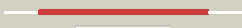



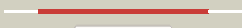














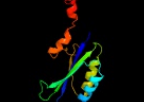







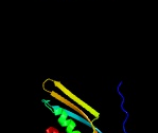
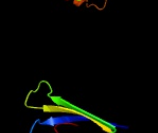


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3838c_pheA_4311882_4312847
Date	Sat Aug 10 22:05:01 BST 2019
Unique Job ID	5b5a7731c76b0ee4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mwbA_	 Alignment		100.0	42	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
2	c3luyA_	 Alignment		100.0	27	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
3	c2qmxB_	 Alignment		100.0	35	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
4	c2qmwA_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
5	c4lubA_	 Alignment		100.0	38	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
6	d2qmw1	 Alignment		100.0	23	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	d2qmw2	 Alignment		99.9	29	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
8	d1phza1	 Alignment		99.9	25	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
9	c2mdaB_	 Alignment		99.9	24	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
10	c5jk5A_	 Alignment		99.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
11	c2phmA_	 Alignment		99.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated

12	c5denA	Alignment		99.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
13	d1ygya3	Alignment		97.8	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
14	c5gzsaA	Alignment		97.5	17	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: structure of vc protein
15	d2f1fa1	Alignment		97.5	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
16	d2pc6a2	Alignment		97.3	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
17	c3ibwA	Alignment		97.3	4	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
18	c1u8sB	Alignment		97.3	13	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
19	c2f1fA	Alignment		97.3	22	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
20	c2nyiB	Alignment		97.3	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
21	c2lvwA	Alignment	not modelled	97.3	17	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
22	d1u8sa2	Alignment	not modelled	97.1	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
23	c2pc6C	Alignment	not modelled	97.1	23	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
24	d2fgca2	Alignment	not modelled	97.1	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
25	c2fgcA	Alignment	not modelled	96.7	18	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
26	d1zpvA1	Alignment	not modelled	96.6	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
27	d2f06a2	Alignment	not modelled	96.6	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
28	d1sc6a3	Alignment	not modelled	96.6	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
						Fold: Ferredoxin-like

29	d2f06a1	Alignment	not modelled	96.6	15	Superfamily: ACT-like Family: BT0572-like
30	c1ygyA_	Alignment	not modelled	96.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
31	c5uscB_	Alignment	not modelled	96.2	15	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
32	c2f06B_	Alignment	not modelled	96.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
33	c3l76B_	Alignment	not modelled	95.4	13	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
34	c4ovrA_	Alignment	not modelled	95.3	15	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 xanthobacter autotrophicus py2, target efi-510329, with bound beta-d-3 galacturonate
35	d1u8sa1	Alignment	not modelled	95.1	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
36	c5yeiG_	Alignment	not modelled	94.9	12	PDB header: transferase Chain: G: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
37	c6dzsD_	Alignment	not modelled	94.8	23	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
38	c4pfrA_	Alignment	not modelled	94.3	14	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3541, target efi-510203), apo open3 partially disordered
39	c3n0vD_	Alignment	not modelled	94.0	9	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
40	c1y7pB_	Alignment	not modelled	93.9	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein af1403; PDBTitle: 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
41	c5lq8A_	Alignment	not modelled	93.9	17	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
42	c1tdjA_	Alignment	not modelled	93.7	16	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
43	c5o2kE_	Alignment	not modelled	93.6	17	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
44	c3mtjA_	Alignment	not modelled	93.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
45	c4pfiA_	Alignment	not modelled	93.4	15	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 marinobacter aquaeolei vt8 (maqu_2829, target efi-510133), apo open3 structure
46	c3un6A_	Alignment	not modelled	93.2	16	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
47	c4nhbB_	Alignment	not modelled	93.0	14	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio desulfuricans (dDes_1525), target efi-510107, with3 bound sn-glycerol-3-phosphate
48	c4ib2B_	Alignment	not modelled	92.6	11	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
49	c3e4rA_	Alignment	not modelled	92.6	20	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
50	c4q0cA_	Alignment	not modelled	92.1	24	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
51	c4z9nB_	Alignment	not modelled	91.6	21	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
52	d1z7me1	Alignment	not modelled	91.4	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
53	c4ef2A	Alignment	not modelled	91.3	11	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
54	c3p7iA	Alignment	not modelled	91.0	14	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
55	c4pbqC	Alignment	not modelled	90.9	9	PDB header: solute-binding protein Chain: C: PDB Molecule: putative trap periplasmic solute binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 haemophilus influenzae rdaw (hicg_00826, target efi-510123) with3 bound l-gulonate
56	c3gxaA	Alignment	not modelled	90.9	15	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
57	c3ix1A	Alignment	not modelled	90.8	9	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
58	c3ix1B	Alignment	not modelled	90.8	9	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
59	d1xs5a	Alignment	not modelled	90.6	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
60	d1ve4a1	Alignment	not modelled	90.6	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
61	c3n5IA	Alignment	not modelled	90.6	18	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
62	c4n8yA	Alignment	not modelled	90.4	20	PDB header: transport protein Chain: A: PDB Molecule: putative trap-type c4-dicarboxylate transport system, PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 bradyrhizobium sp. btai1 b (bbta_0128), target efi-5100563 (bbta_0128), complex with alpha/beta-d-galacturonate
63	c4ovqA	Alignment	not modelled	90.0	20	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate abc transporter, substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans, target efi-510230, with bound beta-d-3 glucuronate
64	c6esvA	Alignment	not modelled	89.8	14	PDB header: signaling protein Chain: A: PDB Molecule: putative periplasmic phosphite-binding-like protein (pbl) PDBTitle: structure of the phosphate-bound form of aix from rhizobium sp. str.2 nt-26
65	c4pcdA	Alignment	not modelled	89.4	14	PDB header: solute-binding protein Chain: A: PDB Molecule: c4-dicarboxylate transport system, substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans och 114 (rd1_1052, target efi-510238) with3 bound l-galactonate
66	c4ln5A	Alignment	not modelled	89.4	20	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 burkholderia ambifaria (bamb_6123), target efi-510059, with bound3 glycerol and chloride ion
67	c3louB	Alignment	not modelled	89.2	7	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
68	c4nn3A	Alignment	not modelled	89.0	14	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 (desal_2161), target efi-510109, with bound3 orotic acid
69	c5me4A	Alignment	not modelled	89.0	14	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
70	c3tviD	Alignment	not modelled	89.0	9	PDB header: transferase Chain: D: PDB Molecule: aspartokinase; PDBTitle: crystal structure of clostridium acetobutylicum aspartate kinase2 (caak): an important allosteric enzyme for industrial amino acids3 production
71	c4ntiA	Alignment	not modelled	88.9	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
						PDB header: transport protein

72	c4mncA	Alignment	not modelled	88.7	21	Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 polaromonas sp. js666 (bpro_4736), target efi-510156, with bound3 benzoyl formate, space group p21
73	c4oteA	Alignment	not modelled	88.6	11	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
74	c3ab4K	Alignment	not modelled	88.3	15	PDB header: transferase Chain: K: PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
75	c4ovpB	Alignment	not modelled	87.7	15	PDB header: solute-binding protein Chain: B: PDB Molecule: c4-dicarboxylate transport system substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 sulfitebacter sp. nas-14.1, target efi-510292, with bound alpha-d-3 manuronate
76	c3ir1F	Alignment	not modelled	87.7	14	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria meningitidis
77	c5yeiF	Alignment	not modelled	86.5	15	PDB header: transferase Chain: F: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
78	c4mx6A	Alignment	not modelled	86.1	8	PDB header: transport protein Chain: A: PDB Molecule: trap-type c4-dicarboxylate:h+ symport system substrate- PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 shewanella oneidensis (so_3134), target efi-510275, with bound3 succinate
79	c3o1lB	Alignment	not modelled	85.9	11	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
80	c2dtjA	Alignment	not modelled	85.6	16	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
81	c3tmgA	Alignment	not modelled	85.5	15	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
82	c4xeqC	Alignment	not modelled	85.4	13	PDB header: transport protein Chain: C: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio vulgaris (deval_0042, target efi-510114) bound to3 copurified (r)-pantoic acid
83	c2pfzA	Alignment	not modelled	85.1	13	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
84	c4ng7A	Alignment	not modelled	84.8	15	PDB header: transport protein Chain: B: PDB Molecule: trap periplasmic solute binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 citrobacter koseri (cko_04899), target efi-510094, apo, open3 structure
85	c3l6gA	Alignment	not modelled	84.8	14	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
86	c4pddA	Alignment	not modelled	84.5	13	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 polaromonas sp js666 (bpro_0088, target efi-510167) bound to d-3 erythronate
87	c1p99A	Alignment	not modelled	83.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus aureus
88	d1p99a	Alignment	not modelled	83.5	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
89	c6jf1A	Alignment	not modelled	83.5	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
90	c3s1tB	Alignment	not modelled	83.3	11	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
91	c5ub6B	Alignment	not modelled	82.9	13	PDB header: metal binding protein Chain: B: PDB Molecule: phosphate-binding protein; PDBTitle: xac2383 from xanthomonas citri bound to pyrophosphate
92	c4mnpA	Alignment	not modelled	82.1	11	PDB header: sugar binding protein Chain: A: PDB Molecule: n-acetylneuraminate-binding protein; PDBTitle: structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586
93	c4pbhA	Alignment	not modelled	82.0	16	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit, putative; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 ruegeria pomeroyi dss-3 (spo1773, target efi-510260)

