Phyre^2

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Description	P0AGC5
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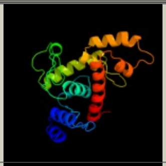
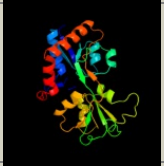
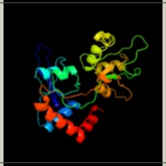
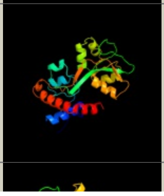
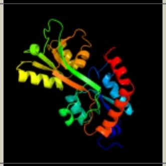
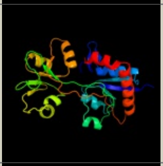
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1slyA_	Alignment		100.0	26	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
2	c2y8pA_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a; **PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
3	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
4	c3k4uA_	Alignment		100.0	24	**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
5	d2a5sa1	Alignment		100.0	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
6	c3hv1A_	Alignment		100.0	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
7	c2ieeB_	Alignment		100.0	15	**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.
8	c2q89A_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter amino acid-binding protein; **PDBTitle:** crystal structure of ehub in complex with hydroxyectoine
9	c3kbrA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
10	d1qsaa2	Alignment		100.0	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
11	c2rc9A_	Alignment		100.0	11	**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

12	c3kzgB_	Alignment		100.0	18	**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
13	d1pb7a_	Alignment		100.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
14	c3r39A_	Alignment		100.0	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
15	c2vhaB_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**periplasmic binding transport protein; **PDBTitle:** debp
16	c2o1mB_	Alignment		100.0	20	**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
17	d1hsla_	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
18	c3i6vA_	Alignment		100.0	17	**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
19	d1lsta_	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
20	c3g41A_	Alignment		100.0	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
21	c2q2aD_	Alignment	not modelled	100.0	18	**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
22	c3h7mA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
23	c2v25B_	Alignment	not modelled	100.0	17	**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
24	c2y7iB_	Alignment	not modelled	100.0	15	**PDB header:**arginine-binding protein **Chain:** B: **PDB Molecule:**stm4351; **PDBTitle:** structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
25	c3delC_	Alignment	not modelled	100.0	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
26	c1xt8B_	Alignment	not modelled	100.0	16	**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
27	d1wdna_	Alignment	not modelled	100.0	20	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
28	c3mplA_	Alignment	not modelled	100.0	16	**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)

29	d1gbsa_	Alignment	not modelled	100.0	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
30	d1mqia_	Alignment	not modelled	100.0	19	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
31	c2yjpB_	Alignment	not modelled	100.0	21	**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
32	c3mgwA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
33	d1xt8a1	Alignment	not modelled	100.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
34	c2pyyB_	Alignment	not modelled	100.0	15	**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
35	d1s50a1	Alignment	not modelled	100.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
36	d1ii5a_	Alignment	not modelled	100.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
37	c2xx7B_	Alignment	not modelled	99.9	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.
38	c3gxkB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9
39	d2f34a1	Alignment	not modelled	99.9	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
40	c2v3tA_	Alignment	not modelled	99.9	12	**PDB header:**receptor **Chain:** A: **PDB Molecule:**glutamate receptor delta-2 subunit synonym **PDBTitle:** structure of the ligand-binding core of the ionotropic2 glutamate receptor-like glurdelta2 in the apo form
41	c1yaeB_	Alignment	not modelled	99.9	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
42	c3kg2A_	Alignment	not modelled	99.9	17	**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
43	c3n5lA_	Alignment	not modelled	99.3	12	**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
44	c2x26A_	Alignment	not modelled	99.2	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
45	c3e4rA_	Alignment	not modelled	99.1	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
46	c3qslA_	Alignment	not modelled	99.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
47	c3uifA_	Alignment	not modelled	99.1	8	**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
48	c3hn0A_	Alignment	not modelled	99.0	12	**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	c3ix1A_	Alignment	not modelled	98.9	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
50	c3ix1B_	Alignment	not modelled	98.9	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
						PDB header:unknown function **Chain:** A: **PDB Molecule:**possible thiamine biosynthesis enzyme;

51	c2x7pA_	Alignment	not modelled	98.9	12	**PDBTitle:** the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
52	c3un6A_	Alignment	not modelled	98.9	11	**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	c3gxaA_	Alignment	not modelled	98.9	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
54	c3k2dA_	Alignment	not modelled	98.8	11	**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
55	c3ir1F_	Alignment	not modelled	98.8	9	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
56	d1qusa_	Alignment	not modelled	98.8	15	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
57	d1xs5a_	Alignment	not modelled	98.7	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
58	c3tqwA_	Alignment	not modelled	98.7	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
59	c3tmgA_	Alignment	not modelled	98.6	11	**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
60	c3l6gA_	Alignment	not modelled	98.6	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
61	d1us5a_	Alignment	not modelled	98.3	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
62	c2g29A_	Alignment	not modelled	98.3	12	**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
63	d1p99a_	Alignment	not modelled	98.2	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
64	c1p99A_	Alignment	not modelled	98.2	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
65	c3bkhA_	Alignment	not modelled	98.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
66	c2qpqC_	Alignment	not modelled	98.2	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
67	c2de4B_	Alignment	not modelled	98.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dibenzothiophene desulfurization enzyme b; **PDBTitle:** crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
68	c3b50A_	Alignment	not modelled	98.1	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sialic acid-binding periplasmic protein siap; **PDBTitle:** structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
69	c2f5xC_	Alignment	not modelled	98.0	16	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
70	c2dvzA_	Alignment	not modelled	97.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
71	c2pfzA_	Alignment	not modelled	97.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
72	c2i4cA_	Alignment	not modelled	97.9	11	**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
73	d1zbma1	Alignment	not modelled	97.9	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
74	c2vpnB_	Alignment	not modelled	97.8	7	**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
						Fold: Periplasmic binding protein-like II

