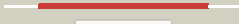



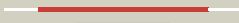





















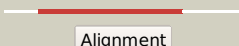

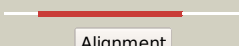

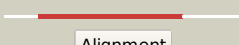

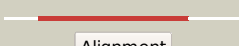







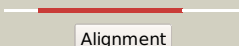



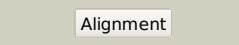

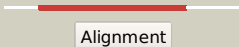


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0510_(hemC)_601860_602789
Date	Fri Jul 26 01:50:05 BST 2019
Unique Job ID	eda70bf17473f84e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4htgA_	 Alignment		100.0	39	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: porphobilinogen deaminase, chloroplastic; PDBTitle: porphobilinogen deaminase from arabidopsis thaliana
2	c2ypnA_	 Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: protein (hydroxymethylbilane synthase); PDBTitle: hydroxymethylbilane synthase
3	c4mlqA_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: crystal structure of bacillus megaterium porphobilinogen deaminase
4	c3eq1A_	 Alignment		100.0	45	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
5	d1pdaa1	 Alignment		100.0	46	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
6	d1gtka2	 Alignment		99.9	43	Fold: dsRBD-like Superfamily: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
7	d1pdaa2	 Alignment		99.9	44	Fold: dsRBD-like Superfamily: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
8	c1p99A_	 Alignment		98.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus aureus
9	d1p99a_	 Alignment		98.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
10	c3tqwA_	 Alignment		97.7	21	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
11	c4gotA_	 Alignment		97.6	14	PDB header: lipid binding protein Chain: A: PDB Molecule: methionine-binding lipoprotein metq; PDBTitle: crystal structure of a putative methionine-binding lipoprotein2 (bsu32730) from bacillus subtilis subsp. subtilis str. 168 at 1.95 a3 resolution

12	c3gxaA_	 Alignment		97.5	17	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
13	c4ntIA_	 Alignment		97.4	13	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein, yaec family; PDBTitle: crystal structure of a lipoprotein, yaec family (ef3198) from2 enterococcus faecalis v583 at 1.80 a resolution
14	c4qhA_	 Alignment		97.3	16	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine
15	c4z9nB_	 Alignment		97.2	18	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
16	c3ir1F_	 Alignment		97.1	20	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria meningitidis
17	c3uifA_	 Alignment		97.0	16	PDB header: transport protein Chain: A: PDB Molecule: sulfonate abc transporter, periplasmic sulfonate-binding PDBTitle: crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
18	c3un6A_	 Alignment		96.9	15	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein saouhsc_00137; PDBTitle: 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
19	c2x26A_	 Alignment		96.7	17	PDB header: transport protein Chain: A: PDB Molecule: periplasmic aliphatic sulphonates-binding protein; PDBTitle: crystal structure of the periplasmic aliphatic sulphonate binding2 protein ssua from escherichia coli
20	d1xs5a_	 Alignment		96.6	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
21	c4ib2B_	 Alignment	not modelled	96.0	14	PDB header: transport protein Chain: B: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (rumgna_00858) from2 ruminococcus gnavus atcc 29149 at 1.76 a resolution
22	c4ef2A_	 Alignment	not modelled	95.6	15	PDB header: methionine-binding protein Chain: A: PDB Molecule: pheromone cob1/lipoprotein, yaec family; PDBTitle: crystal structure of a pheromone cob1 precursor/lipoprotein, yaec2 family (ef2496) from enterococcus faecalis v583 at 2.10 a resolution
23	c3up9A_	 Alignment	not modelled	95.5	15	PDB header: methionine-binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative lipoprotein (actodo_00931) from2 actinomyces odontolyticus atcc 17982 at 2.35 a resolution
24	c6jf1A_	 Alignment	not modelled	95.4	17	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
25	c4oteA_	 Alignment	not modelled	95.4	13	PDB header: protein transport Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (cd630_1653) from2 clostridium difficile 630 at 2.20 a resolution
26	c3kzqB_	 Alignment	not modelled	95.4	10	PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
27	c3e4rA_	 Alignment	not modelled	95.1	18	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes PDB header: glycine betaine-binding protein

28	c3l6gA_	Alignment	not modelled	95.0	8	Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
29	c4k3fA_	Alignment	not modelled	94.6	12	PDB header: transport protein Chain: A: PDB Molecule: probable tonb-dependent receptor; PDBTitle: crystal structure of a putative tonb-dependent receptor (pa5505) from2 pseudomonas aeruginosa pao1 at 1.60 a resolution
30	c4esxA_	Alignment	not modelled	94.5	13	PDB header: transferase Chain: A: PDB Molecule: pyrimidine biosynthesis enzyme thi13; PDBTitle: crystal structure of c. albicans thi5 complexed with plp
31	c3k2dA_	Alignment	not modelled	93.4	13	PDB header: immune system Chain: A: PDB Molecule: abc-type metal ion transport system, periplasmic component; PDBTitle: crystal structure of immunogenic lipoprotein a from vibrio vulnificus
32	c2x7pA_	Alignment	not modelled	92.6	16	PDB header: unknown function Chain: A: PDB Molecule: possible thiamine biosynthesis enzyme; PDBTitle: the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
33	c3hn0A_	Alignment	not modelled	91.6	10	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
34	d2czla1	Alignment	not modelled	91.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
35	c4q0cA_	Alignment	not modelled	90.5	15	PDB header: transferase Chain: A: PDB Molecule: virulence sensor protein bvgs; PDBTitle: 3.1 a resolution crystal structure of the b. pertussis bvgs2 periplasmic domain
36	c5me4A_	Alignment	not modelled	90.1	16	PDB header: transport protein Chain: A: PDB Molecule: probable phosphite transport system-binding protein htxb; PDBTitle: the structure of htxb from pseudomonas stutzeri in complex with2 hypophosphite to 1.52 a resolution
37	c3qsIA_	Alignment	not modelled	90.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
38	d1zbma1	Alignment	not modelled	89.6	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
39	d2ozza1	Alignment	not modelled	89.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
40	c5gzSA_	Alignment	not modelled	87.2	18	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: structure of vc protein
41	c4oz9A_	Alignment	not modelled	87.1	18	PDB header: lyase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
42	c6esvA_	Alignment	not modelled	86.0	18	PDB header: signaling protein Chain: A: PDB Molecule: putative periplasmic phosphite-binding-like protein (pbl) PDBTitle: structure of the phosphate-bound form of aiox from rhizobium sp. str.2 nt-26
43	c4xz6A_	Alignment	not modelled	83.4	25	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/proline abc transporter, periplasmic PDBTitle: tmox in complex with tmao
44	c3g41A_	Alignment	not modelled	83.3	11	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
45	c5o2kE_	Alignment	not modelled	82.9	16	PDB header: transport protein Chain: E: PDB Molecule: probable phosphite transport system-binding protein ptxb; PDBTitle: native apo-structure of pseudomonas stutzeri ptxb to 2.1 a resolution
46	c5y2wA_	Alignment	not modelled	81.6	15	PDB header: transcription Chain: A: PDB Molecule: rubisco operon transcriptional regulator; PDBTitle: structure of synechocystis pcc6803 ccmr regulatory domain in complex2 with 2-pg
47	c3ix1A_	Alignment	not modelled	80.7	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
48	c3ix1B_	Alignment	not modelled	80.7	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
49	c3tmgA_	Alignment	not modelled	80.7	14	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, PDBTitle: crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
50	d2a5sa1	Alignment	not modelled	80.6	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
51	c3delC_	Alignment	not modelled	80.0	11	PDB header: protein binding, transport protein Chain: C: PDB Molecule: arginine binding protein; PDBTitle: the structure of ct381, the arginine binding protein from

						the2 periplasm chlamydia trachomatis
52	c4h67D_	Alignment	not modelled	75.8	16	PDB header: transferase Chain: D: PDB Molecule: pyrimidine precursor biosynthesis enzyme thi5; PDBTitle: crystal structure of hmp synthase thi5 from s. cerevisiae
53	c2q2aD_	Alignment	not modelled	74.6	11	PDB header: transport protein Chain: D: PDB Molecule: artj; PDBTitle: crystal structures of the arginine-, lysine-, histidine-binding2 protein artj from the thermophilic bacterium geobacillus3 stearothermophilus
54	c6h2tA_	Alignment	not modelled	74.3	17	PDB header: signaling protein Chain: A: PDB Molecule: probable glutamine-binding lipoprotein glnh (glnbp); PDBTitle: glnh bound to glu, mycobacterium tuberculosis
55	c4pshA_	Alignment	not modelled	73.1	14	PDB header: protein transport Chain: A: PDB Molecule: abc-type transporter, periplasmic subunit family 3; PDBTitle: structure of holo argbp from t. maritima
56	c2ylnA_	Alignment	not modelled	70.2	12	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
57	c3hv1A_	Alignment	not modelled	70.1	11	PDB header: transport protein Chain: A: PDB Molecule: polar amino acid abc uptake transporter substrate PDBTitle: crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
58	d2nxoa1	Alignment	not modelled	69.2	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
59	c4q5tA_	Alignment	not modelled	65.3	11	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of an atmb (putative membrane lipoprotein) from2 streptococcus mutans ua159 at 1.91 a resolution
60	d1ex2a_	Alignment	not modelled	62.5	28	Fold: Anticodon-binding domain-like Superfamily: TPase-like Family: Maf-like
61	c5b70B_	Alignment	not modelled	59.5	14	PDB header: transcription Chain: B: PDB Molecule: lysr family transcriptional regulator; PDBTitle: oxyr2 e204g regulatory domain from vibrio vulnificus
62	c4p0eB_	Alignment	not modelled	59.0	33	PDB header: unknown function Chain: B: PDB Molecule: maf-like protein yhde; PDBTitle: yhde e33a (p212121 space group)
63	c4h5fB_	Alignment	not modelled	58.5	15	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc superfamily atp binding cassette PDBTitle: crystal structure of an amino acid abc transporter substrate-binding2 protein from streptococcus pneumoniae canada mdr_19a bound to l-3 arginine, form 1
64	c3r39A_	Alignment	not modelled	57.5	8	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
65	c2rejA_	Alignment	not modelled	57.3	23	PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation
66	c2y7iB_	Alignment	not modelled	56.9	9	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
67	c4z7eB_	Alignment	not modelled	56.2	13	PDB header: transport protein Chain: B: PDB Molecule: lmo1422 protein; PDBTitle: soluble binding domain of lmo1422 abc-transporter
68	c2p5xB_	Alignment	not modelled	55.7	34	PDB header: cell cycle Chain: B: PDB Molecule: n-acetylserotonin o-methyltransferase-like protein; PDBTitle: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
69	c5z49A_	Alignment	not modelled	54.1	15	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator cmprr; PDBTitle: crystal structure of the effector-binding domain of synechococcus2 elongatus cmprr in complex with ribulose-1,5-bisphosphate
70	c4ne4A_	Alignment	not modelled	52.9	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein PDBTitle: crystal structure of abc transporter substrate binding protein prox2 from agrobacterium tumefaciens cocrystallized with btb
71	c2pfzA_	Alignment	not modelled	52.7	12	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
72	c4wepA_	Alignment	not modelled	51.9	15	PDB header: transport protein Chain: A: PDB Molecule: putative osmoprotectant uptake system substrate-binding PDBTitle: apo yehz from escherichia coli
73	d1lsta_	Alignment	not modelled	50.5	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c2ieeB_	Alignment	not modelled	50.2	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable abc transporter extracellular-binding protein PDBTitle: crystal structure of yckb_bacsu from bacillus subtilis. northeast2 structural genomics consortium target sr574.

75	c5ub6B_	Alignment	not modelled	49.6	18	PDB header: metal binding protein Chain: B: PDB Molecule: phosphate-binding protein; PDBTitle: xac2383 from xanthomonas citri bound to pyrophosphate
76	c4hebA_	Alignment	not modelled	48.3	33	PDB header: cell cycle Chain: A: PDB Molecule: septum formation protein maf; PDBTitle: the crystal structure of maf protein of bacillus subtilis
77	c5iv1C_	Alignment	not modelled	48.3	16	PDB header: periplasmic binding protein Chain: C: PDB Molecule: ptxb; PDBTitle: 2.12 a resolution structure of ptxb from prochlorococcus marinus (mit2 9301) in complex with phosphite
78	c4oo0B_	Alignment	not modelled	47.6	29	PDB header: hydrolase Chain: B: PDB Molecule: maf-like protein bcal2394; PDBTitle: crystal structure of maf-like protein bcej2315_23540 from burkholderia2 cenocepacia
79	c4jhcA_	Alignment	not modelled	46.6	26	PDB header: cell cycle Chain: A: PDB Molecule: maf-like protein ycef; PDBTitle: crystal structure of the uncharacterized maf protein ycef from e. coli
80	d2amha1	Alignment	not modelled	46.2	33	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
81	c4nm6A_	Alignment	not modelled	46.0	24	PDB header: oxidoreductase/dna Chain: A: PDB Molecule: methylcytosine dioxygenase tet2; PDBTitle: crystal structure of tet2-dna complex
82	c3p7iA_	Alignment	not modelled	44.6	13	PDB header: transport protein Chain: A: PDB Molecule: phnd, subunit of alkylphosphonate abc transporter; PDBTitle: crystal structure of escherichia coli phnd in complex with 2-2 aminoethyl phosphonate
83	c4n6dA_	Alignment	not modelled	44.3	19	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens dsm2638 (desal_3247), target efi-510112,3 phased with i3c, open complex, c-terminus of symmetry mate bound in4 ligand binding site
84	c4ovsB_	Alignment	not modelled	43.5	12	PDB header: solute-binding protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 sulfurospirillum deleyianum dsm 6946 (sdel_0447), target efi-510309,3 with bound succinate
85	c2o1mB_	Alignment	not modelled	43.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable amino-acid abc transporter extracellular-binding PDBTitle: crystal structure of the probable amino-acid abc transporter2 extracellular-binding protein ytmk from bacillus subtilis. northeast3 structural genomics consortium target sr572
86	c3fd3A_	Alignment	not modelled	43.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: chromosome replication initiation inhibitor protein; PDBTitle: structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
87	d1r9la_	Alignment	not modelled	42.3	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
88	c6detA_	Alignment	not modelled	42.2	15	PDB header: transport protein Chain: A: PDB Molecule: tv2483; PDBTitle: the crystal structure of tv2483 bound to l-arginine
89	c5tpiA_	Alignment	not modelled	40.8	22	PDB header: hydrolase Chain: A: PDB Molecule: putative transcriptional regulator (lysr family); PDBTitle: 1.47 angstrom crystal structure of the c-terminal substrate binding2 domain of lysr family transcriptional regulator from klebsiella3 pneumoniae.
90	c3pppA_	Alignment	not modelled	40.7	19	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline-binding protein; PDBTitle: structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
91	d1sw5a_	Alignment	not modelled	36.5	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
92	c5jvbB_	Alignment	not modelled	35.9	13	PDB header: transport protein Chain: B: PDB Molecule: phosphonate abc transporter, periplasmic phosphonate- PDBTitle: 1.95a resolution structure of ptxb from trichodesmium erythraeum2 ims101 in complex with phosphite
93	c6mmvC_	Alignment	not modelled	34.7	12	PDB header: transport protein Chain: C: PDB Molecule: glutamate receptor ionotropic, nmda 1; PDBTitle: triheteromeric nmda receptor glun1/glun2a/glun2a* extracellular domain2 in the '2-knuckle-asymmetric' conformation, in complex with glycine3 and glutamate, in the presence of 1 micromolar zinc chloride, and at4 ph 7.4
94	c5sv6A_	Alignment	not modelled	33.6	18	PDB header: unknown function Chain: A: PDB Molecule: extracellular solute-binding protein, family 3; PDBTitle: crystal structure of mxaj from methlophaga aminisulfidivorans mpt
95	c5t0wA_	Alignment	not modelled	33.4	15	PDB header: transport protein Chain: A: PDB Molecule: anccd-1; PDBTitle: crystal structure of the ancestral amino acid-binding protein anccd-2 1, a precursor of cyclohexadienyl dehydratase
96	c4e14A_	Alignment	not modelled	33.0	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride PDB header: transport protein

97	c3k4uA_	Alignment	not modelled	31.4	12	Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinnella succinogenes dsm 1740 complexed with lysine
98	c4eq9A_	Alignment	not modelled	31.2	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein-amino acid PDBTitle: 1.4 angstrom crystal structure of abc transporter glutathione-binding2 protein gsht from streptococcus pneumoniae strain canada mdr_19a in3 complex with glutathione
99	c3r6uA_	Alignment	not modelled	31.1	17	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opbc from bacillus2 subtilis
100	c2vd3B_	Alignment	not modelled	29.7	19	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
101	c3n5IA_	Alignment	not modelled	28.2	17	PDB header: transport protein Chain: A: PDB Molecule: binding protein component of abc phosphonate transporter; PDBTitle: crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
102	c6onpA_	Alignment	not modelled	27.5	12	PDB header: unknown function Chain: A: PDB Molecule: periplasmic binding protein xoxj; PDBTitle: crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
103	c2hpgB_	Alignment	not modelled	27.2	19	PDB header: ligand binding protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding PDBTitle: the crystal structure of a thermophilic trap periplasmic2 binding protein
104	c5z72B_	Alignment	not modelled	27.2	8	PDB header: transcription Chain: B: PDB Molecule: ccpc; PDBTitle: crystal structure of ccpc regulatory domain in complex with citrate2 from bacillus amyloliquefaciens
105	c4ymxB_	Alignment	not modelled	25.4	14	PDB header: transport protein Chain: B: PDB Molecule: abc-type amino acid transport system, periplasmic PDBTitle: crystal structure of the substrate binding protein of an amino acid2 abc transporter
106	c3ho7A_	Alignment	not modelled	25.0	27	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
107	c5lq8A_	Alignment	not modelled	24.6	15	PDB header: periplasmic binding protein Chain: A: PDB Molecule: putative phosphonate binding protein for abc transporter; PDBTitle: 1.52 a resolution structure of phnd1 from prochlorococcus marinus (mit2 9301) in complex with methylphosphonate
108	c2j18S_	Alignment	not modelled	23.2	15	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l18; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
109	c4nmyA_	Alignment	not modelled	22.8	10	PDB header: transport protein Chain: A: PDB Molecule: abc-type transport system, extracellular solute-binding PDBTitle: crystal structure of the thiamin-bound form of substrate-binding2 protein of abc transporter from clostridium difficile
110	d1i6aa_	Alignment	not modelled	21.8	25	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
111	c2g29A_	Alignment	not modelled	21.7	11	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein nrta; PDBTitle: crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
112	c5iprD_	Alignment	not modelled	21.3	16	PDB header: signaling protein Chain: D: PDB Molecule: ionotropic glutamate receptor subunit nr2b; PDBTitle: cryo-em structure of glun1/glun2b nmda receptor in the dcka/d-apv-2 bound conformation, state 3
113	d1mzga_	Alignment	not modelled	21.1	22	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
114	c2ql3G_	Alignment	not modelled	21.1	15	PDB header: transcription Chain: G: PDB Molecule: probable transcriptional regulator, lysr family protein; PDBTitle: crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
115	c2h9qC_	Alignment	not modelled	21.0	15	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
116	c4euhA_	Alignment	not modelled	20.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ca_c0462; PDBTitle: crystal structure of clostridium acetobutlicum trans-2-enoyl-coa2 reductase apo form
117	c5xp0B_	Alignment	not modelled	20.7	15	PDB header: transcription Chain: B: PDB Molecule: probable csgab operon transcriptional regulatory protein; PDBTitle: crystal structure of master biofilm regulator csgd regulatory domain
118	c5orgA_	Alignment	not modelled	20.5	15	PDB header: octopine-binding protein Chain: A: PDB Molecule: octopine-binding periplasmic protein; PDBTitle: structure of the periplasmic binding protein (pbp) occj from a.2 tumefaciens b6 in complex with octopine.
119	c2f78A_	Alignment	not modelled	20.1	20	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate

