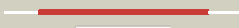























Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0411c_glnH_497317_498303
 Date Tue Jul 23 14:50:48 BST 2019
 Unique Job ID c3ac6a5b22037c07

Detailed template information

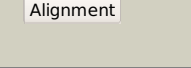
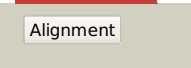
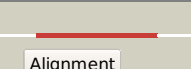
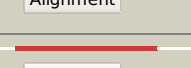
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6h2tA_	 Alignment		100.0	100	PDB header: signaling protein Chain: A: PDB Molecule: probable glutamine-binding lipoprotein glnh (glnbp); PDBTitle: glnh bound to glu, mycobacterium tuberculosis
2	c4z9nB_	 Alignment		100.0	28	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
3	c5eyfA_	 Alignment		100.0	33	PDB header: solute-binding protein Chain: A: PDB Molecule: glutamate abc superfamily atp binding cassette transporter, PDBTitle: crystal structure of solute-binding protein from enterococcus faecium2 with bound glutamate
4	c4h5fB_	 Alignment		100.0	21	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
5	c3vvfA_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, binding protein; PDBTitle: crystal structure of ttc0807 complexed with arginine
6	c6detA_	 Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: tv2483; PDBTitle: the crystal structure of tv2483 bound to l-arginine
7	c2ylnA_	 Alignment		100.0	19	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
8	c3hv1A_	 Alignment		100.0	18	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
9	c4pshA_	 Alignment		100.0	28	PDB header: protein transport Chain: A: PDB Molecule: abc-type transporter, periplasmic subunit family 3; PDBTitle: structure of holo argbp from t. maritima
10	c4ohnA_	 Alignment		100.0	21	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: crystal structure of an abc uptake transporter substrate binding2 protein from streptococcus pneumoniae with bound histidine
11	c4oz9A_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine

12	c4q0cA_	Alignment		100.0	19	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
13	c2vhaB_	Alignment		100.0	22	PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding transport protein; PDBTitle: debp
14	c3kzqB_	Alignment		100.0	26	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
15	c4pp0B_	Alignment		100.0	21	PDB header: transport protein Chain: B: PDB Molecule: nopaline-binding periplasmic protein; PDBTitle: structure of the pbp noct-m117n in complex with pyronopaline
16	c3k4uA_	Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinella succinogenes dsm 1740 complexed with lysine
17	c5hmtA_	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: crystal structure of the cyclohexadienyl dehydratase-like solute-2 binding protein sar11_1068 from candidatus pelagibacter ubique.
18	d2a5sa1	Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
19	c5josA_	Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: crystal structure of an ancestral cyclohexadienyl dehydratase, anccd-2 3(p188l).
20	c1xt8B_	Alignment		100.0	22	PDB header: transport protein Chain: B: PDB Molecule: putative amino-acid transporter periplasmic solute-binding PDBTitle: crystal structure of cysteine-binding protein from campylobacter2 jejuni at 2.0 a resolution
21	c5kuhB_	Alignment	not modelled	100.0	18	PDB header: signaling protein Chain: B: PDB Molecule: glutamate receptor ionotropic, kainate 2; PDBTitle: gluk2em with ly466195
22	c2v25B_	Alignment	not modelled	100.0	27	PDB header: receptor Chain: B: PDB Molecule: major cell-binding factor; PDBTitle: structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
23	c2yjpB_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: B: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the solute receptors for l-cysteine of2 neisseria gonorrhoeae
24	c2ieeB_	Alignment	not modelled	100.0	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.
25	c4i62A_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: 1.05 angstrom crystal structure of an amino acid abc transporter2 substrate-binding protein abpa from streptococcus pneumoniae canada3 mdr_19a bound to l-arginine
26	d1pb7a_	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
27	c3kbrA_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01 PDB header: octopine-binding protein

28	c5orgA	Alignment	not modelled	100.0	22	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.
29	c5t0wA	Alignment	not modelled	100.0	33	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
30	c3g41A	Alignment	not modelled	100.0	19	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
31	d1xt8a1	Alignment	not modelled	100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
32	c5uh0A	Alignment	not modelled	100.0	19	PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: 1.95 angstrom resolution crystal structure of fragment (35-274) of2 membrane-bound lytic murein transglycosylase f from yersinia pestis.
33	c4ymxB	Alignment	not modelled	100.0	29	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
34	c2q89A	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter amino acid-binding protein; PDBTitle: crystal structure of ehub in complex with hydroxyectoine
35	c3r39A	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
36	c2o1mB	Alignment	not modelled	100.0	21	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
37	c2y7iB	Alignment	not modelled	100.0	22	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
38	c3delC	Alignment	not modelled	100.0	21	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
39	c4zv2A	Alignment	not modelled	100.0	32	PDB header: solute-binding protein Chain: A: PDB Molecule: ancqr; PDBTitle: an ancestral arginine-binding protein bound to glutamine
40	c2rc9A	Alignment	not modelled	100.0	22	PDB header: membrane protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit 3a; PDBTitle: crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
41	c3i6vA	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
42	c3h7mA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with similarity2 to periplasmic binding proteins
43	c5l2eB	Alignment	not modelled	100.0	19	PDB header: protein binding Chain: B: PDB Molecule: glutamate receptor ionotropic, delta-2, glutamate receptor PDBTitle: crystal structure of rat glutamate receptor delta-2 extracellular2 domain
44	c4oenA	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: A: PDB Molecule: second substrate binding domain of putative amino acid abc PDBTitle: crystal structure of the second substrate binding domain of a putative2 amino acid abc transporter from streptococcus pneumoniae canada3 mdr_19a
45	c6a80B	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: B: PDB Molecule: putative amino acid-binding periplasmic abc transporter PDBTitle: crystal structure of putative amino acid binding periplasmic abc2 transporter protein from candidatus liberibacter asiaticus in complex3 with cystine
46	c4c0rB	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: B: PDB Molecule: putative amino acid binding protein; PDBTitle: molecular and structural basis of glutathione import in2 gram-positive bacteria via gsht and the cystine abc3 importer tcybc of streptococcus mutans.
47	c4uqqD	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: D: PDB Molecule: glutamate receptor ionotropic, kainate 2; PDBTitle: electron density map of gluk2 desensitized state in complex with 2s,2 4r-4-methylglutamate
48	c4kr5B	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: B: PDB Molecule: glutamine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcus lactis glnp substrate binding domain2 2 (sbd2) in open conformation
49	c4g4pA	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, amino acid-binding/permease PDBTitle: crystal structure of glutamine-binding protein from enterococcus2 faecalis at 1.5 a PDB header: transport protein

50	c2q2aD_	Alignment	not modelled	100.0	27	Chain: D: PDB Molecule: artj; PDBTitle: crystal structures of the arginine-, lysine-, histidine-binding2 protein artj from the thermophilic bacterium geobacillus3 stearothermophilus
51	c4eq9A_	Alignment	not modelled	100.0	19	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
52	d1wdna_	Alignment	not modelled	100.0	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
53	d1lsta_	Alignment	not modelled	100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
54	d1hsla_	Alignment	not modelled	100.0	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
55	c5l9mA_	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: A: PDB Molecule: deoxyfructosyl-amino acid transporter periplasmic binding PDBTitle: structure of agrobacterium tumefaciens b6 strain pbp soca complexed2 with deoxyfructosylglutamine (dfg)
56	c4f3pB_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: B: PDB Molecule: glutamine-binding periplasmic protein; PDBTitle: crystal structure of a glutamine-binding periplasmic protein from2 burkholderia pseudomallei in complex with glutamine
57	c5dtbB_	Alignment	not modelled	100.0	17	PDB header: membrane protein Chain: B: PDB Molecule: cg3822; PDBTitle: crystal structure of the drosophila cg3822 kair1d ligand binding2 domain complex with glutamate
58	c6mmvC_	Alignment	not modelled	100.0	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 at4 ph 7.4
59	c4kptA_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: A: PDB Molecule: glutamine abc transporter permease and substrate binding PDBTitle: crystal structure of substrate binding domain 1 (sbd1) of abc2 transporter glnpq from lactococcus lactis
60	c3mplA_	Alignment	not modelled	100.0	13	PDB header: signaling protein Chain: A: PDB Molecule: virulence sensor protein bvgs; PDBTitle: crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
61	c5dt6A_	Alignment	not modelled	100.0	18	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor 1; PDBTitle: crystal structure of the drosophila glur1a ligand binding domain2 complex with glutamate
62	d1mqia_	Alignment	not modelled	100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
63	c2xx7B_	Alignment	not modelled	100.0	19	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 2; PDBTitle: crystal structure of 1-(4-(1-pyrrolidinylcarbonyl)phenyl)-3-2 (trifluoromethyl)-4,5,6,7-tetrahydro-1h-indazole in complex with3 the ligand binding domain of the rat glua2 receptor and glutamate4 at 2.2a resolution.
64	c4ykiA_	Alignment	not modelled	100.0	15	PDB header: membrane protein Chain: A: PDB Molecule: mI032222a iglur; PDBTitle: mnemiopsis leidyi mI032222a iglur lbd glycine complex
65	c6mmvD_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: D: PDB Molecule: glutamate receptor ionotropic, nmda 2a; 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
66	c5iprD_	Alignment	not modelled	100.0	25	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
67	c4zdmA_	Alignment	not modelled	100.0	16	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor kainate-like protein; PDBTitle: pleurobrachia bachei iglur3 lbd glycine complex
68	c5sv6A_	Alignment	not modelled	100.0	16	PDB header: unknown function Chain: A: PDB Molecule: extracellular solute-binding protein, family 3; PDBTitle: crystal structure of mxaj from methlophaga aminisulfidivorans mpt
69	d1s50a1	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
70	c4wxjB_	Alignment	not modelled	100.0	17	PDB header: membrane protein Chain: B: PDB Molecule: glutamate receptor iib,glutamate receptor iib; PDBTitle: drosophila muscle gluriib complex with glutamate
71	c2pyyB_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: B: PDB Molecule: ionotropic glutamate receptor bacterial homologue; PDBTitle: crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
72	d2f34a1	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like

73	c4io7A_	Alignment	not modelled	100.0	18	PDB header: membrane protein Chain: A: PDB Molecule: avglur1 ligand binding domain; PDBTitle: crystal structure of the avglur1 ligand binding domain complex with2 phenylalanine at 1.9 angstrom resolution
74	d1ii5a_	Alignment	not modelled	100.0	23	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
75	c5bwjC_	Alignment	not modelled	100.0	15	PDB header: signaling protein Chain: C: PDB Molecule: sensory transduction histidine kinase, putative; PDBTitle: structural characterization and modeling of the borrelia burgdorferi2 hybrid histidine kinase hk1 periplasmic sensor
76	c1yaeB_	Alignment	not modelled	100.0	16	PDB header: membrane protein Chain: B: PDB Molecule: glutamate receptor, ionotropic kainate 2; PDBTitle: structure of the kainate receptor subunit glur6 agonist binding domain2 complexed with domoic acid
77	c2v3tA_	Alignment	not modelled	100.0	19	PDB header: receptor Chain: A: PDB Molecule: glutamate receptor delta-2 subunit synonym glurdelta2, glur PDBTitle: structure of the ligand-binding core of the ionotropic glutamate2 receptor-like glurdelta2 in the apo form
78	c5ideA_	Alignment	not modelled	100.0	21	PDB header: signaling protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: cryo-em structure of glua2/3 ampa receptor heterotetramer (model i)
79	c5ikbA_	Alignment	not modelled	100.0	21	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor ionotropic, kainate 4, glutamate receptor PDBTitle: crystal structure of the kainate receptor gluk4 ligand binding domain2 in complex with kainate
80	c6onpA_	Alignment	not modelled	100.0	17	PDB header: unknown function Chain: A: PDB Molecule: periplasmic binding protein xoxj; PDBTitle: crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
81	c5kbuA_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor 2, voltage-dependent calcium channel PDBTitle: cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution
82	c4pe5A_	Alignment	not modelled	100.0	19	PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor ionotropic, nmda 1; PDBTitle: crystal structure of glun1a/glun2b nmda receptor ion channel
83	c4pe5B_	Alignment	not modelled	100.0	19	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor ionotropic, nmda 2b; PDBTitle: crystal structure of glun1a/glun2b nmda receptor ion channel
84	c5gzsA_	Alignment	not modelled	100.0	15	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: structure of vc protein
85	c3kg2A_	Alignment	not modelled	100.0	20	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
86	c4tlmC_	Alignment	not modelled	99.9	26	PDB header: signaling protein Chain: C: PDB Molecule: receptor subunit glun1; PDBTitle: crystal structure of glun1/glun2b nmda receptor, structure 2
87	c6mmiD_	Alignment	not modelled	99.9	25	PDB header: transport protein Chain: D: PDB Molecule: glutamate receptor ionotropic, nmda 2a; PDBTitle: diheteromeric nmda receptor glun1/glun2a in the 'splayed-open'2 conformation, in complex with glycine and glutamate, in the presence3 of 1 millimolar zinc chloride, and at ph 7.4
88	c6qkzA_	Alignment	not modelled	99.9	21	PDB header: membrane protein Chain: A: PDB Molecule: glua1; PDBTitle: full length glua1/2-gamma8 complex
89	c6irfD_	Alignment	not modelled	99.9	21	PDB header: membrane protein Chain: D: PDB Molecule: glutamate receptor ionotropic, nmda 2a; PDBTitle: structure of the human glun1/glun2a nmda receptor in the2 glutamate/glycine-bound state at ph 6.3, class i
90	c6gpcB_	Alignment	not modelled	99.9	33	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	c5uowB_	Alignment	not modelled	99.9	24	PDB header: membrane protein Chain: B: PDB Molecule: n-methyl-d-aspartate receptor subunit nr2a; PDBTitle: triheteromeric nmda receptor glun1/glun2a/glun2b in complex with2 glycine, glutamate, mk-801 and a glun2b-specific fab, at ph 6.5
92	c5jvbB_	Alignment	not modelled	99.8	11	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	c5o2kE_	Alignment	not modelled	99.8	13	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
94	c5me4A_	Alignment	not modelled	99.7	16	PDB header: transport protein Chain: A: PDB Molecule: probable phosphite transport system-binding protein htbx; PDBTitle: the structure of htbx from pseudomonas stutzeri in complex with2 hypophosphite to 1.52 a resolution
95	c5lv1C_	Alignment	not modelled	99.7	12	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

96	c6esvA	 Alignment	not modelled	99.5	13	PDB header: signaling protein Chain: A: PDB Molecule: putative periplasmic phosphite-binding-like protein (pb1) PDBTitle: structure of the phosphate-bound form of aix from rhizobium sp. str.2 nt-26
97	c3n5IA	 Alignment	not modelled	99.4	9	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
98	c3p7IA	 Alignment	not modelled	99.4	12	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
99	c5ub6B	 Alignment	not modelled	99.3	15	PDB header: metal binding protein Chain: B: PDB Molecule: phosphate-binding protein; PDBTitle: xac2383 from xanthomonas citri bound to pyrophosphate
100	c5lq8A	 Alignment	not modelled	99.2	12	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
101	c3e4rA	 Alignment	not modelled	99.0	16	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
102	c2x26A	 Alignment	not modelled	98.9	18	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
103	c3uifA	 Alignment	not modelled	98.9	13	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
104	c3l6gA	 Alignment	not modelled	98.9	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
105	c4oteA	 Alignment	not modelled	98.7	9	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
106	c3ix1B	 Alignment	not modelled	98.7	11	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
107	c4q5tA	 Alignment	not modelled	98.7	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
108	c3ix1A	 Alignment	not modelled	98.7	11	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
109	d1xs5a	 Alignment	not modelled	98.7	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
110	c3qslA	 Alignment	not modelled	98.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
111	c3tqwA	 Alignment	not modelled	98.6	12	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
112	c4ntIA	 Alignment	not modelled	98.6	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
113	c3k2dA	 Alignment	not modelled	98.6	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
114	c6jf1A	 Alignment	not modelled	98.6	12	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
115	c3hn0A	 Alignment	not modelled	98.6	11	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
116	c3tmgA	 Alignment	not modelled	98.5	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
117	c3up9A	 Alignment	not modelled	98.5	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 PDB header: unknown function

118	c3un6A_	Alignment	not modelled	98.4	9	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
119	c4de8A_	Alignment	not modelled	98.3	13	PDB header: membrane protein Chain: A: PDB Molecule: cps2a; PDBTitle: lytr-cps2a-psr family protein with bound octaprenyl monophosphate2 lipid
120	c4ef2A_	Alignment	not modelled	98.3	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