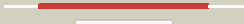



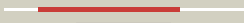



















# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	O34090
Date	Tue Jul 17 17:05:02 BST 2012
Unique Job ID	73b5b93bc6276f95

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ypnA</a>	 Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hydroxymethylbilane synthase); <b>PDBTitle:</b> hydroxymethylbilane synthase
2	<a href="#">c3eq1A</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase; <b>PDBTitle:</b> the crystal structure of human porphobilinogen deaminase at2.8a resolution
3	<a href="#">d1pdaa1</a>	 Alignment		100.0	50	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
4	<a href="#">d1gtka2</a>	 Alignment		99.9	33	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
5	<a href="#">d1pdaa2</a>	 Alignment		99.9	35	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
6	<a href="#">c1p99A</a>	 Alignment		97.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pg110; <b>PDBTitle:</b> 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
7	<a href="#">d1p99a</a>	 Alignment		97.6	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
8	<a href="#">c3gxaA</a>	 Alignment		97.4	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of gna1946
9	<a href="#">c2x26A</a>	 Alignment		97.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic aliphatic sulphonates-binding protein; <b>PDBTitle:</b> crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
10	<a href="#">c3uifA</a>	 Alignment		96.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfonate abc transporter, periplasmic sulfonate-binding <b>PDBTitle:</b> crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
11	<a href="#">c3tqwA</a>	 Alignment		96.9	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-binding protein; <b>PDBTitle:</b> structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii

12	<a href="#">c3ir1F_</a>	Alignment		96.8	16	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
13	<a href="#">c3un6A_</a>	Alignment		96.4	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein saouhsc_00137; <b>PDBTitle:</b> 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
14	<a href="#">d2ozza1</a>	Alignment		96.0	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
15	<a href="#">c3e4rA_</a>	Alignment		95.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
16	<a href="#">c3l6gA_</a>	Alignment		95.1	10	<b>PDB header:</b> glycine betaine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding <b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation
17	<a href="#">d1xs5a_</a>	Alignment		94.8	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
18	<a href="#">c3kzqB_</a>	Alignment		94.3	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> arginine 3rd transport system periplasmic binding <b>PDBTitle:</b> crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
19	<a href="#">c3up9A_</a>	Alignment		93.8	16	<b>PDB header:</b> methionine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (actodo_00931) from2 actinomyces odontolyticus atcc 17982 at 2.35 a resolution
20	<a href="#">d1zbma1</a>	Alignment		93.5	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
21	<a href="#">d2czla1</a>	Alignment	not modelled	91.5	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
22	<a href="#">c3hn0A_</a>	Alignment	not modelled	91.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
23	<a href="#">c3tmgA_</a>	Alignment	not modelled	90.5	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine, l-proline abc transporter, <b>PDBTitle:</b> crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
24	<a href="#">c4ef2A_</a>	Alignment	not modelled	90.4	21	<b>PDB header:</b> methionine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pheromone cob1/lipoprotein, yaec family; <b>PDBTitle:</b> crystal structure of a pheromone cob1 precursor/lipoprotein, yaec2 family (ef2496) from enterococcus faecalis v583 at 2.10 a resolution
25	<a href="#">c3qslA_</a>	Alignment	not modelled	89.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> structure of cae31940 from bordetella bronchiseptica rb50
26	<a href="#">c3k2dA_</a>	Alignment	not modelled	88.8	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type metal ion transport system, periplasmic component; <b>PDBTitle:</b> crystal structure of immunogenic lipoprotein a from vibrio vulnificus
27	<a href="#">c3ix1A_</a>	Alignment	not modelled	85.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methyl pyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-

						methylpyrimidine binding2 protein from bacillus halodurans <b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
28	<a href="#">c3ix1B_</a>	Alignment	not modelled	85.0	15	
29	<a href="#">c3ho7A_</a>	Alignment	not modelled	84.9	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> oxyr; <b>PDBTitle:</b> crystal structure of oxyr from porphyromonas gingivalis
30	<a href="#">c2x7pA_</a>	Alignment	not modelled	84.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiamine biosynthesis enzyme; <b>PDBTitle:</b> the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
31	<a href="#">c2h9bB_</a>	Alignment	not modelled	82.7	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
32	<a href="#">c3n6uA_</a>	Alignment	not modelled	76.8	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
33	<a href="#">c3g41A_</a>	Alignment	not modelled	74.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
34	<a href="#">c3delC_</a>	Alignment	not modelled	73.8	12	<b>PDB header:</b> protein binding, transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine binding protein; <b>PDBTitle:</b> the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
35	<a href="#">d2nxoa1</a>	Alignment	not modelled	73.4	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
36	<a href="#">c2q2aD_</a>	Alignment	not modelled	72.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> artj; <b>PDBTitle:</b> crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
37	<a href="#">d1i6aa_</a>	Alignment	not modelled	70.2	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
38	<a href="#">c3fd3A_</a>	Alignment	not modelled	70.0	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome replication initiation inhibitor protein; <b>PDBTitle:</b> structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
39	<a href="#">d1ixca2</a>	Alignment	not modelled	67.7	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
40	<a href="#">d1ex2a_</a>	Alignment	not modelled	63.2	17	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> Maf-like
41	<a href="#">c2ylnA_</a>	Alignment	not modelled	63.1	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter, periplasmic binding protein, <b>PDBTitle:</b> crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
42	<a href="#">d1zwaya1</a>	Alignment	not modelled	61.7	14	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> YjxX-like
43	<a href="#">d1u5wa1</a>	Alignment	not modelled	60.9	10	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> YjxX-like
44	<a href="#">d1al3a_</a>	Alignment	not modelled	60.1	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
45	<a href="#">c1al3A_</a>	Alignment	not modelled	60.1	13	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> cys regulon transcriptional activator cysb; <b>PDBTitle:</b> cofactor binding fragment of cysb from klebsiella aerogenes
46	<a href="#">c2o1mB_</a>	Alignment	not modelled	57.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable amino-acid abc transporter <b>PDBTitle:</b> crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytnk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
47	<a href="#">c2p5xB_</a>	Alignment	not modelled	56.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylserotonin o-methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
48	<a href="#">c3hv1A_</a>	Alignment	not modelled	52.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polar amino acid abc uptake transporter substrate <b>PDBTitle:</b> crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
49	<a href="#">d2amha1</a>	Alignment	not modelled	47.6	30	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> Maf-like
50	<a href="#">c1twyG_</a>	Alignment	not modelled	43.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae

51	<a href="#">d1twya_</a>	Alignment	not modelled	43.7	18	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
52	<a href="#">d1hsla_</a>	Alignment	not modelled	43.3	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
53	<a href="#">c2vd3B_</a>	Alignment	not modelled	40.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
54	<a href="#">c3n5lA_</a>	Alignment	not modelled	39.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc phosphonate transporter; <b>PDBTitle:</b> crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
55	<a href="#">d1lsta_</a>	Alignment	not modelled	39.2	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
56	<a href="#">c3oxnD_</a>	Alignment	not modelled	38.9	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
57	<a href="#">c2i4cA_</a>	Alignment	not modelled	34.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bicarbonate transporter; <b>PDBTitle:</b> crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
58	<a href="#">c2pfzA_</a>	Alignment	not modelled	33.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
59	<a href="#">c2y7iB_</a>	Alignment	not modelled	33.2	12	<b>PDB header:</b> arginine-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> stm4351; <b>PDBTitle:</b> structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
60	<a href="#">c2ieeB_</a>	Alignment	not modelled	31.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable abc transporter extracellular-binding <b>PDBTitle:</b> crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
61	<a href="#">c3r6uA_</a>	Alignment	not modelled	30.4	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline-binding protein; <b>PDBTitle:</b> crystal structure of choline binding protein opubc from bacillus2 subtilis
62	<a href="#">d1zh8a1</a>	Alignment	not modelled	29.5	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
63	<a href="#">c2uyeA_</a>	Alignment	not modelled	29.4	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> double mutant y110s,f111v dntn from burkholderia sp. strain2 dnt in complex with thiocyanate
64	<a href="#">d1ni7a_</a>	Alignment	not modelled	29.3	15	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
65	<a href="#">c3r39A_</a>	Alignment	not modelled	28.4	8	<b>PDB header:</b> <b>PDB COMPND:</b>
66	<a href="#">c4eq9A_</a>	Alignment	not modelled	28.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter substrate-binding protein-amino acid <b>PDBTitle:</b> 1.4 angstrom crystal structure of putative abc transporter substrate-2 binding protein from streptococcus pneumoniae strain canada mdr_19a3 in complex with glutathione
67	<a href="#">c2h9qC_</a>	Alignment	not modelled	28.2	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a catm2 variant (r156h)
68	<a href="#">c2ql3G_</a>	Alignment	not modelled	27.4	13	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> probable transcriptional regulator, lysr family protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
69	<a href="#">d1tjna_</a>	Alignment	not modelled	26.7	18	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> CbiX-like
70	<a href="#">c1tjnA_</a>	Alignment	not modelled	26.7	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sirohydrochlorin cobaltchelataase; <b>PDBTitle:</b> crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
71	<a href="#">c2f78A_</a>	Alignment	not modelled	26.3	22	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> benm effector binding domain with its effector benzoate
72	<a href="#">c2hxrA_</a>	Alignment	not modelled	25.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator cynr; <b>PDBTitle:</b> structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
73	<a href="#">c2f7cA_</a>	Alignment	not modelled	25.4	13	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> catm effector binding domain with its effector cis,cis-muconate
74	<a href="#">c3zu3A_</a>	Alignment	not modelled	25.1	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase ypo4104/y4119/yp_4011; <b>PDBTitle:</b> structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)

75	<a href="#">d1mzga_</a>	Alignment	not modelled	23.8	27	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
76	<a href="#">c3kosA_</a>	Alignment	not modelled	23.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator ampr; <b>PDBTitle:</b> structure of the ampr effector binding domain from <i>citrobacter2 freundii</i>
77	<a href="#">c3onmB_</a>	Alignment	not modelled	22.6	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator Irha; <b>PDBTitle:</b> effector binding domain of lysr-type transcription factor rovm from <i>y.2 pseudotuberculosis</i>
78	<a href="#">c4ab6A_</a>	Alignment	not modelled	21.8	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> regulatory domain structure of nmb2055 (metr), c103s c106s mutant, a2 lysr family regulator from <i>n. meningitidis</i>
79	<a href="#">d1nn4a_</a>	Alignment	not modelled	21.7	16	<b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB
80	<a href="#">c3cz6A_</a>	Alignment	not modelled	21.6	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein rap1; <b>PDBTitle:</b> crystal structure of the rap1 c-terminus
81	<a href="#">c3vpjF_</a>	Alignment	not modelled	21.1	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> F: <b>PDB Molecule:</b> tse1-specific immunity protein; <b>PDBTitle:</b> crystal structure of type vi effector tse1 from <i>pseudomonas aeruginosa2</i> in complex with immune protein tsi1
82	<a href="#">c2de4B_</a>	Alignment	not modelled	21.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> di-benzothiophene desulfurization enzyme b; <b>PDBTitle:</b> crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfenic acid
83	<a href="#">c1wloA_</a>	Alignment	not modelled	21.1	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sufe protein; <b>PDBTitle:</b> solution structure of the hypothetical protein from <i>thermus2 thermophilus hb8</i>
84	<a href="#">c3k4uA_</a>	Alignment	not modelled	20.6	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding component of abc transporter; <b>PDBTitle:</b> crystal structure of putative binding component of abc transporter2 from <i>wolinella succinogenes dsm 1740</i> complexed with lysine
85	<a href="#">c3jv9B_</a>	Alignment	not modelled	20.4	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> the structure of a reduced form of oxyr from <i>n. meningitidis</i>
86	<a href="#">c4fgiH_</a>	Alignment	not modelled	19.8	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> tsi1; <b>PDBTitle:</b> structure of the effector - immunity system tse1 / tsi1 from <i>2 pseudomonas aeruginosa</i>
87	<a href="#">c4e14A_</a>	Alignment	not modelled	18.4	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
88	<a href="#">d2i6ea1</a>	Alignment	not modelled	18.1	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
89	<a href="#">c2i6eG_</a>	Alignment	not modelled	18.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein dr0370 from <i>deinococcus radiodurans</i> , pfam2 duf178
90	<a href="#">c3hhfB_</a>	Alignment	not modelled	17.3	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga regulatory domain, a lysr-type transcriptional2 regulator from <i>neisseria meningitidis</i> .
91	<a href="#">c1zy8M_</a>	Alignment	not modelled	17.2	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, <b>PDBTitle:</b> the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex.
92	<a href="#">c2f5zK_</a>	Alignment	not modelled	17.2	40	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> K: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
93	<a href="#">d1vhca_</a>	Alignment	not modelled	16.4	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
94	<a href="#">c3pppA_</a>	Alignment	not modelled	16.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline-binding protein; <b>PDBTitle:</b> structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of <i>bacillus3 subtilis abc transporter opuc</i>
95	<a href="#">c3he8A_</a>	Alignment	not modelled	15.9	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> structural study of <i>clostridium thermocellum</i> ribose-5-phosphate2 isomerase b
96	<a href="#">c2wfoA_</a>	Alignment	not modelled	15.5	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycoprotein 1; <b>PDBTitle:</b> crystal structure of machupo virus envelope glycoprotein2 gp1
97	<a href="#">c3k6gA_</a>	Alignment	not modelled	15.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> telomeric repeat-binding factor 2-interacting protein 1; <b>PDBTitle:</b> crystal structure of rap1 and trf2 complex
98	<a href="#">c3mtjA_</a>	Alignment	not modelled	14.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from <i>thiobacillus2 denitrificans</i> to 2.15a <b>PDB header:</b> transcription

99	<a href="#">c2yu3A_</a>	Alignment	not modelled	14.2	21	<b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase iii 39 kda <b>PDBTitle:</b> solution structure of the domain swapped wingedhelix in dna-2 directed rna polymerase iii 39 kda polypeptide
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