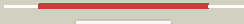



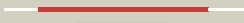



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2537c_aroD_2861158_2861601
 Date Wed Aug 7 12:50:17 BST 2019
 Unique Job ID 9e5e80759b46d734

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lwzC_	 Alignment		100.0	47	PDB header: lyase Chain: C; PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-dehydroquinone2 dehydratase (aroq) from yersinia pestis
2	d1gtza_	 Alignment		100.0	41	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinone dehydratase Family: Type II 3-dehydroquinone dehydratase
3	c3n8kG_	 Alignment		100.0	100	PDB header: lyase Chain: G; PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
4	d1uqra_	 Alignment		100.0	46	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinone dehydratase Family: Type II 3-dehydroquinone dehydratase
5	d2c4va1	 Alignment		100.0	36	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinone dehydratase Family: Type II 3-dehydroquinone dehydratase
6	d1gqoa_	 Alignment		100.0	44	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinone dehydratase Family: Type II 3-dehydroquinone dehydratase
7	c6cv6L_	 Alignment		100.0	42	PDB header: lyase Chain: L; PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: crystal structure of 3-dehydroquinone dehydratase, type ii, from2 burkholderia phymatum stm815
8	c2uygF_	 Alignment		100.0	54	PDB header: lyase Chain: F; PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: crystallographic structure of the typeii 3-dehydroquinase from thermus2 thermophilus
9	c4rhcH_	 Alignment		100.0	49	PDB header: lyase Chain: H; PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: crystal structure of 3-dehydroquinone dehydratase from acinetobacter2 baumannii at 2.68 a resolution
10	d1h05a_	 Alignment		100.0	99	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinone dehydratase Family: Type II 3-dehydroquinone dehydratase
11	c3kipU_	 Alignment		100.0	45	PDB header: lyase Chain: U; PDB Molecule: 3-dehydroquinase, type ii; PDBTitle: crystal structure of type-ii 3-dehydroquinase from c. albicans

12	c4l8lA_	Alignment		100.0	49	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinatase 1; PDBTitle: crystal structure of the type ii dehydroquinase from pseudomonas2 aeruginosa
13	c3u80A_	Alignment		100.0	48	PDB header: unknown function Chain: A: PDB Molecule: 3-dehydroquinatase, type ii; PDBTitle: 1.60 angstrom resolution crystal structure of a 3-dehydroquinatase2 dehydratase-like protein from bifidobacterium longum
14	c4kzkA_	Alignment		96.4	15	PDB header: sugar binding protein Chain: A: PDB Molecule: l-arabinose abc transporter, periplasmic l-arabinose- PDBTitle: the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
15	c4wwhA_	Alignment		95.8	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmeg_1704, target efi-3 510967) with bound d-galactose
16	c4rxuA_	Alignment		95.2	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
17	c4ys6A_	Alignment		95.0	6	PDB header: solute-binding protein Chain: A: PDB Molecule: putative solute-binding component of abc transporter; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentans (cphy_1585, target efi-3 511156) with bound beta-d-glucose
18	c3o1hB_	Alignment		94.7	12	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
19	c3uuqB_	Alignment		94.4	14	PDB header: sugar binding protein Chain: B: PDB Molecule: multiple sugar-binding periplasmic receptor chve; PDBTitle: crystal structure of the periplasmic sugar binding protein chve
20	c5er3A_	Alignment		94.3	14	PDB header: solute-binding protein Chain: A: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of abc transporter system solute-binding protein2 from rhodopirellula baltica sh 1
21	c6dspB_	Alignment	not modelled	93.9	14	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
22	c4wzzA_	Alignment	not modelled	93.8	11	PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentans (cphy_0583, target efi-3 511148) with bound l-rhamnose
23	c4yhsA_	Alignment	not modelled	93.7	17	PDB header: solute-binding protein Chain: A: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from bradyrhizobium sp. btai1 (bbta_2440, target efi-3 511490) with bound bis-tris
24	c5ulbA_	Alignment	not modelled	93.5	18	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
25	c5lg5F_	Alignment	not modelled	93.4	23	PDB header: isomerase Chain: F: PDB Molecule: allantoin racemase; PDBTitle: crystal structure of allantoin racemase from pseudomonas fluorescens2 allr
26	c3h75A_	Alignment	not modelled	93.2	14	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
27	c2qvcC_	Alignment	not modelled	91.8	12	PDB header: transport protein Chain: C: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of a periplasmic sugar abc transporter

						from2 thermotoga maritima
28	d8abpa_	Alignment	not modelled	91.8	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
29	c2fqxA_	Alignment	not modelled	91.6	16	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
30	c6hyhA_	Alignment	not modelled	91.5	11	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucufuranose
31	c3qvjB_	Alignment	not modelled	91.5	22	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
32	c4pz0A_	Alignment	not modelled	91.4	11	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
33	d1tjya_	Alignment	not modelled	90.9	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
34	d1gpma2	Alignment	not modelled	90.6	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	c4ptzC_	Alignment	not modelled	90.3	16	PDB header: oxidoreductase Chain: C: PDB Molecule: fmn reductase ssue; PDBTitle: crystal structure of the escherichia coli alkanesulfonate fmn2 reductase ssue in fmn-bound form
36	c3g1wB_	Alignment	not modelled	90.0	11	PDB header: transport protein Chain: B: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
37	c4y9tA_	Alignment	not modelled	89.9	14	PDB header: solute-binding protein Chain: A: PDB Molecule: abc transporter, solute binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis s4 (avi_5305, target efi-511224)3 with bound alpha-d-glucosamine
38	c3ksmA_	Alignment	not modelled	89.6	13	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system, periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from haella chejuensis
39	c4rxtA_	Alignment	not modelled	89.4	13	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 arad_9553 from agrobacterium radiobacter, target efi-511541, in3 complex with d-arabinose
40	c4rs3A_	Alignment	not modelled	89.1	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, carbohydrate uptake transporter-2 (cut2) PDBTitle: crystal structure of carbohydrate transporter a0qyb3 from2 mycobacterium smegmatis str. mc2 155, target efi-510969, in complex3 with xylitol
41	c4irxA_	Alignment	not modelled	87.6	24	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of caulobacter myo-inositol binding protein bound to2 myo-inositol
42	c5braA_	Alignment	not modelled	87.1	12	PDB header: solute-binding protein Chain: A: PDB Molecule: putative periplasmic binding protein with substrate ribose; PDBTitle: crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3 efi-511085)
43	c3d02A_	Alignment	not modelled	87.0	11	PDB header: sugar binding protein Chain: A: PDB Molecule: putative lacI-type transcriptional regulator; PDBTitle: crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
44	c5hsgA_	Alignment	not modelled	87.0	14	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, nucleotide binding/atpase PDBTitle: crystal structure of an abc transporter solute binding protein from2 klebsiella pneumoniae (kpn_01730, target efi-511059), apo open3 structure
45	c3brsA_	Alignment	not modelled	86.8	17	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
46	c5hqjA_	Alignment	not modelled	86.2	13	PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of abc transporter solute binding protein b1g1h72 from burkholderia graminis c4d1m, target efi-511179, in complex with3 d-arabinose
47	c2p0yA_	Alignment	not modelled	86.1	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
48	c4z0nA_	Alignment	not modelled	85.6	12	PDB header: transcription Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of a periplasmic solute binding protein (ipr025997)2 from streptobacillus moniliformis dsm-12112 (smon_0317, target efi-3 511281) with bound d-galactose PDB header: transcription regulator

49	c3k9cA	Alignment	not modelled	85.0	16	Chain: A: PDB Molecule: transcriptional regulator, lacI family protein; PDBTitle: crystal structure of lacI transcriptional regulator from rhodococcus2 species.
50	c5dkvD	Alignment	not modelled	84.9	15	PDB header: sugar binding protein Chain: D: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein from2 agrobacterium vitis(avis_5339, target efi-511225) bound with alpha-d-3 tagatopyranose
51	c4rk1F	Alignment	not modelled	84.3	15	PDB header: transcription regulator Chain: F: PDB Molecule: ribose transcriptional regulator; PDBTitle: crystal structure of lacI family transcriptional regulator from2 enterococcus faecium, target efi-512930, with bound ribose
52	c4wt7B	Alignment	not modelled	84.3	12	PDB header: transport protein Chain: B: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis (avi_5165, target efi-511223)3 with bound allitol
53	d1ka9h	Alignment	not modelled	84.0	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
54	c5ocpA	Alignment	not modelled	83.9	8	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: the periplasmic binding protein component of the arabinose abc2 transporter from shewanella sp. ana-3 bound to alpha and beta-l-3 arabinofuranose
55	c3bb1A	Alignment	not modelled	83.7	10	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
56	d2fva1	Alignment	not modelled	83.5	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
57	c3clkB	Alignment	not modelled	83.4	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
58	c1wxwA	Alignment	not modelled	83.4	17	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha1280; PDBTitle: crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophilus hb8
59	d2dria	Alignment	not modelled	83.2	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
60	c4ru1C	Alignment	not modelled	82.4	10	PDB header: transport protein Chain: C: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of carbohydrate transporter acei_1806 from2 acidothermus cellulolyticus 11b, target efi-510965, in complex with3 myo-inositol
61	c4o5aA	Alignment	not modelled	81.9	13	PDB header: transcription regulator Chain: A: PDB Molecule: lacI family transcription regulator; PDBTitle: the crystal structure of a lacI family transcriptional regulator from2 bifidobacterium animalis subsp. lactis dsm 10140
62	c4yo7A	Alignment	not modelled	81.7	14	PDB header: solute binding protein Chain: A: PDB Molecule: sugar abc transporter (sugar-binding protein); PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from bacillus halodurans c-125 (bh2323, target efi-3 511484) with bound myo-inositol
63	c4ry0A	Alignment	not modelled	81.4	23	PDB header: transport protein Chain: A: PDB Molecule: probable ribose abc transporter, substrate-binding protein; PDBTitle: crystal structure of ribose transporter solute binding protein2 rhe_pf00037 from rhizobium etli cfn 42, target efi-511357, in complex3 with d-ribose
64	c4kqcA	Alignment	not modelled	80.4	16	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: abc transporter, lacI family transcriptional regulator from2 brachyspira murdochii
65	c3qk7C	Alignment	not modelled	80.3	17	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
66	c4kvfA	Alignment	not modelled	79.8	9	PDB header: transport protein Chain: A: PDB Molecule: rhamnose abc transporter, periplasmic rhamnose-binding PDBTitle: the crystal structure of a rhamnose abc transporter, periplasmic2 rhamnose-binding protein from kribbella flavida dsm 17836
67	c3rotA	Alignment	not modelled	78.9	13	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
68	c3ma0A	Alignment	not modelled	78.2	16	PDB header: sugar binding protein Chain: A: PDB Molecule: d-xylose-binding periplasmic protein; PDBTitle: closed liganded crystal structure of xylose binding protein from2 escherichia coli
69	c2hqbA	Alignment	not modelled	78.2	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comK gene; PDBTitle: crystal structure of a transcriptional activator of comK2 gene from bacillus halodurans
70	c2rjoA	Alignment	not modelled	77.9	13	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway

						signal2 protein from burkholderia phytofirmans
71	d2pjuA1	Alignment	not modelled	76.6	21	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
72	c2vk2A	Alignment	not modelled	75.1	7	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
73	c2zkiH	Alignment	not modelled	75.1	20	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
74	c6j27D	Alignment	not modelled	75.0	16	PDB header: transferase Chain: D: PDB Molecule: n(4)-bis(aminopropyl)spermidine synthase; PDBTitle: crystal structure of the branched-chain polyamine synthase from2 thermus thermophilus (tth-bpsa) in complex with n4-3 aminopropylspermidine and 5'-methylthioadenosine
75	d2g39a1	Alignment	not modelled	74.5	22	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
76	c3h5oB	Alignment	not modelled	74.3	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
77	d2ocda1	Alignment	not modelled	73.1	26	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
78	c4q0mA	Alignment	not modelled	73.0	17	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of pyrococcus furiosus l-asparaginase
79	c4rk5A	Alignment	not modelled	72.8	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcriptional regulator from2 lactobacillus casei, target efi-512911, with bound sucrose
80	c5dteD	Alignment	not modelled	72.2	12	PDB header: transport protein Chain: D: PDB Molecule: monosaccharide-transporting atpase; PDBTitle: crystal structure of an abc transporter periplasmic solute binding2 protein (ipr025997) from actinobacillus succinogenes 130z(asuc_0081,3 target efi-511065) with bound d-allose
81	d1dxya2	Alignment	not modelled	71.9	15	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
82	c3hcwB	Alignment	not modelled	70.6	14	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
83	c2ad5B	Alignment	not modelled	69.6	12	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
84	c3d8uA	Alignment	not modelled	69.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
85	c5ijwA	Alignment	not modelled	68.1	27	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction
86	c5ot0A	Alignment	not modelled	67.4	21	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the thermostable l-asparaginase from thermococcus kodakarensis
87	c3gv0A	Alignment	not modelled	67.3	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
88	d1wxxa2	Alignment	not modelled	67.0	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: hypothetical RNA methyltransferase
89	c3kkeA	Alignment	not modelled	66.4	10	PDB header: transcription regulator Chain: A: PDB Molecule: lacI family transcriptional regulator; PDBTitle: crystal structure of a lacI family transcriptional regulator from2 mycobacterium smegmatis
90	c3tb6B	Alignment	not modelled	66.4	10	PDB header: dna binding protein Chain: B: PDB Molecule: arabinose metabolism transcriptional repressor; PDBTitle: structure of the effector-binding domain of arabinose repressor arar2 from bacillus subtilis
91	c2iksA	Alignment	not modelled	66.1	12	PDB header: transcription Chain: A: PDB Molecule: dna-binding transcriptional dual regulator; PDBTitle: crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
92	c4kq9A	Alignment	not modelled	65.9	15	PDB header: transport protein Chain: A: PDB Molecule: ribose abc transporter, substrate binding protein; PDBTitle: crystal structure of periplasmic ribose abc transporter from2 conexibacter woesei dsm 14684
93	c2x7xA	Alignment	not modelled	65.8	20	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component system2 bt1754
94	c4rymA	Alignment	not modelled	65.6	16	PDB header: transport protein Chain: A: PDB Molecule: possible sugar abc superfamily atp binding cassette

94	c9111A	Alignment	not modelled	65.8	10	PDBTitle: crystal structure of periplasmic abc transporter solute binding2 protein a7jw62 from mannheimia haemolytica phl213, target efi-511105,3 in complex with myo-inositol PDB header: transport protein Chain: A: PDB Molecule: rhamnose abc transporter, rhamnose-binding protein;
95	c5bq3A	Alignment	not modelled	65.5	11	PDBTitle: crystal structure of a sugar abc transporter (actodo_00688) from2 actinomyces odontolyticus atcc 17982 at 2.60 a resolution
96	d1zq1a2	Alignment	not modelled	64.8	19	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
97	c3hfrA	Alignment	not modelled	64.7	21	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes
98	c2jfoB	Alignment	not modelled	64.7	23	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
99	c4yleA	Alignment	not modelled	64.3	6	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from burkholderia multivorans (bmul_1631, target efi-3 511115) with an unknown ligand modelled as alpha-d-erythofuranose
100	c2ppvA	Alignment	not modelled	64.3	39	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
101	c3l49D	Alignment	not modelled	63.8	15	PDB header: transport protein Chain: D: PDB Molecule: abc sugar (ribose) transporter, periplasmic substrate- PDBTitle: crystal structure of abc sugar transporter subunit from rhodobacter2 sphaeroides 2.4.1
102	c4jqoA	Alignment	not modelled	63.5	13	PDB header: transport protein Chain: A: PDB Molecule: abc ribose transporter, periplasmic solute-binding protein; PDBTitle: putative ribose abc transporter, periplasmic solute-binding protein2 from rhodobacter sphaeroides
103	c5do0A	Alignment	not modelled	63.5	18	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
104	c4dmgA	Alignment	not modelled	63.5	16	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein ttha1493; PDBTitle: thermus thermophilus m5c1942 methyltransferase rlmo
105	c5f4bB	Alignment	not modelled	63.3	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
106	c2jfqA	Alignment	not modelled	62.9	23	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of staphylococcus aureus glutamate racemase in2 complex with d- glutamate
107	c1vcnA	Alignment	not modelled	62.9	14	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
108	c2pjuD	Alignment	not modelled	62.6	21	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
109	d1gcaa	Alignment	not modelled	62.5	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
110	c3ctpB	Alignment	not modelled	62.5	14	PDB header: transcription regulator Chain: B: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of periplasmic binding protein/laci transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
111	c2p2dA	Alignment	not modelled	61.9	24	PDB header: transferase Chain: A: PDB Molecule: l-asparaginase i; PDBTitle: crystal structure and allosteric regulation of the cytoplasmic2 escherichia coli l-asparaginase i
112	c5z6vA	Alignment	not modelled	61.8	20	PDB header: protein transport Chain: A: PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
113	d2ffea1	Alignment	not modelled	61.4	19	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
114	c4r81C	Alignment	not modelled	61.2	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase; PDBTitle: nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
115	c6ndiB	Alignment	not modelled	61.1	15	PDB header: sugar binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.60 angstrom resolution crystal structure of periplasmic binding and2 sugar binding domain of lacI family protein from klebsiella3 pneumoniae.
116	c4c76A	Alignment	not modelled	60.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn reductase (nadph); PDBTitle: crystal structure of the fmn-reductase msue from pseudomonas putida2 kt2440.

117	d2hzba1	Alignment	not modelled	60.5	28	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
118	c3s40C_	Alignment	not modelled	60.3	10	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
119	c5n9mA_	Alignment	not modelled	58.5	16	PDB header: transferase Chain: A: PDB Molecule: cobyrinic acid synthase; PDBTitle: crystal structure of gatD - a glutamine amidotransferase from Staphylococcus aureus involved in peptidoglycan amidation
120	c4r8kC_	Alignment	not modelled	57.6	17	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the guinea pig l-asparaginase 1 catalytic domain