75	d2czla1	Alignment	not modelled	97.8	14	**Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
76	c3gyyC_	Alignment	not modelled	97.8	7	**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
77	d1amfa_	Alignment	not modelled	97.8	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
78	c2zzxD_	Alignment	not modelled	97.7	16	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc transporter, solute-binding protein; **PDBTitle:** crystal structure of a periplasmic substrate binding protein in2 complex with lactate
79	c3fxbB_	Alignment	not modelled	97.7	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of the ectoine-binding protein ueha
80	c3muqB_	Alignment	not modelled	97.7	12	**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
81	c3fd3A_	Alignment	not modelled	97.7	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**chromosome replication initiation inhibitor protein; **PDBTitle:** structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
82	c2hpgB_	Alignment	not modelled	97.7	12	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding **PDBTitle:** the crystal structure of a thermophilic trap periplasmic2 binding protein
83	c2pfyA_	Alignment	not modelled	97.7	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
84	c2ql3G_	Alignment	not modelled	97.6	11	**PDB header:**transcription **Chain:** G: **PDB Molecule:**probable transcriptional regulator, lysr family protein; **PDBTitle:** crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
85	d1atga_	Alignment	not modelled	97.6	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
86	c2h5yC_	Alignment	not modelled	97.6	14	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**molybdate-binding periplasmic protein; **PDBTitle:** crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
87	c3n6uA_	Alignment	not modelled	97.4	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
88	d2fyia1	Alignment	not modelled	97.4	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
89	c2rejA_	Alignment	not modelled	97.4	13	**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
90	d2esna2	Alignment	not modelled	97.3	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
91	c2hxrA_	Alignment	not modelled	97.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator cynr; **PDBTitle:** structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
92	c3ho7A_	Alignment	not modelled	97.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
93	c3kn3C_	Alignment	not modelled	97.0	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
94	c3r6uA_	Alignment	not modelled	97.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
95	c3lr1A_	Alignment	not modelled	97.0	13	**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
96	c2hzkB_	Alignment	not modelled	97.0	11	**PDB header:**ligand binding, transport protein **Chain:** B: **PDB Molecule:**trap-t family sorbitol/mannitol transporter, periplasmic **PDBTitle:** crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
97	d2ozza1	Alignment	not modelled	96.9	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
98	d2nxoa1	Alignment	not modelled	96.8	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
99	c1xsfA_	Alignment	not modelled	96.7	22	**PDB header:**cell cycle, hydrolase **Chain:** A: **PDB Molecule:**probable resuscitation-promoting factor rpfb; **PDBTitle:** solution structure of a resuscitation promoting factor2

						domain from mycobacterium tuberculosis
100	d1ixca2	Alignment	not modelled	96.6	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
101	c1al3A_	Alignment	not modelled	96.6	16	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cys regulon transcriptional activator cysb; **PDBTitle:** cofactor binding fragment of cysb from klebsiella aerogenes
102	d1al3a_	Alignment	not modelled	96.6	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
103	c3jv9B_	Alignment	not modelled	96.6	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** the structure of a reduced form of oxyr from n. meningitidis
104	d1i6aa_	Alignment	not modelled	96.5	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
105	d1utha_	Alignment	not modelled	96.5	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
106	d1xsfa1	Alignment	not modelled	96.5	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
107	c3eq1A_	Alignment	not modelled	96.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
108	d1r9la_	Alignment	not modelled	95.8	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
109	c2uyeA_	Alignment	not modelled	95.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein; **PDBTitle:** double mutant y110s,f111v dntr from burkholderia sp. strain2 dnt in complex with thiocyanate
110	c3oxnD_	Alignment	not modelled	95.6	10	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
111	d1b1xa1	Alignment	not modelled	95.5	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
112	d1eh3a_	Alignment	not modelled	95.4	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
113	c3fj7A_	Alignment	not modelled	95.4	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major antigenic peptide peb3; **PDBTitle:** crystal structure of l-phospholactate bound peb3
114	c2vd3B_	Alignment	not modelled	95.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
115	d1dtza1	Alignment	not modelled	95.3	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
116	d1sw5a_	Alignment	not modelled	95.2	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
117	c3eo5A_	Alignment	not modelled	94.9	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
118	c1twyG_	Alignment	not modelled	94.7	11	**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
119	d1twya_	Alignment	not modelled	94.7	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
120	c3pppA_	Alignment	not modelled	94.7	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc