Phyre2

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Description	P0A7V0
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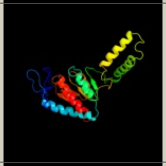
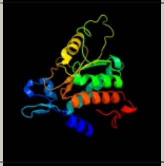
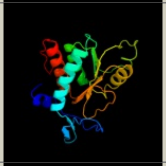
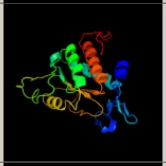
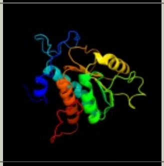
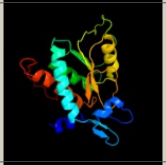
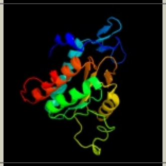
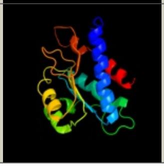
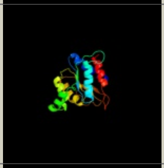
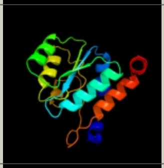
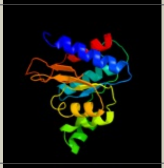
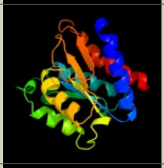
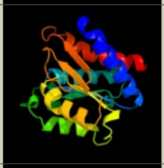
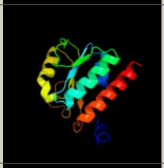
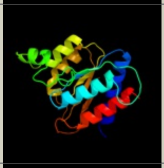
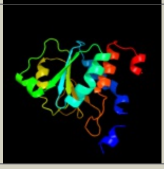
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2uubb1	Alignment		100.0	42	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
2	c3bbnB_	Alignment		100.0	41	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
3	d2gy9b1	Alignment		100.0	100	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
4	c3bchA_	Alignment		100.0	26	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
5	c3iz6A_	Alignment		100.0	28	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
6	d1vi6a_	Alignment		100.0	31	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
7	c2xznB_	Alignment		100.0	29	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rps0e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
8	c3izbA_	Alignment		100.0	27	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein rps0 (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
9	c2zkqb_	Alignment		100.0	24	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
10	c1s1hB_	Alignment		100.0	29	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
11	d1x94a_	Alignment		97.6	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain

12	d1tk9a_	Alignment		97.1	21	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
13	c2x3yA_	Alignment		97.1	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
14	c3shoA_	Alignment		95.8	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
15	d1x92a_	Alignment		95.5	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
16	c1nriA_	Alignment		94.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
17	d1nria_	Alignment		94.5	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
18	d1m3sa_	Alignment		93.6	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
19	c2yvaB_	Alignment		93.1	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
20	c2amlB_	Alignment		92.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
21	d1vima_	Alignment	not modelled	92.1	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
22	c3knzA_	Alignment	not modelled	90.1	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative sugar binding protein; **PDBTitle:** crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
23	c3trjC_	Alignment	not modelled	89.6	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
24	c3fxaA_	Alignment	not modelled	86.2	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
25	c2a3nA_	Alignment	not modelled	85.6	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
26	c2xhzC_	Alignment	not modelled	85.4	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
27	c3c65A_	Alignment	not modelled	83.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain

28	c3cvjB_	Alignment	not modelled	78.6	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
29	c2nrrA_	Alignment	not modelled	75.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal rnaseh endonuclase2 domain of uvrc
30	d1jeoa_	Alignment	not modelled	74.4	24	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
31	c3hgtA_	Alignment	not modelled	73.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hda1 complex subunit 3; **PDBTitle:** structural and functional studies of the yeast class ii hda12 hdac complex
32	d1j5xa_	Alignment	not modelled	72.0	10	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
33	c3etnD_	Alignment	not modelled	71.5	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
34	c3g68A_	Alignment	not modelled	69.4	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
35	d1kzyc2	Alignment	not modelled	66.5	20	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**53BP1
36	c3cf4A_	Alignment	not modelled	61.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
37	c3ga2A_	Alignment	not modelled	60.3	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
38	d1pjqa1	Alignment	not modelled	59.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
39	c2r7aC_	Alignment	not modelled	57.9	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bacterial heme binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
40	d2f9ya1	Alignment	not modelled	55.5	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
41	c2nrzB_	Alignment	not modelled	54.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
42	c2f9iC_	Alignment	not modelled	54.7	33	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
43	c2w36B_	Alignment	not modelled	50.4	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
44	d1l7ba_	Alignment	not modelled	49.3	21	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**DNA ligase
45	d1pixa3	Alignment	not modelled	48.4	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
46	c3gocB_	Alignment	not modelled	44.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
47	c2zj3A_	Alignment	not modelled	44.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
48	c1pixB_	Alignment	not modelled	43.1	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutaconyl-coa decarboxylase a subunit; **PDBTitle:** crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
49	c1xnwD_	Alignment	not modelled	42.3	20	**PDB header:**ligase **Chain:** D: **PDB Molecule:**propionyl-coa carboxylase complex b subunit; **PDBTitle:** acyl-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i
50	d1j6ua1	Alignment	not modelled	42.0	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
51	c2vpiA_	Alignment	not modelled	40.8	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
52	d1p3da1	Alignment	not modelled	40.6	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain

53	c3n6rF_	Alignment	not modelled	40.0	15	**PDB header:**ligase **Chain:** F: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
54	d1l5xa_	Alignment	not modelled	39.8	30	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
55	c3glmD_	Alignment	not modelled	36.6	21	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glutaconyl-coa decarboxylase subunit a; **PDBTitle:** glutaconyl-coa decarboxylase a subunit from clostridium2 symbiosum co-crystallized with crotonyl-coa
56	d1euca1	Alignment	not modelled	34.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
57	d1x9ia_	Alignment	not modelled	34.7	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
58	d2gv8a2	Alignment	not modelled	34.4	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
59	c1keeH_	Alignment	not modelled	34.1	37	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
60	d1xnya1	Alignment	not modelled	33.8	33	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
61	d2jfga1	Alignment	not modelled	33.1	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
62	c1vrgE_	Alignment	not modelled	33.0	28	**PDB header:**ligase **Chain:** E: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution
63	d1k9vf_	Alignment	not modelled	32.8	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
64	d1s3la_	Alignment	not modelled	32.7	26	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
65	c1s3mA_	Alignment	not modelled	32.7	26	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
66	d1on3a1	Alignment	not modelled	32.1	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
67	d1o6ca_	Alignment	not modelled	31.1	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
68	c3tqiB_	Alignment	not modelled	30.8	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
69	c3qk7C_	Alignment	not modelled	30.5	15	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
70	d1xnya2	Alignment	not modelled	30.4	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
71	c2puwA_	Alignment	not modelled	29.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
72	c3u9rB_	Alignment	not modelled	29.5	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**methylcrotonyl-coa carboxylase, beta-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit
73	c3euaD_	Alignment	not modelled	29.4	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
74	d1vrga1	Alignment	not modelled	29.2	39	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
75	d1b74a1	Alignment	not modelled	29.0	22	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
76	d2a7sa2	Alignment	not modelled	28.6	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
77	c3bblA_	Alignment	not modelled	28.4	8	**PDB header:**regulatory protein **Chain:** A: **PDB Molecule:**regulatory protein of laci family; **PDBTitle:** crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
78	d2f9yb1	Alignment	not modelled	26.9	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain

79	c2f9yB_	Alignment	not modelled	26.9	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
80	d2d59a1	Alignment	not modelled	26.8	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
81	d2a7sa1	Alignment	not modelled	26.6	25	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
82	d1ir6a_	Alignment	not modelled	26.5	25	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
83	c1ir6A_	Alignment	not modelled	26.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
84	d1a9xa4	Alignment	not modelled	26.4	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
85	c1x0uB_	Alignment	not modelled	26.3	32	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical methylmalonyl-coa decarboxylase alpha subunit; **PDBTitle:** crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
86	d1vrga2	Alignment	not modelled	26.1	32	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
87	c3cs3A_	Alignment	not modelled	26.0	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
88	c2f9iD_	Alignment	not modelled	26.0	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
89	c1on3E_	Alignment	not modelled	26.0	15	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methylmalonyl-coa carboxyltransferase 12s **PDBTitle:** transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
90	c3o1hB_	Alignment	not modelled	25.2	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
91	c3fijD_	Alignment	not modelled	24.9	37	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
92	c2a7sD_	Alignment	not modelled	24.7	21	**PDB header:**ligase **Chain:** D: **PDB Molecule:**probable propionyl-coa carboxylase beta chain 5; **PDBTitle:** crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis
93	d1pixa2	Alignment	not modelled	24.4	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
94	c1uheA_	Alignment	not modelled	24.3	37	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
95	c1pjtB_	Alignment	not modelled	24.3	15	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
96	d1on3a2	Alignment	not modelled	24.1	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
97	c3r74B_	Alignment	not modelled	22.0	21	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
98	d1ka9h_	Alignment	not modelled	21.8	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
99	d1f0ka_	Alignment	not modelled	21.6	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
100	d1oi7a1	Alignment	not modelled	21.3	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
101	c2v4uA_	Alignment	not modelled	20.9	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
102	c3fkjA_	Alignment	not modelled	20.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution