Phyre^2

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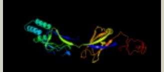
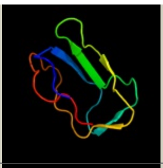
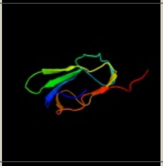
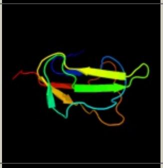
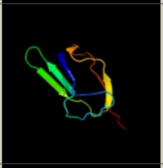
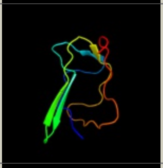
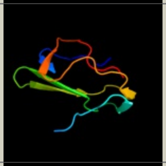
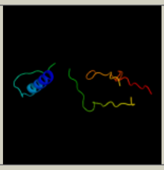
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fppB_	Alignment		100.0	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
2	c3h9iB_	Alignment		100.0	15	**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
3	c2f1mA_	Alignment		99.9	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
4	c3lnnB_	Alignment		99.9	21	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
5	c1t5eB_	Alignment		99.9	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
6	d1vf7a_	Alignment		99.9	21	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
7	c2k33A_	Alignment		99.6	27	**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		98.6	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	c3n6rK_	Alignment		98.5	42	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
10	d1dcza_	Alignment		98.5	54	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
11	c2ejgD_	Alignment		98.4	33	**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

12	d1o78a_	Alignment		98.3	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
13	c2ejmA_	Alignment		98.3	48	**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
14	c2dn8A_	Alignment		98.1	13	**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		98.0	19	**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		98.0	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
17	d1iyua_	Alignment		97.9	34	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
18	d1k8ma_	Alignment		97.9	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
19	d1bdoa_	Alignment		97.9	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
20	d1ghja_	Alignment		97.9	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
21	c2q8iB_	Alignment	not modelled	97.8	52	**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	c2l5tA_	Alignment	not modelled	97.7	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
23	d1y8ob1	Alignment	not modelled	97.7	52	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
24	c2dncA_	Alignment	not modelled	97.6	46	**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	97.5	37	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
26	d1gjxa_	Alignment	not modelled	97.4	34	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
27	d1pmra_	Alignment	not modelled	97.3	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
28	c2dneA_	Alignment	not modelled	97.1	48	**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
29	d1glaf_	Alignment	not modelled	95.9	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
30	d2gpra_	Alignment	not modelled	95.7	32	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
31	d2f3ga_	Alignment	not modelled	95.6	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
32	d1gpra_	Alignment	not modelled	95.4	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
33	d2pnrc1	Alignment	not modelled	95.2	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
34	c2qf7A_	Alignment	not modelled	95.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
35	c2jkuA_	Alignment	not modelled	94.7	20	**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
36	d1uoua3	Alignment	not modelled	93.3	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
37	d1brwa3	Alignment	not modelled	93.0	31	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
38	d2tpta3	Alignment	not modelled	92.0	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
39	c2dsjA_	Alignment	not modelled	91.1	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
40	c1otpA_	Alignment	not modelled	90.3	24	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
41	c3h5qA_	Alignment	not modelled	90.2	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
42	c2j0fC_	Alignment	not modelled	90.2	24	**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
43	c2gu1A_	Alignment	not modelled	90.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
44	c1brwB_	Alignment	not modelled	88.8	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
45	c3fmcC_	Alignment		88.7	17	**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
46	c2qj8B_	Alignment	not modelled	87.9	19	**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
47	c2hsiB_	Alignment	not modelled	86.1	17	**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
48	c2aukA_	Alignment	not modelled	83.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
49	c3cdxB_	Alignment	not modelled	82.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
50	d1qwya_	Alignment	not modelled	82.4	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
51	c3na6A_	Alignment	not modelled	81.8	16	**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

52	d1qpoa2	Alignment	not modelled	79.2	22	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
53	c2xhaB_	Alignment	not modelled	75.8	17	**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)
54	c1tqqC_	Alignment	not modelled	75.5	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**outer membrane protein tolc; **PDBTitle:** structure of tolc in complex with hexamminecobalt
55	d1e2wa2	Alignment	not modelled	75.2	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
56	c2b44A_	Alignment	not modelled	75.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
57	d1wp1a_	Alignment	not modelled	74.7	11	**Fold:**Outer membrane efflux proteins (OEP) **Superfamily:**Outer membrane efflux proteins (OEP) **Family:**Outer membrane efflux proteins (OEP)
58	d1o4ua2	Alignment	not modelled	74.4	15	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
59	d1ci3m2	Alignment	not modelled	73.9	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
60	c1yc9A_	Alignment	not modelled	73.7	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein; **PDBTitle:** the crystal structure of the outer membrane protein vcec from the2 bacterial pathogen vibrio cholerae at 1.8 resolution
61	d1tova_	Alignment	not modelled	73.3	16	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
62	d1ek9a_	Alignment	not modelled	73.1	11	**Fold:**Outer membrane efflux proteins (OEP) **Superfamily:**Outer membrane efflux proteins (OEP) **Family:**Outer membrane efflux proteins (OEP)
63	c3dtpA_	Alignment	not modelled	73.0	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
64	c3nyyA_	Alignment	not modelled	72.8	22	**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
65	d1qapa2	Alignment	not modelled	72.1	10	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
66	c3pikA_	Alignment	not modelled	71.8	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusc; **PDBTitle:** outer membrane protein cusc
67	c3it5B_	Alignment	not modelled	70.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
68	c2xhcA_	Alignment	not modelled	68.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
69	c2aujD_	Alignment	not modelled	68.6	31	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
70	d1ixda_	Alignment	not modelled	68.5	19	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
71	c3d4rE_	Alignment	not modelled	67.8	18	**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
72	d1whla_	Alignment	not modelled	67.6	23	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
73	d2cp2a1	Alignment	not modelled	66.7	19	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
74	d2coya1	Alignment	not modelled	66.7	22	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
75	d2cp6a1	Alignment	not modelled	66.4	21	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
76	d1whma_	Alignment	not modelled	65.2	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
						Fold:SH3-like barrel

77	d1whga_	Alignment	not modelled	64.5	16	**Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
78	c1y4cA_	Alignment	not modelled	63.4	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
79	c3gnnA_	Alignment	not modelled	62.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
80	c3ipkA_	Alignment	not modelled	62.5	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
81	c1h9mB_	Alignment	not modelled	62.0	22	**PDB header:**binding protein **Chain:** B: **PDB Molecule:**molybdenum-binding-protein; **PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
82	c3e1yG_	Alignment	not modelled	61.8	15	**PDB header:**translation **Chain:** G: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding subunit **PDBTitle:** crystal structure of human erf1/erf3 complex
83	c2qqsB_	Alignment	not modelled	61.5	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
84	c1o4uA_	Alignment	not modelled	61.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
85	c3ghgK_	Alignment	not modelled	58.4	6	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
86	d2cp3a1	Alignment	not modelled	58.2	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
87	c1h9sA_	Alignment	not modelled	58.1	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**molybdenum transport protein mode; **PDBTitle:** molybdate bound complex of dimop domain of mode from e.coli
88	c3dlmA_	Alignment	not modelled	57.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setdb1; **PDBTitle:** crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
89	d2ix0a1	Alignment	not modelled	57.9	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
90	c3pajA_	Alignment	not modelled	57.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
91	c1qapA_	Alignment	not modelled	57.1	10	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
92	c1deqF_	Alignment	not modelled	57.0	9	**PDB header:** **PDB COMPND:**
93	d2cp0a1	Alignment	not modelled	56.6	16	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
94	c1e2vB_	Alignment	not modelled	56.5	19	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
95	c3m9bK_	Alignment	not modelled	56.3	12	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
96	c3e20A_	Alignment	not modelled	56.0	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
97	c1ctmA_	Alignment	not modelled	56.0	6	**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
98	d1onla_	Alignment	not modelled	54.6	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
99	c2z0wA_	Alignment	not modelled	54.1	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cap-gly domain-containing linker protein 4; **PDBTitle:** crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
100	c2jxmB_	Alignment	not modelled	53.8	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f;

100		Alignment	not modelled			**PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
101	c3csqC_	Alignment	not modelled	53.8	12	**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
102	c2jbmA_	Alignment	not modelled	53.4	0	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
103	c1zeqX_	Alignment	not modelled	51.8	15	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
104	c2edgA_	Alignment	not modelled	51.8	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
105	c2xdpA_	Alignment	not modelled	51.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 4c; **PDBTitle:** crystal structure of the tudor domain of human jmjd2c
106	c3tqvA_	Alignment	not modelled	51.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
107	d2e3ha1	Alignment	not modelled	50.8	18	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
108	c1tu2B_	Alignment	not modelled	50.5	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
109	c2e4hA_	Alignment	not modelled	49.5	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**restin; **PDBTitle:** solution structure of cytoskeletal protein in complex with2 tubulin tail
110	c2b7pA_	Alignment	not modelled	48.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
111	c1ei3E_	Alignment	not modelled	46.4	8	**PDB header:** **PDB COMPND:**
112	c3l0gD_	Alignment	not modelled	46.3	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
113	c2e75C_	Alignment	not modelled	46.2	19	**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
114	d1tu2b2	Alignment	not modelled	45.5	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
115	c2d3eD_	Alignment	not modelled	45.0	7	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
116	c3ojaB_	Alignment	not modelled	43.1	8	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
117	c2jvvA_	Alignment	not modelled	42.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
118	c2kvqG_	Alignment	not modelled	42.9	26	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
119	c1qpoA_	Alignment	not modelled	41.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
120	d2hqha1	Alignment	not modelled	41.3	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain