Phyre2

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Description	P0AFS9
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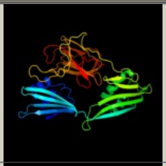
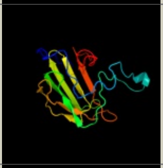
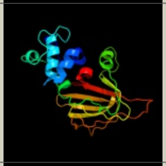
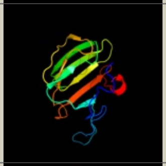
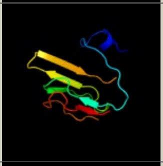
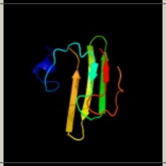
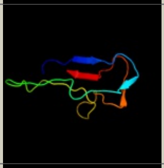
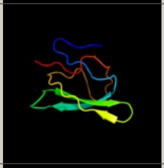
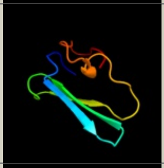
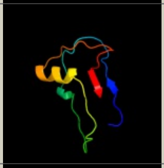
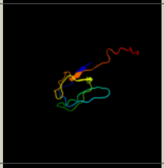
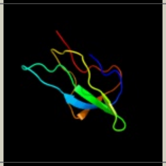
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gu1A_	Alignment		100.0	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
2	c2hsiB_	Alignment		100.0	37	**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
3	c3nyyA_	Alignment		100.0	21	**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
4	d1qwya_	Alignment		100.0	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
5	c2b44A_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
6	c3it5B_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
7	c3csqC_	Alignment		99.9	23	**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
8	d2f3ga_	Alignment		97.1	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
9	d1glaf_	Alignment		97.0	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
10	d2gpra_	Alignment		96.7	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
11	d1gpra_	Alignment		96.7	15	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like

12	c2aukA_	Alignment		95.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
13	d1brwa3	Alignment		93.8	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
14	d1dcza_	Alignment		93.3	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
15	d1ci3m2	Alignment		93.3	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
16	d1e2wa2	Alignment		93.2	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
17	d2tpta3	Alignment		92.5	20	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
18	c2kccA_	Alignment		92.2	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
19	c2ejgD_	Alignment		91.9	21	**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
20	c1otpA_	Alignment		91.6	20	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
21	c2j0fC_	Alignment	not modelled	91.6	25	**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
22	c1e2vB_	Alignment	not modelled	91.4	17	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
23	c1ctmA_	Alignment	not modelled	91.1	17	**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
24	c1q90A_	Alignment	not modelled	90.7	17	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
25	c3h5qA_	Alignment	not modelled	90.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
26	c2jxmB_	Alignment	not modelled	90.2	16	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
27	d1bdoa_	Alignment	not modelled	90.0	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
28	c2b8gA_	Alignment	not modelled	90.0	17	**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)
						Fold:alpha/beta-Hammerhead

29	d1uoua3	Alignment	not modelled	89.9	22	**Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
30	c3n6rK_	Alignment	not modelled	89.5	25	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
31	c2dsjA_	Alignment	not modelled	88.2	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
32	c1tu2B_	Alignment	not modelled	87.2	16	**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
33	d1ghja_	Alignment	not modelled	87.2	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
34	c3lnnB_	Alignment	not modelled	87.1	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
35	c1t5eB_	Alignment	not modelled	86.8	30	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
36	c2k33A_	Alignment	not modelled	86.2	30	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
37	c2f1mA_	Alignment	not modelled	86.1	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
38	c1brwB_	Alignment	not modelled	85.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
39	d1o78a_	Alignment	not modelled	85.2	39	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
40	c3fppB_	Alignment	not modelled	84.7	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
41	d1vf7a_	Alignment	not modelled	84.7	27	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
42	d1iyua_	Alignment	not modelled	84.2	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
43	c2aujD_	Alignment	not modelled	83.4	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
44	d1qjoa_	Alignment	not modelled	83.4	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
45	c2ejmA_	Alignment	not modelled	82.5	13	**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
46	c3camB_	Alignment	not modelled	82.4	23	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cold-shock domain family protein; **PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis
47	c2q8iB_	Alignment	not modelled	81.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
48	d1tu2b2	Alignment	not modelled	80.8	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
49	c2qf7A_	Alignment	not modelled	80.3	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
50	c2dn8A_	Alignment	not modelled	80.1	22	**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
51	c2l5tA_	Alignment	not modelled	79.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
52	d1y8ob1	Alignment	not modelled	79.2	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
53	d1laba_	Alignment	not modelled	78.5	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
						Fold: Barrel-sandwich hybrid

54	d1gjxa_	Alignment	not modelled	77.8	16	**Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
55	c2e75C_	Alignment	not modelled	75.6	17	**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
56	d1k8ma_	Alignment	not modelled	75.3	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
57	c3fmcC_	Alignment	not modelled	75.3	20	**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
58	d2pnrc1	Alignment	not modelled	74.7	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
59	c2qj8B_	Alignment	not modelled	74.2	8	**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
60	c2dneA_	Alignment	not modelled	73.8	30	**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
61	c2dncA_	Alignment	not modelled	73.4	30	**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
62	c3h9iB_	Alignment	not modelled	72.5	22	**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
63	d1h95a_	Alignment	not modelled	72.5	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
64	c3aqqD_	Alignment	not modelled	71.9	20	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**calcium-regulated heat stable protein 1; **PDBTitle:** crystal structure of human crhsp-24
65	c2vbcA_	Alignment	not modelled	69.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
66	c3a0jB_	Alignment	not modelled	68.6	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
67	c2jkuA_	Alignment	not modelled	67.0	37	**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
68	d2es2a1	Alignment	not modelled	66.9	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
69	d1pmra_	Alignment	not modelled	66.3	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
70	c3na6A_	Alignment	not modelled	62.2	27	**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
71	d1mjca_	Alignment	not modelled	59.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
72	d1c9oa_	Alignment	not modelled	58.8	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	c2ytyA_	Alignment	not modelled	57.7	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1; **PDBTitle:** solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein)
74	c3cdxB_	Alignment	not modelled	56.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
75	d1g6pa_	Alignment	not modelled	56.4	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
76	c2bh8B_	Alignment	not modelled	56.2	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
77	c3ozxA_	Alignment	not modelled	56.1	15	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
78	c2k5nA_	Alignment	not modelled	56.1	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cold-shock protein; **PDBTitle:** solution nmr structure of the n-terminal domain of protein2 eca1580 from erwinia carotovora, northeast structural3

						genomics consortium target ewr156a
79	c2q6oB_	Alignment	not modelled	54.7	31	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** sall-y70t with sam and cl
80	c2zbvC_	Alignment	not modelled	54.6	22	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermotoga2 maritima
81	d1o4ua2	Alignment	not modelled	53.7	21	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
82	c2xoaA_	Alignment	not modelled	52.8	34	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1)
83	c1rqrA_	Alignment	not modelled	51.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-fluoro-5'-deoxyadenosine synthase; **PDBTitle:** crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex
84	c1xjvA_	Alignment	not modelled	51.1	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protection of telomeres 1; **PDBTitle:** crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)
85	d1qapa2	Alignment	not modelled	48.3	11	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
86	c3ilaG_	Alignment	not modelled	48.0	34	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
87	c3n9tA_	Alignment	not modelled	46.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pnpc; **PDBTitle:** cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
88	c3trzE_	Alignment	not modelled	46.0	14	**PDB header:**rna binding protein/rna **Chain:** E: **PDB Molecule:**protein lin-28 homolog a; **PDBTitle:** mouse lin28a in complex with let-7d microrna pre-element
89	d1e0ga_	Alignment	not modelled	45.9	31	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
90	c2l9yA_	Alignment	not modelled	45.7	24	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
91	c1wu8B_	Alignment	not modelled	44.6	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph0463; **PDBTitle:** crystal structure of project ph0463 from pyrococcus horikoshii ot3
92	c1wydB_	Alignment	not modelled	44.5	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
93	d2ns0a1	Alignment	not modelled	43.5	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
94	d1qpoa2	Alignment	not modelled	41.5	21	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
95	c3a5dB_	Alignment	not modelled	41.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase alpha chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
96	d1mzya2	Alignment	not modelled	41.3	30	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
97	c1fpyE_	Alignment	not modelled	40.0	35	**PDB header:**ligase **Chain:** E: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
98	c1b8aB_	Alignment	not modelled	39.9	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
99	c1htoB_	Alignment	not modelled	39.2	35	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
100	d1hcza2	Alignment	not modelled	39.0	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
101	c2djpA_	Alignment	not modelled	37.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
102	c3imiB_	Alignment	not modelled	37.5	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
103	c2ywfA_	Alignment	not modelled	36.7	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
104	d2ijob1	Alignment	not modelled	35.7	31	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases

105	c3n7xA_	Alignment	not modelled	35.3	23	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** crystal structure of penaeus stylirostris densovirus capsid
106	c3qr5B_	Alignment	not modelled	35.3	27	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**cardiac ca2+ release channel; **PDBTitle:** structure of the first domain of a cardiac ryanodine receptor mutant2 with exon 3 deleted
107	c3o0mB_	Alignment	not modelled	35.1	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
108	d1f52a2	Alignment	not modelled	35.0	30	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamine synthetase catalytic domain
109	d1rqpa1	Alignment	not modelled	33.9	14	**Fold:**Bacterial fluorinating enzyme, C-terminal domain **Superfamily:**Bacterial fluorinating enzyme, C-terminal domain **Family:**Bacterial fluorinating enzyme, C-terminal domain
110	d1uwfa1	Alignment	not modelled	33.9	23	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
111	d2awna2	Alignment	not modelled	33.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
112	c2kcmA_	Alignment	not modelled	33.8	18	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**cold shock domain family protein; **PDBTitle:** solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
113	d1k82a2	Alignment	not modelled	32.8	14	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
114	c2ghiD_	Alignment	not modelled	32.4	34	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport protein; **PDBTitle:** crystal structure of plasmodium yoelii multidrug resistance2 protein 2
115	c2xhaB_	Alignment	not modelled	32.0	26	**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)
116	d3pccm_	Alignment	not modelled	31.8	20	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
117	c1x65A_	Alignment	not modelled	31.7	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**unr protein; **PDBTitle:** solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
118	c3e3xA_	Alignment	not modelled	31.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bipa; **PDBTitle:** the c-terminal part of bipa protein from vibrio parahaemolyticus rimd2 2210633
119	c2quoA_	Alignment	not modelled	31.1	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**heat-labile enterotoxin b chain; **PDBTitle:** crystal structure of c terminal fragment of clostridium2 perfringens enterotoxin
120	c2j9iL_	Alignment	not modelled	30.7	20	**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.