Phyre2

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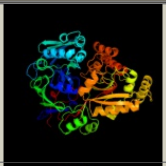
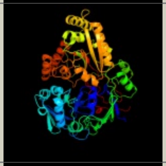
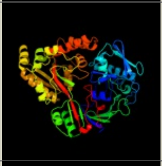
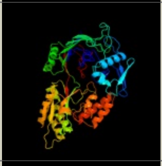
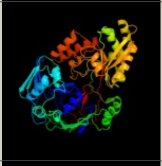
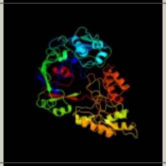
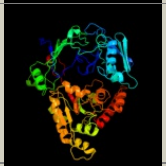
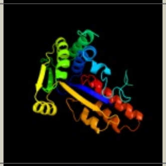
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jeta_	Alignment		100.0	86	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
2	c3o9pA_	Alignment		100.0	49	**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
3	c3tpaA_	Alignment		100.0	25	**PDB header:**heme binding protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** structure of hbpa2 from haemophilus parasuis
4	d1dpea_	Alignment		100.0	24	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
5	c3m8uA_	Alignment		100.0	23	**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)
6	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
7	d1xoca1	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
8	d1zlqa1	Alignment		100.0	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
9	c3t66A_	Alignment		100.0	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
10	d1uqwa_	Alignment		100.0	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
11	c3rqtA_	Alignment		100.0	17	**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

12	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
13	c3ftoA_	Alignment		100.0	20	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**oligopeptide-binding protein oppa; **PDBTitle:** crystal structure of oppa in a open conformation
14	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
15	d1vr5a1	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
16	c2grvC_	Alignment		100.0	18	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
17	c2d5wA_	Alignment		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
18	c3ry3B_	Alignment		100.0	19	**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	19	**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	18	**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	c3chgB_	Alignment	not modelled	96.4	18	**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
23	c3l6gA_	Alignment	not modelled	95.5	19	**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
24	c3tmgA_	Alignment	not modelled	94.5	12	**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
25	d1r9la_	Alignment	not modelled	93.2	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
26	c2rejA_	Alignment	not modelled	92.2	10	**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	c3kn3C_	Alignment	not modelled	81.5	21	**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

28	c3r6uA_	Alignment	not modelled	80.2	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
29	c3nohA_	Alignment	not modelled	72.3	13	**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
30	d1sw5a_	Alignment	not modelled	67.3	2	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
31	c3lr1A_	Alignment	not modelled	65.8	18	**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
32	c3ir1F_	Alignment	not modelled	64.5	16	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
33	c3pppA_	Alignment	not modelled	61.8	16	**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
34	c1tvmA_	Alignment	not modelled	61.4	10	**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
35	c3ombA_	Alignment	not modelled	58.1	11	**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
36	c3kzgB_	Alignment	not modelled	54.5	7	**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
37	c3muqB_	Alignment	not modelled	50.2	20	**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
38	c2e76D_	Alignment	not modelled	48.1	4	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
39	c2rc9A_	Alignment	not modelled	47.2	12	**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
40	c3gxaA_	Alignment	not modelled	44.3	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
41	d1xs5a_	Alignment	not modelled	42.1	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
42	c3hlyA_	Alignment	not modelled	41.6	11	**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.
43	d2p0la1	Alignment	not modelled	41.6	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
44	c3k2dA_	Alignment	not modelled	40.2	17	**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
45	c3ix1A_	Alignment	not modelled	40.2	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
46	c3ix1B_	Alignment	not modelled	40.2	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
47	d1e5da1	Alignment	not modelled	37.9	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
48	c2zykA_	Alignment	not modelled	35.7	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**solute-binding protein; **PDBTitle:** crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
49	d1p99a_	Alignment	not modelled	35.5	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
50	c1p99A_	Alignment	not modelled	35.5	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

51	d2a5sa1	Alignment	not modelled	33.6	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
52	c3un6A_	Alignment	not modelled	31.3	8	**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
53	c2v25B_	Alignment	not modelled	30.7	8	**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	c3tqwA_	Alignment	not modelled	30.0	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
55	d1f4pa_	Alignment	not modelled	27.9	6	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
56	c3k4uA_	Alignment	not modelled	27.5	16	**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
57	c2y7iB_	Alignment	not modelled	27.2	18	**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	d1wdna_	Alignment	not modelled	26.7	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
59	c3r39A_	Alignment	not modelled	26.4	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative periplasmic binding protein; **PDBTitle:** crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
60	d1ycga1	Alignment	not modelled	26.4	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
61	c3i6vA_	Alignment	not modelled	26.2	12	**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
62	c2x26A_	Alignment	not modelled	25.9	13	**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
63	c2ylnA_	Alignment	not modelled	25.8	17	**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
64	c3f6sI_	Alignment	not modelled	25.5	10	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
65	c2xx7B_	Alignment	not modelled	22.9	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.
66	c2q2aD_	Alignment	not modelled	22.0	16	**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	c3delC_	Alignment	not modelled	21.9	9	**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
68	d1xvya_	Alignment	not modelled	20.7	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
69	d1pb7a_	Alignment	not modelled	19.2	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
70	c2o1mB_	Alignment	not modelled	18.6	18	**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
71	c2f5xC_	Alignment	not modelled	18.5	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
72	d1ykga1	Alignment	not modelled	18.5	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
73	c3g41A_	Alignment	not modelled	18.2	11	**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
74	d1hsla_	Alignment	not modelled	17.9	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II

						Family: Phosphate binding protein-like
75	c2uvgA_	Alignment	not modelled	16.2	19	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**abc type periplasmic sugar-binding protein; **PDBTitle:** structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
76	d2fz5a1	Alignment	not modelled	15.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
77	d1twya_	Alignment	not modelled	15.3	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
78	c1twyG_	Alignment	not modelled	15.3	9	**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
79	d1lsta_	Alignment	not modelled	15.2	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
80	c2x7pA_	Alignment	not modelled	14.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**possible thiamine biosynthesis enzyme; **PDBTitle:** the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
81	c3e4rA_	Alignment	not modelled	14.8	14	**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
82	d1g7da_	Alignment	not modelled	14.8	19	**Fold:**ERP29 C domain-like **Superfamily:**ERP29 C domain-like **Family:**ERP29 C domain-like
83	c2ieeB_	Alignment	not modelled	14.3	16	**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.
84	d1eaka1	Alignment	not modelled	14.0	12	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
85	c3qslA_	Alignment	not modelled	13.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
86	c3hn0A_	Alignment	not modelled	13.5	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
87	c2vpnB_	Alignment	not modelled	13.3	13	**PDB header:**transport **Chain:** B: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
88	c2q9uB_	Alignment	not modelled	13.2	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
89	d1mqia_	Alignment	not modelled	13.1	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
90	c3kbrA_	Alignment	not modelled	12.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
91	c2pt1A_	Alignment	not modelled	12.7	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** futa1 synechocystis pcc 6803
92	c3gyyC_	Alignment	not modelled	12.3	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
93	d1elja_	Alignment	not modelled	11.7	5	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
94	d1ii5a_	Alignment	not modelled	11.6	4	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
95	c2qt7B_	Alignment	not modelled	11.5	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**receptor-type tyrosine-protein phosphatase-like **PDBTitle:** crystallographic structure of the mature ectodomain of the2 human receptor-type protein-tyrosine phosphatase ia-2 at3 1.30 angstroms
96	c2gh9A_	Alignment	not modelled	11.3	9	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**maltose/maltodextrin-binding protein; **PDBTitle:** thermus thermophilus maltotriose binding protein bound with2 maltotriose
97	c2qpqC_	Alignment	not modelled	11.1	15	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
98	d1y3na1	Alignment	not modelled	10.1	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						Fold: Periplasmic binding protein-like II

99	d1amfa_	Alignment	not modelled	9.9	15	**Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like