Phyre^2

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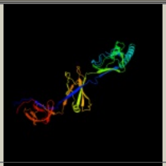
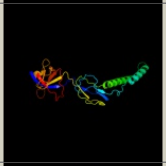
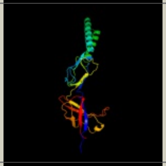
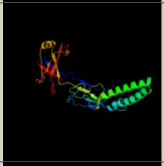
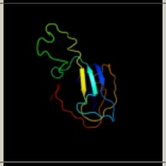
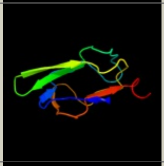
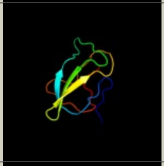
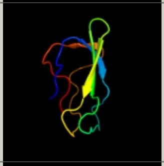
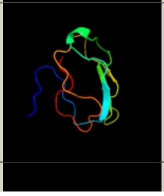
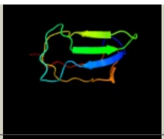
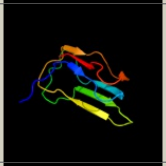
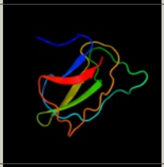
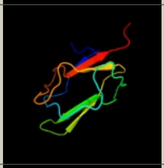
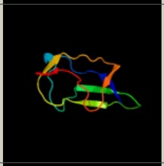
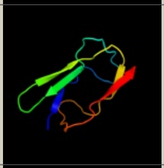
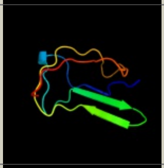
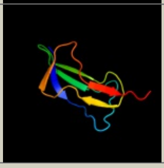
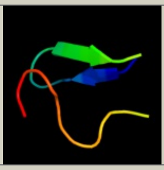
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h9iB_	Alignment		100.0	100	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cation efflux system protein cusb; **PDBTitle:** crystal structure of the membrane fusion protein cusb from escherichia2 coli
2	c2f1mA_	Alignment		99.9	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
3	c3lnnB_	Alignment		99.9	22	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
4	c3fppB_	Alignment		99.9	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
5	c1t5eB_	Alignment		99.9	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
6	d1vf7a_	Alignment		99.9	19	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
7	c2k33A_	Alignment		99.4	17	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
8	c2b8gA_	Alignment		98.5	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein; **PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
9	d1dcza_	Alignment		98.4	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
10	c2ejgD_	Alignment		98.4	27	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
11	d1o78a_	Alignment		98.2	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains

12	c2ejmA_	Alignment		98.1	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
13	c3n6rK_	Alignment		98.0	26	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
14	c2dn8A_	Alignment		98.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
15	c2kccA_	Alignment		97.9	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
16	d1qjoa_	Alignment		97.8	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
17	d1ghja_	Alignment		97.8	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
18	d1k8ma_	Alignment		97.7	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
19	d1bdoa_	Alignment		97.7	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
20	d1iyua_	Alignment		97.7	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
21	c2q8iB_	Alignment	not modelled	97.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
22	d1y8ob1	Alignment	not modelled	97.7	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
23	c2l5tA_	Alignment	not modelled	97.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
24	c2dncA_	Alignment	not modelled	97.5	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
25	d1laba_	Alignment	not modelled	97.4	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
26	d1gjxa_	Alignment	not modelled	97.3	28	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
27	c2dneA_	Alignment	not modelled	97.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
28	d1pmra_	Alignment	not modelled	96.8	15	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains

29	c3fmcC_	Alignment	not modelled	96.0	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
30	c2qj8B_	Alignment	not modelled	95.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
31	c3na6A_	Alignment	not modelled	94.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
32	d2pnrc1	Alignment	not modelled	93.9	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
33	d2tpta3	Alignment	not modelled	93.3	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
34	c2dsjA_	Alignment	not modelled	92.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
35	c2qf7A_	Alignment	not modelled	91.7	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
36	d1uoua3	Alignment	not modelled	91.5	22	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
37	c1otpA_	Alignment	not modelled	91.4	19	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
38	d1brwa3	Alignment	not modelled	91.4	33	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
39	c3iftA_	Alignment	not modelled	89.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
40	d1glaf_	Alignment	not modelled	89.6	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
41	d2gpra_	Alignment	not modelled	89.6	15	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
42	d2f3ga_	Alignment	not modelled	89.2	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
43	c3mxuA_	Alignment	not modelled	89.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
44	c1yuzB_	Alignment		89.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
45	c1brwB_	Alignment	not modelled	88.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
46	c3h5qA_	Alignment	not modelled	87.7	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
47	c2j0fC_	Alignment	not modelled	87.2	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
48	d1gpra_	Alignment	not modelled	86.5	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
49	c1dvbA_	Alignment		85.0	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
50	c2jkuA_	Alignment	not modelled	84.5	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
						PDB header:metal binding protein

51	c2hr5B_	Alignment	not modelled	83.5	23	**Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
52	c3cdxB_	Alignment	not modelled	83.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
53	c2hsiB_	Alignment	not modelled	82.1	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
54	c2gu1A_	Alignment	not modelled	80.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
55	d1qwya_	Alignment	not modelled	76.9	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
56	c2aukA_	Alignment	not modelled	74.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
57	d1o4ua2	Alignment	not modelled	67.7	10	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
58	c2b44A_	Alignment	not modelled	67.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
59	c3d4rE_	Alignment	not modelled	66.4	29	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family; **PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
60	c2xhaB_	Alignment	not modelled	65.9	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
61	d1yuja_	Alignment	not modelled	65.2	18	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
62	d1e2wa2	Alignment	not modelled	64.1	31	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
63	d1ci3m2	Alignment	not modelled	64.1	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
64	d1onla_	Alignment	not modelled	63.3	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
65	d1qpoa2	Alignment	not modelled	62.8	21	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
66	c2edgA_	Alignment	not modelled	62.5	23	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
67	c3it5B_	Alignment	not modelled	61.3	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
68	c1ctmA_	Alignment	not modelled	60.7	16	**PDB header:**electron transport(cytochrome) **Chain:** A: **PDB Molecule:**cytochrome f; **PDBTitle:** crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
69	d1qapa2	Alignment	not modelled	59.5	20	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
70	d1yuza2	Alignment	not modelled	59.0	18	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
71	c2xhcA_	Alignment	not modelled	58.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
72	d1nnqa2	Alignment	not modelled	56.5	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
73	d1hpca_	Alignment	not modelled	55.9	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
74	c3a8jF_	Alignment	not modelled	53.6	23	**PDB header:**transferase/transport protein **Chain:** F: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of et-ehred complex

75	d1dgsa1	Alignment		53.1	33	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
76	d1ep3b1	Alignment	not modelled	49.2	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
77	c3nyyA_	Alignment	not modelled	48.6	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm; **PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
78	c2aujD_	Alignment	not modelled	48.5	44	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
79	d2cu8a1	Alignment	not modelled	43.0	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
80	d1lkoa2	Alignment	not modelled	42.9	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
81	c1e2vB_	Alignment	not modelled	42.5	31	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
82	c2jxmB_	Alignment	not modelled	41.4	38	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
83	c3iynM_	Alignment	not modelled	41.0	22	**PDB header:**virus **Chain:** M: **PDB Molecule:**penton base protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
84	d2i4sa1	Alignment	not modelled	40.7	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
85	c2bldD_	Alignment	not modelled	40.6	22	**PDB header:**virus **Chain:** D: **PDB Molecule:**penton protein; **PDBTitle:** the quasi-atomic model of human adenovirus type 52 capsid (part 1)
86	c2zpmA_	Alignment	not modelled	40.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
87	d1krha1	Alignment	not modelled	40.5	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
88	c3csqC_	Alignment	not modelled	39.8	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
89	c2owoA_	Alignment	not modelled	38.9	25	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
90	d2j01q1	Alignment	not modelled	38.5	10	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
91	c2kjpA_	Alignment	not modelled	38.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ylbl; **PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
92	c3ndjA_	Alignment	not modelled	37.8	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
93	c1v9pB_	Alignment	not modelled	37.4	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
94	c1q90A_	Alignment	not modelled	36.7	31	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
95	c1tu2B_	Alignment	not modelled	36.7	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**apocytochrome f; **PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
96	d1pvma3	Alignment	not modelled	36.2	24	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
97	c1dgsB_	Alignment	not modelled	35.0	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
98	d2i6va1	Alignment	not modelled	33.8	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
99	d2gmga1	Alignment	not modelled	33.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family:PF0610-like
100	c2e75C_	Alignment	not modelled	32.8	25	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**apocytochrome f; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
101	c2ftcl_	Alignment	not modelled	31.6	15	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**mitochondrial ribosomal protein l16; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
102	d1qfja1	Alignment	not modelled	29.9	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
103	d1hf2a1	Alignment	not modelled	29.7	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Cell-division inhibitor MinC, C-terminal domain **Family:**Cell-division inhibitor MinC, C-terminal domain
104	d1tu2b2	Alignment	not modelled	29.4	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
105	c3bboO_	Alignment	not modelled	29.2	14	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**ribosomal protein l16; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
106	d1sota1	Alignment	not modelled	29.1	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
107	c2kl1A_	Alignment	not modelled	26.9	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ylbl protein; **PDBTitle:** solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
108	c2k5cA_	Alignment	not modelled	26.4	33	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
109	d1akya2	Alignment	not modelled	25.5	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
110	d2ak3a2	Alignment	not modelled	25.3	23	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
111	c3i18A_	Alignment	not modelled	25.0	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2051 protein; **PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b
112	d1hcza2	Alignment	not modelled	24.7	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
113	d1jj2h_	Alignment	not modelled	24.5	4	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
114	d1e4va2	Alignment	not modelled	24.4	23	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
115	d1ky9a1	Alignment	not modelled	24.4	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
116	d1j1la_	Alignment	not modelled	23.7	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
117	c1w8xP_	Alignment	not modelled	22.9	19	**PDB header:**virus **Chain:** P: **PDB Molecule:**protein p16; **PDBTitle:** structural analysis of prd1
118	d2epqa1	Alignment	not modelled	22.7	30	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
119	d1ffkf_	Alignment	not modelled	21.4	0	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
120	d1uwfa1	Alignment	not modelled	21.1	18	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits