Phyre2

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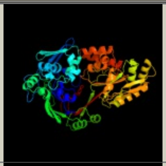
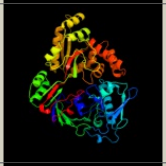
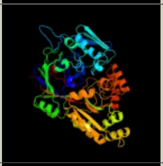
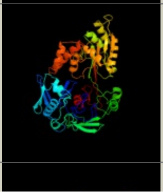
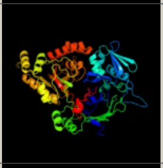
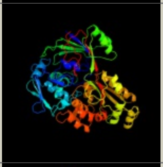
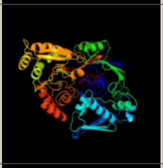
Unique Job ID	17165df8f4660b02

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dpea_	Alignment		100.0	36	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
2	c3tpaA_	Alignment		100.0	34	**PDB header:**heme binding protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** structure of hbpa2 from haemophilus parasuis
3	c3m8uA_	Alignment		100.0	36	**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)
4	d1jeta_	Alignment		100.0	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
5	d1zlqa1	Alignment		100.0	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
6	c3o9pA_	Alignment		100.0	19	**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
7	c2wokA_	Alignment		100.0	20	**PDB header:**peptide binding protein/peptide **Chain:** A: **PDB Molecule:**clavulanic acid biosynthesis oligopeptide **PDBTitle:** clavulanic acid biosynthesis oligopeptide2 binding protein 2 complexed with bradykinin
8	d1xoca1	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
9	d1uqwa_	Alignment		100.0	28	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	c3t66A_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
11	c1ztyA_	Alignment		100.0	19	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein

12	c2o7jA_	Alignment		100.0	19	**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
13	d1vr5a1	Alignment		100.0	20	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
14	c2grvC_	Alignment		100.0	16	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
15	c3ftoA_	Alignment		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
16	c3rqtA_	Alignment		100.0	18	**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
17	c2d5wA_	Alignment		100.0	19	**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
18	c3ry3B_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative solute-binding protein; **PDBTitle:** putative solute-binding protein from yersinia pestis.
19	c3lvuB_	Alignment		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
20	c3pamB_	Alignment		100.0	17	**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
21	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
22	c3tmgA_	Alignment	not modelled	95.5	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
23	c3nohA_	Alignment	not modelled	95.1	14	**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
24	c3l6gA_	Alignment	not modelled	95.1	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
25	c3chgB_	Alignment	not modelled	93.9	17	**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
26	c2rejA_	Alignment	not modelled	93.7	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
27	d1r9la_	Alignment	not modelled	91.4	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like

28	c3r6uA_	Alignment	not modelled	91.4	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
29	d1sw5a_	Alignment	not modelled	86.4	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
30	c3pppA_	Alignment	not modelled	85.6	9	**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
31	c3ir1F_	Alignment	not modelled	72.0	14	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
32	c3hlyA_	Alignment	not modelled	71.5	14	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
33	c2o1mB_	Alignment	not modelled	67.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable amino-acid abc transporter **PDBTitle:** crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
34	c3kzgB_	Alignment	not modelled	65.5	11	**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
35	d1xs5a_	Alignment	not modelled	65.2	4	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
36	d1ycga1	Alignment	not modelled	63.4	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
37	d1e5da1	Alignment	not modelled	63.2	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
38	c3gxaA_	Alignment	not modelled	61.3	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
39	c3un6A_	Alignment	not modelled	57.9	5	**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
40	c3k2dA_	Alignment	not modelled	57.1	18	**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
41	d2vv5a2	Alignment	not modelled	55.7	16	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
42	c3tqwA_	Alignment	not modelled	53.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
43	c3f6sI_	Alignment	not modelled	52.4	13	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
44	c2rc9A_	Alignment	not modelled	51.6	7	**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
45	d1f4pa_	Alignment	not modelled	50.6	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
46	c3kn3C_	Alignment	not modelled	46.7	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative periplasmic protein; **PDBTitle:** crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
47	d1s8na_	Alignment	not modelled	40.9	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	c3hn0A_	Alignment	not modelled	40.8	18	**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
49	d2p0la1	Alignment	not modelled	40.4	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
50	d1p99a_	Alignment	not modelled	40.2	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
51	c1p99A_	Alignment	not modelled	40.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
52	c3r39A_	Alignment	not modelled	39.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative periplasmic binding protein;

