Phyre^2

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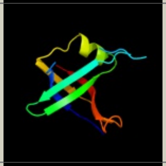
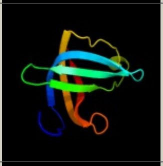
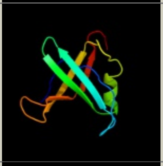
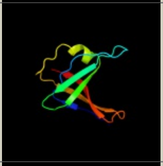
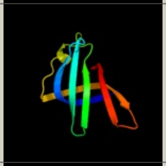
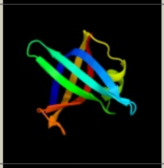
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kf6A_	Alignment		96.8	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
2	c1z9fA_	Alignment		96.4	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
3	c3bfjK_	Alignment		96.3	25	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
4	c3f2cA_	Alignment		95.9	20	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
5	c3ox4D_	Alignment		95.9	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
6	d1oj7a_	Alignment		95.9	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
7	d1vlja_	Alignment		95.9	19	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
8	d1v1qa_	Alignment		95.7	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
9	c2iheA_	Alignment		95.4	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
10	c3okfA_	Alignment		95.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
11	d1rrma_	Alignment		95.4	21	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase

12	d1o2da_	Alignment		95.3	26	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
13	d1bbua1	Alignment		95.2	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
14	c3qvjB_	Alignment		95.2	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
15	c3e0eA_	Alignment		95.1	24	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a; **PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
16	d1l0wa1	Alignment		95.0	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
17	d1gm5a2	Alignment		95.0	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
18	c3bjuB_	Alignment		95.0	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
19	c3hl0B_	Alignment		94.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
20	d1e1oa1	Alignment		94.7	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
21	c3jzdA_	Alignment	not modelled	94.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
22	d1jq5a_	Alignment	not modelled	94.7	22	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
23	d1n9wa1	Alignment	not modelled	94.6	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
24	c3tqyA_	Alignment	not modelled	94.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii
25	d1c0aa1	Alignment	not modelled	94.5	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
26	c3eivB_	Alignment	not modelled	94.4	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein 2; **PDBTitle:** crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor
27	c3gjzB_	Alignment	not modelled	94.4	8	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
28	d1ujna_	Alignment	not modelled	94.3	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS

29	c2ihfA_	Alignment	not modelled	94.1	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
30	c3fduF_	Alignment	not modelled	93.7	17	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
31	c2xgtB_	Alignment	not modelled	93.6	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
32	c3k8aA_	Alignment	not modelled	93.6	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative primosomal replication protein; **PDBTitle:** neisseria gonorrhoeae prib
33	d1eova1	Alignment	not modelled	93.4	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
34	d1ue1a_	Alignment	not modelled	93.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
35	c2eq5D_	Alignment	not modelled	93.4	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
36	c3en2A_	Alignment	not modelled	93.4	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
37	d2nu7b1	Alignment		93.4	18	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
38	c2vlbC_	Alignment	not modelled	93.3	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
39	d1txya_	Alignment	not modelled	93.2	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
40	c3moyA_	Alignment	not modelled	93.2	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
41	c2pi2A_	Alignment	not modelled	93.0	19	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
42	c3gkbA_	Alignment	not modelled	92.8	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis
43	c2vw9B_	Alignment	not modelled	92.6	21	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
44	c2qq3F_	Alignment	not modelled	92.6	20	**PDB header:**lyase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase subunit i; **PDBTitle:** crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426
45	c3uhjE_	Alignment	not modelled	92.6	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
46	d2pi2a1	Alignment	not modelled	92.5	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
47	c3ce9A_	Alignment	not modelled	92.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
48	c3iv7B_	Alignment	not modelled	92.1	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase iv; **PDBTitle:** crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
49	c1ta9A_	Alignment	not modelled	92.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
50	c3e9hB_	Alignment	not modelled	91.8	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
51	d1se8a_	Alignment	not modelled	91.8	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
52	c1se8A_	Alignment	not modelled	91.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein;

						PDBTitle: structure of single-stranded dna-binding protein (ssb) from d.2 radiodurans
53	c3mybA_	Alignment	not modelled	91.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase mycobacterium smegmatis
54	c1gm5A_	Alignment	not modelled	91.2	18	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
55	d1q52a_	Alignment	not modelled	91.2	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
56	c2ej5B_	Alignment	not modelled	91.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase subunit ii; **PDBTitle:** crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
57	c2iexA_	Alignment	not modelled	91.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxynapthoic acid synthetase; **PDBTitle:** crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
58	d1b8aa1	Alignment	not modelled	90.9	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
59	c3clhA_	Alignment	not modelled	90.7	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
60	c1rjnC_	Alignment	not modelled	90.6	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**menb; **PDBTitle:** the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa
61	d1uiya_	Alignment	not modelled	90.5	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
62	c2x58B_	Alignment	not modelled	90.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
63	d1ef8a_	Alignment	not modelled	90.4	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
64	d1qvca_	Alignment	not modelled	90.3	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
65	c3dm3A_	Alignment	not modelled	90.3	23	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor a; **PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
66	d1wdka4	Alignment	not modelled	90.3	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
67	c2issF_	Alignment	not modelled	90.2	24	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
68	c3h0uB_	Alignment	not modelled	90.2	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase from2 streptomyces avermitilis
69	d2nv0a1	Alignment	not modelled	90.2	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
70	c2ppyE_	Alignment	not modelled	90.0	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
71	c1ue7A_	Alignment	not modelled	90.0	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
72	d1eyga_	Alignment	not modelled	89.9	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
73	d1szoa_	Alignment	not modelled	89.9	31	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
74	c2vx2D_	Alignment	not modelled	89.8	26	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**enoyl-coa hydratase domain-containing protein 3; **PDBTitle:** crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)
75	c3h81A_	Alignment	not modelled	89.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa8; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
76	d3ulla_	Alignment	not modelled	89.8	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
77	d2auna2	Alignment	not modelled	89.7	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
						Fold: ClpP/crotonase

78	d2a7ka1	Alignment	not modelled	89.7	22	**Superfamily:**ClpP/crotonase **Family:**Crotonase-like
79	c2q35A_	Alignment	not modelled	89.7	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curf; **PDBTitle:** crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula
80	c3rf7A_	Alignment	not modelled	89.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
81	c2gruB_	Alignment	not modelled	89.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-deoxy-scyllo-inosose synthase; **PDBTitle:** crystal structure of 2-deoxy-scyllo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
82	c2fbmB_	Alignment	not modelled	89.5	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**y chromosome chromodomain protein 1, telomeric isoform b; **PDBTitle:** acetyltransferase domain of cdy1
83	c3lkeA_	Alignment	not modelled	89.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus2 halodurans
84	c3hrxD_	Alignment	not modelled	89.3	24	**PDB header:**lyase **Chain:** D: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of phenylacetic acid degradation protein paag
85	d1jvna2	Alignment	not modelled	89.1	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
86	c3g64A_	Alignment	not modelled	89.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
87	c3omeE_	Alignment	not modelled	89.0	26	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
88	c3rsiA_	Alignment	not modelled	88.9	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
89	d1hzda_	Alignment	not modelled	88.8	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
90	d1zl0a2	Alignment	not modelled	88.5	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
91	c3pgzB_	Alignment	not modelled	88.4	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of a single strand binding protein (ssb) from2 bartonella henselae
92	c2k50A_	Alignment	not modelled	88.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
93	c2kenA_	Alignment	not modelled	88.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
94	c3kojA_	Alignment	not modelled	88.0	5	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ycf41; **PDBTitle:** crystal structure of the ssb domain of q5n255_synp6 protein2 from synechococcus sp. northeast structural genomics3 consortium target snr59a.
95	c2j5gL_	Alignment	not modelled	87.9	29	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**alr4455 protein; **PDBTitle:** the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120
96	d1xx4a_	Alignment	not modelled	87.9	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
97	c3kklA_	Alignment	not modelled	87.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
98	c1zrsB_	Alignment	not modelled	87.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
99	c3bptA_	Alignment	not modelled	87.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyryl-coa hydrolase; **PDBTitle:** crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin
100	c3lgjA_	Alignment	not modelled	87.6	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
101	d1rjma_	Alignment	not modelled	87.4	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
102	d1nzya_	Alignment	not modelled	87.3	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
						PDB header:isomerase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase/isomerase family

103	c3kqfC_	Alignment	not modelled	86.8	17	protein; **PDBTitle:** 1.8 angstrom resolution crystal structure of enoyl-coa hydratase from2 bacillus anthracis.
104	d1eucb1	Alignment	not modelled	86.8	12	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
105	c3njbA_	Alignment	not modelled	86.8	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak
106	d1t3ta2	Alignment	not modelled	86.8	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
107	c3peaD_	Alignment	not modelled	86.6	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus anthracis str.2 'ames ancestor'
108	c3p5mB_	Alignment	not modelled	86.6	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
109	d1krta_	Alignment	not modelled	86.6	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
110	d2fw2a1	Alignment	not modelled	86.6	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
111	c1n9wA_	Alignment	not modelled	86.2	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
112	c2ywjA_	Alignment	not modelled	86.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
113	c3q1tB_	Alignment	not modelled	86.2	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium avium
114	c3l3sF_	Alignment	not modelled	86.2	19	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of an enoyl-coa hydrotase/isomerase family2 protein from silicibacter pomeroyi
115	c3sllC_	Alignment	not modelled	86.1	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
116	c3m4qA_	Alignment	not modelled	85.9	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
117	c2d3tB_	Alignment	not modelled	85.8	20	**PDB header:**lyase, oxidoreductase/transferase **Chain:** B: **PDB Molecule:**fatty oxidation complex alpha subunit; **PDBTitle:** fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
118	d2f6qa1	Alignment	not modelled	85.8	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
119	c1e22A_	Alignment	not modelled	85.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
120	c3r6hA_	Alignment	not modelled	85.5	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa3; **PDBTitle:** crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum