



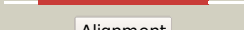

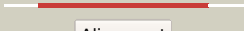









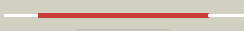







Phyre2


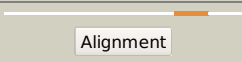
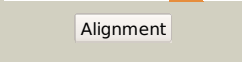
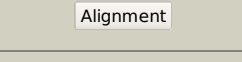
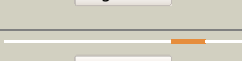
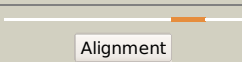
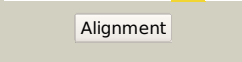
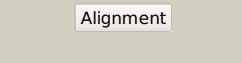
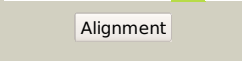
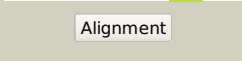
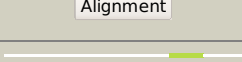
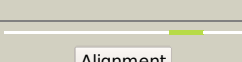
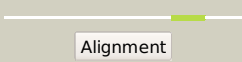
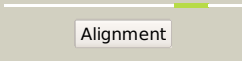
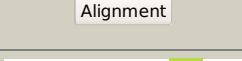
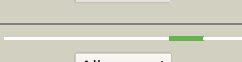
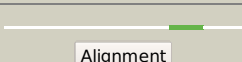
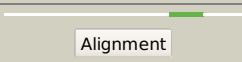
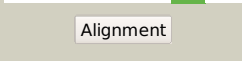
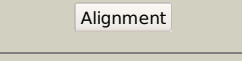
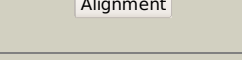

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Date	Wed Jul 31 22:05:37 BST 2019
Unique Job ID	fd7b73ccf5235a2b

Detailed template information


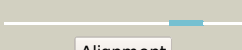
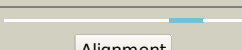


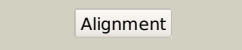
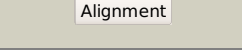
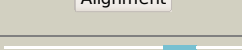
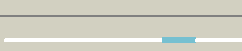

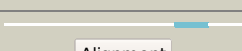
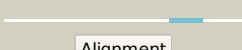

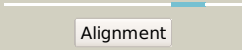
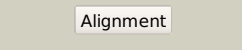

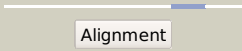
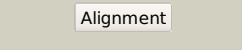
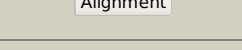
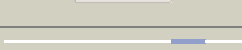

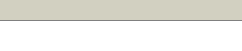

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4onyB_	 Alignment		100.0	19	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein family 5; PDBTitle: crystal structure of a abc transporter, periplasmic substrate-binding2 protein from brucella melitensis
2	c5icqA_	 Alignment		100.0	19	PDB header: periplasmic binding protein Chain: A: PDB Molecule: methylocystis parvus obbp mbne; PDBTitle: methanobactin periplasmic binding protein
3	c2grvC_	 Alignment		100.0	24	PDB header: biosynthetic protein Chain: C: PDB Molecule: !lpqw; PDBTitle: crystal structure of lpqw
4	c4oerA_	 Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: nika protein; PDBTitle: crystal structure of nika from brucella suis, unliganded form
5	d1xoca1	 Alignment		100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
6	c5isuA_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: !lmo0135 protein; PDBTitle: 2.2 angstrom crystal structure of abc transporter substrate binding2 protein ctap (!lmo0135) from listeria monocytogenes.
7	c3tpaA_	 Alignment		100.0	17	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
8	d1dpea_	 Alignment		100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
9	c4qfkG_	 Alignment		100.0	15	PDB header: peptide binding protein Chain: G: PDB Molecule: abc transporter periplasmic peptide-binding protein; PDBTitle: crystal structure of dipeptide binding protein from pseudoalteromonas2 sp. sm9913
10	d1zlqa1	 Alignment		100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
11	c2wokA_	 Alignment		100.0	18	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: clavulanic acid biosynthesis oligopeptide binding protein PDBTitle: clavulanic acid biosynthesis oligopeptide binding protein 2 complexed2 with bradykinin

12	c4oetA_	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: putative peptide abc-transport system periplasmic peptide- PDBTitle: crystal structure of nikz from campylobacter jejuni, unliganded form
13	c5yheA_	Alignment		100.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: nickel abc transporter substrate-binding protein; PDBTitle: the crystal structure of staphylococcus aureus cnta in complex with2 staphylopine and cobalt
14	d1jeta_	Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
15	c1ztyA_	Alignment		100.0	16	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligasaccharide binding2 protein
16	c3o9pA_	Alignment		100.0	17	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: periplasmic murein peptide-binding protein; PDBTitle: the structure of the escherichia coli murein tripeptide binding2 protein mppa
17	c5u4oA_	Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: a 2.05a x-ray structureof a bacterial extracellular solute-binding2 protein, family 5 for bacillus anthracis str. ames
18	c3ftoA_	Alignment		100.0	21	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide-binding protein oppa; PDBTitle: crystal structure of oppa in a open conformation
19	c3m8uA_	Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
20	c6dtfA_	Alignment		100.0	14	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: crystal structure of haemophilus influenzae oppa complex with kkk
21	c3t66A_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: nickel abc transporter (nickel-binding protein); PDBTitle: crystal structure of nickel abc transporter from bacillus halodurans
22	c6hlxA_	Alignment	not modelled	100.0	19	PDB header: transport protein Chain: A: PDB Molecule: agaa; PDBTitle: structure of the pbp agaa in complex with agropinic acid from2 a.tumefacien r10
23	c3zs6A_	Alignment	not modelled	100.0	19	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: the structural characterization of burkholderia pseudomallei oppa.
24	c4zebA_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (agrocinopines a PDBTitle: pbp acca from a. tumefaciens c58 in complex with agrocinopine a
25	c2o7jA_	Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic PDBTitle: the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
26	c6npaA_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: oligopeptide abc transporter, oligopeptide-binding protein; PDBTitle: crystal structure of oligopeptide abc transporter from bacillus2 anthracis str. ames (substrate-binding domain)
27	c3rqtA_	Alignment	not modelled	100.0	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
		Alignment				PDB header: peptide binding protein Chain: A: PDB Molecule: abc transporter, substrate-binding protein,

28	c6i3gA_	Alignment	not modelled	100.0	17	family 5; PDBTitle: crystal structure of a putative peptide binding protein oppa from 2 clostridium difficile
29	d1uqwa_	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
30	c4fajA_	Alignment	not modelled	100.0	15	PDB header: peptide binding protein Chain: A: PDB Molecule: prgz; PDBTitle: structure and mode of peptide binding of pheromone receptor prgz
31	d1vr5a1_	Alignment	not modelled	100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
32	c4wedA_	Alignment	not modelled	100.0	19	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, periplasmic solute-binding protein; PDBTitle: crystal structure of abc transporter substrate-binding protein from 2 sinorhizobium meliloti
33	c6epzA_	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A: PDB Molecule: periplasmic alpha-galactoside-binding protein; PDBTitle: structure of the periplasmic binding protein melb (atu4661) in complex2 with melibiose from agrobacterium fabrum c58
34	c4pfwA_	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: crystal structure of mannohexaose bound oligopeptide abc transporter,2 periplasmic oligopeptide-binding protein (tm1226) from thermotoga3 maritima at 2.2 a resolution
35	c3ry3B_	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.
36	c2d5wA_	Alignment	not modelled	100.0	21	PDB header: peptide binding protein Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
37	c5yybA_	Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: putative abc transporter periplasmic binding protein; PDBTitle: crystal structure of sialic acid binding protein from haemophilus2 ducreyi with neu5gc
38	c5jpwA_	Alignment	not modelled	100.0	22	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic oligopeptide- PDBTitle: oligopeptide-binding protein oppa
39	c5kztB_	Alignment	not modelled	100.0	17	PDB header: peptide binding protein Chain: B: PDB Molecule: peptide/nickel transport system substrate-binding protein; PDBTitle: listeria monocytogenes oppa bound to peptide
40	c4gl8B_	Alignment	not modelled	100.0	17	PDB header: protein transport Chain: B: PDB Molecule: oligopeptide abc transporter oppaiv; PDBTitle: x-ray crystal structure of a periplasmic oligopeptide-binding2 protein/oligopeptide abc transporter(oppaiv) from borrelia3 burgdorferi
41	c3lvuB_	Alignment	not modelled	100.0	21	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
42	c3pamB_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
43	c3o6pA_	Alignment	not modelled	100.0	24	PDB header: protein binding Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: crystal structure of peptide abc transporter, peptide-binding protein
44	c3l6gA_	Alignment	not modelled	94.7	12	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
45	c3chgB_	Alignment	not modelled	94.5	11	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
46	c3tmgA_	Alignment	not modelled	94.3	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
47	c2rejA_	Alignment	not modelled	93.4	12	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
48	c4xz6A_	Alignment	not modelled	90.4	14	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/proline abc transporter, periplasmic PDBTitle: tmox in complex with tmao
49	d1r9la_	Alignment	not modelled	88.4	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
50	c3r6uA_	Alignment	not modelled	87.2	14	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis

51	c6esvA	 Alignment	not modelled	85.0	18	PDB header: signaling protein Chain: A: PDB Molecule: putative periplasmic phosphite-binding-like protein (pb1) PDBTitle: structure of the phosphate-bound form of aixx from rhizobium sp. str.2 nt-26
52	d1ycga1	 Alignment	not modelled	83.3	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
53	c3nohA	 Alignment	not modelled	83.1	11	PDB header: peptide binding protein Chain: A: PDB Molecule: putative peptide binding protein; PDBTitle: crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
54	d1sw5a	 Alignment	not modelled	82.8	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
55	c6jf1A	 Alignment	not modelled	82.0	14	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
56	c3gxaA	 Alignment	not modelled	81.2	16	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
57	c3ir1F	 Alignment	not modelled	80.8	16	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria meningitidis
58	c3up9A	 Alignment	not modelled	71.0	13	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
59	c3ombA	 Alignment	not modelled	69.0	15	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: crystal structure of extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
60	c3pppA	 Alignment	not modelled	68.0	13	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
61	c4nt1A	 Alignment	not modelled	67.8	18	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
62	d2p0la1	 Alignment	not modelled	67.8	17	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
63	c4oteA	 Alignment	not modelled	66.5	14	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
64	c4z7eB	 Alignment	not modelled	65.6	13	PDB header: transport protein Chain: B: PDB Molecule: lmo1422 protein; PDBTitle: soluble binding domain of lmo1422 abc-transporter
65	c4ef2A	 Alignment	not modelled	65.3	19	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
66	d1e5da1	 Alignment	not modelled	64.5	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
67	c1p99A	 Alignment	not modelled	61.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus aureus
68	d1p99a	 Alignment	not modelled	61.3	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
69	c4wepA	 Alignment	not modelled	58.3	13	PDB header: transport protein Chain: A: PDB Molecule: putative osmoprotectant uptake system substrate-binding PDBTitle: apo yehz from escherichia coli
70	c3k2dA	 Alignment	not modelled	56.8	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
71	c5I9pA	 Alignment	not modelled	55.8	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of the pbp mota from a. tumefaciens b6
72	c4ne4A	 Alignment	not modelled	54.8	11	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
73	d1f4pa	Alignment	not modelled	54.2	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
74	c3e4rA	Alignment	not modelled	53.4	12	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

75	d1xs5a_	Alignment	not modelled	52.5	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
76	c3hlyA_	Alignment	not modelled	51.9	14	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from <i>synechococcus</i> sp2 q5mzp6_syp6 protein. northeast structural genomics consortium target3 snr135d.
77	c3nbmA_	Alignment	not modelled	51.6	13	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 <i>streptococcus pneumoniae</i> .
78	c4gotA_	Alignment	not modelled	51.4	15	PDB header: lipid binding protein Chain: A: PDB Molecule: methionine-binding lipoprotein metq; PDBTitle: crystal structure of a putative methionine-binding lipoprotein2 (bsu32730) from <i>bacillus subtilis</i> subsp. <i>subtilis</i> str. 168 at 1.95 a3 resolution
79	c4r6kA_	Alignment	not modelled	50.5	12	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of abc transporter substrate-binding protein yeso2 from <i>bacillus subtilis</i> , target efi-510761, an open conformation
80	c4heqB_	Alignment	not modelled	49.8	11	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from <i>desulfovibrio gigas</i>
81	c5b3kA_	Alignment	not modelled	47.7	13	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from <i>pseudomonas aeruginosa</i>
82	c2l2qA_	Alignment	not modelled	45.2	16	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from <i>borrelia burgdorferi</i>
83	c5o2kE_	Alignment	not modelled	45.0	20	PDB header: transport protein Chain: E: PDB Molecule: probable phosphite transport system-binding protein ptxb; PDBTitle: native apo-structure of <i>pseudomonas stutzeri</i> ptxb to 2.1 a resolution
84	c4h2dB_	Alignment	not modelled	44.9	7	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
85	c4ib2B_	Alignment	not modelled	44.1	18	PDB header: transport protein Chain: B: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (rumgna_00858) from2 <i>ruminococcus gnavus</i> atcc 29149 at 1.76 a resolution
86	c3kzqB_	Alignment	not modelled	44.0	9	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 <i>legionella pneumophila</i>
87	c4yo3G_	Alignment	not modelled	43.8	24	PDB header: transport protein Chain: G: PDB Molecule: tssa; PDBTitle: enteroaggregative <i>escherichia coli</i> tssa n-terminal fragment
88	c3f6sl_	Alignment	not modelled	43.2	11	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: <i>desulfovibrio desulfuricans</i> (atcc 29577) oxidized flavodoxin alternate2 conformers
89	d2fz5a1	Alignment	not modelled	42.2	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
90	c6gpcB_	Alignment	not modelled	41.8	17	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: crystal structure of the arginine-bound form of domain 1 from tmargbp
91	c4k3fA_	Alignment	not modelled	40.4	15	PDB header: transport protein Chain: A: PDB Molecule: probable tonb-dependent receptor; PDBTitle: crystal structure of a putative tonb-dependent receptor (pa5505) from2 <i>pseudomonas aeruginosa</i> pao1 at 1.60 a resolution
92	d1vmea1	Alignment	not modelled	39.1	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
93	c4mgeB_	Alignment	not modelled	38.8	17	PDB header: transferase Chain: B: PDB Molecule: pts system, cellobiose-specific iib component; PDBTitle: 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from <i>bacillus anthracis</i> .
94	c3hn0A_	Alignment	not modelled	38.8	16	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of an abc transporter (bdi_1369) from2 <i>parabacteroides distasonis</i> at 1.75 a resolution
95	c5lq8A_	Alignment	not modelled	38.2	13	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 <i>prochlorococcus marinus</i> (mit2 9301) in complex with methylphosphonate
96	c3tqwA_	Alignment	not modelled	38.1	16	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from <i>coxiiella burnetii</i>
97	d1ja1a2	Alignment	not modelled	38.0	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like

98	c5my5A_	 Alignment	not modelled	38.0	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic substrate-binding protein; PDBTitle: tungstate binding protein - tupa - from desulfovibrio alaskensis g20
99	c3p7iA_	 Alignment	not modelled	37.8	15	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
100	c4qhqa_	 Alignment	not modelled	35.9	9	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine
101	c4fuuA_	 Alignment	not modelled	35.3	13	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a leucine aminopeptidase precursor (bt_2548) from2 bacteroides thetaiotaomicron vpi-5482 at 1.30 a resolution
102	d2f06a2	 Alignment	not modelled	35.3	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
103	c4q5tA_	 Alignment	not modelled	35.3	17	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
104	c6h2tA_	 Alignment	not modelled	35.2	12	PDB header: signaling protein Chain: A: PDB Molecule: probable glutamine-binding lipoprotein glnh (glhbp); PDBTitle: glnh bound to glu, mycobacterium tuberculosis
105	c5k2xA_	 Alignment	not modelled	33.7	12	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter permease; PDBTitle: crystal structure of m. tuberculosis uspc (tetragonal crystal form)
106	c2ek8A_	 Alignment	not modelled	33.6	10	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
107	c3tc8A_	 Alignment	not modelled	32.8	17	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a zn-dependent exopeptidase (bdi_3547) from2 parabacteroides distazonis atcc 8503 at 1.06 a resolution
108	c4h67D_	 Alignment	not modelled	32.3	5	PDB header: transferase Chain: D: PDB Molecule: pyrimidine precursor biosynthesis enzyme thi5; PDBTitle: crystal structure of hmp synthase thi5 from s. cerevisiae
109	c5vegC_	 Alignment	not modelled	32.3	12	PDB header: electron transport Chain: C: PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment
110	c5jvbB_	 Alignment	not modelled	31.9	20	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
111	c4kysA_	 Alignment	not modelled	31.7	12	PDB header: transferase Chain: A: PDB Molecule: thiamine pyridinylase i; PDBTitle: clostridium botulinum thiaminase i in complex with thiamin
112	c3qslA_	 Alignment	not modelled	31.3	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
113	c6qqbB_	 Alignment	not modelled	30.9	14	PDB header: transferase Chain: B: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of porphyromonas gingivalis glutaminyl cyclase
114	c3n5iA_	 Alignment	not modelled	29.0	13	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
115	c5t0wA_	 Alignment	not modelled	28.9	26	PDB header: transport protein Chain: A: PDB Molecule: anccdt-1; PDBTitle: crystal structure of the ancestral amino acid-binding protein anccdt-2 1, a precursor of cyclohexadienyl dehydratase
116	c2m6rA_	 Alignment	not modelled	27.0	10	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: apo_yqca
117	c6g7cF_	 Alignment	not modelled	26.9	29	PDB header: transport protein Chain: F: PDB Molecule: impa-related domain protein; PDBTitle: nt2-ctd domains of the tssa component from the type vi secretion2 system of aeromonas hydrophila.
118	c6onpA_	 Alignment	not modelled	26.8	9	PDB header: unknown function Chain: A: PDB Molecule: periplasmic binding protein xoxj; PDBTitle: crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
119	c4pshA_	 Alignment	not modelled	26.7	17	PDB header: protein transport Chain: A: PDB Molecule: abc-type transporter, periplasmic subunit family 3; PDBTitle: structure of holo argbp from t. maritima
120	c5me4A_	 Alignment	not modelled	26.4	19	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