52	c3r39A_	Alignment	not modelled	39.6	10	**PDBTitle:** crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
53	c2v25B_	Alignment	not modelled	39.5	14	**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
54	d2a9pa1	Alignment	not modelled	38.7	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
55	c3o66A_	Alignment	not modelled	38.1	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline abc transporter; **PDBTitle:** crystal structure of glycine betaine/carnitine/choline abc transporter
56	c3muqB_	Alignment	not modelled	37.2	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
57	c2y7iB_	Alignment	not modelled	35.3	9	**PDB header:**arginine-binding protein **Chain:** B: **PDB Molecule:**stm4351; **PDBTitle:** structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
58	c3ix1B_	Alignment	not modelled	35.2	10	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
59	c3ix1A_	Alignment	not modelled	35.2	10	**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
60	c2ylnA_	Alignment	not modelled	34.6	20	**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
61	d2a5sa1	Alignment	not modelled	34.6	5	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
62	d1xhfa1	Alignment	not modelled	34.2	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	c2j48A_	Alignment	not modelled	33.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
64	c3n5lA_	Alignment	not modelled	32.9	14	**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
65	d1wdna_	Alignment	not modelled	32.4	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
66	c2q2aD_	Alignment	not modelled	30.8	20	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**artj; **PDBTitle:** crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
67	c3kbrA_	Alignment	not modelled	30.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
68	c3lr1A_	Alignment	not modelled	30.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tungstate abc transporter, periplasmic tungstate- **PDBTitle:** the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
69	d1mb3a_	Alignment	not modelled	30.5	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	d1zgza1	Alignment	not modelled	30.0	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	c3g41A_	Alignment	not modelled	29.6	17	**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
72	d1twya_	Alignment	not modelled	29.6	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
73	c1twyG_	Alignment	not modelled	29.6	12	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
74	c3k4uA_	Alignment	not modelled	29.5	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
75	c2f5xC_	Alignment	not modelled	29.3	10	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd

76	c2l2qA_	Alignment	not modelled	28.8	8	**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 borrelia burgdorferi
77	c3ombA_	Alignment	not modelled	28.6	14	**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
78	d1mvoa_	Alignment	not modelled	28.6	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
79	d2fz5a1	Alignment	not modelled	27.6	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
80	c3d7nA_	Alignment	not modelled	27.1	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
81	d1ys7a2	Alignment	not modelled	26.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	c1xt8B_	Alignment	not modelled	26.2	14	**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
83	c2l6nA_	Alignment	not modelled	26.2	13	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_001092504.1; **PDBTitle:** nmr solution structure of the protein yp_001092504.1
84	c3hv1A_	Alignment	not modelled	26.1	17	**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
85	c3delC_	Alignment	not modelled	25.5	19	**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
86	c2yjpB_	Alignment	not modelled	25.1	17	**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
87	d1hsla_	Alignment	not modelled	25.0	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
88	c2ek8A_	Alignment	not modelled	24.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** aminopeptidase from aneurinibacillus sp. strain am-1
89	c3khtA_	Alignment	not modelled	22.5	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
90	c3guxA_	Alignment	not modelled	22.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zn-dependent exopeptidase; **PDBTitle:** crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
91	d1uxya2	Alignment	not modelled	22.3	9	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
92	c2f06B_	Alignment	not modelled	22.3	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
93	c3t6kB_	Alignment	not modelled	22.2	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator receiver; **PDBTitle:** crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
94	c2x26A_	Alignment	not modelled	22.1	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic aliphatic sulphonates-binding protein; **PDBTitle:** crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
95	c3i6vA_	Alignment	not modelled	22.0	11	**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
96	c2ieeB_	Alignment	not modelled	22.0	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable abc transporter extracellular-binding **PDBTitle:** crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
97	c2xx7B_	Alignment	not modelled	21.6	14	**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.

98	d1lsta_	Alignment	not modelled	21.6	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
99	d1zh2a1	Alignment	not modelled	21.6	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
100	c3e4rA_	Alignment	not modelled	21.3	13	**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
101	c2oqrA_	Alignment	not modelled	21.3	14	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
102	c3f6cB_	Alignment	not modelled	21.3	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
103	d5nula_	Alignment	not modelled	21.3	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
104	c3a0rB_	Alignment	not modelled	20.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
105	c1tvmA_	Alignment	not modelled	20.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system