Phyre2

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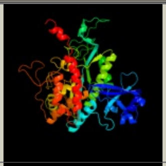
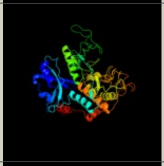
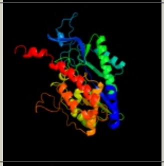
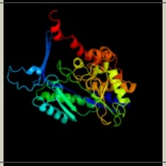
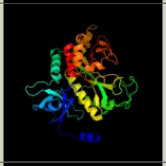
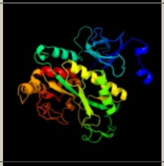
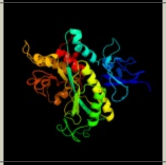
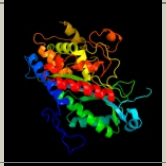
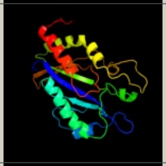
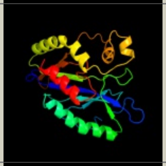
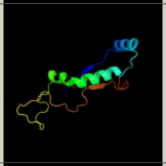
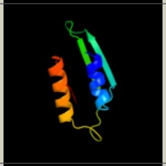
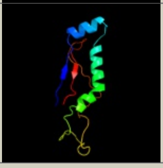
Description	P0A9C5
Date	Thu Jan 5 11:09:53 GMT 2012
Unique Job ID	e9961bc2c0d05e33

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fpyE_	Alignment		100.0	98	**PDB header:**ligase **Chain:** E: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
2	c3ng0A_	Alignment		100.0	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
3	c1htoB_	Alignment		100.0	52	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
4	c2j9iL_	Alignment		100.0	28	**PDB header:**ligase **Chain:** L: **PDB Molecule:**glutamate-ammonia ligase domain-containing **PDBTitle:** lengsin is a survivor of an ancient family of class i2 glutamine synthetases in eukaryotes that has undergone3 evolutionary re-engineering for a tissue-specific role4 in the vertebrate eye lens.
5	d1f52a2	Alignment		100.0	97	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamine synthetase catalytic domain
6	d2bvca2	Alignment		100.0	54	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamine synthetase catalytic domain
7	c2qc8J_	Alignment		100.0	26	**PDB header:**ligase **Chain:** J: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
8	c2d3aJ_	Alignment		100.0	20	**PDB header:**ligase **Chain:** J: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
9	c3fkyD_	Alignment		100.0	22	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
10	c3o6xC_	Alignment		100.0	23	**PDB header:**ligase **Chain:** C: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
11	d1f52a1	Alignment		99.9	100	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Glutamine synthetase, N-terminal domain **Family:**Glutamine synthetase, N-terminal domain

12	d2bvca1	Alignment		99.9	45	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Glutamine synthetase, N-terminal domain **Family:**Glutamine synthetase, N-terminal domain
13	c1tt4B_	Alignment		99.0	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
14	d1tt4a_	Alignment		98.9	23	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase family 2 (GCS2)
15	d1r8ga_	Alignment		98.9	24	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase family 2 (GCS2)
16	c2gwcE_	Alignment		97.9	17	**PDB header:**ligase **Chain:** E: **PDB Molecule:**glutamate cysteine ligase; **PDBTitle:** crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
17	c3ln7A_	Alignment		65.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
18	c2p6yA_	Alignment		39.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein vca0587; **PDBTitle:** x-ray structure of the protein q9km02_vibch from vibrio cholerae at2 the resolution 1.63 a. northeast structural genomics consortium3 target vcr80.
19	d1u8sa2	Alignment		27.5	5	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
20	c3ln6A_	Alignment		25.6	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
21	c1a8pA_	Alignment	not modelled	24.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
22	c3it5B_	Alignment	not modelled	24.6	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
23	d1prtb1	Alignment	not modelled	20.3	13	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
24	c3hwuA_	Alignment	not modelled	19.9	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of putative dna-binding protein (yp_299413.1) from2 ralstonia eutropha jmp134 at 1.30 a resolution
25	c3htnA_	Alignment	not modelled	17.2	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative dna binding protein; **PDBTitle:** crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
26	c2qw5B_	Alignment	not modelled	16.9	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
27	d1xv2a_	Alignment	not modelled	16.3	33	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**Alpha-acetolactate decarboxylase-like
28	c2z2yA_	Alignment	not modelled	16.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688;

28	c2z2vA_	Alignment	not modelled	16.0	15	**PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
29	d2z1ea1	Alignment	not modelled	15.6	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
30	c2f59B_	Alignment	not modelled	15.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
31	d1z2la2	Alignment	not modelled	13.6	8	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
32	c2gu1A_	Alignment	not modelled	13.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
33	d1a8pa2	Alignment	not modelled	13.1	23	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
34	d1ysja2	Alignment	not modelled	12.8	18	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
35	c3r1kA_	Alignment	not modelled	12.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**enhanced intracellular survival protein; **PDBTitle:** crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
36	c1bcpH_	Alignment	not modelled	11.8	13	**PDB header:**toxin **Chain:** H: **PDB Molecule:**pertussis toxin; **PDBTitle:** binary complex of pertussis toxin and atp
37	d2h6la1	Alignment	not modelled	11.8	20	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**AF0104-like
38	d1u8sa1	Alignment	not modelled	11.6	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
39	c2dt4A_	Alignment	not modelled	11.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph0802; **PDBTitle:** crystal structure of pyrococcus horikoshii a plant- and prokaryote-2 conserved (ppc) protein at 1.60 resolution
40	d1d4oa_	Alignment	not modelled	11.0	25	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
41	c2jy5A_	Alignment	not modelled	10.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
42	d1jqoa_	Alignment	not modelled	10.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
43	c1jqoA_	Alignment	not modelled	10.7	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
44	c1pt9B_	Alignment	not modelled	10.4	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
45	d1c41a_	Alignment	not modelled	10.2	7	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
46	c2hv2D_	Alignment	not modelled	9.8	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of conserved protein of unknown function from2 enterococcus faecalis v583 at 2.4 a resolution, probable n-3 acyltransferase
47	c2bruC_	Alignment	not modelled	9.8	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
48	d1pnoa_	Alignment	not modelled	9.6	33	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
49	c2pebB_	Alignment	not modelled	9.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative dioxygenase; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
50	d1owxa_	Alignment	not modelled	9.4	20	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
51	c3ixzB_	Alignment	not modelled	9.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
52	c3mpoD_	Alignment	not modelled	9.2	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
						PDB header:structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23;

53	c2hsiB_	Alignment	not modelled	9.2	31	**PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
54	d1zpva1	Alignment	not modelled	8.8	7	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
55	c3hzrD_	Alignment	not modelled	8.8	10	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
56	c3zvkG_	Alignment	not modelled	8.7	17	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
57	c1u8sB_	Alignment	not modelled	8.5	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
58	c3ke2A_	Alignment	not modelled	8.5	38	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
59	d1nqua_	Alignment	not modelled	8.3	11	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
60	c3fpkB_	Alignment	not modelled	8.2	4	**PDB header:**flavoprotein, oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
61	d1jjcb2	Alignment	not modelled	8.2	22	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
62	d1ejba_	Alignment	not modelled	8.2	14	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
63	c2btwA_	Alignment	not modelled	8.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alr0975 protein; **PDBTitle:** crystal structure of alr0975
64	c3mz2A_	Alignment	not modelled	7.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdi_3922) from parabacteroides distasonis atcc 8503 at 1.55 a3 resolution
65	d1di0a_	Alignment	not modelled	7.0	11	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
66	d1rvv1_	Alignment	not modelled	7.0	11	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
67	d1e4ia_	Alignment	not modelled	7.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
68	c2kjwA_	Alignment	not modelled	6.9	17	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
69	d2hq9a1	Alignment	not modelled	6.8	23	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
70	d1aq0a_	Alignment	not modelled	6.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
71	c3bzjA_	Alignment	not modelled	6.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
72	c2vxeA_	Alignment	not modelled	6.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cg10686-pa; **PDBTitle:** solution structure of the lsm domain of drosophila2 melanogaster tral (trailer hitch)
73	d2hv2a2	Alignment	not modelled	6.5	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
74	c2eq7C_	Alignment	not modelled	6.4	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
75	d1prtc1	Alignment	not modelled	6.4	20	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
76	d2cyua1	Alignment	not modelled	6.3	10	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
77	d1m5wa_	Alignment	not modelled	6.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
						PDB header:transferase **Chain:** H: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase

78	c2obxH_	Alignment	not modelled	6.1	19	1; **PDBTitle:** lumazine synthase ribh2 from mesorhizobium loti (gene mll7281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
79	c2nyiB_	Alignment	not modelled	6.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
80	c3b8eB_	Alignment	not modelled	6.0	17	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
81	c3gk0H_	Alignment	not modelled	5.9	12	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
82	c3tr3A_	Alignment	not modelled	5.9	5	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola; **PDBTitle:** structure of a bola protein homologue from coxiella burnetii
83	c3dcgF_	Alignment	not modelled	5.8	63	**PDB header:**ligase/viral protein **Chain:** F: **PDB Molecule:**virion infectivity factor; **PDBTitle:** crystal structure of the hiv vif bc-box in complex with human elonginb2 and elonginc
84	c3n7zD_	Alignment	not modelled	5.7	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase from bacillus anthracis
85	c2k6xA_	Alignment	not modelled	5.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
86	d2cyga1	Alignment	not modelled	5.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
87	d1gvha3	Alignment	not modelled	5.4	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
88	c2k4vA_	Alignment	not modelled	5.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1076; **PDBTitle:** solution structure of uncharacterized protein pa1076 from2 pseudomonas aeruginosa. northeast structural genomics3 consortium (nesg) target pat3, ontario center for4 structural proteomics target pa1076 .
89	d1t3ba2	Alignment	not modelled	5.4	7	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
90	d2bu3a1	Alignment	not modelled	5.4	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Phytochelatin synthase
91	c2ig6B_	Alignment	not modelled	5.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nimc/nima family protein; **PDBTitle:** crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
92	d1wzca1	Alignment	not modelled	5.3	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
93	d2i00a2	Alignment	not modelled	5.3	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
94	d1ug6a_	Alignment	not modelled	5.2	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
95	d1wmxb_	Alignment	not modelled	5.2	50	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
96	d2c0ra1	Alignment	not modelled	5.2	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
97	d1eeja2	Alignment	not modelled	5.2	19	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
98	c1xs3A_	Alignment	not modelled	5.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein xc975; **PDBTitle:** solution structure analysis of the xc975 protein
99	d1jqna_	Alignment	not modelled	5.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase