Phyre^2

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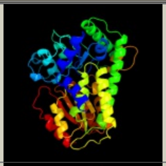
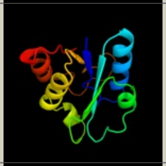
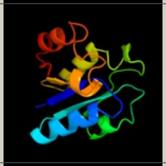
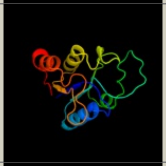
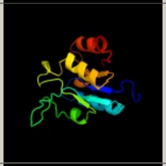
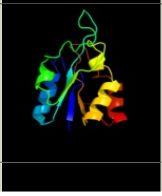
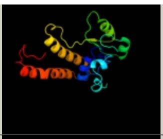
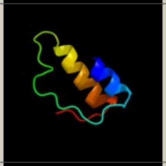
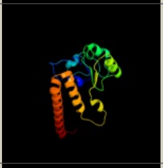
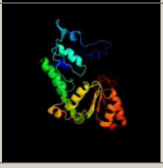
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3o3nB_	Alignment		100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
2	c3o3nA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
3	c2dwcB_	Alignment		91.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
4	c3ouzA_	Alignment		90.4	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
5	c2vpqA_	Alignment		89.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
6	c3g8cB_	Alignment		87.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
7	c2gpwC_	Alignment		87.4	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
8	d1m1nb_	Alignment		86.6	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
9	c1kjjA_	Alignment		86.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
10	c2pn1A_	Alignment		86.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
11	c1ulzA_	Alignment		83.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase

12	c3pshA_	Alignment		82.8	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein hi_1472; **PDBTitle:** classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)
13	d1n2za_	Alignment		81.4	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
14	c3pdiB_	Alignment		79.4	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
15	d1wo8a1	Alignment		78.0	20	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
16	c2dzdB_	Alignment		76.1	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
17	d1nu0a_	Alignment		73.9	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
18	c2r79A_	Alignment		73.7	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein from2 pseudomonas aeruginosa
19	c1m6vE_	Alignment		73.0	19	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
20	d1qh8b_	Alignment		71.0	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
21	c3gidB_	Alignment	not modelled	68.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a
22	c3u9sE_	Alignment	not modelled	67.8	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
23	c2vlbC_	Alignment	not modelled	67.6	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
24	d1m1na_	Alignment	not modelled	67.0	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
25	c2dgdD_	Alignment	not modelled	66.1	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
26	d1qh8a_	Alignment	not modelled	63.5	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
27	d1pq4a_	Alignment	not modelled	63.2	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
28	c2xdqA_	Alignment	not modelled	61.2	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex

29	d1a9xa4	Alignment	not modelled	59.9	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
30	d1tr9a_	Alignment	not modelled	57.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**NagZ-like
31	c3qg5D_	Alignment	not modelled	57.3	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
32	c2xecD_	Alignment	not modelled	55.9	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
33	c2yvqA_	Alignment	not modelled	55.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
34	d2phza1	Alignment	not modelled	54.6	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
35	c2phzA_	Alignment	not modelled	54.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-uptake system-binding protein; **PDBTitle:** crystal structure of iron-uptake system-binding protein2 feua from bacillus subtilis. northeast structural genomics3 target sr580.
36	d1uf3a_	Alignment	not modelled	54.6	8	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
37	d1vhxa_	Alignment	not modelled	54.3	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
38	c3bg5C_	Alignment	not modelled	54.1	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
39	c3opyH_	Alignment	not modelled	53.8	20	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
40	c3opyB_	Alignment	not modelled	53.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
41	c3s81A_	Alignment	not modelled	52.6	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
42	c3ke8A_	Alignment	not modelled	51.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
43	c2r7aC_	Alignment	not modelled	51.0	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bacterial heme binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
44	c2ip4A_	Alignment	not modelled	50.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
45	d2ajta2	Alignment	not modelled	48.8	10	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**AraA N-terminal and middle domain-like
46	d1iv0a_	Alignment	not modelled	48.2	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
47	c2hjwA_	Alignment	not modelled	47.6	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
48	d1m0wa1	Alignment	not modelled	46.1	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Eukaryotic glutathione synthetase, substrate-binding domain
49	d1j6xa_	Alignment	not modelled	44.7	27	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
50	c3t1iC_	Alignment	not modelled	43.2	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
51	c3gfvA_	Alignment	not modelled	42.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized abc transporter solute-binding **PDBTitle:** crystal structure of petrobactin-binding protein yclq from2 bacillu subtilis
52	c3n6rK_	Alignment	not modelled	41.4	11	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
53	c3cx3A_	Alignment	not modelled	41.2	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
54	c3rxyA	Alignment	not modelled	40.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nif3 protein;

54	c3fxyA_	Alignment	not modelled	40.8	18	**PDBTitle:** crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
55	c3lp8A_	Alignment	not modelled	38.8	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
56	d2j9ga2	Alignment	not modelled	38.7	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
57	c3md9A_	Alignment	not modelled	38.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hemin-binding periplasmic protein hmut; **PDBTitle:** structure of apo form of a periplasmic heme binding protein
58	c1gsoA_	Alignment	not modelled	38.0	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
59	c2xd4A_	Alignment	not modelled	37.8	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
60	c3dloC_	Alignment	not modelled	37.5	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
61	d1a9xa2	Alignment	not modelled	37.0	12	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
62	d1tq8a_	Alignment	not modelled	36.9	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
63	d2z3va1	Alignment	not modelled	36.4	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
64	c1fuiB_	Alignment	not modelled	36.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
65	d1mioa_	Alignment	not modelled	35.1	8	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
66	c3eiwA_	Alignment	not modelled	35.1	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**htsa protein; **PDBTitle:** crystal structure of staphylococcus aureus lipoprotein, htsa
67	c2a7vA_	Alignment	not modelled	34.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2
68	d2a7va1	Alignment	not modelled	34.2	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
69	c3cqyA_	Alignment	not modelled	33.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
70	c3qvjB_	Alignment	not modelled	33.6	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
71	d2auna1	Alignment	not modelled	33.5	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LD-carboxypeptidase A C-terminal domain-like **Family:**LD-carboxypeptidase A C-terminal domain-like
72	c3kalB_	Alignment	not modelled	32.8	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**homoglutathione synthetase; **PDBTitle:** structure of homoglutathione synthetase from glycine max in2 closed conformation with homoglutathione, adp, a sulfate3 ion, and three magnesium ions bound
73	c2ys6A_	Alignment	not modelled	32.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
74	c1w96B_	Alignment	not modelled	32.6	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
75	c3aerB_	Alignment	not modelled	32.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
76	c2ixaA_	Alignment	not modelled	31.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
77	c2ov3A_	Alignment	not modelled	31.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
78	c3opyE_	Alignment	not modelled	31.2	16	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
79	c1m0tB_	Alignment	not modelled	31.2	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutathione synthetase; **PDBTitle:** yeast glutathione synthase

80	c3hjtB_	Alignment	not modelled	31.1	15	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
81	c3hgmD_	Alignment	not modelled	30.8	10	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
82	c2qk4A_	Alignment	not modelled	30.6	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
83	c3g23A_	Alignment	not modelled	30.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ld-carboxypeptidase a; **PDBTitle:** crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
84	c2xdqB_	Alignment	not modelled	29.7	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
85	d1w3ia_	Alignment	not modelled	29.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
86	c3m4xA_	Alignment	not modelled	29.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
87	d1kjqa2	Alignment	not modelled	28.4	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
88	c2q8pA_	Alignment	not modelled	28.1	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron-regulated surface determinant e; **PDBTitle:** crystal structure of selenomethionine labelled s. aureus isde2 complexed with heme
89	c3gv0A_	Alignment	not modelled	27.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
90	c2xmoB_	Alignment	not modelled	27.7	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
91	d1vmda_	Alignment	not modelled	27.2	20	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
92	c3q9cF_	Alignment	not modelled	26.9	11	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetylpolyamine amidohydrolase; **PDBTitle:** crystal structure of h159a apah complexed with n8-acetylspermidine
93	c3ovkD_	Alignment	not modelled	26.9	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**aminopeptidase p, xaa-pro dipeptidase; **PDBTitle:** crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
94	c3opyG_	Alignment	not modelled	26.8	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
95	c3m6wA_	Alignment	not modelled	26.5	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
96	c3qocD_	Alignment	not modelled	26.3	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative metallopeptidase; **PDBTitle:** crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
97	c1b74A_	Alignment	not modelled	26.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
98	c3r1fO_	Alignment	not modelled	26.1	16	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
99	c3il0B_	Alignment	not modelled	25.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminopeptidase p; xaa-pro aminopeptidase; **PDBTitle:** the crystal structure of the aminopeptidase p,xaa-pro aminopeptidase2 from streptococcus thermophilus
100	d1lfpa_	Alignment	not modelled	25.6	11	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
101	c1k97A_	Alignment	not modelled	25.5	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
102	d1pv8a_	Alignment	not modelled	25.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
103	c2nytB_	Alignment	not modelled	25.4	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
104	d1jvna1	Alignment	not modelled	25.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel

						Family: Histidine biosynthesis enzymes
105	c1zrsB_	Alignment	not modelled	25.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
106	c3pn9C_	Alignment	not modelled	25.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proline dipeptidase; **PDBTitle:** crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
107	c2jfqA_	Alignment	not modelled	24.6	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
108	c1lw7A_	Alignment	not modelled	24.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulator nadr; **PDBTitle:** nadr protein from haemophilus influenzae
109	c2k4mA_	Alignment	not modelled	23.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium target3 tr8
110	d3bofa2	Alignment	not modelled	23.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
111	c3menC_	Alignment	not modelled	23.3	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**acetylpolyamine aminohydrolase; **PDBTitle:** crystal structure of acetylpolyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
112	c3dx5A_	Alignment	not modelled	23.2	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
113	c3av0A_	Alignment	not modelled	22.7	11	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
114	d1chma1	Alignment	not modelled	22.5	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
115	c1zp9A_	Alignment	not modelled	22.4	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rio1 kinase; **PDBTitle:** crystal structure of full-legnth a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
116	d1t6ca1	Alignment	not modelled	22.2	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
117	c2frxD_	Alignment	not modelled	22.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
118	c2jvrA_	Alignment	not modelled	22.0	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 3; **PDBTitle:** segmental isotope labeling of npl3p
119	d2d13a1	Alignment	not modelled	21.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
120	c3hfrA_	Alignment	not modelled	21.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes