





















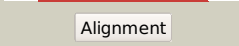







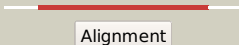

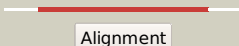

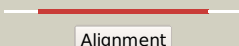



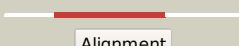



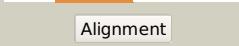



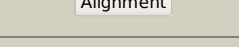
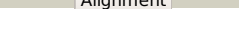


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1315_(murA)_1470327_1471583
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	662c6ef5fc59993d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3r38A_</a>	 Alignment		100.0	48	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; <b>PDBTitle:</b> 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e
2	<a href="#">c5u4hB_</a>	 Alignment		100.0	46	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> 1.05 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from acinetobacter baumannii in covalently3 bound complex with (2r)-2-(phosphonoxy)propanoic acid.
3	<a href="#">c5wi5C_</a>	 Alignment		100.0	47	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; <b>PDBTitle:</b> 2.0 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from streptococcus pneumoniae in complex3 with uridine-diphosphate-2(n-acetylglucosaminy) butyric acid, (2r)-4 2-(phosphonoxy)propanoic acid and magnesium.
4	<a href="#">c5uj5B_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> 2.45 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from campylobacter jejuni.
5	<a href="#">d1uaea_</a>	 Alignment		100.0	45	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
6	<a href="#">c5bq2C_</a>	 Alignment		100.0	44	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 (udp-n-acetylglucosamine enolpyruvyl transferase, ept) from3 pseudomonas aeruginosa
7	<a href="#">d1ejda_</a>	 Alignment		100.0	44	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
8	<a href="#">c2yvva_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 from aquifex aeolicus vf5
9	<a href="#">c3zh3A_</a>	 Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> crystal structure of s. pneumoniae d39 native mura1
10	<a href="#">c4fqdA_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> niko protein; <b>PDBTitle:</b> crystal structure of the enolpyruvyl transferase niko from2 streptomyces tendae
11	<a href="#">c3rmtB_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase 1; <b>PDBTitle:</b> crystal structure of putative 5-enolpyruvoylshikimate-3-phosphate2 synthase from bacillus halodurans c-125

12	<a href="#">d1g6sa_</a>	 Alignment		100.0	20	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
13	<a href="#">c3roiA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> 2.20 angstrom resolution structure of 3-phosphoshikimate 1-2 carboxyvinyltransferase (aroa) from coxiella burnetii
14	<a href="#">c5xwbB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> crystal structure of 5-enolpyruvylshikimate-3-phosphate synthase from2 a psychrophilic bacterium, colwellia psychrerythraea
15	<a href="#">c2o0zA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> mycobacterium tuberculosis epsp synthase in complex with product (eps)
16	<a href="#">c5bufA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> 2.37 angstrom structure of epsp synthase from acinetobacter baumannii
17	<a href="#">c2pqaA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> a100g cp4 epsps liganded with (r)-difluoromethyl tetrahedral reaction2 intermediate analog
18	<a href="#">d1rf6a_</a>	 Alignment		100.0	23	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
19	<a href="#">d1p88a_</a>	 Alignment		100.0	19	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
20	<a href="#">d1qmh2</a>	 Alignment		97.3	18	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> RNA 3'-terminal phosphate cyclase, RTPC
21	<a href="#">c1qmiC_</a>	 Alignment	not modelled	95.4	16	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> rna 3'-terminal phosphate cyclase; <b>PDBTitle:</b> crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology
22	<a href="#">c4o8jB_</a>	 Alignment	not modelled	95.2	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rna 3'-terminal phosphate cyclase; <b>PDBTitle:</b> crystal structure of rtca, the rna 3'-terminal phosphate cyclase from2 pyrococcus horikoshii, in complex with racaaa3'phosphate and adenine.
23	<a href="#">c3pqvD_</a>	 Alignment	not modelled	85.4	12	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> rcl1 protein; <b>PDBTitle:</b> cyclase homolog
24	<a href="#">c3g0tA_</a>	 Alignment	not modelled	56.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
25	<a href="#">c4gtnA_</a>	 Alignment	not modelled	47.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
26	<a href="#">c1o17A_</a>	 Alignment	not modelled	45.3	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyl-transferase (trpd)
27	<a href="#">c4muoB_</a>	 Alignment	not modelled	43.5	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ybib; <b>PDBTitle:</b> the trpd2 enzyme from e.coli: ybib
28	<a href="#">c2hzfA_</a>	 Alignment	not modelled	40.7	16	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1; <b>PDBTitle:</b> crystal structures of a poxviral glutaredoxin in the

						oxidized and2 reduced states show redox-correlated structural changes
29	<a href="#">d1w2za3</a>	Alignment	not modelled	37.7	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
30	<a href="#">c3gmgB_</a>	Alignment	not modelled	25.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein rv1825/mt1873; <b>PDBTitle:</b> crystal structure of an uncharacterized conserved protein from2 mycobacterium tuberculosis
31	<a href="#">c2dsjA_</a>	Alignment	not modelled	21.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside (thymidine) phosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0128 from thermus thermophilus hb8
32	<a href="#">c1v8gB_</a>	Alignment	not modelled	20.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
33	<a href="#">c5kinD_</a>	Alignment	not modelled	19.6	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
34	<a href="#">c4kjeA_</a>	Alignment	not modelled	17.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> atomic resolution structure of pfgrx1
35	<a href="#">c3pnxF_</a>	Alignment	not modelled	16.5	0	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> putative sulfurtransferase dsre; <b>PDBTitle:</b> crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
36	<a href="#">c4j8cA_</a>	Alignment	not modelled	14.8	23	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of the dimerization domain of hsc70-interacting2 protein
37	<a href="#">c4j8cB_</a>	Alignment	not modelled	14.8	23	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of the dimerization domain of hsc70-interacting2 protein
38	<a href="#">c2bpqB_</a>	Alignment	not modelled	14.1	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
39	<a href="#">d1v8za1</a>	Alignment	not modelled	14.1	16	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
40	<a href="#">c4ga5H_</a>	Alignment	not modelled	13.7	13	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> putative thymidine phosphorylase; <b>PDBTitle:</b> crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
41	<a href="#">d2o8ra3</a>	Alignment	not modelled	13.3	11	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
42	<a href="#">c5fqIA_</a>	Alignment	not modelled	13.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> iduronate-2-sulfatase; <b>PDBTitle:</b> insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
43	<a href="#">d1o17a2</a>	Alignment	not modelled	12.9	10	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
44	<a href="#">c2cb1A_</a>	Alignment	not modelled	12.8	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetyl homoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
45	<a href="#">d1jcb2</a>	Alignment	not modelled	12.4	24	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
46	<a href="#">c3juxA_</a>	Alignment	not modelled	12.0	8	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> structure of the translocation atpase seca from thermotoga2 maritima
47	<a href="#">c3h5qA_</a>	Alignment	not modelled	12.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
48	<a href="#">c3nr6A_</a>	Alignment	not modelled	11.9	13	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> protease p14; <b>PDBTitle:</b> crystal structure of xenotropic murine leukemia virus-related virus2 (xmrv) protease
49	<a href="#">c4i2uA_</a>	Alignment	not modelled	10.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of the reduced glutaredoxin from chlorella2 sorokiniana t-89 in complex with glutathione
50	<a href="#">d1jhba_</a>	Alignment	not modelled	10.7	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
51	<a href="#">c3dinB_</a>	Alignment	not modelled	10.7	8	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
52	<a href="#">c2gjhA_</a>	Alignment	not modelled	9.7	29	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7) <b>PDB header:</b> lyase

53	<a href="#">c5tchH_</a>	Alignment	not modelled	9.6	20	<b>Chain:</b> H: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
54	<a href="#">c1khdD_</a>	Alignment	not modelled	9.5	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.9 resolution3 (current name, pectobacterium carotovorum)
55	<a href="#">d1nh2a1</a>	Alignment	not modelled	9.1	18	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
56	<a href="#">d2dy1a4</a>	Alignment	not modelled	9.1	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
57	<a href="#">d1lxja_</a>	Alignment	not modelled	9.0	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
58	<a href="#">d1cdwa1</a>	Alignment	not modelled	8.7	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
59	<a href="#">c5nofB_</a>	Alignment	not modelled	8.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase from thermococcus kodakaraensis
60	<a href="#">d1in0a2</a>	Alignment	not modelled	7.5	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> YajQ-like <b>Family:</b> YajQ-like
61	<a href="#">d1qnaa1</a>	Alignment	not modelled	7.3	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
62	<a href="#">c2o8rA_</a>	Alignment	not modelled	7.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyphosphate kinase; <b>PDBTitle:</b> crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
63	<a href="#">c1nl3B_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca 1 subunit; <b>PDBTitle:</b> crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
64	<a href="#">d1x9za_</a>	Alignment	not modelled	6.8	27	<b>Fold:</b> DNA mismatch repair protein MutL <b>Superfamily:</b> DNA mismatch repair protein MutL <b>Family:</b> DNA mismatch repair protein MutL
65	<a href="#">c4pwyA_</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin-lysine n-methyltransferase; <b>PDBTitle:</b> crystal structure of a calmodulin-lysine n-methyltransferase fragment
66	<a href="#">d1yqha1</a>	Alignment	not modelled	6.7	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
67	<a href="#">c3ndnC_</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> o-succinylhomoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
68	<a href="#">c2cxiA_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of an n-terminal fragment of the phenylalanyl-trna2 synthetase beta-subunit from pyrococcus horikoshii
69	<a href="#">c6ic4H_</a>	Alignment	not modelled	6.4	23	<b>PDB header:</b> protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> abc transporter permease; <b>PDBTitle:</b> cryo-em structure of the a. baumannii mia complex at 8.7 a resolution
70	<a href="#">c2epiA_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0045 protein mj1052; <b>PDBTitle:</b> crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannascii (form 2)
71	<a href="#">c5zvlB_</a>	Alignment	not modelled	5.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of wheat glutaredoxin
72	<a href="#">c3mjsA_</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amphb; <b>PDBTitle:</b> structure of a-type ketoreductases from modular polyketide synthase
73	<a href="#">c3nbxX_</a>	Alignment	not modelled	5.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava; <b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
74	<a href="#">d1nh8a2</a>	Alignment	not modelled	5.7	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
75	<a href="#">c4gduB_</a>	Alignment	not modelled	5.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of sulfate-bound human l-asparaginase protein
76	<a href="#">c4uaqA_</a>	Alignment	not modelled	5.6	11	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit seca 2; <b>PDBTitle:</b> crystal structure of the accessory translocation atpase, seca2, from2 mycobacterium tuberculosis
77	<a href="#">d1ttea1</a>	Alignment	not modelled	5.5	24	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
78	<a href="#">c4n0bA_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulatory protein gabr; <b>PDBTitle:</b> crystal structure of bacillus subtilis gabr, an autorepressor

					and2 transcriptional activator of gabt
79	<a href="#">c1otpA_</a>	Alignment	not modelled	5.2	16 <b>PDB header:</b> phosphorylase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine phosphorylase; <b>PDBTitle:</b> structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
80	<a href="#">c3h8qB_</a>	Alignment	not modelled	5.2	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 3; <b>PDBTitle:</b> crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
81	<a href="#">c3s8iA_</a>	Alignment	not modelled	5.2	8 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ddi1 homolog 1; <b>PDBTitle:</b> the retroviral-like protease (rvp) domain of human ddi1
82	<a href="#">c2k6xA_</a>	Alignment	not modelled	5.2	17 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
83	<a href="#">c3ke2A_</a>	Alignment	not modelled	5.1	17 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yp_928783.1; <b>PDBTitle:</b> crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution