4_2480	signal-peptide containing hypothetical proteins hypothetical protein with a signal peptide, gene within locus of			1			1	2.488
cgd4_2510	signal-peptide containing hypothetical proteins hypothetical protein with a signal peptide, gene within locus of signal-peptide containing hypothetical proteins		1				1	1.984
cgd4_2520	hypothetical protein with a signal peptide, gene within locus of signal-peptide containing hypothetical proteins				1		1	17.848
cgd4_2570	WD repeat protein			1			1	3.278
cgd4_260	WD repeat protein				1		1	10.152
cgd4 2610	hypothetical protein				1		1	9.421
cgd4_2620	hypothetical protein		1		-		1	1.455
cgd4_2630	hypothetical protein				1		1	16.559
cgd4_2640	hypothetical protein				1		1	18.862
	, ,							
cgd4_2650 cqd4_2660	hypothetical protein similarity at COOH terminus with programmed cell death protein		1	- '				3.247 1.650
-3	2							
cgd4_2690	sec7 domain containing protein, possibly of plant origin	1					1	0.405
cgd4_2730	predicted coiled-coil protein	1					1	0.518
cgd4_2760	hypothetical protein	1					1	0.371
cgd4_2800	hypothetical protein having a signal peptide		1				1	1.356
cgd4 2810	hypothetical protein, signal peptide	1					1	0.327
cgd4_2880	hypothetical protein				1		1	6.438
cgd4_2920	hypothetical protein	1					1	0.401
cgd4_2950	, ,			1			1	3.814
-	hypothetical protein RhoGAP domain containing protein with a Sec14D domain at			- '		4		33.744
cgd4_2980	the N-terminus					1	'1	33.744
cgd4_30	hypothetical protein		1				1	1.625
cgd4_3010	hypothetical protein		·		4		1	16.478
	1 51 1			4			1	
cgd4_3020	hypothetical protein with a signal peptide			1				3.341
cgd4_3030	hypothetical protein with a signal peptide			l	1		1	9.488
cgd4_3050	hypothetical protein			l		1	1	232.621
cgd4_3060	hypothetical protein	1		I			1	0.258
cgd4_3070	hypothetical protein			1			1	2.330
cgd4_31	hypothetical protein	1		l			1	0.498
cgd4_3140	WD repeat protein		1				1	1.628
cgd4_32	hypothetical protein		1	l			1	2.021
cgd4_3200	hypothetical protein			l	1		1	16.066
cgd4_3210	hypothetical protein			1			1	2.913
cgd4_3230	hypothetical protein with a signal peptide			- '	1		1	27.260
cgd4_3240	possible NLI interacting factor CTD-like phosphatase	1					1	0.363
	, ,	1				4		
cgd4_3280	hypothetical protein					1	1	52.507
cgd4 330	hypothetical protein				1		1	23.099
-	li area es					1	1	
cgd4_3330 cgd4_3350	hypothetical protein hypothetical protein	1					1	64.007 0.449

cgd4_3360	WD repeat protein			4		1	1	67.441
cgd4_3370 cgd4_3390	hypothetical protein neutral sphingomyelinase activation associated factor-like			1			1	5.206 2.456
cgd4_340	BEACH domain containing protein protein with possible conserved beta tubulin folding factor	1					1	0.397
cgd4_3430	domain hypothetical protein with signal peptide and central coiled-coil				1		1	13.655
-	region, within large locus of signal peptide containing proteins				'			
cgd4_3500	hypothetical protein	1					1	0.290
cgd4_3510	hypothetical protein	1					1	0.390
cgd4_3530	large hypothetical protein with signal peptide, within large locus of signal peptide containing proteins		1				1	1.767
cgd4 3560	hypothetical protein					1	1	30.768
cgd4_3600	hypothetical protein with possible signal peptide, 'HCD					1	1	42.823
cgd4 3610	family'paralog hypothetical protein with signal peptide				- 1		1	10.442
cgd4_3620	immunodominant antigen 23393226					1	1	787.563
cgd4_3640	hypothetical protein					1	1	112.981
cgd4_3660	hypothetical protein	1				-	1	0.372
cgd4 3670	uncharacterized low complexity protein				1		1	9.023
cgd4_3680	hypothetical protein				1		1	11.611
cgd4_3690	large glycine-rich repeat low complexity protein					1	1	28.345
cgd4 3720	possible 2 TPR domains at N-terminus	1					1	0.472
cgd4_3730	hypothetical protein		1				1	1.856
cgd4_3750	hypothetical protein with signal peptide				1		1	6.132
cgd4_3760	hypothetical protein		1				1	1.417
cgd4_3780	hypothetical protein	1	'		1		2	3.769
cgd4_3760 cgd4_3820	hypothetical protein	1			- '		1	0.422
cgd4_3830	Ank repeat protein with possible signal peptide	1					1	0.382
1	Ank, ankyrin repeats containing protein with 9 transmembrane	1					1	0.338
cgd4_3840	domains at C-terminus						'	0.556
cgd4_3870	large protein with signal peptide	1					1	0.419
cgd4_3890	hypothetical protein	1					1	0.299
cgd4_3900	hypothetical protein	1					1	0.309
cgd4_3910	hypothetical protein					1	1	44.273
cgd4_3960	hypothetical protein	1					1	0.426
cgd4_3980	hypothetical protein	•		1			1	2.863
cgd4_400	protein with possible 2 TPR domains	1		<u> </u>			1	0.395
cgd4_4000	possible ribosomal-protein-alanine acetyltransferase	1					1	0.448
cgd4_4030	hypothetical protein	•	1				1	2.267
cgd4_4060	B-box zinc finger domain containing protein	1					1	0.560
cgd4 4070	hypothetical protein	1					1	0.367
cgd4_410	protein with 4xEZ heat domains	-				1	1	51.034
cgd4_4100	hypothetical protein	1					1	0.309
cgd4_4130	hypothetical protein	1					1	0.331
cgd4_4150	hypothetical protein	1					1	0.327
cgd4_4170	hypothetical protein	1					1	0.432
cgd4_4180	hypothetical protein	1					1	0.102
cgd4_4190	hypothetical protein with signal peptide	1					1	0.389
cgd4_4130	hypothetical protein	1					1	0.279
cgd4_4250	hypothetical protein	•	1				1	1.650
cgd4_4270	hypothetical protein		'	1			1	2.633
cgd4_4310	ring finger domain containing protein			۱ ۱		1	1	481.612
cgd4_4330	hypothetical protein		1			'	1	1.509
cgd4_4350	hypothetical protein	1	1				2	1.009
cgd4_4360	ring finger domain containing protein	1	'				1	0.313
cgd4_4370	hypothetical protein	1					1	0.313
cgd4_4380	1 11	1					1	0.305
	hypothetical protein, signal peptide					1	1	73.638
cgd4_4400	hypothetical protein		1			'		
cgd4_4410	2x PHD domain containing protein			1			1	2.093
cgd4_4420	hypothetical protein			1			1	5.465
cgd4_4440	hypothetical protein	4		- '			1	2.500
cgd4_4450	possible transporter with 11 transmembrane domains	1					1	0.337
cgd4_450	very large low complexity protein	1					1	0.494
cgd4_4500	signal peptide containing cysteine rich protein, gene anchored to telomere.				1		1	15.850
cgd4_460	hypothetical protein			1			1	2.496
cgd4_480	hypothetical protein	1					1	0.473
cgd4_490	hypothetical protein				1		1	20.780
logat too	hypothetical protein	1					1	0.453
	1 11		1				1	1.599
cgd4_50	mypothetical protein	1	ı 'l				1	0.497
cgd4_50 cgd4_510	hypothetical protein hypothetical protein	1	'					
cgd4_50 cgd4_510 cgd4_520	hypothetical protein						1	0.343
cgd4_50 cgd4_510 cgd4_520 cgd4_550	hypothetical protein hypothetical protein	1					1	0.343 0.397
cgd4_50 cgd4_510 cgd4_520 cgd4_550 cgd4_560	hypothetical protein hypothetical protein hypothetical protein	1					1	0.397
cgd4_50 cgd4_510 cgd4_520 cgd4_550 cgd4_560 cgd4_600	hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1					1	0.397 0.525
cgd4_50 cgd4_510 cgd4_520 cgd4_550 cgd4_560 cgd4_600 cgd4_610	hypothetical protein hypothetical protein hypothetical protein hypothetical protein MJ050-like PP-loop ATpase	1	1				1 1 1	0.397 0.525 0.379
cgd4_50 cgd4_510 cgd4_520 cgd4_550 cgd4_560 cgd4_600	hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1	1				1	0.397 0.525

Depth   Dept	cgd4_760	possible ASF1 anti-silencing function 1 like protein	1		ı	1	ı	1	0.446
agod, 800 agog, protein with signal peptide goods agog, 900 hypothetical protein goods agog, 901 agog, 901 agog, 901 agog, 901 agog, 902 agog, 902 agog, 902 agog, 903	cgd4_770	Low complexity protein with large Glu repeat	1					1	0.294
cgd4 900 younger for the first protein cydf4 900 younger for the first protein cydf4 900 younger for the first protein cydf4 900 younger for first protein protein cydf4 900 younger for first protein protein cydf4 900 younger for first protein protein cydf4 900 younger for first protein protein cydf4 900 younger for first protein protein cydf4 900 younger for first protein cydf4 900 younger for first protein protein cydf4 900 younger for first protein protein cydf4 900 younger for first protein having a signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal peptide cydf4 900 younger for first protein with signal	cgd4_820	WD repeat protein	1					1	0.470
ogd4-900 (V) propeat containing protein (1) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	cgd4_850	large protein with signal peptide	1					1	0.441
cgd4 900  Will repeat containing protein cgd4 900 cgd4 900 cgd4 900 cgd5 1900 cgd5 191	cgd4_860	possible WWE domain				1		1	10.894
1   1   1   1   1   1   1   1   1   1	cgd4_90	hypothetical protein					1	1	38.676
### APP Company Compan	cgd4_900	WD repeat containing protein				1		1	9.413
1   1   5   5   5   5   5   5   5   5	cgd4_940	hypothetical protein				1		1	12.471
Lagds 1,010 (apds	cgd4_950	WD repeat protein	1					1	0.342
agd5 1950 hypothetical protein protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein family / small nuclear ribonucleoprotein   1	cgd5_10	signal peptide containing protein					1	1	596.842
god5 1,050 hypothetical protein (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein having a signal peptide (255 1,050 hypothetical protein (255 1,050 hypothetical protei	cgd5_1010	hypothetical protein			1			1	4.613
Company   Comp	cgd5_1040	arfgap'arfgap like finger domain containing protein'	1					1	0.611
ggd5_1190	cgd5_1050	hypothetical protein	1					1	0.372
C2H2 finger domain containing protein gd5_1120 DNMAP1 like Myb domain WD-40 repeat protein family / small nuclear ribonucleoprotein Prp4-prelated gd5_1180 PO2 domain protein that is fused to a MATH domain at its N- terminus gd5_1120 Importential protein gd5_1200 Importential protein gd5_1200 Importential protein gd5_1200 Importential protein gd5_1200 Importential protein gd5_1200 Importential protein gd5_1200 Importential protein gd5_1200 Importential protein gd5_1200 Importential protein gd5_1400 Importential protein with signal peptide gd5_1400 Importential protein with signal peptide gd5_1400 Importential protein with signal peptide gd5_1400 Importential protein with signal peptide gd5_1500 Importential protein with signal peptide gd5_1500 Importential protein having a signal peptide gd5_1500 Importential protein having a signal peptide gd5_1600 Importential protein having a signal peptide gd5_1600 Importential protein having a signal peptide gd5_1600 Importential protein pytochretical protein pytochretical protein pytochretical protein pytochretical protein pytochretical protein pytochretical protein gd5_1600 Importential protein gd5_1600 Importential protein gd5_1600 Importential protein gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein with signal peptide gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein with signal peptide and acidic stretch gd5_1600 Importential protein gd5_1600 Importential	cgd5_1060	hypothetical protein	1	1				2	0.957
DNNAP1   Ike Myb domain	cgd5_1080	hypothetical protein				1		1	7.228
WD-40 repeat protein family / small nuclear ribonucleoprotein   1   1   1   1   1   1   1   1   1	cgd5_1110	C2H2 finger domain containing protein	1					1	0.490
prp4-prelated cogd5_1150 Prp4-prelated cogd5_1160 ProZ domain protein that is fused to a MATH domain at its N-time in the subsection of th	cgd5_1120	DNMAP1 like Myb domain	1					1	0.566
cgd5_1150 cgd5_1150 cgd5_1210 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_1220 cgd5_140 cgd5_140 cgd5_140 cgd5_140 cgd5_1420 cgd5_1420 cgd5_1420 cgd5_1420 cgd5_1420 cgd5_1420 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_1450 cgd5_160	cgd5_1130	WD-40 repeat protein family / small nuclear ribonucleoprotein	1					1	0.428
POZ domain protein that is fused to a MATH domain at its N-terminus capds 1,220.		1 ' '							
terminus   terminus	1			1					2.024
cgd5 1200 inig finger and box containing protein, putative cgd5 1200 (gd5 1200 hypothetical protein hypothetical protein hypothetical protein hypothetical protein cgd5 1400 hypothetical protein cgd5 1400 hypothetical protein cgd5 1400 hypothetical protein cgd5 1400 hypothetical protein cgd5 1400 hypothetical protein with signal peptide cgd5 1440 hypothetical protein with signal peptide cgd5 1440 hypothetical protein with signal peptide cgd5 1480 hypothetical protein with signal peptide hypothetical protein with signal peptide cgd5 1480 hypothetical protein with signal peptide hypothetical protein having a signal peptide hypothetical protein having a signal peptide cgd5 1530 hypothetical protein having a signal peptide cgd5 1530 hypothetical protein having a signal peptide cgd5 1580 hypothetical protein having a signal peptide cgd5 1680 hypothetical protein having a signal peptide cgd5 1680 hypothetical protein protein cgd5 1620 hypothetical protein with signal peptide cgd5 1620 hypothetical protein with sort conserved N-terminal motif, possible cysteine binding domain MoRN repeat protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothetical protein with signal peptide cgd5 1680 hypothet	cgd5_1160		1					1	0.403
Company   Comp	cad5 1200					1		4	23.380
cgd5_1370 hypothetical protein cgd5_1400 (cgd5_1400 hypothetical protein phypothetical protein cgd5_1400 hypothetical protein cgd5_1400 hypothetical protein cgd5_1400 hypothetical protein cgd5_1400 hypothetical protein with signal peptide cgd5_1440 hypothetical protein with signal peptide hypothetical protein with signal peptide cgd5_1400 hypothetical protein with signal peptide cgd5_1400 hypothetical protein with signal peptide cgd5_1400 hypothetical protein with signal peptide cgd5_1400 hypothetical protein with signal peptide cgd5_1500 hypothetical protein with signal peptide cgd5_1530 hypothetical protein hypothetical protein cgd5_1530 hypothetical protein phypothetical protein hypothetical protein mypothetical protein with sort conserved N-terminal motif, possible cysteine binding domain MORN repeat protein with sort conserved N-terminal motif, possible cysteine binding domain MORN repeat protein with sort conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4b keep in hypothetical protein with sort conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4b keep in hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein hypothetical protein with RIM domain hypothetical protein with RIM domain hypothetical pro	1		1	4		'			0.881
cgd5_140 ARF GFPase activating protein, putative cgd5_1400 hypothetical protein cgd5_1420 cgd5_1420 hypothetical protein cgd5_1450 hypothetical protein with signal peptide cgd5_1460 hypothetical protein with signal peptide cgd5_1460 hypothetical protein with signal peptide cgd5_1460 hypothetical protein having a signal peptide cgd5_1500 hypothetical protein having a signal peptide cgd5_1500 hypothetical protein having a signal peptide cgd5_1580 hypothetical protein having a signal peptide cgd5_1580 hypothetical protein having a signal peptide cgd5_1580 hypothetical protein having a signal peptide cgd5_1610 hypothetical protein having a signal peptide cgd5_1610 hypothetical protein having a signal peptide cgd5_1610 hypothetical protein having a signal peptide cgd5_1610 hypothetical protein having a signal peptide cgd5_1610 hypothetical protein having a signal peptide cgd5_1620 cgd5_1640 hypothetical protein having a signal peptide cgd5_1650 hypothetical protein having a signal peptide cgd5_1650 hypothetical protein having a signal peptide cgd5_1660 cgd5_1670 hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with a n-terminal domain shared with the TOG/ALp4p ke microthuble associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	1 **		1 1					1.296
cgd5_1400 cgd5_1400 cgd5_1400 cgd5_1400 cgd5_1400 cgd5_1400 cgd5_1400 cgd5_1440 cgd5_1440 cgd5_1440 cgd5_1460 cgd5_1480 cgd5_1480 cgd5_1480 cgd5_1480 cgd5_1530 cgd5_1530 cgd5_1530 cgd5_1530 cgd5_1530 cgd5_1580 cgd5_1580 cgd5_1580 cgd5_1580 cgd5_160 cgd5_1580 cgd5_160 cgd5_160 cgd5_160 cgd5_160 cgd5_160 cgd5_160 cgd5_1600 cgd	1	1 21 1		'	4				5.073
cgd5_1400 hypothetical protein (cgd5_1450) hypothetical protein with signal peptide (cgd5_1450) hypothetical protein with signal peptide (cgd5_1450) hypothetical protein with signal peptide (cgd5_1450) hypothetical protein with signal peptide (cgd5_1480) cysteine rich protein with signal peptide (cgd5_1480) hypothetical protein with signal peptide (cgd5_1480) hypothetical protein with signal peptide (cgd5_1500) hypothetical protein with signal peptide (cgd5_1580) hypothetical protein having a signal peptide (cgd5_1580) hypothetical protein hypothetical protein (cgd5_1580) hypothetical protein (cgd5_1580) hypothetical protein (cgd5_1580) hypothetical protein (cgd5_1580) hypothetical protein (cgd5_1580) hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain (cgd5_160) hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain (cgd5_1650) hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with some served apicomplexan domain (cgd5_1600) hypothetical protein with signal peptide hypothetical protein with signal peptide (cgd5_1600) hypothetical protein with signal peptide (cgd5_1800) hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein with protein with a pleckstrin homology (PH) domain hypothetical protein protein with prot	1	1 **	1		- '				
cgd5_1420   putative secreted protein   cgd5_1440   large protein with signal peptide   cgd5_1450   hypothetical protein with signal peptide   cgd5_1460   hypothetical protein with signal peptide   cgd5_1460   cgd5_1500   hypothetical protein having a signal peptide   cgd5_1530   hypothetical protein having a signal peptide   cgd5_1530   hypothetical protein   hypothetical protein   cgd5_1590   hypothetical protein   hypothetical		j							0.574
Single Protein with signal peptide		1 **		4					0.378
cgd5_1450	1	i.	4						1.446 0.443
Cgd5_1460	1				4			1	
cgd5_1480 cysteine rich protein having a signal peptide	1	1		4	1				3.570
cgd5_1500 hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain MCRN repeat protein hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain MCRN repeat protein hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p if ke microtubule associated protein hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p if ke microtubule associated protein hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at hypothetical protein hypotheti	1	1 21 1 1		1					1.719
cgd5_1530 hypothetical protein having a signal peptide hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with short conserved hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain MORN repeat protein with short conserved N-terminal motif, possible cysteine binding domain MORN repeat protein hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p ike microtubule associated proteins hypothetical protein with signal peptide norgofi. Protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein hypothetical	1	1	4		1				2.252
cgd5_1580 hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with conserved apicomplexan domain protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at lact the N-terminus hypothetical protein hypotheti	1	1 **							0.466
cgd5_1590 hypothetical protein hypothetical protein hypothetical protein possibly apicomplexan conserved hypothetical protein possibly apicomplexan conserved hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain MORN repeat protein with short conserved N-terminal motif, possible cysteine binding domain MORN repeat protein hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein little N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RIO domain within N-terminal region protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_200 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothet	1	1	1						0.563
cgd5_160 hypothetical protein (possibly apicomplexan conserved hypothetical protein, possibly apicomplexan conserved (pdf_1620) hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain (pdf_1630) hypothetical protein (pdf_1630) hypothetical protein (pdf_1630) hypothetical protein with signal peptide and acidic stretch (pdf_1630) hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p (pdf_1730) hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p (pdf_1730) hypothetical protein with signal peptide (pdf_1730) hypothetical protein with signal peptide (pdf_1730) hypothetical protein with signal peptide (pdf_1730) hypothetical protein with signal peptide (pdf_1730) hypothetical protein with signal peptide (pdf_1730) hypothetical protein with signal peptide (pdf_1730) hypothetical protein (pdf	1	1 **					1		177.577
cgd5_1610 hypothetical protein, possibly apicomplexan conserved hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain cgd5_1650 hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain hypothetical protein with conserved apicomplexan domain hypothetical protein with an N-terminal domain shared with the TOG/ALp4p it microtrouble associated proteins it microtrouble associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with an N-terminal domain shared with the TOG/ALp4p it microtrouble associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein hypothetical protein hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein with RRM domain hypothetical protein hypothetical protein hypo	1	1 **		1					1.878
gd5_1620 hypothetical protein with short conserved N-terminal motif, possible cysteine binding domain MORN repeat protein MORN repeat protein hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein hypo	1	1 **					1		28.240
possible cysteine binding domain cgd5_1640 MORN repeat protein lypothetical protein hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain cgd5_1680 possible cysteine with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein cgd5_170 hypothetical protein cgd5_180 hypothetical protein with signal peptide hypothetical protein with signal peptide cgd5_180 hypothetical protein cgd5_1810 cgd5_1840 Vir superfamily protein cgd5_1870 LETM1/MRS7 family protein with a transmembrane region at the N-terminus hypothetical protein cgd5_1890 hypothetical protein with end of the protein with a pleckstrin homology (PH) domain hypothetical protein hypothetical protein cgd5_1980 hypothetical protein hypothetical protein cgd5_1980 hypothetical protein hypothetical protein cgd5_1980 hypothetical protein cgd5_1980 hypothetical protein hypothetical protein cgd5_200 cgd5_200 cgd5_200 cgd5_200 cgd5_200 cgd5_200 cgd5_200 protein with RIO domain within N-terminal region cgd5_200 cgd5_2080 FCH domain containing protein lypothetical prot	1				1				4.965
cgd5_1640 MCRN repeat protein hypothetical protein with signal peptide and acidic stretch hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain cgd5_1680 protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein hypotheti	cgd5_1620	1 **				1		1	22.852
cgd5_1650 hypothetical protein hypothetical protein with signal peptide and acidic stretch hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein with RIO domain within N-terminal region protein with RIO domain within N-terminal region protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus protein hypothetical protein hypo	cad5 1640				1			1	3.186
cgd5_1660 hypothetical protein with signal peptide and acidic stretch cgd5_1670 hypothetical protein with conserved apicomplexan domain protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide cgd5_1780 hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein hypothetical protein signal peptide containing protein 1 cgd5_1890 hypothetical protein hypothetical protein 1 cgd5_1990 cgd5_1900 hypothetical protein 1 cgd5_1990 cgd5_200 hypothetical protein 1 cgd5_200 hypothetical protein 1 cgd5_200 hypothetical protein 1 cgd5_200 cgd5_200 rotein with RIO domain within N-terminal region protein with RIO domain within N-terminal region protein with PID finger and a nipped-B/Mis4/Scc2 like domain 1 at the C-terminus cgd5_2100 hypothetical protein 1 cgd5_2100 rotein with PID finger and a nipped-B/Mis4/Scc2 like domain 1 at the C-terminus containing protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 rotein with PID finger and a nipped-B/Mis4/Scc2 like domain 1 at the C-terminus containing protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2100 hypothetical protein 1 cgd5_2200 hypothetical protein 1 cgd5_2200 hypothetical protein 1 cgd5_2200 hypothetical protein 1 cgd5	1				- 1				4.511
cgd5_1680 protein with an N-terminal domain shared with the TOG/ALp4p ike microtubule associated proteins hypothetical protein with signal peptide cgd5_1780 hypothetical protein with signal peptide cgd5_180 hypothetical protein with signal peptide cgd5_1800 hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a pleckstrin homology (PH) domain cgd5_1970 hypothetical protein with a pleckstrin homology (PH) domain cgd5_1990 cgd5_200 cgd5_200 protein with RIO domain within N-terminal region protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2120 hypothetical protein hypothetical protein in hypothetical protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2140 hypothetical protein hypothetical protein in hypothetical protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2120 hypothetical protein hypothetical protein in hypothetica	1	1 ***		1	۱'				1.767
cgd5_1680 protein with an N-terminal domain shared with the TOG/ALp4p like microtubule associated proteins hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein hypothetical protein with a pleckstrin homology (PH) domain hypothetical protein with RIO domain within N-terminal region and possible central coiled coil domain protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus FCH domain containing protein hypothetical protein hypot	1	1 **		'	1				2.710
ike microtubule associated proteins hypothetical protein upothetical protein with signal peptide hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a transmembrane region at the N-terminus hypothetical protein with a pleckstrin homology (PH) domain cgd5_1890 hypothetical protein with a pleckstrin homology (PH) domain cgd5_1990 hypothetical protein with a pleckstrin homology (PH) domain cgd5_1990 hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RIO domain within N-terminal region cgd5_200 gradien with RIO domain within N-terminal region cgd5_2050 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus FCH domain cgd5_2100 hypothetical protein hypothetical protein hypothetical protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2100 hypothetical protein hypotheti	1		1		- 1			1	0.568
cgd5_170         hypothetical protein         1         2         2         1<	cguo_1000	li i i						'	0.000
cgd5_1800 hypothetical protein with signal peptide hypothetical protein with signal peptide hypothetical protein with signal protein cgd5_1810 SMART 2xt_SNARE domain containing protein cgd5_1810 Vir superfamily protein cgd5_1840 Vir superfamily protein cgd5_1870 LETM1/MRS7 family protein with a transmembrane region at the N-terminus hypothetical protein hypothetical protein cgd5_1890 hypothetical protein with a pleckstrin homology (PH) domain cgd5_1970 AtPH1 like protein with a pleckstrin homology (PH) domain cgd5_1990 hypothetical protein hypothetical protein limited containing protein hypothetical protein limited cgd5_200 gignal peptide containing protein limited cgd5_200 protein with RIO domain within N-terminal region cgd5_2000 protein with forkhead associated (FHA) domain within N-terminal region and possible central coiled coil domain lat the C-terminus regd5_2000 protein with FHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus regd5_2100 hypothetical protein limited hypothetical protein limited hypothetical protein limited hypothetical protein limited hypothetical protein limited large low complexity protein with proline/alanine-rich repeat large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexity protein with RRM domain limited large low complexi	cgd5 170	· ·			1			1	3.481
cgd5_180 hypothetical protein with signal peptide	cgd5 1780	MJ1625/yease Yp1009cp-like HhH domain					1	1	85.961
cgd5_1800 hypothetical protein cgd5_1810 SMART 2xt_SNARE domain containing protein cgd5_1840 Vir superfamily protein cgd5_1870 LETM1/MRS7 family protein with a transmembrane region at the N-terminus hypothetical protein cgd5_1890 hypothetical protein cgd5_1930 hypothetical protein cgd5_1940 hypothetical protein cgd5_1970 AtPH1 like protein with a pleckstrin homology (PH) domain cgd5_1980 hypothetical protein cgd5_1980 hypothetical protein cgd5_1990 hypothetical protein cgd5_1990 hypothetical protein cgd5_20 signal peptide containing protein cgd5_20 signal peptide containing protein cgd5_20 protein with RIO domain within N-terminal region cgd5_200 protein with RIO domain within N-terminal region and possible central coiled coil domain cgd5_200 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_210 hypothetical protein cgd5_210 hypothetical protein cgd5_210 hypothetical protein cgd5_210 hypothetical protein cgd5_2110 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_220 T8M16_190-plant like protein with RRM domain	1	hypothetical protein with signal peptide				1		1	7.055
cgd5_1840		hypothetical protein	1					1	0.512
cgd5_1840 Vir superfamily protein cgd5_1870 LETM1/MRS7 family protein with a transmembrane region at the N-terminus cgd5_1890 hypothetical protein cgd5_1930 hypothetical protein with a pleckstrin homology (PH) domain cgd5_1970 AtPH1 like protein with a pleckstrin homology (PH) domain hypothetical protein cgd5_1980 hypothetical protein cgd5_1990 hypothetical protein cgd5_200 signal peptide containing protein cgd5_200 protein with RIO domain within N-terminal region cgd5_200 protein with rorkhead associated (FHA) domain within N- terminal region and possible central coiled coil domain cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2120 hypothetical protein cgd5_2120 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with RRM domain cgd5_2200 T8M16_190-plant like protein with RRM domain 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	cgd5 1810	SMART 2xt SNARE domain containing protein	1					1	0.543
cgd5_1870 LETM1/MRS7 family protein with a transmembrane region at the N-terminus hypothetical protein hypothetical protein cgd5_1930 hypothetical protein with a pleckstrin homology (PH) domain cgd5_1970 AtPH1 like protein with a pleckstrin homology (PH) domain cgd5_1980 hypothetical protein cgd5_1990 hypothetical protein cgd5_200 signal peptide containing protein cgd5_200 protein with RIO domain within N-terminal region protein with forkhead associated (FHA) domain within N-terminal region and possible central coiled coil domain cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus FCH domain containing protein hypothetical protein hypothetical protein hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_2200 T8M16_190-plant like protein with RRM domain 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1						1		30.925
the N-terminus hypothetical protein hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical	1	1	1					1	0.275
cgd5_1930 hypothetical protein cgd5_1970 AtPH1 like protein with a pleckstrin homology (PH) domain cgd5_1980 hypothetical protein cgd5_1990 hypothetical protein cgd5_20 signal peptide containing protein hypothetical protein cgd5_200 protein with RIO domain within N-terminal region cgd5_2050 protein with forkhead associated (FHA) domain within N-terminal region and possible central coiled coil domain cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_210 hypothetical protein cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_2200 T8M16_190-plant like protein with RRM domain	-								
cgd5_1970 AtPH1 like protein with a pleckstrin homology (PH) domain cgd5_1980 hypothetical protein cgd5_1990 hypothetical protein cgd5_20 signal peptide containing protein hypothetical protein cgd5_200 protein with RIO domain within N-terminal region cgd5_2050 protein with forkhead associated (FHA) domain within N-terminal region and possible central coiled coil domain cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2100 hypothetical protein cgd5_210 hypothetical protein cgd5_2110 hypothetical protein cgd5_2140 hypothetical protein cgd5_2140 hypothetical protein cgd5_2150 large low complexity protein with proline/alanine-rich repeat cgd5_2200 T8M16_190-plant like protein with RRM domain	cgd5_1890	hypothetical protein			1			1	5.989
cgd5_1980 hypothetical protein cgd5_1990 hypothetical protein cgd5_20 signal peptide containing protein cgd5_200 hypothetical protein cgd5_200 protein with RIO domain within N-terminal region cgd5_2050 protein with forkhead associated (FHA) domain within N- terminal region and possible central coiled coil domain cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2100 hypothetical protein cgd5_210 hypothetical protein cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_2200 T8M16_190-plant like protein with RRM domain	cgd5_1930	hypothetical protein	1					1	0.479
cgd5_1990 hypothetical protein cgd5_20 signal peptide containing protein hypothetical protein cgd5_200 protein with RIO domain within N-terminal region cgd5_2050 protein with FIO domain within N-terminal region cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_210 hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein cgd5_2120 hypothetical protein hypothetical protein hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_2200 T8M16_190-plant like protein with RRM domain	cgd5_1970	AtPH1 like protein with a pleckstrin homology (PH) domain			1			1	3.580
cgd5_20 signal peptide containing protein cgd5_200 hypothetical protein cgd5_2000 protein with RIO domain within N-terminal region cgd5_2050 protein with forkhead associated (FHA) domain within N- terminal region and possible central coiled coil domain protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2090 FCH domain containing protein cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_2200 T8M16_190-plant like protein with RRM domain	cgd5_1980	hypothetical protein			1			1	6.009
cgd5_200 hypothetical protein cgd5_2000 protein with RIO domain within N-terminal region cgd5_2050 protein with forkhead associated (FHA) domain within N- terminal region and possible central coiled coil domain protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2090 FCH domain containing protein cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_220 T8M16_190-plant like protein with RRM domain	cgd5_1990	hypothetical protein			1			1	2.889
cgd5_2000 protein with RIO domain within N-terminal region cgd5_2050 protein with forkhead associated (FHA) domain within N- terminal region and possible central coiled coil domain cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2090 FCH domain containing protein cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_220 T8M16_190-plant like protein with RRM domain	cgd5_20	signal peptide containing protein			1			1	2.466
cgd5_2050 protein with forkhead associated (FHA) domain within N-terminal region and possible central coiled coil domain protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2090 FCH domain containing protein 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	cgd5_200	hypothetical protein	1					1	0.312
terminal region and possible central coiled coil domain cgd5_2080 protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus cgd5_2090 FCH domain containing protein cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_220 hypothetical protein cgd5_220 T8M16_190-plant like protein with RRM domain	cgd5_2000	protein with RIO domain within N-terminal region					1	1	46.919
cgd5_2080         protein with PHD finger and a nipped-B/Mis4/Scc2 like domain at the C-terminus         1	cgd5_2050	protein with forkhead associated (FHA) domain within N-	1	1				2	1.409
at the C-terminus cgd5_2090 FCH domain containing protein cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2170 large low complexity protein with proline/alanine-rich repeat cgd5_220 hypothetical protein cgd5_220 T8M16_190-plant like protein with RRM domain									
cgd5_2090     FCH domain containing protein     1       cgd5_210     hypothetical protein     1       cgd5_2120     hypothetical protein     1       cgd5_2140     hypothetical protein     1       cgd5_2170     hypothetical protein     1       cgd5_2180     large low complexity protein with proline/alanine-rich repeat     1       cgd5_220     hypothetical protein     1       cgd5_2200     T8M16_190-plant like protein with RRM domain     1	cgd5_2080			1				1	1.904
cgd5_210 hypothetical protein cgd5_2120 hypothetical protein cgd5_2140 hypothetical protein cgd5_2140 hypothetical protein cgd5_2170 hypothetical protein cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_220 hypothetical protein cgd5_220 T8M16_190-plant like protein with RRM domain	cade 2000		- 1					4	0.335
cgd5_2120 hypothetical protein	1	j .							0.335
cgd5_2140 hypothetical protein	1	1 **	1						0.355
cgd5_2170     hypothetical protein     1     1       cgd5_2180     large low complexity protein with proline/alanine-rich repeat     1     1       cgd5_220     hypothetical protein     1     1       cgd5_2200     T8M16_190-plant like protein with RRM domain     1     1		1 **		1			4		1.611
cgd5_2180 large low complexity protein with proline/alanine-rich repeat cgd5_220 hypothetical protein 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	1 **			إ		1		61.975
cgd5_220 hypothetical protein 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	1 **			1				2.401
cgd5_2200 T8M16_190-plant like protein with RRM domain 1 1	1						1		61.504
	1	1 **	1						0.347
	1					1			8.952
		1 **			ا	1			5.962
cgd5_2260 Low complexity hypothetical protein	1	1 1 2 21 1			1		4		5.479
cgd5_2310   Sin3 like paired amphipathic helix containing protein   1 1	cga5_2310	Sins like paired amphipathic helix containing protein			-		1	1	24.474

cgd5_2340	possible SET domain containing protein			1			1 1	5.046
cgd5_240	G patch domain containing protein			1			1	3.844
cgd5_2540	WD repeat protein	4	1				1	1.486
cgd5_2560	MutL family ATpase	1		1			1 1	0.369
cgd5_2570 cgd5_260	hypothetical protein hypothetical protein	1		'			1	5.281 0.451
cgd5_2600	putative leucine aminopeptidase; of possible plant or bacterial	'	1				'	1.390
cgu5_2000	origin		' '				'	1.590
cgd5_2620	penguin protein containing pumolio repeats				1		1	19.644
cgd5_2640	little finger (CxxCCxxC) domain containing protein		1				1	1.827
cgd5 2650	hypothetical protein	1					1	0.423
cgd5_2660	hypothetical protein	1					1	0.408
cgd5_2700	hypothetical protein with a signal peptide				1		1	19.761
cgd5_2720	large protein containing a signal peptide					1	1	266.329
cgd5 2730	hypothetical protein			1			1	4.324
cgd5_2750	hypothetical protein, signal peptide			1			1	2.431
cgd5_2760	hypothetical protein					1	1	62.000
cgd5_2770	ARF like small GTpase	1					1	0.381
cgd5_2850	hypothetical protein	1					1	0.358
cgd5_2860	hypothetical protein			1			1	5.630
cgd5_2890	hypothetical protein		1				1	2.025
cgd5_2920	hypothetical protein	1	· 'I				1	0.522
cgd5_2920 cgd5_2930	hypothetical protein					1		41.689
	1 **			1		'	1	4.980
cgd5_2970	hypothetical protein				4		l I	
cgd5_2980	hypothetical protein				1	1	1	15.738
cgd5_30	hypothetical protein	,				1	1	161.352
cgd5_300	hypothetical protein	1					1	0.444
cgd5_3010	hypothetical protein with possible plus3 domain		1				1	2.234
cgd5_3020	hypothetical protein	1					1	0.389
cgd5_3060	hypothetical protein	1					1	0.354
cgd5_3100	hypothetical protein	1					1	0.440
cgd5_3120	hypothetical protein		1				1	1.506
cgd5_3190	hypothetical protein	1					1	0.307
cgd5_3210	large hypothetical protein with signal peptide	1					1	0.356
cgd5_330	hypothetical protein	1					1	0.345
cgd5_3300	large protein with 4 PHD domains				1		1	23.238
cgd5_3310	WD repeat protein					1	1	67.521
cgd5_3320	hypothetical protein			1			1	3.140
cgd5_3350	hypothetical protein				1		1	6.550
cgd5_3370	hypothetical protein		1				1	1.711
cgd5_3380	protein with signal peptide and possible kazal domain	1	1				2	1.160
cgd5_3390	very large hypothetical protein	1					1	0.395
cgd5_3440	hypothetical protein	1					1	0.336
cgd5 3470	E. coli yfiP family protein			1			1	3.325
cgd5 3480	hypothetical protein with possible conserved HGG motif					1	1	105.595
cgd5_3490	hypothetical protein with signal peptide					1	1	125.868
cgd5 350	hypothetical protein			1			1	2.522
cgd5_3570	putative secreted protein	1					1	0.366
cgd5_3600	predicted secreted protein	1					1	0.387
cgd5_3620	hypothetical protein	1					1	0.502
cgd5_3640	hypothetical protein		1				1	1.828
cgd5 3650	hypothetical protein					1	1	191.631
cgd5_3670	hypothetical protein	1					1	0.430
cgd5_3680	WD repeat containing protein	1					1	0.309
cgd5_370	predicted coiled coil protein				1		1	6.495
cgd5_3700	Sec1 family	1			'		1	0.354
cgd5_3760	hypothetical protein				1			12.585
cgu3_3700	priypotrietical protein				1			8.113
loadE 2700	by notherinal protein with a possible systems rich domain (PROY				<u>'</u>		'	0.113
cgd5_3780	hypothetical protein with a possible cysteine-rich domain (BBOX						1	0.304
	zinc finger?)							
cgd5_3800	zinc finger?) hypothetical protein	1	1.				l I	
cgd5_3800 cgd5_3830	zinc finger?) hypothetical protein hypothetical protein	1	1				1	1.414
cgd5_3800 cgd5_3830 cgd5_3860	zinc finger?) hypothetical protein hypothetical protein hypothetical protein	1	1				1 1	1.414 0.284
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3880	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1	1				1 1 1	1.414 0.284 0.523
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3880 cgd5_3900	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus	1 1 1	1				1 1 1 1	1.414 0.284 0.523 0.253
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3880 cgd5_3900 cgd5_3910	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein	1 1 1	1				1 1 1 1	1.414 0.284 0.523 0.253 0.346
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3880 cgd5_3900 cgd5_3910 cgd5_3930	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein	1 1 1	1			1	1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3880 cgd5_3900 cgd5_3910 cgd5_3930 cgd5_40	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches	1 1 1 1 1	1			1	1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3880 cgd5_3900 cgd5_3910 cgd5_3930	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated	1 1 1	1			1	1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3900 cgd5_3910 cgd5_3930 cgd5_40 cgd5_400	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus	1 1 1 1 1	1			1	1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3990 cgd5_3910 cgd5_3930 cgd5_40 cgd5_400 cgd5_400	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus hypothetical protein	1 1 1 1 1	1			1	1 1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3990 cgd5_3910 cgd5_3930 cgd5_40 cgd5_400 cgd5_4000 cgd5_4010	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus hypothetical protein	1 1 1 1 1 1 1	1			1	1 1 1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309 0.290 0.399
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3990 cgd5_3910 cgd5_3930 cgd5_40 cgd5_400 cgd5_400 cgd5_4010 cgd5_4010	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1 1 1	1			1	1 1 1 1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309 0.290 0.399 0.427
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3900 cgd5_3910 cgd5_3930 cgd5_40 cgd5_400 cgd5_400 cgd5_4010 cgd5_4010 cgd5_4020 cgd5_4030	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1 1 1 1	1			1	1 1 1 1 1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309 0.290 0.399 0.427 0.316
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3900 cgd5_3910 cgd5_3930 cgd5_40 cgd5_400 cgd5_400 cgd5_4010 cgd5_4010 cgd5_4020 cgd5_4030 cgd5_4040	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1 1 1 1	1			1	1 1 1 1 1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309 0.290 0.399 0.427 0.316 0.370
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3880 cgd5_3900 cgd5_3910 cgd5_400 cgd5_400 cgd5_400 cgd5_4010 cgd5_4010 cgd5_4020 cgd5_4030 cgd5_4040 cgd5_4040 cgd5_4070	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1 1 1 1	1			1	1 1 1 1 1 1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309 0.290 0.399 0.427 0.316 0.370 0.400
cgd5_3800 cgd5_3830 cgd5_3860 cgd5_3860 cgd5_3900 cgd5_3910 cgd5_3930 cgd5_40 cgd5_400 cgd5_400 cgd5_4010 cgd5_4010 cgd5_4020 cgd5_4030 cgd5_4040	zinc finger?) hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein with RING finger domain at C-terminus hypothetical protein hypothetical protein signal peptide containing large protein with proline stretches protein with 4 PHD domains plus a SET domain and associated cysteine cluster at the C-terminus hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1 1 1 1 1 1 1 1 1 1	1 1 1 1 1			1	1 1 1 1 1 1 1 1 1 1	1.414 0.284 0.523 0.253 0.346 1.954 100.741 0.309 0.290 0.399 0.427 0.316

1   1   1   1   1   1   1   1   1   1	cgd5_4120 cgd5_4130	hypothetical protein with a signal peptide hypothetical protein having a signal peptide and transmembrane	1 1					1	0.310 0.420
1   1   1   1   1   1   1   1   1   1	cad5 4240	domain near C-terminus	1					1	0.417
ogd5_43400   hypothetical protein   1   1   2.5.399   cgd5_4300   large protein with possible RING domain   1   1   3.380   cgd5_4300   large protein with 2 CaP (CARP) domains, possible adenyl cyclase-associated protein   1   1   3.380   cgd5_4400   region with 2 CaP (CARP) domains, possible adenyl cyclase-associated protein   1   1   1.970   cgd5_4410   region with 2 CaP (CARP) domains, possible adenyl cyclase-associated protein   1   1   1.970   cgd5_4400   region   region   1   1   1.970   cgd5_4400   region   region   1   1   2.6.620   cgd5_4400   region   region   region   1   1   2.6.620   cgd5_4400   region		1 **					1		
ogd5_4300         Injochtectaal protein         1         1         1         25.399           ogd5_440         protein with 2 CAP (CARP) domains, possible adenyl cyclase-associated protein         1         1         1         3.380           ogd5_440         RIKEN cDNA 2610011N19 gen         1         1         1         1.970           ogd5_4400         WOM2 repeat protein         1         1         1         2.683           ogd5_4401         Orgonal protein         1         1         1         2.682           ogd5_4401         Orgonal protein         1         1         1         2.683           ogd5_4401         Orgonal protein         1         1         0.383         1         0.383           ogd5_4401         Orgonal protein         1         1         0.383         1         0.383           ogd5_4501         Orgonal protein         1         1         0.383         1         0.383           ogd5_501         Orgonal protein         1         1         0.347         1         0.347           ogd5_605         Orgonal protein         1         1         0.383         1         0.383           ogd5_605         Orgonal protein         1         0.			1				'		
ogd5_4400  Gd5_4410  Gd6_4410  Gd6_4	" -	1 21	'				1		
1   1   1   6.338		1 ***			1		'		
Capd. 4-410   Gagd. 4-410		1 9 1			۱'	1			
1   1   1   1   1   1   1   1   1   1	C903_440					'		'	0.550
agd5_4410         Mypothelestal protein         1         1         24.820           agd5_4460         Rogd5_4460         Rogd5_4600         Rogd5_4700         R	cqd5 4400			1				1	1.970
cgdf. 4400         WD40 repeat protein         1         1         6.831           cgdf. 4480         large low complexity protein, possible apicomplexan-specific cydf. 4480         1         0.391           cgdf. 4500         possible via couls protein of god and protein cydf. 4500         1         1         0.391           cgdf. 4500         possible via couls protein sorting associated protein (VPS)         1         1         2.086           cgdf. 4501         possible via couls protein sorting associated protein (VPS)         1         0.473           cgdf. 4701         pycothecical protein         1         1         0.473           cgdf. 5401         hypothecical protein         1         1         0.473           cgdf. 5401         hypothecical protein         1         1         0.303           cgdf. 5402         hypothecical protein         1         1         0.303           cgdf. 560         hypothecical protein         1         1         0.399           cgdf. 760         hypothecical protein         1         0.495         1         0.495           cgdf. 801         hypothecical protein         1         0.495         1         0.495         1         0.495           cgdf. 801         hypothecical protein		hypothetical protein					1	1	24.620
0gd5.4480         hypothetical protein         1         0.357           0gd5.4490         rage low complexity protein, possible apicomplexan-specific         1         0.383           0gd5.4500         possible ring domain protein         1         0.383           0gd5.4510         possible vacuular protein sorting associated protein (VPS)         1         0.383           0gd5.470         hypothetical protein         1         1         0.318           0gd5.471         hypothetical protein         1         1         0.318           0gd5.471         hypothetical protein         1         1         1         0.378           0gd5.571         hypothetical protein         1         1         2         0.397           0gd5.572         hypothetical protein         1         1         2         0.997           0gd5.778         hypothetical protein         1         1         3.398         1         1         0.358           0gd5.80         hypothetical protein         1         1         0.358         1         0.359         1         0.359         1         0.359         1         0.359         1         0.359         1         0.359         1         0.359         1         0.359		WD40 repeat protein				1		1	6.831
cgd5.4480         large low complexity protein, possible apicomplexan-specific         1         0.391         0.391           cgd5.450         possible vincular protein         1         1         2.886         0.391         1         2.886         0.391         1         1         2.886         0.391         1         0.381         1         0.381         1         0.381         1         0.381         1         0.381         1         0.381         1         0.382         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.374         1         0.373         1         0.303         0.992         1         1         0.303         0.992         1         1         0.303         0.992         1         1         0.303         0.992         1         1         0.303         0.992         1         1         0.303         0.992         1         1         0.303         1         0.992         1         1         0.992         1	" -		1					1	0.357
cgd5.490         pspoelbeid protein         1         0.383           cgd5.4500         psselbe in go anmain protein         1         1         0.388           cgd5.4510         psselbe in go anmain protein         1         0.318         1         0.318           cgd5.4710         pspoelbeid protein         1         1         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.318         1         0.325         740         1         0.326         740         1         0.326         740         1         0.327         740         1         0.327         740         1         0.338         1         1         0.339         1         0.358         1         0.328         740         1         0.339         1         0.339         1         0.339         1         0.339         1         0.339         1         0.339         1         0.329         1         0.32		1 **						1	
cgd5.4500         possible ring domain protein         1         1         2.0889         2.085         2.	" -								
cgd5, 4500         possible vacuolar protein sorting associated protein (VPS)         1         0.318         0.318         0.354         0.364         470         0.319         0.348		1 **				1			
cgdf_4.610         hypothelical protein         1         1         0.473         2         1.037         0.352         1.037         0.352         1.037         0.352         0.997         1.037         0.997         1.037         0.997         1.037         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.039         0.997         1.049	1	Transfer of the second	1						
cgd5_470         hypothetical protein         1         1         1         2         1         0.303           cgd5_401         hypothetical protein         1         1         1         2         0.303           cgd5_503         hypothetical protein         1         1         1         0.303           cgd5_706         hypothetical protein         1         1         0.309           cgd5_707         hypothetical protein         1         0.405           cgd5_708         hypothetical protein         1         0.405           cgd5_801         hypothetical protein         1         0.401           cgd5_801         hypothetical protein         1         1         1.252,323           cgd5_801         hypothetical protein         1         1         1.252,323           cgd5_802         hypothetical protein         1         1         1.252,323           cgd5_801         hypothetical protein         1         1         1.879           cgd5_802         hypothetical protein         1         1         1.879           cgd5_801         hypothetical protein         1         1         1.356           cgd5_901         hypothetical protein         1 <td< td=""><td> </td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>									
cgd5, 470         hypothetical protein         1         1         1         0.303         20         0.997         0.998         0.999         0.998         0.998         0.999		1 **		1					
cgd5_540         hypothetical protein         1         1         1         2         0.997           cgd5_530         protein with 4 ankyrin repeats plus a bromodomain.         1         1         1         3.0981           cgd5_740         WD repeat protein         1         0.945         1         0.945           cgd5_780         hypothetical protein         1         0.945         1         0.945           cgd5_80         hypothetical protein         1         1         0.939         1         0.939           cgd5_80         hypothetical protein         1         1         1         0.401         0.903           cgd5_80         hypothetical protein         1         1         1         1.859         1         1         1.859         1         1         1.859         1         1         1         1.859         1         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859         1         1.859		1 51							
cgd5_650         hypothetical protein         1         1         0.399           cgd5_670         protein with 4 ankyrin repeats plus a bromodomain.         1         1         1         3.0981           cgd5_780         hypothetical protein         1         1         0.985         3.0981           cgd5_870         hypothetical protein         1         1         0.985         3.0981           cgd5_801         hypothetical protein         1         1         1         0.0805           cgd5_810         leucine-rich repeat protein         1         1         1         2.5323           cgd5_810         leucine-rich repeat protein         1         1         0.659         1         1         0.589           cgd5_810         leucine-rich repeat protein         1         1         0.589         1         0.589           cgd5_810         lypothetical protein         1         1         1         0.589         1         0.589           cgd5_90         lypothetical protein protein         1         1         1         1         0.374           cgd5_90         lypothetical protein with signal peptide and cysteine rich region at the C-terminus         1         1         1         1         5.25219		1 ***		1					
cgd5_300         protein with 4 ankyrin repeats plus a bromodomain.         1         1         1         3.09.91           cgd5_760         Nypothetical protein         1         0.495         1         0.495           cgd5_760         Nypothetical protein         1         0.495         1         0.495           cgd5_80         Nypothetical protein         1         1         0.493         1           cgd5_80         Nypothetical protein         1         1         1.252         3           cgd5_80         Nypothetical protein         1         1         1.859         1           cgd5_80         Nypothetical protein         1         1         1.859         1         0.589           cgd5_80         Nypothetical protein         1         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879         1         1.879 <td>  " -</td> <td>1</td> <td></td> <td>  ' </td> <td></td> <td></td> <td></td> <td></td> <td></td>	" -	1		'					
cgd5_760         WD repeat protein         1         0.495           cgd5_780         hypothetical protein         1         0.365           cgd5_80         hypothetical protein         1         0.363           cgd5_80         hypothetical protein         1         1         0.401           cgd5_810         leucine-rich repeat protein         1         1         1.582           cgd5_80         hypothetical protein         1         1         1.589           cgd5_80         hypothetical protein         1         1         0.589           cgd5_80         hypothetical protein         1         1         0.589           cgd5_80         hypothetical protein         1         1         0.377           cgd5_80         hypothetical protein         1         1         1.334           cgd5_90         hypothetical protein own containing protein         1         1         1.344           cgd5_91         Ox7 pi like TLDc domain containing protein         1         1         1.565           cgd5_90         Ox7 pi like TLDc domain containing protein         1         1         5.252           cgd5_100         cgd6_100         hypothetical protein with signal peptide         1         1 <td< td=""><td> </td><td>1 **</td><td></td><td></td><td></td><td></td><td>4</td><td></td><td></td></td<>		1 **					4		
cgd5_760         hypothetical protein         1         0.365         265_780         hypothetical protein         1         0.393         393         2945_80         1         0.401 <td< td=""><td>1 - 1 - 1</td><td>The state of the s</td><td></td><td></td><td></td><td></td><td>- 1</td><td></td><td></td></td<>	1 - 1 - 1	The state of the s					- 1		
cgd5_80         hypothetical protein         1         0.333           cgd5_80         hypothetical protein         1         1         0.401           cgd5_810         leucine-rich repeat protein         1         1         1.55.23           cgd5_810         leucine-rich repeat protein         1         1         1.58.93           cgd5_80         PPZC like phosphatase         1         1         1.87.97           cgd5_80         hypothetical protein         1         1         1.87.97           cgd5_80         virRVirH family protein         1         1         1.37.4           cgd5_90         hypothetical protein         1         1         1.37.4           cgd5_90         Ox7 plike TLDc domain containing protein         1         1         2.157           cgd5_90         Ox7 plike TLDc domain containing protein         1         1         3.565           cgd5_91         Ox7 plike TLDc domain containing protein         1         1         5.5521           cgd5_91         Ox7 plike TLDc domain containing protein         1         1         5.5521           cgd5_100         leucine rich repeat (LRR) protein         1         1         5.5521           cgd6_101         hypothetical protein with sign	1								
Cgd5_80		1 **							
cgd5_800         hypothetical protein         1         1         1         25.232           cgd5_801         leucine-rich repeat protein         1         1         1,859         cgd5_800         1         0.589           cgd5_800         hypothetical protein         1         1         1,377         0.073         cgd5_800         1         1,8797         0.073         cgd5_90         1         1         1,334         0.073         1         1,394         1         1,394         0.073         1         1,394         1         1,394         0.073         1         1,394 <td> </td> <td>1</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>		1							
Equipment   Equi		1 21	1						
Cgd5_840	" -	1				1			
cgd5_860   hypothetical protein   1   1   1   3.737	cgd5_810	leucine-rich repeat protein		1					
cgd5_880	cgd5_840	PP2C like phosphatase							0.589
cgd5_880         VirRV/Irl family protein         1         1         1         1,344         1,394	cgd5_860	hypothetical protein	1					1	0.377
Cgd5   90	cgd5_870	hypothetical protein				1		1	8.797
Cgd5_90	cgd5_880	VirR/VirH family protein		1				1	1.394
cgd5_910         protein with conserved domain that is fused in vertebrates to neuralized domain repeats         1         1         0.523           cgd5_980         Cyd7 [pi like TLDc domain containing protein         1         1         1         3.565           cgd6_100         hypothetical protein with signal peptide and cysteine rich region at the C-terminus         1         1         5.25.219           cgd6_100         hypothetical protein with signal peptide         1         1         1         3.401           cgd6_1030         hypothetical protein with signal peptide         1         1         1.861         1         1         1.861           cgd6_1130         hypothetical protein with signal peptide         1         1         1.0336         1         1.0473         3.361         1         1.967         1.962         1         1.967         1.962         1         1.967         1.962         1         1.962         1.962         1         1.962         1.962         1         1.962         1.962         1         1.962         1.962         1         1.962         1.962         1         1.962         1.962         1         1.962         1.962         1         1.962         1         1.962         1         1.962         1 <t< td=""><td>cgd5_890</td><td>hypothetical protein</td><td>1</td><td></td><td></td><td></td><td></td><td>1</td><td>0.374</td></t<>	cgd5_890	hypothetical protein	1					1	0.374
Capd5_980   Cxr1p like TLDc domain containing protein   1   1   3.565	cgd5_90	hypothetical protein		1				1	2.157
cgd5_960	cgd5 910	protein with conserved domain that is fused in vertebrates to	1					1	0.523
1	-	neuralized domain repeats							
Cgd6_10	cgd5_960	Oxr1p like TLDc domain containing protein			1			1	3.565
at the C-terminus	cgd5_990	hypothetical protein		1				1	1.669
cgd6_100         leucine rich repeat (LRR) protein         1         1         52.251           cgd6_1000         hypothetical protein with signal peptide         1         1         3.401           cgd6_1060         protein with spectrin repeats, CG12008-like         1         1         0.473           cgd6_1170         signal peptide-containing protein         1         1         0.336           cgd6_1130         hypothetical protein with signal peptide         1         1         1.945           cgd6_1160         hypothetical protein         1         1         1.945           cgd6_1160         hypothetical protein         1         1         1.945           cgd6_1210         hypothetical protein         1         1         0.289           cgd6_1210         hypothetical protein         1         1         0.289           cgd6_1220         hypothetical protein         1         1         0.313           cgd6_1220         hypothetical protein         1         1         0.322           cgd6_1250         hypothetical protein         1         0.341         0.341           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1330 <td< td=""><td>cgd6_10</td><td>hypothetical protein with signal peptide and cysteine rich region</td><td></td><td></td><td></td><td></td><td>1</td><td>1</td><td>525.219</td></td<>	cgd6_10	hypothetical protein with signal peptide and cysteine rich region					1	1	525.219
Cgd6_1000         hypothetical protein with signal peptide         1         1         3.401           cgd6_1030         hypothetical protein with signal peptide         1         1         1.861           cgd6_1100         signal peptide-containing protein         1         0.473           cgd6_1110         signal peptide-containing protein         1         0.336           cgd6_1130         hypothetical protein with signal peptide         1         1         0.369           cgd6_1140         hypothetical protein         1         1         1         1.945           cgd6_1150         hypothetical protein         1         1         1         0.289           cgd6_1180         large protein with signal peptide         1         1         0.289           cgd6_1210         hypothetical protein         1         1         0.426           cgd6_1220         hypothetical protein         1         1         0.322           cgd6_1220         hypothetical protein         1         1         0.322           cgd6_1260         hypothetical protein with one or more transmembrane domain         1         1         0.432           cgd6_1260         hypothetical protein with one or more transmembrane domain         1         1         0.431		at the C-terminus							
cgd6_1030         hypothetical protein with signal peptide         1         1         1.861           cgd6_1060         protein with spectrin repeats, CG12008-like         1         1         0.473           cgd6_1110         signal peptide-containing protein         1         1         0.336           cgd6_1130         hypothetical protein with signal peptide         1         1         1.945           cgd6_1140         hypothetical protein         1         1         1         1.945           cgd6_1150         hypothetical protein         1         1         1         1.945           cgd6_1180         large protein with signal peptide         1         1         0.289           cgd6_1210         hypothetical protein         1         1         0.426           cgd6_1220         hypothetical protein         1         1         0.328           cgd6_1220         hypothetical protein         1         1         0.322           cgd6_1250         hypothetical protein with one or more transmembrane domain         1         1         0.322           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         1         0.326           cgd6_1330         SCCH domain containing protein         1 <td>cgd6_100</td> <td>leucine rich repeat (LRR) protein</td> <td></td> <td></td> <td></td> <td></td> <td>1</td> <td></td> <td></td>	cgd6_100	leucine rich repeat (LRR) protein					1		
cgd6_1060         protein with spectrin repeals, CG12008-like         1         0.473           cgd6_1110         signal peptide-containing protein         1         0.336           cgd6_1130         hypothetical protein with signal peptide         1         1         1.945           cgd6_1150         hypothetical protein         1         1         1.945           cgd6_1150         hypothetical protein         1         1         1.945           cgd6_1180         large protein with signal peptide         1         1         0.289           cgd6_1210         hypothetical protein         1         1         3.288           cgd6_1220         hypothetical protein         1         1         0.426           cgd6_1220         hypothetical protein         1         1         0.313           cgd6_1220         hypothetical protein         1         1         0.328           cgd6_1230         hypothetical protein with one or more transmembrane domain         1         1         0.345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         1         0.431           cgd6_1300         3CCCH domain containing protein         1         1         1         0.447           c	cgd6_1000	hypothetical protein with signal peptide			1			1	3.401
cgd6_1110         signal peptide-containing protein         1         0.336           cgd6_1130         hypothetical protein with signal peptide         1         1         0.369           cgd6_1140         hypothetical protein         1         1         1,945         1         1,942         1         1,942         1         1,942         1         1,942         1         1,942         1         1,942         1         1,942         1         1,942         1         1,942         <	cgd6_1030	hypothetical protein with signal peptide		1				1	1.861
cgd6_1130         hypothetical protein with signal peptide         1         0.369           cgd6_1140         hypothetical protein         1         1         1.945           cgd6_1160         hypothetical protein         1         1         1.915           cgd6_1180         large protein with signal peptide         1         1         0.289           cgd6_1180         large protein with signal peptide         1         1         0.426           cgd6_1210         hypothetical protein         1         1         0.426           cgd6_1220         hypothetical protein         1         1         0.313           cgd6_1240         hypothetical protein         1         1         0.341           cgd6_1250         hypothetical protein         1         1         0.322           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         1         0.431           cgd6_1280         cgd6_1330         3CCCH domain containing protein         1         1         0.431           cgd6_1400         hypothetical protein         1         1         0.543           cgd6_1470         hypothetical protein         1         1         1         0.447           cgd6_1500	cgd6_1060	protein with spectrin repeats, CG12008-like	1						0.473
cgd6_1140         hypothetical protein         1         1         1,945           cgd6_1150         hypothetical protein         1         1         9,157           cgd6_1180         large protein with signal peptide         1         0,289           cgd6_1210         hypothetical protein         1         1         3,288           cgd6_1220         hypothetical protein         1         1         3,288           cgd6_1220         hypothetical protein         1         1         0,313           cgd6_1240         hypothetical protein         1         1         0,313           cgd6_1250         hypothetical protein         1         1         0,345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0,345           cgd6_1280         ropothetical protein with one or more transmembrane domain         1         0,345           cgd6_1280         rocCH domain containing protein         1         0,343           cgd6_1330         CCCH domain containing protein         1         0,447           cgd6_1400         Sec14 domain containing protein         1         0,447           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane         1         1	cgd6_1110	signal peptide-containing protein	1					1	0.336
cgd6_1150         hypothetical protein         1         1         9.157           cgd6_1160         hypothetical protein         1         0.289           cgd6_1180         large protein with signal peptide         1         0.426           cgd6_1210         hypothetical protein         1         1         0.426           cgd6_1220         hypothetical protein         1         1         0.313           cgd6_1240         hypothetical protein         1         0.442           cgd6_1250         hypothetical protein         1         0.322           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.431           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.322           cgd6_1330         3CCCH domain containing protein         1         0.543           cgd6_1400         bect-14 domain containing protein         1         1         0.447           cgd6_1540         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain	cgd6_1130	hypothetical protein with signal peptide	1					1	0.369
cgd6_1160         nypothetical protein         1         0.289           cgd6_1180         large protein with signal peptide         1         0.426           cgd6_1210         hypothetical protein         1         1         0.426           cgd6_1220         hypothetical protein         1         0.313         0.313           cgd6_1240         hypothetical protein         1         0.442         0.322         0.362         0.362         0.322         0.366         0.362         0.322         0.366         1         0.345         0.322         0.366         1         0.345 <td>cgd6_1140</td> <td>hypothetical protein</td> <td></td> <td>1</td> <td></td> <td></td> <td></td> <td>1</td> <td>1.945</td>	cgd6_1140	hypothetical protein		1				1	1.945
cgd6_1180         large protein with signal peptide         1         0.426           cgd6_1210         hypothetical protein         1         1         3.288           cgd6_1220         hypothetical protein         1         0.313         1         0.342           cgd6_1240         hypothetical protein         1         1         0.342         1         0.322           cgd6_1250         hypothetical protein with one or more transmembrane domain         1         1         0.325           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         1         0.431           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         1         0.431           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         1         0.431           cgd6_1330         3CCCH domain containing protein         1         1         0.543           cgd6_1400         hypothetical protein         1         1         0.447           cgd6_1470         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1 <td>cgd6_1150</td> <td>hypothetical protein</td> <td></td> <td></td> <td></td> <td>1</td> <td></td> <td>1</td> <td>9.157</td>	cgd6_1150	hypothetical protein				1		1	9.157
cgd6_1210         hypothetical protein         1         1         3.288           cgd6_1220         hypothetical protein         1         0.313           cgd6_1240         hypothetical protein         1         0.442           cgd6_1250         hypothetical protein         1         0.322           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.431           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1330         3CCCH domain containing protein         1         0.543           cgd6_1400         hypothetical protein         1         0.447           cgd6_1400         hypothetical protein         1         1         0.447           cgd6_1400         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         1         1         0.379           cgd6_1500         ryu2p / cwf16-like; Zn finger         1         1         1 <td>cgd6_1160</td> <td>hypothetical protein</td> <td>1</td> <td></td> <td></td> <td></td> <td></td> <td>1</td> <td>0.289</td>	cgd6_1160	hypothetical protein	1					1	0.289
cgd6_1210         hypothetical protein         1         1         3.288           cgd6_1220         hypothetical protein         1         0.313           cgd6_1240         hypothetical protein         1         0.442           cgd6_1250         hypothetical protein         1         0.322           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.431           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1330         3CCCH domain containing protein         1         0.543           cgd6_1400         hypothetical protein         1         0.447           cgd6_1400         hypothetical protein         1         1         0.447           cgd6_1400         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         1         1         0.379           cgd6_1500         ryu2p / cwf16-like; Zn finger         1         1         1 <td> </td> <td>1 **</td> <td>1</td> <td></td> <td></td> <td></td> <td></td> <td>1</td> <td>0.426</td>		1 **	1					1	0.426
cgd6_1220         hypothetical protein         1         0.313           cgd6_1240         hypothetical protein         1         0.442           cgd6_1250         hypothetical protein         1         0.442           cgd6_1260         hypothetical protein         1         0.322           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1280         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_12700         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1400         hypothetical protein         1         1         0.447           cgd6_1400         Sec14 domain containing protein         1         1         1         0.447           cgd6_1470         postein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         1         0.961				1	1				
cgd6_1240         hypothetical protein         1         0.442           cgd6_1250         hypothetical protein         1         0.322           cgd6_1260         hypothetical protein         1         0.345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.431           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         1         0.431           cgd6_1330         3CCCH domain containing protein         1         1         0.543           cgd6_1400         hypothetical protein         1         0.447           cgd6_1460         Sec14 domain containing protein         1         1         0.447           cgd6_1460         Sec14 domain containing protein         1         1         1         6.961           cgd6_1470         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         1         3.545           cgd6_1540         possible histone mRNA hairpin-binding protein <td> </td> <td>1 21</td> <td>1</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>		1 21	1						
cgd6_1250         hypothetical protein         1         0.322           cgd6_1260         hypothetical protein         1         0.345           cgd6_1280         hypothetical protein with one or more transmembrane domain         1         0.345           cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1330         3CCCH domain containing protein         1         1         0.543           cgd6_1400         hypothetical protein         1         1         0.447           cgd6_1460         Sec14 domain containing protein         1         1         1         1.626           cgd6_1470         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         3.545           cgd6_1540         possible histone mRNA hairpin-binding protein         1         1         0.379           cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         1.504           cgd6_1610         hypothetical protein         1         1         0.345           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plu		1 **							
cgd6_1260		1 21							
cgd6_1280		1 ***							
cgd6_1290         ring finger, membrane associated, possible signal peptide         1         0.326           cgd6_1330         3CCCH domain containing protein         1         0.543           cgd6_1400         hypothetical protein         1         0.447           cgd6_1460         Sec14 domain containing protein         1         1         1.626           cgd6_1470         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         3.545           cgd6_1540         possible histone mRNA hairpin-binding protein         1         1         0.379           cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         0.345           cgd6_1600         hypothetical protein         1         1         0.345           cgd6_1610         hypothetical protein         1         1         0.326           cgd6_1700         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1710         Mcm10p-like; Mcm10p-like*         1         1         1         0.508           cgd6_1740         Tra1p-like		1 **							
cgd6_1330         3CCCH domain containing protein         1         0.543           cgd6_1400         hypothetical protein         1         0.447           cgd6_1460         Sec14 domain containing protein         1         1         1.626           cgd6_1470         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         0.374           cgd6_1540         possible histone mRNA hairpin-binding protein         1         1         0.379           cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         0.345           cgd6_1600         hypothetical protein         1         1         0.345           cgd6_1610         hypothetical protein         1         1         0.326           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         1         2.541           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         2.182		1 * '							
cgd6_1400         hypothetical protein         1         0.447           cgd6_1460         Sec14 domain containing protein         1         1         1         1.626           cgd6_1470         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         3.545           cgd6_1540         possible histone mRNA hairpin-binding protein         1         1         0.379           cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         1.504           cgd6_1600         hypothetical protein         1         1         0.345           cgd6_1610         hypothetical protein         1         1         3.332           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         1         2.541           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         2.182           cgd6_17700         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus									
Cgd6_1460		0,							
cgd6_1470         protein with SET domain flanked by cysteine clusters plus a C-terminal PHD domain         1         1         6.961           cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         3.545           cgd6_1540         possible histone mRNA hairpin-binding protein         1         1         0.379           cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         1.504           cgd6_1600         hypothetical protein         1         1         0.345           cgd6_1610         hypothetical protein         1         1         3.332           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         1         2.541           cgd6_1710         Mcm10p-like; Mcm10p-like'         1         1         1         2.541           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         0.417           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         0.417		1 21	7	ار ا					
terminal PHD domain cgd6_1500 cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown) cgd6_1540 possible histone mRNA hairpin-binding protein cgd6_1560 Yju2p / cwf16-like; Zn finger cgd6_1600 hypothetical protein cgd6_1610 hypothetical protein cgd6_1610 MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS cgd6_1700 RRM domain containing protein cgd6_1710 Mcm10p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein cgd6_1770 protein with C2H2 Zn finger, ASR2B-like N- and C-terminus  1		9.		1					
cgd6_1500         cytoachrome c oxidase subunit III with 6 transmembrane domains (Note: unknown)         1         1         3.545           cgd6_1540         possible histone mRNA hairpin-binding protein         1         1         0.379           cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         1.504           cgd6_1600         hypothetical protein         1         1         0.345           cgd6_1610         hypothetical protein         1         1         1         3.332           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         2.541           cgd6_1710         Mcm10p-like'Mcm10p-like'         1         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         1         0.417           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417	сда6_1470					1		1	6.961
domains (Note: unknown)   cgd6_1540   possible histone mRNA hairpin-binding protein   1   1   0.379   cgd6_1560   Yju2p / cwf16-like; Zn finger   1   1   1   1.504   cgd6_1600   hypothetical protein   1   1   0.345   cgd6_1610   hypothetical protein   1   1   3.332   cgd6_1670   MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG   1   1   0.326   family plus RNA binding domain TGS   cgd6_1700   RRM domain containing protein   1   1   2.541   cgd6_1710   Mcm10p-like'Mcm10p-like'   1   1   0.508   cgd6_1740   Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein   cgd6_1770   protein with C2H2 Zn finger, ASR2B-like N- and C-terminus   1   1   0.417   1   0.417	cad6 1500				4			4	2 545
cgd6_1540         possible histone mRNA hairpin-binding protein         1         0.379           cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         1.504           cgd6_1600         hypothetical protein         1         1         0.345           cgd6_1610         hypothetical protein         1         1         3.332           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         2.541           cgd6_1710         Mcm10p-like Mcm10p-like'         1         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         2.182           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417	Cyuo_1500				- '			'	3.545
cgd6_1560         Yju2p / cwf16-like; Zn finger         1         1         1.504           cgd6_1600         hypothetical protein         1         1         0.345           cgd6_1610         hypothetical protein         1         1         1         3.332           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         1         2.541           cgd6_1710         Mcm10p-like'Mcm10p-like'         1         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         1         2.182           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417	cad6 1540		1					1	0.379
cgd6_1600         hypothetical protein         1         0.345           cgd6_1610         hypothetical protein         1         1         3.332           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         1         2.541           cgd6_1710         Mcm10p-like'Mcm10p-like'         1         1         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         2.182           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417		, , ,		1					
cgd6_1610         hypothetical protein         1         3.332           cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         1         0.326           cgd6_1700         RRM domain containing protein         1         1         2.541           cgd6_1710         Mcm10p-like'Mcm10p-like'         1         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         1         2.182           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417			1	'					
cgd6_1670         MJ1332/Ygr210cp-like GTP binding protein; GTpase OBG family plus RNA binding domain TGS         1         0.326           cgd6_1700         RRM domain containing protein         1         1         2.541           cgd6_1710         Mcm10p-like'Mcm10p-like'         1         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         2.182           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417		1 **	,		4				
family plus RNA binding domain TGS   cgd6_1700   RRM domain containing protein   1   1   2.541   cgd6_1710   Mcm10p-like' Mcm10p-like'   1   1   0.508   cgd6_1740   Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein   cgd6_1770   protein with C2H2 Zn finger, ASR2B-like N- and C-terminus   1   1   0.417		1 21	- 1		'				
cgd6_1700         RRM domain containing protein         1         1         2.541           cgd6_1710         Mcm10p-like'Mcm10p-like'         1         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         2.182           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417	Cguo_16/0							'	0.326
cgd6_1710         Mcm10p-like'Mcm10p-like'         1         0.508           cgd6_1740         Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein         1         1         2.182           cgd6_1770         protein with C2H2 Zn finger, ASR2B-like N- and C-terminus         1         1         0.417	cad6 1700				1			1	2 541
cgd6_1740 Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein cgd6_1770 protein with C2H2 Zn finger, ASR2B-like N- and C-terminus 1 1 0.417		9,	1		- '				
kinase domain; very large protein cgd6_1770 protein with C2H2 Zn finger, ASR2B-like N- and C-terminus 1 0.417				1	- 1				0.000
cgd6_1770 protein with C2H2 Zn finger, ASR2B-like N- and C-terminus 1 0.417	cgd6_1710	l ·		- 1	- !	- 1		11	2 182
	cgd6_1710	Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-		1				1	2.182
	cgd6_1710 cgd6_1740	Tra1p-like; C-terminal FAT domain plus phoshoinositide 3-kinase domain; very large protein	1	1					

cogd. 1,870         cggd. 1,870         CGG06, 1,880         CGG0286/Bcpt pBRCA and CDKN41-interacting protein isoform         1         1         2.328           cggb. 1,880         CGG0286/Bcpt pBRCA and CDKN41-interacting protein isoform         1         1         1         2.328           cggb. 1,980         Phyphothecial protein client inchromorphy proteins in common the common street in comm	cgd6 180	hypothetical protein	1		ı	1	ı	1	0.533
1	cgd6_1810	hypothetical protein	1					1	0.431
Calika   Cagill   1900   Injury probetical predicted protein, unknown function   1	cgd6_1870	signal recognition particle SPR19			1			1	2.326
1   1   1   1   1   1   1   1   1   1	cgd6_1880						1	1	28.430
cgd8_10         Mypothetical protein         1         0.418           cgd8_10         130         1         0.368           cgd8_10         140         1         0.368           cgd8_100         1,000         1         1         0.340           cgd8_2010         120         1         1         1.515           cgd8_2010         120         1         1         1.326           cgd8_2200         120         1         1         1.326           cgd8_2220         120         1         1         1.326           cgd8_2220         120         1         1.426         1.326           cgd8_2220         120         1         1.426         1.436           cgd8_2210         120         1.436         1.436         1.436           cgd8_2220         120         1.436         1.436         1.438           cgd8_2230         120         1.436         1.438         1.388           cgd8_2270         120         1.436         1.438         1.388           cgd8_2270         120         1.438         1.438         1.438           cgd8_2330         120         1.438         1.438         1.438<	cad6 1890					4		1	10.542
1		1 **	1			'			
cgd6_1980         hypotheteal protein with a signal peptide         1         2         148         0         <	1	1 21							0.366
cgdb 1980         hypothetecla protein with a signal peptide         1         1         1.1.5.15           cgdb 2910         19C         cydb 2910         15C         domain containing protein         1         1         1.3.52           cgdb 2200         cgdb 2240         protein with N-terminal apicomplexan-specific globular domain protein         1         1         2.44         1         1.55         1         1.45         1         1.55         1         1.45         1         1.55         <	1	•							0.340
cgdb 2190         Text Commain containing protein         1         1         1         1.352           cgdb 2200         leucine-rich repeats protein         1         1         2.48         2.48           cgdb 2240         leucine-rich repeats protein         1         1.552         1.555         2.68         2.27         1         1.555         2.68         2.27         1         1.552         1.555         1.555         2.68         2.27         1         1.552         1.555	1	1 2.		1					1.510
cgdg 2240         gucine-the repeats protein         1         1         2,148         1         1,248         1         1,248         1         1,248         1         1,248         1         1,248         1         1,248         1,248         1         1,248         1         1,248         1,248         1         1,248         1,248         1         1,248 <td< td=""><td>1</td><td>1</td><td></td><td>1</td><td></td><td></td><td></td><td>1</td><td>1.352</td></td<>	1	1		1				1	1.352
cgd6 2240   potein with N-terminal apicomplexan-specific globular domain my proto-oncogene protein, putative global protein my proto-oncogene protein my proto-oncogene protein my protein my proto-oncogene protein my protein my proto-oncogene protein my my protein my	cgd6_2190	TBC domain containing protein	1					1	0.384
puls PHD domain	cgd6_2200	leucine-rich repeats protein		1				1	2.148
cgd6_2250         myb proto-oncogene protein, putative         1         1         0.418         1.0387           cgd6_2230         cgd6_2310         1         1         1         1.0387           cgd6_2330         cgd6_2370         cgd7_2370         cgd7_2370<	cgd6_2240			1				1	1.555
1   1   1   1   1   1   1   1   1   1	and6 2250	1'	1						0.410
December   Transmembrane domains   December   Decembe	-		- 1			4			
	cguo_zzro	1 **				'		'	10.507
cgd6 2330 cgd6 2370 cgd6 2400 cgd6 2400 cgd6 2400 cgd6 2400 cgd6 2400 cgd6 2400 cgd6 2400 cgd6 2400 cgd6 2500 cgd6 2400 cgd6 2500 cgd6 2400 cgd6 2500 cgd6 2400 cgd6 2500 cgd	cgd6_2320		1					1	0.331
cgd6 2370         Sect-1-family protein         1         0.288           cgd6 2410         ogd6 2410         hypothetical protein         1         0.502           cgd6 250         hypothetical protein with possible signal peptide         1         0.348           cgd6 2500         hypothetical protein with possible signal peptide         1         1.2.053           cgd6 2500         hypothetical protein of low complexity         1         1.2.053           cgd6 2600         hypothetical protein of low complexity         1         1.7.96           cgd6 2601         hypothetical protein         1         1.2.053           cgd6 2602         cgd6 2600         hypothetical protein         1         1.2.053           cgd6 2601         hypothetical protein         1         1.2.053           cgd6 2702         cgd6 2700         1         1.2.028           cgd6 2701         hypothetical protein         1         1.2.238           cgd6 2702         hypothetical protein         1         1.2.38           cgd6 2700         hypothetical protein         1         1.2.38           cgd6 2700         hypothetical protein         1         1.2.461           cgd6 2801         hypothetical protein with signal peptide and transmembrane									
cgd6 2400         Nypothetical protein         1         0.502           cgd6 2510         possible CuA1 divialent ion tolerance protein         1         0.376           cgd6 250         hypothetical protein with possible signal peptide         1         1         0.376           cgd6 2520         hypothetical protein with possible signal peptide         1         1         1.2706           cgd6 2570         MORN domain repeat containing protein         1         1         1.2706           cgd6 2630         population of the complexity         1         1.799           cgd6 2630         population of the complexity protein of low complexity         1         1.799           cgd6 270         population of the complexity protein of low complexity         1         1.799           cgd6 2800         population of the complexity protein of low complexity         1         1.379           cgd6 2870         population of low complexity protein of low complexity         1         1.322           cgd6 2800         population of low complexity protein of low complexity         1         1.322           cgd6 2710         low complexity protein possible apicomplexan conserved         1         1.322           cgd6 2720         low complexity protein possible apicomplexan conserved         1         1.322	-	1 1 1				1			
agdf 2410         cgd8 250         hypothetical protein         1         0.378           agd 2620         hypothetical protein in hypothetical protein hypothetical protein hypothetical protein in hypothetical protein of low complexity         1         1         0.248           agd 2630         hypothetical protein of low complexity         1         1.270         2.035           agd 2630         hypothetical protein of low complexity         1         1.379         1.379           agd 2630         hypothetical protein         1         1.208         1.372         1.372           agd 2630         hypothetical protein         1         1.208         1.372 <t< td=""><td>1</td><td>1</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>	1	1							
cgd6_250         hypothetical protein with possible signal peptide         1         1         1         1         3.413         2.065         2570         hypothetical protein with possible signal peptide         1         1         1         1.2706         2.065         2570         MORN domain repeat containing protein         1         1         1.2706         2.065         2600         2600         2600         MORN domain repeat containing protein         1         1         1.2056         2.065         2600		1 2.							
cgd6_2500         hypothetical protein with possible signal peptide         1         2         0.05         2         0.05	-	i,							
cgd6_2530         Nypothelical protein         1         1         1         1         1         1         1         2.053           cgd6_2800         Nypothelical protein of low complexity         1         1         3.7215         2.053           cgd6_2800         Nypothelical protein of low complexity         1         1         3.7215         3.7215           cgd6_2800         Nypothelical protein         1         1         0.520         3.7215 <td>1</td> <td>1 2.</td> <td>'</td> <td></td> <td>1</td> <td></td> <td></td> <td></td> <td></td>	1	1 2.	'		1				
cgd6_2570         MORN domain repeat containing protein         1         1         2.055           cgd6_2580         hypothetical protein of low complexity         1         1         1.759           cgd6_2630         hypothetical protein         1         1         0.520           cgd6_2630         hypothetical protein         1         0.520           cgd6_2700         cgd6_2710         hypothetical protein         1         0.282           cgd6_2710         hypothetical protein         1         0.211         1         0.411           cgd6_2710         hypothetical protein possible apicomplexan conserved         1         1         1.138         1         1.248           cgd6_2710         hypothetical protein having a signal peptide and transmembrane domain within C- terminus         1         1         1.244         1         1.448         1         1.244         1         1.444         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.244         1         1.		1			'	1			
1	1	1 2.		1					
Cgd6_2800	-	, , , , , , , , , , , , , , , , , , , ,		1 1					1.795
cgd6_2830	1	1 **					1		337.215
cgd6_270	1	1 2.	1					1	0.520
cgd6_2700	cgd6_2670	hypothetical protein	1					1	0.282
Cgd6_2700	cgd6_2680	hypothetical protein	1					1	0.411
cgd6_2710         hypothetical protein having a signal peptide and transmembrane domain within C- terminus         1         1         2.136           cgd6_2720         hypothetical protein having a signal peptide and transmembrane domain within C- terminus         1         1         1         124.481           cgd6_2800         cgdf-2810         hypothetical protein         1         1         0.350           cgd6_2820         cgdf-181         hypothetical protein         1         1         0.397           cgd6_2820         hypothetical protein         1         1         0.397           cgd6_2820         hypothetical protein         1         1         0.431           cgd6_2820         hypothetical protein         1         1         1.791           cgd6_2890         hypothetical protein with signal peptide         1         1         0.418           cgd6_2920         hypothetical protein with signal peptide         1         1         0.398           cgd6_2920         hypothetical protein with signal peptide         1         1         1.291           cgd6_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein protein with conserved cysteines as in riboflavin-binding protein protein with conserved cysteines as in riboflavin-binding protein protein with conserved cysteines as in riboflavin-binding protein	cgd6_270	hypothetical protein		1				1	1.398
cgd6_2720         hypothetical protein having a signal peptide and transmembrane dodd.         1         1         124.461           cgd6_280         hypothetical protein hypothetical protein putative         1         0.356           cgd6_2810         hypothetical protein putative         1         1         0.356           cgd6_2850         hypothetical protein         1         1         0.236           cgd6_2860         cgd6_2870         hypothetical protein         1         1         0.431           cgd6_2880         hypothetical protein         1         1         1         1.418           cgd6_2890         hypothetical protein with signal peptide         1         1         1         1.791           cgd6_2990         hypothetical protein with signal peptide         1         1         0.337           cgd6_2990         hypothetical protein with signal peptide         1         1         1.291           cgd6_2990         hypothetical protein with signal peptide with 6 or more transmembrane domains         1         1         3.965           cgd6_2990         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         1         5.870           cgd6_300         hypothet	cgd6_2700	Low complexity protein, possible apicomplexan conserved		1					1.848
domain within C- terminus   1	1	1 2.		1					2.136
cgd6_2760         hypothetical protein         1         1         4.0847           cgd6_2800         124f1.1 protein, putative         1         1         0.350           cgd6_2810         124f1.1 protein, putative         1         1         2.238           cgd6_2850         hypothetical protein         1         1         0.350           cgd6_2860         hypothetical protein         1         1         0.431           cgd6_2880         hypothetical protein         1         1         1.418           cgd6_2880         hypothetical protein         1         1         1.791           cgd6_2890         hypothetical protein with signal peptide         1         1         0.418           cgd6_2920         hypothetical protein with signal peptide         1         1         1.291           cgd6_2950         gd6_2950         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         1.291           cgd6_2990         hypothetical protein         1         1         0.426           cgd6_3030         protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         0.426	cgd6_2720						1	1	124.461
cgd6_280         hypothetical protein         1         0.350           cgd6_2810         t24f1.1 protein, putative         1         1         0.397           cgd6_2850         hypothetical protein         1         1         0.397           cgd6_2860         hypothetical protein         1         1         0.431           cgd6_2880         hypothetical protein         1         1         1.418           cgd6_2880         hypothetical protein         1         1         1.791           cgd6_2890         hypothetical protein         1         1         1.791           cgd6_2910         hypothetical protein with signal peptide         1         1         0.418           cgd6_2920         hypothetical protein with signal peptide         1         1         0.378           cgd6_2920         hypothetical protein with signal peptide         1         1         1.291           cgd6_2920         cgd6_2960         Bax inhibitor-1 (BI-1) integral membrane protien with 6 or more transmembrane domains         1         1         1.299           cgd6_2980         cgd6_3080         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible CPI archor         1         1         5.870	cad6 2760						1	1	40 847
cgd6_2800         t24f1.1 protein, putative         1         1         0.397           cgd6_2810         hypothetical protein         1         1         2.238           cgd6_28260         hypothetical protein         1         1         0.435           cgd6_28260         uncharacterized coiled coil protein         1         1         1.418           cgd6_28260         hypothetical protein         1         1         1.148           cgd6_28290         hypothetical protein         1         1         1.179           cgd6_2910         hypothetical protein with signal peptide         1         1         0.418           cgd6_2920         cgd6_2950         large low complexity with PFL0380c_pfal like Znfinger         1         1         1.291           cgd6_2960         large low complexity with PFL0380c_pfal like Znfinger         1         1         1.291           cgd6_2980         large low complexity with PFL0380c_pfal like Znfinger         1         1         1         1.291           cgd6_2980         large low complexity with PFL0380c_pfal like Znfinger         1         1         1         1.291           cgd6_3030         cgd6_3030         cgd6_3030         large low complexity with Protein with conserved cysteines as in riboflavin-binding protein protein protei	1	1	1				•		
cgd6_2810         hypothetical protein         1         2.238           cgd6_2850         cgd6_2860         hypothetical protein         1         0.431           cgd6_2870         hypothetical protein         1         1         0.453           cgd6_2880         hypothetical protein         1         1         1.791           cgd6_2890         hypothetical protein         1         1         1.791           cgd6_2910         hypothetical protein with signal peptide         1         1         0.378           cgd6_2950         large low complexity with PFL0360c_pfal like Znfinger         1         1         1         3.965           cgd6_2960         large low complexity with PFL0360c_pfal like Znfinger         1         1         1         3.965           cgd6_2980         large low complexity with PFL0360c_pfal like Znfinger         1         1         1         1         3.965           cgd6_2980         large low complexity with Order transmembrane domains         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         1         5.870           cgd6_3030         cgd6_3030         protein with C-terminal RCC1 domain         1         1         1         0.426	1	1 2.							
cgd6_2850         hypothetical protein         1         0.433           cgd6_2860         cgd6_2870         thypothetical protein         1         1         1.418         0.556           cgd6_2880         hypothetical protein         1         1         1.418         1.791           cgd6_2890         hypothetical protein with signal peptide         1         1         0.418         1         0.248           cgd6_2910         hypothetical protein with signal peptide         1         1         0.378         1         0.281           cgd6_2920         large low complexity with PFL0360c_pfal like Znfinger         1         1         0.390         1         1.291         1         1         0.390         1         1.291         1         1.31.965         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.291         1         1.292         1         1.292         1				1				1	2.239
cgd6_2870         hypothetical protein         1         1.418           cgd6_2880         hypothetical protein         1         1.791           cgd6_2890         hypothetical protein         1         1         0.418           cgd6_2910         hypothetical protein with signal peptide         1         1         0.281           cgd6_2920         hypothetical protein with signal peptide         1         1         0.390           cgd6_2950         Bax inhibitor-1 (BI-1). integral membrane protien with 6 or more transmembrane domains         1         1         1         31.965           cgd6_2960         Bax inhibitor-1 (BI-1). integral membrane protien with 6 or more transmembrane domains         1         1         1         31.965           cgd6_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         1         5.870           cgd6_2990         hypothetical protein         1         1         0.426         1         1         0.426         1         1         0.426         1         1         0.505         1         1         1         0.505         1         1         0.506         1         1         0.426         1         0.426	1	hypothetical protein	1					1	0.431
1	cgd6_2860	uncharacterized coiled coil protein	1					1	0.556
cg66_2880         hypothetical protein         1         0.419           cg66_2910         hypothetical protein with signal peptide         1         0.281           cg66_2920         hypothetical protein with signal peptide         1         0.378           cg66_2950         large low complexity with PFL0360c_pfal like Znfinger         1         1         1.291           cg66_2960         Bax inhibitor-1 (Bl-1). integral membrane protien with 6 or more transmembrane domains         1         1         31.965           cg66_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         5.870           cg66_2990         hypothetical protein         1         1         0.426           cg66_3030         hypothetical protein         1         1         0.426           cg66_3030         hypothetical protein         1         1         0.426           cg66_3030         hypothetical protein with a signal peptide         1         1         1         0.456           cg66_3050         hypothetical protein with a signal peptide         1         1         1         1.768           cg66_3070         hypothetical protein with a signal peptide         1         1         1	cgd6_2870	hypothetical protein		1				1	1.418
cgd6_290         hypothetical protein lypothetical protein with signal peptide         1         1         0.281           cgd6_2920         hypothetical protein with signal peptide         1         1         0.378           cgd6_2950         large low complexity with PFL0360c_pfal like Znfinger         1         1         1.291           cgd6_2960         Bax inhibitor-1 (BI-1). integral membrane protien with 6 or more transmembrane domains         1         1         31.965           cgd6_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         1         5.870           cgd6_2990         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         0.426           cgd6_300         hypothetical protein         1         1         0.426           cgd6_300         hypothetical protein         1         1         0.459           cgd6_3030         protein with C-terminal RCC1 domain         1         1         0.459           cgd6_3040         hypothetical protein with a signal peptide         1         1         1.768           cgd6_3050         hypothetical protein with a signal peptide         1         1 <td>cgd6_2880</td> <td>hypothetical protein</td> <td></td> <td>1</td> <td></td> <td></td> <td></td> <td>1</td> <td>1.791</td>	cgd6_2880	hypothetical protein		1				1	1.791
cgd6_2910         hypothetical protein with signal peptide         1         0.378           cgd6_2920         hypothetical protein with signal peptide         1         0.390           cgd6_2960         large low complexity with PFL0360c_pfal like Znfinger         1         1         1.291           cgd6_2980         Bax inhibitor-1 (BI-1). Integral membrane protien with 6 or more transmembrane domains hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor hypothetical protein         1         1         1         5.870           cgd6_2990         hypothetical protein         1         1         0.426         1         0.42	-	1 2.							0.419
cgd6_2920         hypothetical protein with signal peptide         1         0.390           cgd6_2960         large low complexity with PFL0360c_pfal like Znfinger         1         1         1.291           cgd6_2960         Bax inhibitor-1 (BI-1). integral membrane protien with 6 or more transmembrane domains         1         1         1.291           cgd6_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         5.870           cgd6_2990         hypothetical protein         1         0.426         1         0.426           cgd6_3030         protein with C-terminal RCC1 domain hypothetical protein with a signal peptide         1         1         0.456           cgd6_3040         hypothetical protein with a signal peptide         1         1         1.768           cgd6_3050         hypothetical protein with a signal peptide         1         1         1.768           cgd6_3070         hypothetical protein with a signal peptide         1         1         1.764           cgd6_3080         hypothetical protein with a signal peptide         1         1         1.764           cgd6_3100         hypothetical protein         1         1         2.799           cgd6_3100         hypothet	cgd6_290	1 2.	1					1	0.281
cgd6_2950         large low complexity with PFL0360c_pfal like Znfinger         1         1         1.291           cgd6_2960         Bax inhibitor-1 (Bl-1). integral membrane protien with 6 or more transmembrane domains         1         1         31.965           cgd6_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         1         5.870           cgd6_2990         hypothetical protein         1         1         0.426         1         0.505           cgd6_300         protein with C-terminal RCC1 domain         1         1         0.505         1		1	1					1	0.378
cgd6_2960         Bax inhibitor-1 (BI-1). integral membrane protien with 6 or more transmembrane domains         1         1         31.965           cgd6_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor hypothetical protein         1         1         1         5.870           cgd6_2990         hypothetical protein         1         1         0.426         1         0.505         1         0.505         1         0.505         1         0.505         1         0.505         1         0.505         1         0.505         1         0.505         1         0.505         1         0.505         1         0.505         0.505         1         0.505 <t< td=""><td></td><td>1 1 1</td><td>1</td><td></td><td></td><td></td><td></td><td></td><td></td></t<>		1 1 1	1						
transmembrane domains	1			1			4		
cgd6_2980         hypothetical protein with conserved cysteines as in riboflavin-binding protein precursor (RBP), contains signal peptide plus possible GPI anchor         1         1         5.870           cgd6_2990         hypothetical protein         1         0.426         1         0.426           cgd6_300         hypothetical protein         1         0.505         1         0.505           cgd6_3030         protein with C-terminal RCC1 domain         1         1         0.459           cgd6_3040         hypothetical protein with a signal peptide         1         1         0.459           cgd6_3050         hypothetical protein with a signal peptide         1         1         1         7.640           cgd6_3070         hypothetical protein with a signal peptide         1         1         7.640         1         7.640           cgd6_3080         hypothetical protein with a signal peptide         1         1         7.640         1         7.640           cgd6_3090         hypothetical protein         1         1         7.640         1         1         7.640           cgd6_310         hypothetical protein         1         1         1         0.266         1         1         1         0.266         1         1         0.412         <	cga6_2960						- 1	1	31.965
binding protein precursor (RBP), contains signal peptide plus possible GPI anchor   1	cgd6 2980					1		1	5.870
cgd6_2990         hypothetical protein         1         0.426           cgd6_300         hypothetical protein         1         0.505           cgd6_3030         protein with C-terminal RCC1 domain         1         0.397           cgd6_3040         hypothetical protein         1         0.459           cgd6_3050         hypothetical protein with a signal peptide         1         1         0.218           cgd6_3070         hypothetical protein with a signal peptide         1         1         7.640           cgd6_3080         hypothetical protein with a signal peptide         1         1         2.798           cgd6_3090         hypothetical protein with a signal peptide         1         1         2.798           cgd6_310         hypothetical protein         1         1         0.266           cgd6_310         hypothetical protein         1         0.346           cgd6_3110         hypothetical protein         1         0.270           cgd6_3120         hypothetical protein         1         0.270           cgd6_3150         hypothetical protein         1         1         0.342           cgd6_3170         Sel1 protein, putative         1         1         0.538           cgd6_3200         <	-								
cgd6_300         hypothetical protein         1         0.505           cgd6_3030         protein with C-terminal RCC1 domain         1         0.397           cgd6_3040         hypothetical protein         1         0.458           cgd6_3050         hypothetical protein with a signal peptide         1         1         1         1.768           cgd6_3070         hypothetical protein with a signal peptide         1         1         1         1.7640           cgd6_3080         hypothetical protein with a signal peptide         1         1         1.7640           cgd6_3080         hypothetical protein with a signal peptide         1         1         1.7640           cgd6_3090         hypothetical protein with a signal peptide         1         1         1.7640           cgd6_310         hypothetical protein         1         1         1.7640           cgd6_310         hypothetical protein         1         1         1.7640           cgd6_310         hypothetical protein         1         1         0.266           cgd6_310         hypothetical protein         1         1         0.342           cgd6_3120         hypothetical protein         1         1         1         0.538           cgd6_3200 <td>10.0000</td> <td>1.</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>0.400</td>	10.0000	1.							0.400
cgd6_3030         protein with C-terminal RCC1 domain         1         0.397           cgd6_3040         hypothetical protein with a signal peptide         1         1         0.459           cgd6_3050         hypothetical protein with a signal peptide         1         1         1         1.768           cgd6_3060         hypothetical protein with a signal peptide         1         1         1         2.798           cgd6_3080         hypothetical protein with a signal peptide         1         1         1         2.799           cgd6_3090         hypothetical protein with a signal peptide         1         1         1         2.799           cgd6_310         hypothetical protein         1         1         0.266           cgd6_3110         hypothetical protein         1         1         0.346           cgd6_3120         hypothetical protein         1         1         0.270           cgd6_3130         hypothetical protein         1         1         1         0.342           cgd6_3160         large low complexity protein         1         1         1         0.342           cgd6_320         hypothetical protein         1         1         0.538           cgd6_330         hypothetical protein	-	1 2.							
cgd6_3040         hypothetical protein         1         0.459           cgd6_3050         hypothetical protein with a signal peptide         1         1         1.768           cgd6_3060         hypothetical protein with a signal peptide         1         1         1         1.7680           cgd6_3070         hypothetical protein with a signal peptide         1         1         1         2.799           cgd6_3080         hypothetical protein with a signal peptide         1         1         1         2.799           cgd6_3090         hypothetical protein         1         1         0.266           cgd6_310         hypothetical protein         1         1         0.346           cgd6_3110         hypothetical protein         1         1         0.412           cgd6_3120         hypothetical protein         1         1         0.270           cgd6_3130         hypothetical protein         1         1         0.342           cgd6_3160         large low complexity protein         1         1         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497         0.538           cgd6_3320         hypothetical protein         1         1         0.38	1	1							
cgd6_3050         hypothetical protein with a signal peptide         1         1         1.768           cgd6_3060         hypothetical protein with a signal peptide         1         1         1         1.768           cgd6_3070         hypothetical protein with a signal peptide         1         1         1         2.799           cgd6_3080         hypothetical protein with a signal peptide         1         1         1         2.799           cgd6_3090         hypothetical protein         1         1         0.266         1         0.266           cgd6_310         hypothetical protein         1         1         0.346         1         0.346           cgd6_3120         hypothetical protein         1         1         0.270         1         0.270         1         0.270         1         0.270         1         0.270         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1         0.342         1		I <sup>*</sup>							
cgd6_3060         hypothetical protein         1         0.218           cgd6_3070         hypothetical protein with a signal peptide         1         1         7.640           cgd6_3080         hypothetical protein with a signal peptide         1         1         1         2.799           cgd6_3090         hypothetical protein         1         1         0.266         1         0.266           cgd6_310         hypothetical protein         1         1         0.346         1         0.412           cgd6_3110         hypothetical protein         1         1         0.412         1         0.270           cgd6_3120         hypothetical protein         1         1         1         0.270           cgd6_3150         hypothetical protein         1         1         1         0.342           cgd6_3160         large low complexity protein         1         1         1         0.342           cgd6_3170         Sel1 protein, putative         1         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497           cgd6_330         hypothetical protein         1         1         0.382           cgd6_3300         Yir323cp/Cwc24 p fami	-	1	'	1					
cgd6_3070         hypothetical protein with a signal peptide         1         1         7.640           cgd6_3080         hypothetical protein with a signal peptide         1         1         2.799           cgd6_3090         hypothetical protein         1         0.266           cgd6_310         hypothetical protein         1         0.346           cgd6_3110         hypothetical protein         1         0.412           cgd6_3120         hypothetical protein         1         0.270           cgd6_3130         hypothetical protein         1         1         50.680           cgd6_3150         hypothetical protein         1         1         0.340           cgd6_3160         large low complexity protein         1         1         1         0.340           cgd6_3170         Sel1 protein, putative         1         1         0.538         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497         1         0.382           cgd6_330         hypothetical protein         1         1         0.382         1         0.382           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365         1		1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	1	'					
cgd6_3080         hypothetical protein with a signal peptide         1         1         2.799           cgd6_3090         hypothetical protein         1         0.266           cgd6_310         hypothetical protein         1         0.346           cgd6_3110         hypothetical protein         1         1         0.412           cgd6_3120         hypothetical protein         1         1         0.270           cgd6_3150         hypothetical protein         1         1         1         0.342           cgd6_3160         large low complexity protein         1         1         1         0.538           cgd6_3200         hypothetical protein, putative         1         1         0.497           cgd6_3200         hypothetical protein         1         0.497           cgd6_3350         hypothetical protein         1         0.382           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335         1         0.335		1 55				1			
cgd6_3090         hypothetical protein         1         0.266           cgd6_310         hypothetical protein         1         0.346           cgd6_3110         hypothetical protein         1         0.412           cgd6_3120         hypothetical protein         1         0.270           cgd6_3130         hypothetical protein         1         1         0.270           cgd6_3150         hypothetical protein         1         1         0.342           cgd6_3160         large low complexity protein         1         1         0.538           cgd6_3170         Sel1 protein, putative         1         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         0.382           cgd6_330         Yir323cp/Cwc24 p familly; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         1         0.335	-	1			1				
cgd6_310         hypothetical protein         1         0.346           cgd6_3110         hypothetical protein         1         0.412           cgd6_3120         hypothetical protein         1         0.270           cgd6_3130         hypothetical protein         1         1         50.680           cgd6_3150         hypothetical protein         1         1         0.342           cgd6_3160         large low complexity protein         1         1         2.261           cgd6_3170         Sel1 protein, putative         1         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         1         0.382           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335	1	1	1						
cgd6_3110         hypothetical protein         1         0.412           cgd6_3120         hypothetical protein         1         0.270           cgd6_3130         hypothetical protein         1         1         0.270           cgd6_3150         hypothetical protein         1         1         0.342           cgd6_3160         large low complexity protein         1         1         2.261           cgd6_3170         Sel1 protein, putative         1         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         1         0.382           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335	1	1 2.							0.346
cgd6_3120         hypothetical protein         1         0.270           cgd6_3130         hypothetical protein         1         1         50.680           cgd6_3150         hypothetical protein         1         1         0.342           cgd6_3160         large low complexity protein         1         1         2.261           cgd6_3170         Sel1 protein, putative         1         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         1         1.034           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335	1	1	1					1	0.412
cgd6_3130         hypothetical protein         1         1         50.680           cgd6_3150         hypothetical protein         1         1         0.342           cgd6_3160         large low complexity protein         1         1         2.261           cgd6_3170         Sel1 protein, putative         1         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         11.034           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335	1	1	1					1	0.270
cgd6_3160         large low complexity protein         1         1         2.261           cgd6_3170         Sel1 protein, putative         1         0.538           cgd6_3200         hypothetical protein         1         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         11.034           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335	cgd6_3130	hypothetical protein					1	1	50.680
cgd6_3170         Sel1 protein, putative         1         0.538           cgd6_3200         hypothetical protein         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         1.034           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335	1	1	1					1	0.342
cgd6_3200         hypothetical protein         1         0.497           cgd6_3250         hypothetical protein         1         1         0.382           cgd6_330         hypothetical protein         1         1         11.034           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         0.335	cgd6_3160	large low complexity protein		1				1	2.261
cgd6_3250         hypothetical protein         1         0.382           cgd6_330         hypothetical protein         1         1         1.034           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         1         0.335	cgd6_3170	Sel1 protein, putative	1					1	0.538
cgd6_330         hypothetical protein         1         1         11.034           cgd6_3300         Yir323cp/Cwc24 p family; CCCH+ringfinger domains         1         1         0.365           cgd6_3310         hypothetical protein with signal peptide         1         1         0.335	1	1							0.497
cgd6_3300 Yir323cp/Cwc24 p family; CCCH+ringfinger domains 1 0.365 cgd6_3310 hypothetical protein with signal peptide 1 0.335	1	1	1						0.382
cgd6_3310 hypothetical protein with signal peptide 1 0.335	1	1				1			11.034
	1								0.365
CG00_332U   Inyportnetical protein   1   1   0.257	1	1 2							0.335
	cga6_3320	Inypotnetical protein	1		I	I		1	0.257

cgd6_3430	RRM (2xRRMs) domaincontaining protein		1	- 1	1	1	1.448
cgd6_3440	hypothetical protein				1	1	13.023
cgd6_3450	EBNA1 binding protein 2; nucleolar protein p40				1	1	138.327
cgd6_3460	hypothetical protein			1		1	3.152
cgd6_3470	hypothetical protein				1	1	30.420
cgd6_3480	hypothetical protein				1	1	46.390
cgd6_3490	RNA-binding protein, putative				1	1	9.166
cgd6_350	hypothetical protein	1				1	0.342
cgd6_3500	hypothetical protein			1		1	6.298
cgd6_3510	hypothetical protein			1		1	4.376
cgd6_3520	hypothetical protein				1	1	15.332
cgd6_360	hypothetical protein	1				1	0.368
cgd6_3610	hypothetical predicted WD-40 repeat protein, unknown function			1		1	5.595
cgd6_3650	signal peptide, large secreted protein with N terminal ankyrin	1				1 1	0.543
3	repeats + 8+ transmembrane domain						
cgd6_3660	hypothetical protein		1			1	1.346
cgd6_3670	hypothetical protein	1				1	0.253
cgd6_3680	Low complexity hypothetical protein	1				1	0.425
cgd6_3740	41-2 protein antigen precursor			1		1	3.381
cgd6_3760	hypothetical protein				1	1	113.466
cgd6_3770	hypothetical protein	1				1	0.426
cgd6_380	hypothetical protein with signal peptide and 4 transmembrane	1				1	0.289
	domains, possible apicomplexan conserved						
cgd6_3810	NUDIX domain protein; mRNA cleavage factor-like protein Im			1		1	4.787
	like, plant+animal group						
cgd6_3840	SET domain containing protein			1		1	3.366
cgd6_3890	hypothetical protein	1				1	0.598
cgd6_390	hypothetical protein	1		- ]		1	0.511
cgd6_3900	hypothetical protein			1		1	2.364
cgd6_3920	hypothetical protein with signal peptide				1	1	1,276.224
cgd6_3930	hypothetical protein		1			1	2.404
cgd6_3940	hypothetical protein			1		1	3.502
cgd6_3950	uncharacterized protein	1				1 1	0.358
cgd6_3980	hypothetical protein	-			1	1 1	16.534
cgd6_4000	hypothetical protein having a signal peptide		1			1 1	1.864
cgd6_4010	hypothetical protein	1	'				0.434
	uncharacterized apicomplexan-specific protein	1					0.419
cgd6_4050	1 ' ' ' '	'		1			
cgd6_4070	hypothetical protein	4		'		'	2.339
cgd6_4090	hypothetical low complexity protein	1			4		0.333
cgd6_4110	hypothetical protein					1	55.956
cgd6_4140	coiled coil protein	1				1	0.275
cgd6_4160	EF-hands domain containing protein				1	1	19.666
cgd6_4170	hypothetical protein				1	1	6.004
cgd6_4230	hypothetical protein containing a signal peptide				1	1	27.021
cgd6_4240	MO25 protein	1				1	0.296
cgd6_4260	Low complexity protein			1		1	4.521
cgd6_4280	hypothetical protein having a signal peptide				1	1	56.925
cgd6_4290	large protein having a MATH plus possible UBC hydrolase plus			1		1	3.691
	type I pseurousyn plus hexapeptide						
cgd6_4300	uncharacterized coiled coil protein	1				1	0.505
cgd6_4360	hypothetical protein having a signal peptide and 4		1			1	1.677
10 4000	transmembrane domains						0.500
cgd6_4390	hypothetical low complexity protein	1				1	0.529
cgd6_4430	hypothetical protein	1				1	0.394
cgd6_4460	large protein with ARM repeats				1	1	19.317
cgd6_4470	hypothetical low complexity protein with signal peptide				1	1 1	53.627
cgd6_450	hypothetical protein		1			1	1.370
cgd6_4520	hypothetical protein	1				1	0.460
cgd6_4590	ankyrin-related protein, putative				1	1	9.386
cgd6_460	hypothetical protein	1	1			2	1.033
cgd6_4640	hypothetical protein	1				1	0.347
cgd6_4690	SAC3/GANP/Rpn12p family				1	1	8.863
cgd6_470	hypothetical protein	1				1	0.284
cgd6_4720	hypothetical protein				1	1	7.312
cgd6_4790	predicted degraded Zn-finger +bbox Zn finger protein	1				1	0.372
cgd6_480	hypothetical protein	1					0.392
cgd6_4800	hypothetical protein	1				'	0.330
	1 2	1		J		'	0.338
cgd6_4810	hypothetical protein					1 1	
cgd6_4820	hypothetical protein	1		ار		1 1	0.346
cgd6_4870	hypothetical protein			1		1	3.241
cgd6_4950	hypothetical protein				1		114.487
cgd6_50	hypothetical protein	1		J		1	0.599
cgd6_5010	hypothetical protein		1	- ]		1	1.590
cgd6_5020	protein with WD40 repeats		1			1	1.837
cgd6_5030	hypothetical protein			- ]	1	1	10.895
	1			- 1		1	0.000
cgd6_5050	hypothetical protein	1	Į.		l l	'	0.368

cgd6_5120	protein with two PHD Zn fingers that is probably involved in chromatin function			1			1	3.547
cgd6_5150	ring finger protein	1					1	0.434
cgd6_5160	hypothetical protein with conserved carboxy terminal region (KIAA1078 protein)	1					1	0.495
cgd6_5170	hypothetical protein	1					1	0.412
cgd6_5180	hypothetical protein having a transmembrane domain within N-terminus	1					1	0.444
cgd6_5220	cysteine-rich protein with zinc finger	1					1	0.286
cgd6_5230	hypothetical protein	1					1	0.294
cgd6_5270	hypothetical protein with possible signal peptide		1				1	1.682
cgd6_5280	hypothetical protein with signal peptide		1				1	1.537
cgd6_530	Low complexity protein having signal peptide and glycine-rich repeat at C-terminal region			1			1	4.522
cgd6_5300	hypothetical protein	1					1	0.319
cgd6_5310	hypothetical protein with signal peptide		1				1	2.057
cgd6_5360	hypothetical protein with signal peptide	1					1	0.361
cgd6_5370	hypothetical protein	1					1	0.374
cgd6_5390	hypothetical protein, signal peptide		1				1	1.771
cgd6_5420	hypothetical protein, signal peptide		1				1	1.454
cgd6_5440	hypothetical protein, signal peptide, paralogs				1		1	18.558
cgd6_600	hypothetical protein	1					1	0.314
cgd6_770	hypothetical protein				1		1	6.692
cgd6_810	swift like BRCT domain	1					1	0.479
cgd6_820	predicted secreted low complexity protein with a signal peptide		1				1	2.042
cgd6_840	shanti/Ykl100cp/Minor histocompatibility antigen H13-like;	1					1	0.558
	presenilin, signal peptide peptidase family, with 10							
0046 060	transmembrane domains and a signal peptide		4				1	1.384
cgd6_860	hypothetical protein		'			1	1	36.922
cgd6_940	pescadillo containing BRCT domain		1			- 1	1	
cgd6_950	Pdr17p-like Sec14 domain containing protein	1	'				1	2.092 0.472
cgd6_970	hypothetical protein	'				1	1	31.885
cgd7_10	hypothetical protein				1	- 1	1	
cgd7_100	ring domain-containing protein		1		'			9.033
cgd7_1000	F27M3_19 plant like RRM plus AlkB domain containing protein		1				1	1.991
cgd7_1010	very large low complexity protein		1				1	1.997
cgd7_1020	G10 protein			1			1	3.007
cgd7_1030	hypothetical protein		1		4		1	1.512
cgd7_1050	hypothetical protein	1			1		1	15.256
cgd7_1090	hypothetical protein	1			1		1	0.292
cgd7_1120	3CCCH domain containing protein				'	4		7.978
cgd7_1170	protein containing ringfinger+4xC2H2+littlefinger domains	1				1	1	45.442
cgd7_1210	hypothetical protein containing a signal peptide	1			1		1	0.457
cgd7_1220	hypothetical protein containing a signal peptide		_		- 1		1	9.343
cgd7_1230	hypothetical protein		1				1	1.962
cgd7_1270	large hypothetical protein			1			1	2.567
cgd7_1280	hypothetical protein			1			1	4.180
cgd7_1290	hypothetical protein containing a signal peptide			1			1	2.501
cgd7_1300	hypothetical protein containing a signal peptide	1					1	0.507
cgd7_1360	protein with signal peptide and Sec14d domain, probably secreted				1		1	16.514
cgd7_1370	hypothetical protein			1			1	4.150
cgd7_1400	signal peptide containing protein		1				1	1.406
cgd7_1420	hypothetical protein					1	1	83.928
cgd7_1440	protein with 5 TPR domains			1			1	2.511
cgd7_1450	hypothetical protein		1				1	2.045
cgd7 1470	hypothetical protein		1				1	1.691
cgd7_1480	hypothetical protein			1			1	2.881
cgd7_1510	hypothetical protein		1	1			1	2.009
cgd7_1550	uncharacterized protein			1			1	2.550
cgd7_1570	hypothetical protein			1			1	3.179
cgd7_1580	mbl domain containing protein	1					1	0.577
cgd7_1610	uncharacterized low complexity protein	1					1	0.374
cgd7_170	hypothetical protein				1		1	9.088
cgd7_1740	Ing1 like PHD finger protein				1		1	6.957
cgd7_1770	hypothetical protein	1					1	0.496
cgd7_1790	protein with BRIGHT domain like HTH domain at N-terminus		1				1	1.774
	hypothetical protein		1				1	1.895
	1 **	1					1	0.395
cgd7_180	TOIVIC4 OIVIC4. CHIOHIOSOMAI ATDASE WILL CHAIL COILEO COIL						'	0.000
	SMC4'SMC4, chromosomal ATpase with giant coiled coil regions'							
cgd7_180		1					1	0.383
cgd7_180 cgd7_1850	regions'	1			1		1	0.383 13.547
cgd7_180 cgd7_1850 cgd7_1870	regions' hypothetical protein	1			1			
cgd7_180 cgd7_1850 cgd7_1870 cgd7_1890	regions' hypothetical protein KH domain protein				1		1	13.547
cgd7_180 cgd7_1850 cgd7_1870 cgd7_1890 cgd7_190	regions' hypothetical protein KH domain protein hypothetical protein	1		1	1		1	13.547 0.313
cgd7_180 cgd7_1850 cgd7_1870 cgd7_1890 cgd7_190 cgd7_1920	regions' hypothetical protein KH domain protein hypothetical protein hypothetical protein	1		1	1	1	1 1 1	13.547 0.313 0.491
cgd7_180 cgd7_1850 cgd7_1870 cgd7_1890 cgd7_190 cgd7_1920 cgd7_1990	regions' hypothetical protein KH domain protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	1		1	1	1	1 1 1 1	13.547 0.313 0.491 4.679

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907 2200 hypothetical protein signal peptide 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical singular protein 907 2210 pothetical protein 907 2210 pothetical singular protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical protein 907 2210 pothetical 907 221		· ·	1					
907 2220 hypotheteal protein of graphide, possible secreted protein of graphide protei		1 2		1				
937 2230 collect ooli protein signal peptide, possible secreted protein 937 2240 pyrothetical protein signal peptide 937 2240 pyrothetical protein signal peptide 937 2240 pyrothetical protein 938 2240 pyrothetical protein 938 2240 pyrothetical protein 938 2240 pyrothetical protein 938 2240 pyrothetical protein 938 2240 pyrothetical small peptide 938 2240 pyrothetical small peptide 938 2240 pyrothetical protein 938 2240 pyrothetical pyr	" -	1 **				1		
937 2240 hypothetical invocamplexity protein org. 272 hypothetical invocamplexity protein org. 272 hypothetical invocamplexity protein org. 272 hypothetical		1 2			1			
937 2270 hypothetical protein 937 2294 937 2394				1				
agd7 2290         hypothetical protein         1         1         40 785           agd7 2340         agd7 2350         hypothetical small protein, possible signal peptide         1         0.387           agd7 2350         agd7 2340         hypothetical small protein, possible signal peptide         1         0.487           agd7 240         signal peptide, secreted low complexity protein         1         1         4.059           agd7 240         signal peptide, secreted low complexity protein         1         1         1         2.055           agd7 240         signal peptide, secreted low complexity protein         1         1         1         3.881           agd7 250         Skp1 family protein, putative         1         1         1         3.881           agd7 250         Use complexity protein, putative         1         1         1         3.881           agd7 270         SkSCS Mc Sye bromosomal ABC ATpase*         1         1         5.648           agd7 2710         SkSCS Mc Sye bromosomal ABC ATpase*         1         0.515           agd7 2720         agd7 2800         1         0.615           agd7 281         agd7 2800         1         0.617           agd7 2820         agd7 2800         1         0.617 <td> </td> <td>1 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>		1 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1						
2007   2340   a gree secreted protein, signal peptide   1   0.387		1 2.						
0.967   2.350		1 **				1		
cgd7 240	1	, , , , , , , , , , , , , , , , , , , ,						
		1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3						
2007 2400   apinal peptide, secreted low complexity protein         1   4.059	cgd7_2360		1				1	0.457
0g07_2440         ginan lepetide, secreted low complexity protein         1         1         26.511           0g7_2450         Skp1 family protein, putative         1         1         3.881           0g7_2500         Skp1 family protein, putative         1         1         3.881           0g7_2500         Low complexity protein, putative         1         1         4.334           0g7_2610         Dec-Yekich domain protein with kelch repeats at the C-terminus         1         1         4.334           0g7_2720         SMC33MC type chromosomal ABC ATpase'         1         1         5.645           0g7_2720         SMC33MC type chromosomal ABC ATpase'         1         0.555           0g7_2720         FALZ protein         1         0.482           0g7_2720         FALZ protein         1         0.482           0g7_2720         FALZ protein         1         0.482           0g7_2720         FALZ protein         1         1         0.482           0g7_2800         uncharacterized brotein with predicted coiled coil regions         1         1         0.482           0g7_2800         uncharacterized brotein with predicted coiled coil regions         1         0.427         1         0.207           0g7_2800         p	cad7 240				4		1	4.050
1   1.992   1.997   2.440   2.997   2.990		1 2			١.	1		
6gd7 2500         Skpt family protein, putative         1         1         3.881           0gd7 2501         Dypothetical protein         1         1         5.948           0gd7 2610         POZ-kelch domain protein with kelch repeats at the C-terminus         1         1         4.134           0gd7 2610         POZ-kelch domain protein with kelch repeats at the C-terminus         1         0.473           0gd7 2700         SMG3SMC type chromosomal ABC ATpase'         1         0.555           0gd7 2710         SMG3SMC type chromosomal ABC ATpase'         1         0.555           0gd7 2710         SMG3SMC type chromosomal ABC ATpase'         1         0.555           0gd7 27210         Challed Sandaria Prated and with protein (RNA processing phosphatase/ATpase domain)         1         0.555           0gd7 2710         Challed Sandaria Prated box complexity protein uncharacterized low complexity protein uncharacterized low complexity protein uncharacterized low complexity protein uncharacterized protein with predicted coiled	" -	1 3		1		'		
1   1   5   5.948				'	1			
cgd7_2600         Low complexity protein, putative         1         1         4.134         4.134         6.967_2640         1         0.473         1         0.473         1         0.473         1         0.473         1         0.473         1         0.473         1         0.473         1         1         5.6445         1         0.565         445         445         1         0.565         445         1         0.565         2         1         1         0.565         2         1         0.565         2         1         1         0.565         2         1         0.565         2         2         1         0.565         2         2         2		1 ' ' '			١'	1		
Ggd7 2610   POZ-Hecht domain protein with kelch repeats at the C-terminus		1 **			1	'		
cgd7_2800         TPR repeat protein         1         1         56.445           cgd7_2710         SMG2SMC type chromosomal ABC ATpase*         1         0.555           cgd7_2720         Cgd7_2720         1         0.515           cgd7_2720         Cgd7_2720         1         0.617           cgd7_2720         Cgd7_2720         1         0.627           cgd7_2720         Cgd7_2720         1         0.627           cgd7_2720         Cgd7_2720         1         0.627           cgd7_2720 <td> </td> <td></td> <td>1</td> <td></td> <td>١.</td> <td></td> <td></td> <td></td>			1		١.			
SMC2SNC type chromosomal ABC ATpase	1		'			1		
Cgd7   2710   attaxinz related mudix domain protein (RNA processing hypothesis phases/Arpsaes domain)   1		· · ·	1			'		
Disphalase/ATpase domain		I						
Capt	cgu/_2/10		'				'	0.515
Ggd7_2740   WD40 protein   1   0.394	cad7 2720	l; ; ;	1				1	0.482
cgd7_2770		l ·						
cgd7   2790		· ·					1	
cgd7 _ 2850   putative	1			1			1	
cgd7_2860	-94	1 9					-	
cgd7   2870   uncharacterized low complexity protein   1	cgd7_2830	hypothetical low complexity protein		1			1	2.091
cgd7_2880	cgd7_2860	uncharacterized protein with predicted coiled coil regions	1				1	0.427
Cgd7_2890   SLBP family of RNA binding proteins   1	cgd7_2870	uncharacterized low complexity protein			1		1	2.529
cgd7_2930         hypothetical protein         1         1         0.510           cgd7_29860         hypothetical protein         1         0.454           cgd7_2990         Low complexity protein witha potential C2C2 zinc ribbon         1         1         0.302           cgd7_2990         hypothetical protein         1         1         1.2247           cgd7_300         hypothetical protein         1         1         1.2247           cgd7_3010         cysteine-rich protein         1         1         1.37.047           cgd7_3080         hypothetical protein         1         1         1.2247           cgd7_3010         ucharacterized low complexity protein         1         1         0.296           cgd7_3030         uncharacterized low complexity protein         1         1         0.476           cgd7_3030         uncharacterized low complexity protein         1         1         0.476           cgd7_3010         uncharacterized low complexity protein         1         1         0.476           cgd7_3150         uncharacterized low complexity protein         1         1         0.342           cgd7_3210         hypothetical protein         1         1         3.255           cgd7_3220 <td< td=""><td>cgd7_2880</td><td>hypothetical protein</td><td>1</td><td></td><td></td><td></td><td>1</td><td>0.414</td></td<>	cgd7_2880	hypothetical protein	1				1	0.414
Cgd7_2960	cgd7_2890	SLBP family of RNA binding proteins	1				1	0.421
Codd	cgd7_2930	hypothetical protein	1				1	0.510
Cgd7   2990   hypothetical protein   1   1   1   2.247     cgd7   300   hypothetical protein   1   1   1   1.5.229     cgd7   3010   hypothetical protein   1   1   1   1.5.229     cgd7   3080   hypothetical protein   1   1   1   419.549     cgd7   3080   hypothetical protein   1   1   1   0.296     cgd7   3090   uncharacterized low complexity protein   1   1   0.296     cgd7   3150   uncharacterized low complexity protein   1   1   0.342     cgd7   3190   protein with 3   CCCH domains   1   1   1   35.565     cgd7   3210   hypothetical protein   1   1   1   35.565     cgd7   3230   SUBB domain protein   1   1   1   1   5.512     cgd7   3230   SWIB domain protein   1   1   1   1   5.572     cgd7   3280   JAB domain containing protein   1   1   1   1.760     cgd7   3310   hypothetical protein   1   1   1   1.760     cgd7   3340   hypothetical protein   1   1   1   3.285     cgd7   3420   hypothetical protein   1   1   1   3.285     cgd7   3420   hypothetical protein   1   1   3.3885     cgd7   3460   hypothetical protein   1   1   3.3885     cgd7   3500   hypothetical protein   1   1   3.3885     cgd7   3500   hypothetical protein   1   1   3.3885     cgd7   3500   hypothetical protein   1   1   1   3.3885     cgd7   3640   hypothetical protein   1   1   1   3.3885     cgd7   3640   hypothetical protein   1   1   1   3.3885     cgd7   3640   hypothetical protein   1   1   1   3.3885     cgd7   3760   hypothetical protein   1   1   1   3.3885     cgd7   3770   hypothetical protein   1   1   1   3.385     cgd7   3890   hypothetical protein   1   1   1   3.385     cgd7   3990   hypothetical protein   1   1   1   3.385     cgd7   3990   hypothetical protein   1   1   1   1   3.385     cgd7   3990   hypothetical protein   1   1   1   1   3.385     cgd7   3990   hypothetical protein   1   1   1   1   1   3.385     cgd7   3990   hypothetical	cgd7_2960	hypothetical protein	1				1	0.454
cgd7_30         large uncharacterized protein         1         1         15.229           cgd7_3000         hypothetical protein         1         419.549           cgd7_3080         hypothetical protein         1         419.549           cgd7_3090         uncharacterized low complexity protein         1         0.296           cgd7_3190         eukaryote specific membrane proteins signal peptide plus 8 transmembrane domain         1         1         35.565           cgd7_3210         hypothetical protein         1         1         35.565           cgd7_3220         SLBP family of RNA binding proteins         1         1         0.572           cgd7_3280         SWIB domain protein         1         1         1.760           cgd7_3280         SWB domain containing protein         1         1         1.760           cgd7_3310         hypothetical protein         1         1         1.760           cgd7_3320         hypothetical protein         1         1         1.760           cgd7_3320         hypothetical protein         1         1         1.3165           cgd7_3420         hypothetical protein         1         1         1.3585           cgd7_3420         hypothetical protein         1	cgd7_2980	Low complexity protein witha potential C2C2 zinc ribbon	1				1	0.302
cgd7_3000         hypothetical protein         1         37.047           cgd7_3010         cysteine-rich protein         1         1         419.549           cgd7_3080         hypothetical protein         1         0.296           cgd7_3090         uncharacterized low complexity protein         1         0.296           cgd7_3150         eukaryote specific membrane proteins signal peptide plus 8 transmembrane domain         1         1         0.342 transmembrane domain           cgd7_3210         hypothetical protein         1         1         1         3.5565           cgd7_3210         hypothetical protein         1         1         1         3.225           cgd7_3220         SWIB domain protein         1         1         1         0.512           cgd7_3280         JAB domain containing protein         1         1         1         1.760           cgd7_3320         ring finger protein         1         1         1         1.760           cgd7_3340         hypothetical protein         1         1         1         3.212           cgd7_3420         hypothetical protein         1         1         1.3321           cgd7_3470         hypothetical protein         1         1         0.430	cgd7_2990	hypothetical protein			1		1	2.247
cgd7_3010         cysteine-rich protein         1         419.549           cgd7_3080         hypothetical protein         1         0.296           cgd7_3090         uncharacterized low complexity protein         1         0.296           cgd7_3190         eukaryote specific membrane proteins signal peptide plus 8 transmembrane domain         1         1         3.565           cgd7_3210         hypothetical protein         1         1         1         3.565           cgd7_3230         SLBP family of RNA binding proteins         1         1         0.572           cgd7_3260         SWIB domain protein         1         1         1.760           cgd7_3270         hypothetical protein         1         1         1.760           cgd7_3280         hypothetical protein         1         1         1.760           cgd7_3310         hypothetical protein         1         1         1.760           cgd7_3320         rig finger protein         1         1         1.760           cgd7_3320         hypothetical protein         1         1         1.325           cgd7_3420         hypothetical protein         1         1         1.3585           cgd7_3420         hypothetical protein         1 <td< td=""><td>cgd7_30</td><td>large uncharacterized protein</td><td></td><td></td><td></td><td>1</td><td>1</td><td>15.229</td></td<>	cgd7_30	large uncharacterized protein				1	1	15.229
Cgd7_3080         nypothetical protein         1         0.296           cgd7_3090         uncharacterized low complexity protein         1         0.476           cgd7_3150         eukaryote specific membrane proteins signal peptide plus 8 transmembrane domain         1         1         0.342           cgd7_3190         protein with 3 CCCH domains         1         1         1         3.5565           cgd7_3230         SLBP family of RNA binding proteins         1         1         0.572           cgd7_3280         SWIB domain protein         1         1         0.572           cgd7_3290         JAB domain containing protein         1         1         1.760           cgd7_3310         hypothetical protein         1         1         1.760           cgd7_3320         ing finger protein         1         1         1.760           cgd7_3310         hypothetical protein         1         1         1.760           cgd7_3320         ing finger protein         1         1         1.760           cgd7_3420         hypothetical protein         1         1         1.325           cgd7_3440         hypothetical protein         1         1         3.285           cgd7_3500         hypothetical protein	cgd7_3000	hypothetical protein				1	1	37.047
Cgd7_3090         uncharacterized low complexity protein         1         0.476           cgd7_3150         eukaryote specific membrane proteins signal peptide plus 8 transmembrane domain         1         1         0.342           cgd7_3190         protein with 3 CCCH domains         1         1         1         35.565           cgd7_3230         SLBP family of RNA binding proteins         1         1         1         0.572           cgd7_3280         SWB domain protein         1         1         1         1.760           cgd7_3280         JAB domain containing protein         1         1         1         1.760           cgd7_3310         hypothetical protein         1         1         1         1.760           cgd7_3320         ing finger protein         1         1         1         1.3165           cgd7_3320         hypothetical protein         1         1         1         3.212           cgd7_3420         hypothetical protein         1         1         3.3212           cgd7_3420         hypothetical protein         1         1         3.3832           cgd7_3470         hypothetical protein         1         1         0.430           cgd7_350n         hypothetical protein	cgd7_3010	cysteine-rich protein				1	1	419.549
Cgd7_3150         eukaryote specific membrane proteins signal peptide plus 8 transmembrane domain protein with 3 CCCH domains         1         0.342 transmembrane domain protein with 3 CCCH domains         1         1         35,565 cgd7_3210 hypothetical protein         1         1         3,5565 cgd7_3230 SLBP family of RNA binding proteins         1         1         1         3,225 cgd7_3260 SWIB domain protein         1         1         0.572 cgd7_3260 JAB domain containing protein         1         1         1,760 cgd7_3310 hypothetical protein         1         1         1,760 cgd7_3320 ring finger protein         1         1         1,760 cgd7_3320 ring finger protein         1         1         1,760 cgd7_3340 ring finger protein         1         1         1,365 cgd7_3340 ring finger protein         1         1         1,365 cgd7_3340 ring finger protein         1         1         1,365 cgd7_3340 ring finger protein         1         1         1,358 cgd7_3340 ring finger protein         1         1         1,358 cgd7_3440 ring finger protein         1         1         1,358 cgd7_3460 ring finger protein         1         1         1,358 cgd7_3460 ring finger protein         1         1         1,358 cgd7_3560 ring finger protein         1         1         1,358 cgd7_3570 ring finger protein         1         1         1,368 cgd7_3560 ring finger protein         1         1         1,368 cgd7_3680 ring finger protein         1<	cgd7_3080	hypothetical protein	1				1	0.296
transmembrane domain cgd7_3190 protein with 3 CCH domains hypothetical protein	cgd7_3090	uncharacterized low complexity protein	1				1	0.476
cgd7_3190         protein with 3 CCCH domains         1         1         35.565           cgd7_3210         hypothetical protein         1         1         3.225           cgd7_3230         SLBP family of RNA binding proteins         1         1         0.572           cgd7_3280         SWIB domain protein         1         1         1.760           cgd7_3280         JAB domain containing protein         1         1         1.760           cgd7_3310         hypothetical protein         1         1         1.760           cgd7_3320         fing finger protein         1         1         61.043           cgd7_3420         hypothetical protein         1         1         1.3.585           cgd7_3420         hypothetical protein         1         1         3.3.212           cgd7_3460         hypothetical protein, potential zinc ribbon         1         1         0.334           cgd7_3500         hypothetical protein         1         1         1.769           cgd7_3570         hypothetical protein         1         1         1.769           cgd7_3680         kelch repeats protein         1         1         1.3.080           cgd7_3700         rocked neck protein HAT repeats         1	cgd7_3150	eukaryote specific membrane proteins signal peptide plus 8	1				1	0.342
cgd7_3210         hypothetical protein         1         3.225           cgd7_3230         SLBP family of RNA binding proteins         1         0.572           cgd7_3280         SWIB domain protein         1         0.512           cgd7_3280         JAB domain containing protein         1         1         1.760           cgd7_3310         hypothetical protein         1         1         1.760           cgd7_3320         hypothetical protein         1         1         61.043           cgd7_3340         hypothetical protein         1         1         0.457           cgd7_3420         hypothetical protein         1         1         33.212           cgd7_3420         hypothetical protein         1         1         3.2585           cgd7_3420         hypothetical protein         1         1         3.321           cgd7_3420         hypothetical protein         1         1         3.3212           cgd7_3420         hypothetical protein         1         1         3.3212           cgd7_3420         hypothetical protein         1         1         0.3324           cgd7_3420         hypothetical protein         1         1         0.430           cgd7_3520		transmembrane domain						
cgd7_3230         SLBP family of RNA binding proteins         1         0.572           cgd7_3260         SWIB domain protein         1         0.512           cgd7_3280         JAB domain containing protein         1         1         1.760           cgd7_3210         hypothetical protein         1         1         1.3165           cgd7_3320         ing finger protein         1         1         1.0457           cgd7_3340         hypothetical protein         1         1         0.457           cgd7_3440         hypothetical protein         1         1         3.212           cgd7_3460         hypothetical protein         1         1         0.334           cgd7_3470         large low comlexity protein, potential zinc ribbon         1         1         0.430           cgd7_3500         hypothetical protein         1         1         0.430           cgd7_3520         hypothetical protein         1         1         0.473           cgd7_3570         kelch repeats protein         1         1         0.473           cgd7_3680         rpr repeat protein         1         1         1         0.470           cgd7_3700         protein with a conserved N-terminal region         1 <td< td=""><td>cgd7_3190</td><td>protein with 3 CCCH domains</td><td></td><td></td><td></td><td>1</td><td>1</td><td>35.565</td></td<>	cgd7_3190	protein with 3 CCCH domains				1	1	35.565
cgd7_3260         SWIB domain protein         1         0.512 <td>cgd7_3210</td> <td>hypothetical protein</td> <td></td> <td></td> <td>1</td> <td></td> <td>1</td> <td>3.225</td>	cgd7_3210	hypothetical protein			1		1	3.225
cgd7_3280         JAB domain containing protein         1         1         1.760           cgd7_3310         hypothetical protein         1         1         3.165           cgd7_3320         ing finger protein         1         1         61.043           cgd7_3320         hypothetical protein         1         0.457           cgd7_3420         hypothetical protein         1         1         3.212           cgd7_3420         hypothetical protein         1         1         3.381           cgd7_3420         hypothetical protein         1         1         0.334           cgd7_3400         hypothetical protein, potential zinc ribbon         1         1         0.334           cgd7_3500         hypothetical protein         1         1         1.358           cgd7_3500         hypothetical protein         1         1         1.3769           cgd7_3500         hypothetical protein         1         1         1.398           cgd7_3500         hypothetical protein         1         1         1.398           cgd7_3500         hypothetical protein         1         1         1.308           cgd7_3500         hypothetical protein         1         1         3.080	cgd7_3230	SLBP family of RNA binding proteins	1				1	0.572
cgd7_3310         hypothetical protein         1         3.165           cgd7_3320         ring finger protein         1         1         61.043           cgd7_3340         hypothetical protein         1         0.457         1         0.457           cgd7_3420         hypothetical protein         1         1         3.3212         1         3.3585           cgd7_3460         hypothetical protein         1         1         0.430         1         0.430           cgd7_3470         large low comlexity protein, potential zinc ribbon         1         1         0.430         1         0.430           cgd7_3500         hypothetical protein         1         1         1.769         1         1         0.430           cgd7_3520         hypothetical protein         1         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769         1         1.769	cgd7_3260	SWIB domain protein	1				1	0.512
cgd7_3320         ring finger protein         1         61.043           cgd7_3340         hypothetical protein         1         0.457           cgd7_3420         hypothetical protein         1         1         33.212           cgd7_3440         hypothetical protein         1         1         3.585           cgd7_3470         large low comlexity protein, potential zinc ribbon         1         1         0.430           cgd7_3500         hypothetical protein         1         1         6.395           cgd7_3520         hypothetical protein         1         1         6.395           cgd7_3570         hypothetical protein         1         1         0.473           cgd7_3580         kelch repeats protein         1         1         0.473           cgd7_3570         hypothetical protein         1         1         3.080           cgd7_3680         rcooked neck protein HAT repeats         1         1         1         4.188           cgd7_3700         rcooked neck protein HAT repeats         1         1         5.916           cgd7_3710         hypothetical protein         1         1         5.916           cgd7_3770         hypothetical protein         1         1 <t< td=""><td>cgd7_3280</td><td>JAB domain containing protein</td><td></td><td>1</td><td></td><td></td><td>1</td><td>1.760</td></t<>	cgd7_3280	JAB domain containing protein		1			1	1.760
cgd7_3340         hypothetical protein         1         0.457           cgd7_3420         hypothetical protein         1         1         33.212           cgd7_3440         hypothetical protein         1         1         3.585           cgd7_3470         large low comlexity protein, potential zinc ribbon         1         1         0.430           cgd7_3500         hypothetical protein         1         1         6.395           cgd7_3520         hypothetical protein         1         1         1.769           cgd7_3570         hypothetical protein         1         1         0.473           cgd7_3580         kelch repeats protein         1         1         1.3080           cgd7_3640         Yipe Family of predicted nucleotide binding proteins         1         1         1.3080           cgd7_3680         TPR repeat protein         1         1         1.3080           cgd7_3780         crooked neck protein HAT repeats         1         1         0.470           cgd7_370         hypothetical protein         1         1         5.916           cgd7_3710         hypothetical protein         1         1         0.321           cgd7_380         hypothetical protein         1 <t< td=""><td>cgd7_3310</td><td>hypothetical protein</td><td></td><td></td><td>1</td><td></td><td>1</td><td>3.165</td></t<>	cgd7_3310	hypothetical protein			1		1	3.165
cgdf_3420         hypothetical protein         1         1         33.212           cgd7_3440         hypothetical protein         1         1         3.585           cgd7_3460         hypothetical protein         1         0.334           cgd7_3470         large low comlexity protein, potential zinc ribbon         1         1         0.430           cgd7_3500         hypothetical protein         1         1         6.395           cgd7_3520         hypothetical protein         1         1         1.769           cgd7_3570         hypothetical protein         1         1         0.473           cgd7_3580         kelch repeats protein         1         1         1         3.080           cgd7_3640         YjeF family of predicted nucleotide binding proteins         1         1         4.188           cgd7_3680         TPR repeat protein         1         1         4.188           cgd7_3690         crooked neck protein HAT repeats         1         1         5.916           cgd7_370         hypothetical protein         1         1         5.916           cgd7_3710         LRR protein         1         1         1.342           cgd7_3850         hypothetical protein         1	cgd7_3320	ring finger protein				1	1	61.043
cgd7_3440         hypothetical protein         1         3.585           cgd7_3460         hypothetical protein         1         0.334           cgd7_3470         large low comlexity protein, potential zinc ribbon         1         0.430           cgd7_3500         hypothetical protein         1         1         0.430           cgd7_3520         hypothetical protein         1         1         1.769           cgd7_3570         hypothetical protein         1         1         0.473           cgd7_3580         kelch repeats protein         1         1         1         3.080           cgd7_3640         YjeF family of predicted nucleotide binding proteins         1         1         1         4.188           cgd7_3680         TPR repeat protein         1         1         0.317         1         1         0.317           cgd7_3690         crooked neck protein HAT repeats         1         1         0.470         1         5.916           cgd7_3700         hypothetical protein         1         1         0.321         1         1         0.321           cgd7_3710         LRR protein         1         1         1         1.481         1         1         1         1 <t< td=""><td>cgd7_3340</td><td>hypothetical protein</td><td>1</td><td></td><td></td><td></td><td>1</td><td>0.457</td></t<>	cgd7_3340	hypothetical protein	1				1	0.457
cgd7_3460	cgd7_3420	hypothetical protein				1	1	33.212
cgd7_3470   large low comlexity protein, potential zinc ribbon   1	cgd7_3440	hypothetical protein			1		1	3.585
cgd7_3500         hypothetical protein         1         1         6.395           cgd7_3520         hypothetical protein         1         1         1.769           cgd7_3570         hypothetical protein         1         1         0.473           cgd7_3580         kelch repeats protein         1         1         3.080           cgd7_3640         YjeF family of predicted nucleotide binding proteins         1         1         4.188           cgd7_3680         TPR repeat protein         1         1         0.317           cgd7_3690         crooked neck protein HAT repeats         1         1         0.470           cgd7_370         protein with a conserved N-terminal region         1         1         5.916           cgd7_3700         hypothetical protein         1         1         0.321           cgd7_3710         LRR protein         1         1         0.342           cgd7_3770         hypothetical protein         1         1         1.481           cgd7_380         hypothetical protein         1         1         1.481           cgd7_380         hypothetical protein         1         1         1.400           cgd7_3930         hypothetical protein         1         1	cgd7_3460	hypothetical protein	1				1	0.334
cgd7_3520         hypothetical protein         1         1.769           cgd7_3570         hypothetical protein         1         0.473           cgd7_3580         kelch repeats protein         1         1         3.080           cgd7_3640         YjeF family of predicted nucleotide binding proteins         1         1         4.188           cgd7_3680         TPR repeat protein         1         1         0.317           cgd7_3690         crooked neck protein HAT repeats         1         1         0.470           cgd7_370         protein with a conserved N-terminal region         1         1         5.916           cgd7_3700         hypothetical protein         1         1         0.321           cgd7_3710         LRR protein         1         1         1.481           cgd7_3770         hypothetical protein         1         1         1.481           cgd7_3780         hypothetical protein         1         1         1.481           cgd7_380         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         1.747 <td>cgd7_3470</td> <td>large low comlexity protein, potential zinc ribbon</td> <td>1</td> <td></td> <td></td> <td></td> <td>1</td> <td>0.430</td>	cgd7_3470	large low comlexity protein, potential zinc ribbon	1				1	0.430
1	cgd7_3500	hypothetical protein				1	1	6.395
cgd7_3580         kelch repeats protein         1         3.080           cgd7_3640         YjeF family of predicted nucleotide binding proteins         1         1         4.188           cgd7_3680         TPR repeat protein         1         1         0.317           cgd7_3690         crooked neck protein HAT repeats         1         1         0.470           cgd7_370         protein with a conserved N-terminal region         1         1         5.916           cgd7_3700         hypothetical protein         1         1         0.321           cgd7_3710         LRR protein         1         1         0.342           cgd7_3770         hypothetical protein         1         1         1.481           cgd7_380         hypothetical protein         1         1         2.011           cgd7_380         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         1	cgd7_3520	hypothetical protein		1			1	1.769
1	cgd7_3570	hypothetical protein	1				1	0.473
cgd7_3680         TPR repeat protein         1         0.317           cgd7_3690         crooked neck protein HAT repeats         1         0.470           cgd7_370         protein with a conserved N-terminal region         1         1         5.916           cgd7_3700         hypothetical protein         1         1         0.321           cgd7_3710         LRR protein         1         1         1.481           cgd7_3800         hypothetical protein         1         1         1.481           cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         1.747           cgd7_3980         PX and WD40 domain protein         1         1         0.531	cgd7_3580	kelch repeats protein			1		1	3.080
cgd7_3680         TPR repeat protein         1         0.317           cgd7_3690         crooked neck protein HAT repeats         1         0.470           cgd7_370         protein with a conserved N-terminal region         1         1         5.916           cgd7_3700         hypothetical protein         1         1         0.321           cgd7_3710         LRR protein         1         1         1.342           cgd7_3770         hypothetical protein         1         1         1.481           cgd7_3770         hypothetical protein         1         1         1.481           cgd7_3700         hypothetical protein         1         1         1.481           cgd7_380         hypothetical protein         1         1         1.400           cgd7_380         hypothetical protein         1         1         1.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         1         0.531	cgd7 3640	YjeF family of predicted nucleotide binding proteins			1		1	4.188
cgd7_370         protein with a conserved N-terminal region         1         1         5.916           cgd7_3700         hypothetical protein         1         0.321           cgd7_3710         LRR protein         1         1         0.342           cgd7_3770         hypothetical protein         1         1         1.481           cgd7_380         hypothetical protein         1         1         2.011           cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	cgd7_3680	TPR repeat protein	1				1	0.317
cgd7_370         protein with a conserved N-terminal region         1         1         5.916           cgd7_3700         hypothetical protein         1         0.321           cgd7_3710         LRR protein         1         1         1.3481           cgd7_380         hypothetical protein         1         1         2.011           cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	1	crooked neck protein HAT repeats	1				1	0.470
cgd7_3700         hypothetical protein         1         0.321           cgd7_3710         LRR protein         1         0.342           cgd7_3770         hypothetical protein         1         1         1.481           cgd7_380         hypothetical protein         1         1         2.011           cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531		i i				1	1	
cgd7_3710         LRR protein         1         0.342           cgd7_3770         hypothetical protein         1         1.481           cgd7_380         hypothetical protein         1         1         2.011           cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	1	ļ	1					
cgd7_3770         hypothetical protein         1         1.481           cgd7_380         hypothetical protein         1         2.011           cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	1	1 2						
cgd7_380         hypothetical protein         1         2.011           cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	1	I -		1				
cgd7_3850         hypothetical protein         1         1         1.400           cgd7_3900         hypothetical protein         1         1         0.339           cgd7_3920         hypothetical protein         1         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	1	1 **		1				
cgd7_3900         hypothetical protein         1         0.339           cgd7_3920         hypothetical protein         1         1.747           cgd7_3930         hypothetical protein         1         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	1	1 2						
cgd7_3920       hypothetical protein       1       1       1.747         cgd7_3930       hypothetical protein       1       0.535         cgd7_3980       PX and WD40 domain protein       1       0.531	1	1 **	1	'				
cgd7_3930         hypothetical protein         1         0.535           cgd7_3980         PX and WD40 domain protein         1         0.531	1	1 2	,	1				
cgd7_3980   PX and WD40 domain protein   1   0.531	1	1 2	1	'				
	1	1 **						
1-9	1	· ·	'			1		
	1-9-1 -0000	J. 7F	ı l	1	ı	•	.1	30., 30

cgd7_400   hypothetical protein, signal peptide   1   1   1	
	1.895
cgd7_4000   hypothetical coiled coil protein   1   1   1	18.186
cgd7_4030 hypothetical low complexity protein 1 1	4.739
cgd7_4040   hypothetical protein   1   1	13.507
cgd7_4060 signal recognition particle SPR72	13.736
cgd7 410 hypothetical protein 1	1.857
	3.457
cgd7_4100   Ssm4 ring finger fused to a forkhead associated (FHA) domain   1   1   1   1   1   1   1   1   1	3.457
cgd7 4140 WD40 domain protein 1	2.068
1	1.451
-9a	· .
	0.520
cgd7_420 protein with DEXDc plus ring plus HELICc; possible SNF2	5.453
domain	0.404
	1.848
cgd7_4280 signal peptide, large secreted protein	7.912
cgd7_4300 Low complexity protein with coiled coil regions	42.191
cgd7_4320   signal peptide, secreted protein   1 1 1	32.552
cgd7_4330 glycoprotein, putative 1 1 1	3.015
cgd7_4340 very large secreted protein, signal peptide 1 1	0.420
cgd7_4360 hypothetical protein 1 1	43.413
cgd7_4400 coronin-type WD40 protein	1.401
cgd7 4480 T8M16 190 RRM protein of possible plant origin	15.767
cgd7 4490 signal peptide-containing protein with transmembrane domain 1	0.506
cgd7_4500 sgnal peptide, large secreted protein 1 1	0.420
1.5 = 1.1   1.5   1.7   1.5   1	1.499
cgd7_4560   gigantic extracellular protein with interesting sushi (9x) and   1   1   1   1   1   1   1   1   1	1.433
signal peptide-CRYPB(3x)-sushi (9x)-archaeoglobus type	
repeats (2x)	
cgd7_4570 DID domain proteins (DID4/DID2 family) 1	0.443
cgd7_4630 hypothetical protein 1 1	28.015
lean = 1000 librarionem krotem	0.342
	l I
cgd7_4670   hypothetical protein   1   1	0.492
cgd7_4700 ring finger domain protein and 2 transmembrane domains	0.370
cgd7_4720   hypothetical protein   1   1	3.911
cgd7_4750   hypothetical protein   1   1	4.721
cgd7_4830   membrane proteins related to the mechanosensitive ion channel   1   1	0.403
cgd7_4850   hypothetical protein   1   1   1	1.170
cgd7_4860 uncharacterized protein	7.463
cgd7_4870 hypothetical protein 1 1 1	3.173
cgd7_4890 hypothetical protein 1	0.456
cgd7_490 hypothetical protein 1 1	34.212
cgd7_4960 Not4hp/Mot2p, RING finger+RRM domains	6.481
cgd7_500 hypothetical protein 1 1	47.761
cgd7_5030 uncharacterized low complexity protein 1	0.458
1.0. =	l
1.0. = 1.1.   1.1	0.470
cgd7_505   hypothetical protein   1   1	1.780
cgd7_5090 SET domain protein with MYND insert (Skm/BOP family) 1	2.774
cgd7_5110   hypothetical low complexity protein   1   1	1.447
cgd7_5190 uncharacterized protein with coiled coil regions 1 1 1	2.104
cgd7_5240 uncharacterized protein 1 1 1	3.565
cgd7_5290   hedgehog-type HINT domain protein, possible animal horizontal   1   1	0.442
transfer, signal peptide	
cgd7_5320 Cwf5-like with 2 ZnR domains (CCCH and RRM domains	39.267
missing)	
cgd7_5360 uncharacterized protein 1 1 1	7.696
cgd7_5370 LigT, 2 H domain protein, involved in RNA processing	0.483
cgd7_5380   CtIP type zinc knuckle (C2H2)   1   1   2	2.062
cgd7_540 hypothetical protein with signal peptide and 8 or more 1 1	0.381
transmembrane domains	
cgd7_5410   WD40 protein   1   1   1	2.340
cgd7_5420 uncharacterized protein 1 1	0.404
cgd7_5440 very large low complexity protein, probably membrane	0.571
associated	
cgd7_5470 uncharacterized protein 1 1 1	17.188
cgd7_5500 large secreted protein	0.442
cgd7_5520   serine/threonine rich low complexity protein 1 1	8.666
cgd7_5530   hypothetical protein   1   1	0.326
cgd7_560 hypothetical protein 1 1	0.320
	l I
	7.043
cgd7_600 hypothetical protein 1	0.297
cgd7_620 Sec14d domain containing protein 1 1	7.669
cgd7_680 hypothetical protein with a signal peptide 1 1	2.365
cgd7_710 possible helicase 1 1 1	0.400
	8.938
cgd7_760 bruno-like protein with 2 RRM domains 1	0.930
	0.426
cgd7_760 bruno-like protein with 2 RRM domains	0.426

cgd7_800	hypothetical protein	Ш	1				1	1.935
cgd7_850	putative patched family protein	1					1	0.477
cgd7_860	large protein with possible conserved (animals and fungi) N-				1		1	17.045
cgd7_870	terminal and C-terminal regions hypothetical protein	1					1	0.324
	hypothetical protein	1					1	0.423
cgd7_890	protein with 2 possible TPR domains, possible n-terminal			1			1	2.548
cgd7_920	acetyltransferase			'			'	2.540
cgd7_970	Syf1p. protein with 8 HAT domains	1					1	0.455
cgd7_980	protein with MYND plus SET domains plus 5 Ank repeats		1				1	1.717
cgd7_990	hypothetical protein		-	1			1	2.532
cgd8_10	uncharacterized protein	1		-			1	0.391
cgd8_100	hypothetical protein	1					1	0.306
cgd8_1000	hypothetical protein	1					1	0.392
cgd8_1010	hypothetical protein	1					1	0.317
cgd8_1010	hypothetical protein	1					1	0.479
	Lift and the second sec	1					1	0.479
cgd8_1040	hypothetical protein		4				1	1.692
cgd8_1090	hypothetical protein		1					
cgd8_1140	Sec14d domain containing protein		1	4			1	1.851
cgd8_1180	coronin like WD40 repeat protein			1	_		1	3.110
cgd8_1190	hypothetical protein				1		1	5.818
cgd8_120	hypothetical protein	1					1	0.382
cgd8_1220	uncharacterized protein with threonine repeats	1					1	0.415
cgd8_1260	hypothetical protein	1					1	0.494
cgd8_1310	hypothetical protein	1					1	0.448
cgd8_1360	hypothetical protein				1		1	13.676
cgd8_1380	hypothetical protein				1		1	5.564
cgd8_1450	11x WD40 repeats containing protein of plant origin					1	1	47.471
cgd8_1470	hypothetical protein				1		1	12.307
cgd8_1500	FH2 domain containing protein				1		1	7.457
cgd8_1520	coiled coil protein	1					1	0.337
cgd8_1540	coiled coil, low complexity protein	1					1	0.602
cgd8_1590	uncharacterized protein	1					1	0.327
cgd8_1630	hypothetical protein	1					1	0.370
cgd8_1680	hypothetical protein	•			1		1	8.481
cgd8_1690	hypothetical protein	1			'		1	0.359
	Lift and the second sec				1		1	13.960
cgd8_1710	hypothetical protein	1			'		1	0.518
cgd8_1740	predicted secrete protein, paralog within GGC gene family of secreted cryptospordium proteins	1					'	0.516
cgd8_1760	secreted protein, signal peptide			1			1	2.679
cgd8_1770	HxYxP motif containing repeats seen only in C. elegans					1	1	121.562
""	F29G6.3b, signal peptide							.2002
cgd8_1780	hypothetical protein, signal peptide	1					1	0.356
cgd8_180	hypothetical protein				1		1	9.192
cgd8 1810	hypothetical protein					1	1	61.027
cgd8_1830	pelota/Dom34; pelota like RNA binding domain		1				1	1.996
cgd8_1860	LisH domain at N + WD40 repeats				1		1	23.827
cgd8 1890	hypothetical protein			1			1	4.716
cgd8_1930	large protein with a GCN1 domain	1		-			1	0.343
cgd8_1960	hypothetical protein	1					1	0.332
cgd8_2040	POZ domain protein, related to tetramerization domain of K	•	1				1	1.692
cguo_2040	channel		' '				١.	1.002
cgd8_2120	hypothetical protein	1					1	0.537
cgd8 2140	hypothetical protein	1					1	0.350
cgd8_2150	proliferating cell nuclear antigen PCNA	1					1	0.417
cgd8_2160	shares a domain with poly(ADP) ribose glycohydrolases, some	1					1	0.348
0940_2100	protein kinase A anchoring proteins and baculovirus HzNV						.1	0.010
	Orf103, possible transmembrane domain within N-terminus							
cgd8_2230	hypothetical protein	1					1	0.299
cgd8_2290	hypothetical protein		1				1	2.556
cgd8_2300	brahma like protein with a HSA domain, SNF2 like helicase and		1				1	1.468
" -	a bromo domain							
cgd8_2310	hypothetical protein	1					1	0.470
cgd8_2400	hypothetical protein	1					1	0.388
cgd8_2460	hypothetical protein with possible SAP domain	1					1	0.462
cgd8_2530	sushi-domain containing secreted protein; with a signal peptide,		1				1	1.921
-	low complexity region followed by a sushi domain							
cgd8_2570	hypothetical protein	1					1	0.352
cgd8_2590	hypothetical protein	1					1	0.403
cgd8_260	hypothetical protein	1					1	0.576
cgd8_2600	hypothetical protein	1					1	0.362
	hypothetical protein		1				1	1.871
cgd8_2620	le and a second				1		1	13.192
cgd8_2620 cgd8_2660	hypothetical protein					1		
	hypothetical protein hypothetical secreted protein, signal peptide	1					1	0.551
cgd8_2660 cgd8_2680	hypothetical secreted protein, signal peptide	1	1				1	0.551 1.860
cgd8_2660 cgd8_2680 cgd8_2690	1 **	1	1					
cgd8_2660 cgd8_2680 cgd8_2690 cgd8_2740	hypothetical secreted protein, signal peptide hypothetical protein hypothetical protein		1	1			1	1.860
cgd8_2660 cgd8_2680 cgd8_2690	hypothetical secreted protein, signal peptide hypothetical protein		1	1			1	1.860 0.359

cgd8_2980	hypothetical protein		1				1	1.514
cgd8_30	signal peptide, predicted secreted protein of cryptosprodidium- specific SKSR gene family			1			1	3.067
cgd8_3010	Smc ABC ATpase	1					1	0.424
cgd8_3020	hypothetical protein	1					1	0.388
cgd8_3030	hypothetical protein, signal peptide, secreted protein	1					1	0.529
cgd8_3050	hypothetical protein				1		1	21.755
cgd8_3080	Swr1p like SWI/SNF2 family ATpase with a HSA domain at the N-terminus probably involved in chromatin remodelling	1					1	0.427
cgd8_310	hypothetical protein		1				1	1.760
cgd8_3110	12x WD40 repeat containing protein					1	1	123.457
cgd8_3160	hypothetical protein			1			1	5.056
cgd8_3170	hypothetical protein	1					1	0.438
cgd8_320	hypothetical protein	1	1				2	1.092
cgd8_330	hypothetical protein	1		1			2	1.696
cgd8_3410	hypothetical protein	1					1	0.469
cgd8_3490	hypothetical protein				1		1	9.775
cgd8_3500	hypothetical protein			1			1	4.821
cgd8_3530	predicted secreted protein				1		1	16.731
cgd8_3540	predicted secreted protein					1	1	54.426
cgd8_3550	hypothetical protein			1			1	2.390
cgd8_3560	predicted secreted protein				1		1	6.427
cgd8_3570	predicted secreted protein			1			1	4.477
cgd8_3580	hypothetical protein, signal peptide, paralogs				1		1	9.708
cgd8_3590	predicted secreted protein				1		1	12.880
cgd8_3650	predicted DM-LD37668p			1			1	4.149
cgd8_3700	hypothetical protein				1		1	6.749
cgd8_3710	hypothetical protein				1		1	8.772
cgd8_3720	D441/Mpe1p like protein with a zinc knuckle (C2HC) and PhD					1	1	35.163
cad9 3750	Zn finger domain predicted secreted protein					1	1	343.094
cgd8_3750 cgd8_3780	hypothetical protein	1				'	1	0.541
cgd8_3790	Sec14'Sec14'	1					1	0.523
cgd8_3800	hypothetical protein	'				1	1	94.614
cgd8_3810	hypothetical protein				1	'	1	15.164
cgd8_3830	hypothetical protein				1		1	18.637
cgd8_3840	hypothetical protein		1		'		1	1.306
cgd8_390	hypothetical protein		<u>'</u>	1			1	2.521
cgd8_3930	LepA like TRAFAC class GTpase, 2 transmembrane domain	1		- '			1	0.438
cguo_5950	near C						'1	0.430
cgd8_3960	RIKEN cDNA 9430077D24 gene, putative	1					1	0.339
cgd8_3980	hypothetical protein	1					1	0.395
cgd8_4020	hypothetical protein		1				1	1.597
cgd8_4070	SANT domain containing protein	1					1	0.337
cgd8_4080	WD-repeat protein	1					1	0.421
cgd8 410	possible secreted protein with long stretch of threonines,					1	1	39.095
_	putative mucin							
cgd8_4110	hypothetical protein	1					1	0.519
cgd8_4190	uncharacterized glycine-rich low complexity protein	1					1	0.313
cgd8_420	Low complexity coiled coil protein	1					1	0.473
cgd8_4200	uncharacterized protein with several coiled-coil regions				1		1	8.164
cgd8_4280	zz domain protein				1		1	7.415
cgd8_4300	hypothetical protein		1				1	1.468
cgd8_4310	hypothetical protein		1				1	2.230
cgd8_4380	SNW family nuclear protein			1			1	5.523
cgd8_4390	hypothetical protein			1			1	3.044
cgd8_4420	WD40 repeat and RING finger domain-containing protein				1		1	19.626
cgd8_4450	hypothetical protein		1				1	1.924
cgd8_4470	hypothetical protein	1					1	0.583
cgd8_4510	hypothetical protein				1		1	11.685
cgd8_4520	large protein with possible domain of nucleoporin, Non-		1				1	2.142
	repetitive/WGA-negative nucleoporin		4					4 000
cgd8_4540	predicted coiled coil protein		1				1	1.668
cgd8_4590	hypothetical protein	1					1	0.327
cgd8_4600	hypothetical protein	1					1	0.430
cgd8_4610	hypothetical protein	1				1	1	0.405
cgd8_4620	ISWI related chromatinic protein with an apicomplexan specific domain architecture composed of 3x PHD+SNF2					1	1	48.753
	ATpase+2xPHD							
cgd8_4640	WD40 repeat				1		1	18.713
cgd8_4660	hypothetical protein, signal peptide		1				1	1.447
cgd8_470	MRG/Alp3 like proteini with a chromodomain and an MRG	1					1	0.316
<u> </u>	domain							
cgd8_4700	hypothetical protein	1					1	0.307
	hypothetical protein					1	1	71.536
cgd8_4710	1 21						. 1	
cgd8_4710 cgd8_4770 cgd8_4780	hypothetical protein	1				I	1	0.500

cgd8_4840   repeat and Q repeat at the C-terminus   1		cgd8_4800	SSM4 like ring finger with a forkhead associated (FHA) domain (apicomplexan-specific architecture)		1				1	1.933
cgd8_440		cad8 4820		1					1	0.375
repeat and Q repeat at the C-terminus cgd8_490 cgd8_4920 cgd8_4920 cgd8_4920 cgd8_4920 cgd8_4980 cgd8_4980 cgd8_4980 cgd8_5020 cgd8_4980 cgd8_501 cgd8_501 cgd8_501 cgd8_501 cgd8_501 cgd8_5020 cgd8_5020 cgd8_5020 cgd8_5020 cgd8_5040 cgd8_5010 cgd8_5100 cgd8_5290 cgd8_5290 cgd8_5290 cgd8_5290 cgd8_5290 cgd8_5200 cgd8_5300 cgd8_5400 cgd8_5500 cgd8_6200 cgd8_770 cgd8_8300 cgd8_770 cgd8_770 cgd8_8300 cgd8_770 cgd8_770 cgd8_770 cgd			*!			1				5.452
Cgd8_4920   Cgd8_4960   Cgd8_4960   Cgd8_4960   Cgd8_4960   Cgd8_4960   Cgd8_4960   Cgd8_4960   Cgd8_500   Cgd8_5010   Cgd8_		cguo_+o+o				'			'	0.402
cgd8_4960		cgd8_490	uncharacterized large low complexity coiled coil protein	1					1	0.372
cgd8_4980		cgd8_4920	WD repeats containing protein	1					1	0.288
Signal peptide predicted secreted protein of cryptosprodidium-specific FGLN gene family hypothetical protein   1   1   1   1   1   1   1   1   1		cgd8_4960	hypothetical protein, signal peptide				1		1	9.100
Specific FGLN gene family		cgd8_4980	hypothetical protein	1					1	0.483
Starch binding domain containing protein, possible plant origin   1		cgd8_50				1			1	4.918
cgd8_5040   hypothetical protein   1   1   1   1   1   1   1   1   1		cgd8_5010	hypothetical protein				1		1	19.586
cgd8_5070		cgd8_5020	starch binding domain containing protein, possible plant origin	1					1	0.409
cgd8_5100		cgd8_5040	hypothetical protein	1					1	0.299
cgd8_5170		-	hypothetical protein	1					1	0.467
Cgd8_5170   hypothetical protein   cgd8_5180   hypothetical protein   hypothetical protei		cgd8_5100	hypothetical protein			1			1	2.796
Cgd8_5180		cgd8_5110	hypothetical protein				1		1	6.575
cgdd_5190   large protein with central conserved domain, possible BCRT   domain   cgd8_5250   protein with 2x PHD domains   large protein with possible signal peptide and acidic plus glycine repeats   large protein with possible signal peptide and acidic plus glycine repeats   signal peptide containing protein   1   1   1   1   1   1   1   1   1		cgd8_5170	hypothetical protein	1					1	0.289
domain   cgd8_5250   large protein with 2x PHD domains   1   1   1   1   1   1   1   1   1		cgd8_5180	hypothetical protein	1					1	0.444
cgd8_5290   large protein with possible signal peptide and acidic plus glycine repeats   1		cgd8_5190	• •	1					1	0.443
repeats signal peptide containing protein cgd8_5300 signal peptide containing protein cgd8_5310 signal peptide containing protein cgd8_5330 hypothetical protein cgd8_5340 coiled coil protein cgd8_550 large uncharacterized protein cgd8_620 hypothetical protein cgd8_660 large low complexity protein cgd8_700 predicted secreted protein, signal peptide with several threonines, possible mucin cgd8_740 prefoldin like molecular chaperone cgd8_740 predicted secreted protein, 1 or more transmembrane domain, signal peptide cgd8_770 hypothetical protein cgd8_770 predicted secreted protein, 1 or more transmembrane domain, signal peptide cgd8_770 hypothetical protein cgd8_830 hypothetical protein cgd8_870 VPS13 like protein involved in vacuolar protein trafficking Unknown Total		cgd8_5250	protein with 2x PHD domains	1					1	0.346
cgd8_5310   signal peptide containing protein   1   1   1   2   2   2   2   2   2   2		cgd8_5290				1			1	2.282
cgd8_5330		cgd8_5300	signal peptide containing protein			1			1	5.676
cgd8_5340         coiled coil protein         1         1         7           cgd8_550         large uncharacterized protein         1         1         0           cgd8_620         hypothetical protein         1         1         0           cgd8_660         large low complexity protein         1         1         0           cgd8_700         predicted secreted protein, signal peptide with several threonines, possible mucin         1         1         1           cgd8_720         hypothetical protein         1         1         1         0           cgd8_740         prefoldin like molecular chaperone         1         1         1         0           cgd8_760         predicted secreted protein, 1 or more transmembrane domain, signal peptide         1         1         1         0           cgd8_770         hypothetical protein         1         1         1         0           cgd8_830         hypothetical protein         1         1         1         0           cgd8_970         VPS13 like protein involved in vacuolar protein trafficking         1         1         1         0           Unknown Total         0         1         1         1         1         1         0		cgd8_5310	signal peptide containing protein		1				1	1.431
cgd8_550         large uncharacterized protein         1         1         1         0		cgd8_5330	hypothetical protein				1		1	24.100
cgd8_620         hypothetical protein         1         1         1         0           cgd8_660         large low complexity protein         1         1         1         0           cgd8_700         predicted secreted protein, signal peptide with several threonines, possible mucin         1         1         1         1         0           cgd8_720         hypothetical protein         1         1         1         1         0		cgd8_5340	coiled coil protein					1	1	71.171
cgd8_660 large low complexity protein cgd8_700 predicted secreted protein, signal peptide with several threonines, possible mucin cgd8_720 hypothetical protein cgd8_740 prefoldin like molecular chaperone cgd8_760 predicted secreted protein, 1 or more transmembrane domain, signal peptide cgd8_770 hypothetical protein cgd8_830 hypothetical protein cgd8_830 hypothetical protein cgd8_970 VPS13 like protein involved in vacuolar protein trafficking  Unknown Total		cgd8_550	large uncharacterized protein	1					1	0.438
Cgd8_700   predicted secreted protein, signal peptide with several threonines, possible mucin   Cgd8_720   hypothetical protein   Cgd8_740   prefoldin like molecular chaperone   Cgd8_760   predicted secreted protein, 1 or more transmembrane domain, signal peptide   Cgd8_770   hypothetical protein   Cgd8_830   hypothetical protein   Cgd8_830   hypothetical protein   Cgd8_970   VPS13 like protein involved in vacuolar protein trafficking   Cgd8_170   Cgd8_970   VPS13 like protein involved in vacuolar protein trafficking   Cgd8_170   Cgd8_970   VPS13 like protein involved in vacuolar protein trafficking   Cgd8_170   Cgd8_		cgd8_620	hypothetical protein	1					1	0.398
threonines, possible mucin cgd8_720 hypothetical protein cgd8_740 prefoldin like molecular chaperone cgd8_760 predicted secreted protein, 1 or more transmembrane domain, signal peptide cgd8_770 hypothetical protein cgd8_830 hypothetical protein cgd8_970 VPS13 like protein involved in vacuolar protein trafficking  Unknown Total  threonines, possible mucin 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		cgd8_660	large low complexity protein	1					1	0.494
cgd8_740		cgd8_700	, , , , ,	1					1	0.457
cgd8_760 predicted secreted protein, 1 or more transmembrane domain, signal peptide cgd8_770 hypothetical protein 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		-	1 * ' ' '	1					1	0.281
Signal peptide   Cgd8_770   hypothetical protein   1   1   0   0   0   0   0   0   0   0		cgd8_740	prefoldin like molecular chaperone	1					1	0.337
cgd8_770   hypothetical protein   1   1   0   1   0   0   0   0   0   0		cgd8_760	l' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '	1					1	0.512
cgd8_830       hypothetical protein       1       1       1       0       0       1       0       0       1       0		cgd8 770		1					1	0.384
cgd8_970   VPS13 like protein involved in vacuolar protein trafficking   1   1   0   1   1   0   1   1   0   1   1			*!	1					1	0.487
Unknown Total 612 211 196 185 148 1352 10			*!	1					1	0.438
	Uı	<b>-</b> _		612	211	196	185	148	1352	16.705
301 200 212 201 210 1010 2	Unknown Total			801	293	272	267	216	1849	20.490
Grand Total ### 481 481 481 481 3137 20	Grand Total			###	481	481	481	481	3137	26.292