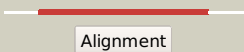

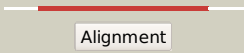



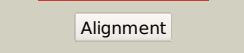



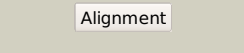

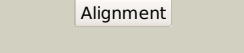



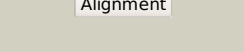

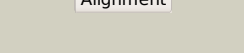

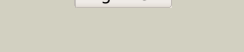



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3666c_(dppA)_4105637_4107262
Date	Fri Aug 9 18:20:35 BST 2019
Unique Job ID	bdb57c02a823450e

Detailed template information

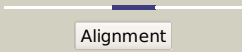
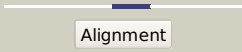

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3o9pA_	 Alignment		100.0	23	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: periplasmic murein peptide-binding protein; PDBTitle: the structure of the escherichia coli murein tripeptide binding2 protein mppa
2	d1jeta_	 Alignment		100.0	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c3zs6A_	 Alignment		100.0	21	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: the structural characterization of burkholderia pseudomallei oppa.
4	c3tpaA_	 Alignment		100.0	19	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
5	c4qfkG_	 Alignment		100.0	20	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
6	d1dpea_	 Alignment		100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	c6dtfA_	 Alignment		100.0	22	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: crystal structure of haemophilus influenzae oppa complex with kkk
8	c3m8uA_	 Alignment		100.0	19	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)
9	c6npoA_	 Alignment		100.0	18	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)
10	c2wokA_	 Alignment		100.0	19	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
11	c4oerA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: nika protein; PDBTitle: crystal structure of nika from brucella suis, unliganded form

12	d1uqwa_	Alignment		100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
13	c6hlxA_	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: agaa; PDBTitle: structure of the pbp agaa in complex with agropinic acid from2 a.tumefacien r10
14	c3t66A_	Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: nickel abc transporter (nickel-binding protein); PDBTitle: crystal structure of nickel abc transporter from bacillus halodurans
15	c5u4oA_	Alignment		100.0	18	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
16	c4gl8B_	Alignment		100.0	20	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
17	d1zlqa1	Alignment		100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
18	d1xoca1	Alignment		100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
19	c4fajA_	Alignment		100.0	19	PDB header: peptide binding protein Chain: A: PDB Molecule: prgz; PDBTitle: structure and mode of peptide binding of pheromone receptor prgz
20	c5isuA_	Alignment		100.0	19	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.
21	c5yheA_	Alignment	not modelled	100.0	14	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
22	c5kztB_	Alignment	not modelled	100.0	19	PDB header: peptide binding protein Chain: B: PDB Molecule: peptide/nickel transport system substrate-binding protein; PDBTitle: listeria monocytogenes oppa bound to peptide
23	c4oetA_	Alignment	not modelled	100.0	20	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
24	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
25	c4onyB_	Alignment	not modelled	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
26	c4zebA_	Alignment	not modelled	100.0	18	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
27	c6i3gA_	Alignment	not modelled	100.0	18	PDB header: peptide binding protein Chain: A: PDB Molecule: abc transporter, substrate-binding protein, family 5;

						PDBTitle: crystal structure of a putative peptide binding protein oppa from2 clostridium difficile
28	c5yybA_	Alignment	not modelled	100.0	18	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
29	c1ztyA_	Alignment	not modelled	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
30	c5icqA_	Alignment	not modelled	100.0	17	PDB header: periplasmic binding protein Chain: A: PDB Molecule: methylcystis parvus obbp mbne; PDBTitle: methanobactin periplasmic binding protein
31	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
32	c3ftoA_	Alignment	not modelled	100.0	16	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide-binding protein oppa; PDBTitle: crystal structure of oppa in a open conformation
33	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 from2 sinorhizobium melliloti
34	c4pfaA_	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	d1vr5a1	Alignment	not modelled	100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
36	c2grvC_	Alignment	not modelled	100.0	16	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
37	c3ry3B_	Alignment	not modelled	100.0	21	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.
38	c2d5wA_	Alignment	not modelled	100.0	20	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
39	c6epzA_	Alignment	not modelled	100.0	16	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
40	c5ipwA_	Alignment	not modelled	100.0	18	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic oligopeptide-binding protein oppa
41	c3lvuB_	Alignment	not modelled	100.0	18	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	22	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	c5sv6A_	Alignment	not modelled	60.2	12	PDB header: unknown function Chain: A: PDB Molecule: extracellular solute-binding protein, family 3; PDBTitle: crystal structure of mxaj from methlophaga aminisulfivorans mpt
45	c3chgB_	Alignment	not modelled	49.6	8	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	c6esvA_	Alignment	not modelled	44.8	11	PDB header: signaling protein Chain: A: PDB Molecule: putative periplasmic phosphite-binding-like protein (pbl) PDBTitle: structure of the phosphate-bound form of aixo from rhizobium sp. str.2 nt-26
47	c3hlyA_	Alignment	not modelled	41.1	10	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_synp6 protein. northeast structural genomics consortium target3 snr135d.
48	c3un6A_	Alignment	not modelled	41.0	14	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
49	c6onpA_	Alignment	not modelled	40.1	14	PDB header: unknown function Chain: A: PDB Molecule: periplasmic binding protein xoxj; PDBTitle: crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
						PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic

50	c3kzgb_	Alignment	not modelled	34.6	10	binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila PDB header: transport protein
51	c4qhqA_	Alignment	not modelled	33.5	16	Chain: A: PDB Molecule: lipoprotein; PDBTitle: the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine
52	c2o1mB_	Alignment	not modelled	33.4	16	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
53	c6jf1A_	Alignment	not modelled	33.2	10	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
54	c4q0cA_	Alignment	not modelled	32.5	13	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
55	c4yo3G_	Alignment	not modelled	31.5	19	PDB header: transport protein Chain: G: PDB Molecule: tssa; PDBTitle: enteroaggregative escherichia coli tssa n-terminal fragment
56	c3hn0A_	Alignment	not modelled	29.7	16	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
57	c3tqwA_	Alignment	not modelled	27.0	15	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
58	c6g7cF_	Alignment	not modelled	24.5	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.
59	c3ombA_	Alignment	not modelled	22.9	5	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	d1g7da_	Alignment	not modelled	21.5	19	Fold: ERP29 C domain-like Superfamily: ERP29 C domain-like Family: ERP29 C domain-like
61	c5dt6A_	Alignment	not modelled	19.2	8	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	c4kptA_	Alignment	not modelled	18.4	14	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
63	c5l9mA_	Alignment	not modelled	17.6	15	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)
64	c5e3eA_	Alignment	not modelled	17.5	30	PDB header: toxin Chain: A: PDB Molecule: cdii immunity protein; PDBTitle: crystal structure of cdia-ct/cdii complex from y. kristensenii 33638
65	c3l6gA_	Alignment	not modelled	16.9	10	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
66	c3f6sl_	Alignment	not modelled	15.6	10	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
67	c6h2tA_	Alignment	not modelled	14.9	9	PDB header: signaling protein Chain: A: PDB Molecule: probable glutamine-binding lipoprotein glnh (glnhp); PDBTitle: glnh bound to glu, mycobacterium tuberculosis
68	d1f4pa_	Alignment	not modelled	14.3	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
69	c2i4cA_	Alignment	not modelled	14.2	15	PDB header: transport protein Chain: A: PDB Molecule: bicarbonate transporter; PDBTitle: crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
70	c6detA_	Alignment	not modelled	13.5	11	PDB header: transport protein Chain: A: PDB Molecule: tv2483; PDBTitle: the crystal structure of tv2483 bound to l-arginine
71	c2rejA_	Alignment	not modelled	13.3	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
72	c4m6tA_	Alignment	not modelled	13.1	57	PDB header: transcription regulator Chain: A: PDB Molecule: rna polymerase ii-associated factor 1 homolog, linker, rna PDBTitle: structure of human paf1 and leo1 complex
73	d1r9la_	Alignment	not modelled	12.9	6	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like PDB header: transport protein

74	c4h5fB	Alignment	not modelled	12.3	13	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
75	c1xofA	Alignment	not modelled	12.3	28	PDB header: de novo protein Chain: A: PDB Molecule: bbahett1; PDBTitle: heterooligomeric beta beta alpha miniprotein
76	c3kbrA	Alignment	not modelled	12.1	11	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
77	c5uc2C	Alignment	not modelled	12.1	31	PDB header: hydrolase Chain: C: PDB Molecule: domain of unknown function duf1849; PDBTitle: crystal structure of beta-barrel-like, putative atp binding protein of2 domain of unknown function duf1849 from brucella abortus
78	d2f06a2	Alignment	not modelled	12.0	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
79	c6mjpC	Alignment	not modelled	12.0	5	PDB header: lipid transport Chain: C: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: lptb(e163q)fgc from vibrio cholerae
80	c5uh0A	Alignment	not modelled	11.9	7	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.
81	c2qt7B	Alignment	not modelled	11.8	4	PDB header: hydrolase Chain: B: PDB Molecule: receptor-type tyrosine-protein phosphatase-like n; PDBTitle: crystallographic structure of the mature ectodomain of the human2 receptor-type protein-tyrosine phosphatase ia-2 at 1.30 angstroms
82	c5b3kA	Alignment	not modelled	11.8	12	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
83	c4q5tA	Alignment	not modelled	11.7	6	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
84	c3qslA	Alignment	not modelled	11.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
85	c5l9pA	Alignment	not modelled	11.6	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of the pbp mota from a. tumefaciens b6
86	c3ix1B	Alignment	not modelled	11.1	13	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
87	c3ix1A	Alignment	not modelled	11.1	13	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
88	c3tmgA	Alignment	not modelled	11.1	10	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
89	c2g29A	Alignment	not modelled	11.0	11	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein nrta; PDBTitle: crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
90	c2x26A	Alignment	not modelled	11.0	9	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
91	c3e4rA	Alignment	not modelled	10.9	10	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
92	c3r39A	Alignment	not modelled	10.8	17	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
93	d1pb7a	Alignment	not modelled	9.9	8	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
94	c1xt8B	Alignment	not modelled	9.5	9	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
95	c3g41A	Alignment	not modelled	9.1	20	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
96	c5cd2A	Alignment	not modelled	8.7	8	PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-d-glucanase; PDBTitle: the crystal structure of endo-1,4-d-glucanase from vibrio

					fischeri2 es114
97	c4eq9A_		not modelled	8.7	17 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
98	c4z9nB_		not modelled	8.6	16 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
99	c2ieeB_		not modelled	8.2	12 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.