Phyre^2

Email	l.a.kelley@imperial.ac.uk
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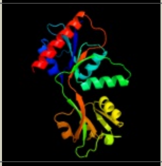
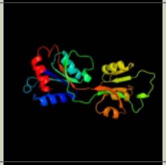
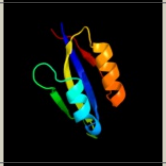
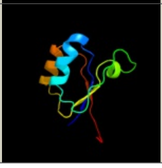
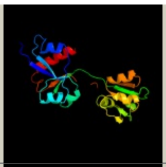
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1q1kA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
2	c2vd3B_	Alignment		100.0	37	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
3	c1nh7A_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
4	d1h3da1	Alignment		100.0	100	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
5	c2vd2A_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the crystal structure of hisg from b. subtilis
6	d1nh8a1	Alignment		100.0	31	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
7	d1ve4a1	Alignment		100.0	34	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
8	d1o63a_	Alignment		100.0	30	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
9	d1z7me1	Alignment		100.0	32	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	d1nh8a2	Alignment		99.9	33	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
11	d1h3da2	Alignment		99.9	100	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain

12	c3uifA_	Alignment		98.0	18	**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
13	c3ix1A_	Alignment		98.0	15	**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
14	c3ix1B_	Alignment		98.0	17	**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
15	c3qslA_	Alignment		97.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
16	c3e4rA_	Alignment		97.5	18	**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
17	c2x26A_	Alignment		97.4	19	**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
18	c3hn0A_	Alignment		97.3	14	**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
19	c3un6A_	Alignment		96.8	9	**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
20	d2nxoa1	Alignment		96.7	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
21	c2de4B_	Alignment	not modelled	96.6	19	**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
22	c2x7pA_	Alignment	not modelled	96.4	12	**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
23	c1p99A_	Alignment	not modelled	96.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
24	d1p99a_	Alignment	not modelled	96.2	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
25	d2czla1	Alignment	not modelled	95.8	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
26	c3n5lA_	Alignment	not modelled	95.3	11	**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
27	d1zbma1	Alignment	not modelled	95.1	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						PDB header:transport protein

28	c2pfzA_	Alignment	not modelled	95.0	12	**Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
29	c3fxbB_	Alignment	not modelled	94.4	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of the ectoine-binding protein ueha
30	c3tmgA_	Alignment	not modelled	94.4	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
31	c3b50A_	Alignment	not modelled	92.0	13	**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.
32	c3l6gA_	Alignment	not modelled	91.2	9	**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
33	c3kzgB_	Alignment	not modelled	90.4	15	**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
34	c2hpgB_	Alignment	not modelled	89.4	17	**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
35	c2zzxD_	Alignment	not modelled	88.9	13	**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
36	c2hzkB_	Alignment	not modelled	88.5	13	**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
37	c2rd5D_	Alignment	not modelled	88.1	11	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
38	c2pfyA_	Alignment	not modelled	88.0	14	**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
39	c3ir1F_	Alignment	not modelled	87.5	14	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
40	c2g29A_	Alignment	not modelled	87.0	13	**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
41	c3gxaA_	Alignment	not modelled	86.0	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
42	d1vm0a_	Alignment	not modelled	82.7	34	**Fold:**IF3-like **Superfamily:**AlbA-like **Family:**Hypothetical protein At2g34160
43	d1us5a_	Alignment	not modelled	81.5	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
44	c3l7pA_	Alignment	not modelled	80.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii; **PDBTitle:** crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
45	c2q3vB_	Alignment	not modelled	80.3	34	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein at2g34160; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g34160
46	c2vpnB_	Alignment	not modelled	79.2	17	**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
47	c3gyyC_	Alignment	not modelled	77.6	17	**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
48	c3bzqA_	Alignment	not modelled	75.7	9	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
49	d1xs5a_	Alignment	not modelled	73.9	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
50	c2j9dG_	Alignment	not modelled	73.8	8	**PDB header:**membrane transport **Chain:** G: **PDB Molecule:**hypothetical nitrogen regulatory pii-like **PDBTitle:** structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
51	d1qy7a_	Alignment	not modelled	73.7	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
						PDB header:signaling protein

52	c3mhyC_	Alignment	not modelled	72.5	18	**Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
53	c3tqwA_	Alignment	not modelled	72.3	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
54	d2ns1b1	Alignment	not modelled	72.3	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
55	d2piia_	Alignment	not modelled	68.8	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
56	c3ho7A_	Alignment	not modelled	68.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
57	c3o8wA_	Alignment	not modelled	67.8	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-1); **PDBTitle:** archaeoglobus fulgidus glnk1
58	d1ul3a_	Alignment	not modelled	65.8	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
59	c2hxrA_	Alignment	not modelled	65.6	14	**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
60	d1hwua_	Alignment	not modelled	64.9	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
61	d1eh3a_	Alignment	not modelled	62.1	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
62	c2f5xC_	Alignment	not modelled	61.7	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
63	c2i4cA_	Alignment	not modelled	59.1	19	**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
64	c2rc9A_	Alignment	not modelled	58.3	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
65	c3c7bA_	Alignment	not modelled	55.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
66	c3gmgB_	Alignment	not modelled	54.2	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
67	d1dtza1	Alignment	not modelled	53.5	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
68	d1i6aa_	Alignment	not modelled	52.4	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
69	d3c7bb2	Alignment	not modelled	47.8	13	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
70	d2cz4a1	Alignment	not modelled	46.8	24	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
71	c3ncpD_	Alignment	not modelled	43.7	25	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-2); **PDBTitle:** glnk2 from archaeoglobus fulgidus
72	c3ce8A_	Alignment	not modelled	43.1	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative pii-like nitrogen regulatory protein; **PDBTitle:** crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
73	d1ryoa_	Alignment	not modelled	41.8	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
74	d1ce2a1	Alignment	not modelled	41.4	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
75	d2dy1a5	Alignment	not modelled	39.6	17	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
76	c3mstA_	Alignment	not modelled	39.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative nitrate transport protein; **PDBTitle:** crystal structure of a putative nitrate transport protein (tvn0104)2 from thermoplasma volcanium at 1.35 a resolution
77	c3k2dA_	Alignment	not modelled	37.9	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
						PDB header:transport protein

78	c2dvzA_	Alignment	not modelled	37.7	16	**Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
79	c2ylnA_	Alignment	not modelled	36.6	10	**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
80	c3onmB_	Alignment	not modelled	36.3	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator lrha; **PDBTitle:** effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
81	d1h76a1	Alignment	not modelled	36.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
82	d1pb7a_	Alignment	not modelled	35.4	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
83	c2qpqC_	Alignment	not modelled	35.0	7	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
84	d1ieja_	Alignment	not modelled	32.9	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
85	c3kbrA_	Alignment	not modelled	31.4	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
86	c2pyyB_	Alignment	not modelled	29.9	19	**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
87	d1ufra_	Alignment	not modelled	29.8	45	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
88	d1w30a_	Alignment	not modelled	29.3	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
89	d1b1xa1	Alignment	not modelled	29.0	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
90	c3i31A_	Alignment	not modelled	27.6	13	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** hera helicase rna binding domain is an rrm fold
91	d2hava1	Alignment	not modelled	27.2	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
92	d1a3ca_	Alignment	not modelled	25.8	45	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
93	d1vcha1	Alignment	not modelled	25.7	45	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
94	d1cjba_	Alignment	not modelled	25.6	45	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
95	d2fyia1	Alignment	not modelled	25.5	19	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
96	d1g9sa_	Alignment	not modelled	25.2	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
97	d1jw1a1	Alignment	not modelled	24.9	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
98	d2igba1	Alignment	not modelled	24.0	45	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
99	d1tc1a_	Alignment	not modelled	23.7	45	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
100	d1vfja_	Alignment	not modelled	23.3	27	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
101	c3kb8A_	Alignment	not modelled	23.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
102	d1z7ga1	Alignment	not modelled	22.9	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
103	d1e0ta3	Alignment	not modelled	22.8	27	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
104	d1fsga_	Alignment	not modelled	22.6	55	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

105	c3m70A_	Alignment	not modelled	22.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
106	d1nula_	Alignment	not modelled	22.5	64	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
107	d1hgxa_	Alignment	not modelled	22.3	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
108	d1p17b_	Alignment	not modelled	21.9	45	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
109	c3o7mD_	Alignment	not modelled	21.8	36	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
110	c2jbhA_	Alignment	not modelled	21.8	55	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1; **PDBTitle:** human phosphoribosyl transferase domain containing 1
111	d2g50a3	Alignment	not modelled	21.8	35	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
112	c2o1mB_	Alignment	not modelled	21.8	14	**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
113	d1g2qa_	Alignment	not modelled	21.7	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
114	d1ii5a_	Alignment	not modelled	21.6	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
115	d1vdma1	Alignment	not modelled	20.5	43	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
116	c2ywtA_	Alignment	not modelled	20.5	55	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
117	d1gnla_	Alignment	not modelled	20.2	17	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Hybrid cluster protein (prismane protein)