						with bound3 benzoic acid
94	c3hn0A_	Alignment	not modelled	81.8	15	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
95	c3c1nA_	Alignment	not modelled	81.8	14	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
96	c5oeiA_	Alignment	not modelled	81.6	14	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein family upf0065:tat pathway signal; PDBTitle: r. palustris rpa4515 with oxoadipate
97	c6hkeB_	Alignment	not modelled	80.7	19	PDB header: transport protein Chain: B: PDB Molecule: possible tctc subunit of the tripartite tricarboxylate PDBTitle: matc (rpa3494) from rhodopseudomonas palustris with bound malate
98	c1ybaC_	Alignment	not modelled	80.4	20	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
99	c4magA_	Alignment	not modelled	80.3	10	PDB header: sugar binding protein Chain: A: PDB Molecule: sialic acid binding protein; PDBTitle: crystal structure of the periplasmic sialic acid binding protein from2 vibrio cholerea
100	c4o8mA_	Alignment	not modelled	80.3	12	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein2 actinobacillus succinogenes 130z, target efi-510004, with bound l-3 galactonate
101	c2hpgB_	Alignment	not modelled	80.0	14	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
102	c3fxbB_	Alignment	not modelled	79.8	9	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
103	c4n91A_	Alignment	not modelled	79.5	10	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
104	c2j0wA_	Alignment	not modelled	79.5	17	PDB header: transferase Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
105	c4p47A_	Alignment	not modelled	79.3	14	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 ochrobactrum anthropi (oant_4429), target efi-510151, c-terminus bound3 in ligand binding pocket
106	c3tqwA_	Alignment	not modelled	79.2	11	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
107	c2cdaB_	Alignment	not modelled	79.1	16	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
108	c3nrbD_	Alignment	not modelled	78.9	14	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
109	c4pakA_	Alignment	not modelled	78.2	11	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 verminephrobacter eiseniae efi01-2 (veis_3954, target efi-510324) a3 nephridial symbiont of the earthworm eisenia foetida, bound to (r)-4 pantoic acid
110	c3w7bB_	Alignment	not modelled	75.7	19	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
111	c4x9tA_	Alignment	not modelled	75.6	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein upf0065; PDBTitle: crystal structure of a tctc solute binding protein from polaromonas2 (bpro_3516, target efi-510338), no ligand
112	c4rleA_	Alignment	not modelled	74.4	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yaaq; PDBTitle: crystal structure of the c-di-amp binding pii-like protein dara
113	c4qhqa_	Alignment	not modelled	73.9	14	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine
114	c4n6dA_	Alignment	not modelled	73.9	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
						PDB header: transport protein Chain: A: PDB Molecule: trap-t family transporter, dctp (periplasmic

115	c4pf8A_	Alignment	not modelled	73.8	14	binding) PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Sulfitobacter</i> sp. nas-14.1 (target efi-510299) with bound beta-d-3 galacturonate
116	d2nv0a1	Alignment	not modelled	73.7	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
117	c4ovsB_	Alignment	not modelled	73.7	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 from <i>Sulfurospirillum deleyianum</i> DSM 6946 (sdel_0447), target efi-510309,3 with bound succinate
118	d1nh8a1	Alignment	not modelled	73.1	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
119	c2x26A_	Alignment	not modelled	72.7	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 <i>Escherichia coli</i>
120	c6mmvC_	Alignment	not modelled	72.5	19	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 at pH 7.4