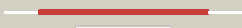
































# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2391_(nirA)_2684689_2686380
Date	Mon Aug 5 13:25:54 BST 2019
Unique Job ID	c0cd21d8ebcd7dfa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zj8B_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable ferredoxin-dependent nitrite reductase nirA; <b>PDBTitle:</b> structure of mycobacterium tuberculosis nirA protein
2	<a href="#">c5h92A_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [ferredoxin], chloroplastic; <b>PDBTitle:</b> crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal
3	<a href="#">c3b0nA_</a>	 Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite reductase; <b>PDBTitle:</b> q448k mutant of assimilatory nitrite reductase (nii3) from tobacco2 leaf
4	<a href="#">c2akjA_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nitrite reductase, chloroplast; <b>PDBTitle:</b> structure of spinach nitrite reductase
5	<a href="#">c5aopA_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase hemoprotein; <b>PDBTitle:</b> sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1
6	<a href="#">c2v4jA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
7	<a href="#">c2v4jE_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
8	<a href="#">c3c7bE_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
9	<a href="#">d1zj8a2</a>	 Alignment		100.0	100	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
10	<a href="#">c3c7bA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
11	<a href="#">d1zj8a4</a>	 Alignment		100.0	100	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like

12	<a href="#">d1aopa3</a>	Alignment		100.0	25	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
13	<a href="#">d2akja4</a>	Alignment		100.0	31	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
14	<a href="#">d2akja2</a>	Alignment		100.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
15	<a href="#">d1zj8a3</a>	Alignment		100.0	100	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
16	<a href="#">d1aopa4</a>	Alignment		100.0	25	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
17	<a href="#">d3c7bb3</a>	Alignment		100.0	17	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
18	<a href="#">d2v4jb3</a>	Alignment		100.0	17	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
19	<a href="#">d3c7ba3</a>	Alignment		100.0	20	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
20	<a href="#">d2akja3</a>	Alignment		100.0	34	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
21	<a href="#">d2v4ja3</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
22	<a href="#">d3c7bb2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
23	<a href="#">d1zj8a1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
24	<a href="#">d2v4jb2</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
25	<a href="#">d1aopa1</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
26	<a href="#">d1aopa2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
27	<a href="#">d2akja1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
28	<a href="#">c3noyA</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
29	<a href="#">c3noyD</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl

29	<a href="#">c2yvlD_</a>	Alignment	not modelled	98.3	29	diphosphate synthase; <b>PDBTitle:</b> structure of gcpe (ispg) from thermus thermophilus hb27
30	<a href="#">d3c7ba2</a>	Alignment	not modelled	97.9	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
31	<a href="#">d2v4ja2</a>	Alignment	not modelled	96.7	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
32	<a href="#">c5lnk2_</a>	Alignment	not modelled	75.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 2: <b>PDB Molecule:</b> mitochondrial complex i, 24 kda subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
33	<a href="#">c5lc5E_</a>	Alignment	not modelled	74.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nahd dehydrogenase [ubiquinone] flavoprotein 2, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
34	<a href="#">d1xdpa1</a>	Alignment	not modelled	69.9	19	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PPK N-terminal domain-like <b>Family:</b> PPK N-terminal domain-like
35	<a href="#">c4h7wA_</a>	Alignment	not modelled	69.8	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> supf0406 protein c16orf57; <b>PDBTitle:</b> crystal structure of human c16orf57
36	<a href="#">d2fug21</a>	Alignment	not modelled	57.3	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> NQO2-like
37	<a href="#">d2o8ra1</a>	Alignment	not modelled	55.2	15	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PPK N-terminal domain-like <b>Family:</b> PPK N-terminal domain-like
38	<a href="#">c6gcsH_</a>	Alignment	not modelled	54.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> 24-kda subunit (nuhm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
39	<a href="#">c6fnuA_</a>	Alignment	not modelled	54.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methylenetetrahydrofolate reductase 1; <b>PDBTitle:</b> structure of s. cerevisiae methylenetetrahydrofolate reductase 1,2 catalytic domain
40	<a href="#">c1xdoB_</a>	Alignment	not modelled	52.2	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyphosphate kinase; <b>PDBTitle:</b> crystal structure of escherichia coli polyphosphate kinase
41	<a href="#">c6hl2C_</a>	Alignment	not modelled	50.3	18	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> nahd-quinone oxidoreductase subunit e; <b>PDBTitle:</b> wild-type nuoef from aquifex aeolicus - oxidized form
42	<a href="#">d1p4xa2</a>	Alignment	not modelled	48.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
43	<a href="#">c1b4aA_</a>	Alignment	not modelled	45.5	17	<b>PDB header:</b> repressor <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> structure of the arginine repressor from bacillus stearothermophilus
44	<a href="#">c3nqoB_</a>	Alignment	not modelled	45.4	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
45	<a href="#">c3ereD_</a>	Alignment	not modelled	44.3	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
46	<a href="#">d3broa1</a>	Alignment	not modelled	43.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
47	<a href="#">c5eriA_</a>	Alignment	not modelled	43.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132
48	<a href="#">c4fhtA_</a>	Alignment	not modelled	41.6	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pcav transcriptional regulator; <b>PDBTitle:</b> crystal structure of the pcav transcriptional regulator from streptomyces coelicolor in complex with its natural ligand
49	<a href="#">c3j4rA_</a>	Alignment	not modelled	40.0	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ca-kinase anchor protein 18; <b>PDBTitle:</b> pseudo-atomic model of the akap18-pka complex in a linear conformation2 derived from electron microscopy
50	<a href="#">c2pjuD_</a>	Alignment	not modelled	40.0	13	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
51	<a href="#">c4qboA_</a>	Alignment	not modelled	39.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nuclease; <b>PDBTitle:</b> vrr_nuc domain
52	<a href="#">c4xrfA_</a>	Alignment	not modelled	39.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of mepr like protein complexed with pseudoligands
53	<a href="#">c2v79B_</a>	Alignment	not modelled	39.2	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication protein dnad; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad from bacillus2 subtilis
54	<a href="#">c4mnuA_</a>	Alignment	not modelled	38.6	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> slya-like transcription regulator; <b>PDBTitle:</b> crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes
55	<a href="#">d1s3ja_</a>	Alignment	not modelled	38.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators

56	<a href="#">d1p9qc3</a>	Alignment	not modelled	38.4	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
57	<a href="#">c5abrB</a>	Alignment	not modelled	38.0	17	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin, 2fe-2s; <b>PDBTitle:</b> structure of fesi protein from azotobacter vinelandii
58	<a href="#">c5jlsA</a>	Alignment	not modelled	37.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
59	<a href="#">c3bjaA</a>	Alignment	not modelled	37.2	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
60	<a href="#">c1b8aA</a>	Alignment	not modelled	36.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase processivity component; <b>PDBTitle:</b> sliding clamp, dna polymerase
61	<a href="#">c1vdxA</a>	Alignment	not modelled	36.0	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0099; <b>PDBTitle:</b> crystal structure of a pyrococcus horikoshii protein with2 similarities to 2'5' rna-ligase
62	<a href="#">c6jbxB</a>	Alignment	not modelled	34.9	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna
63	<a href="#">d1ghha</a>	Alignment	not modelled	34.6	9	<b>Fold:</b> DNA damage-inducible protein DinI <b>Superfamily:</b> DNA damage-inducible protein DinI <b>Family:</b> DNA damage-inducible protein DinI
64	<a href="#">d1f37b</a>	Alignment	not modelled	33.4	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioredoxin-like 2Fe-2S ferredoxin
65	<a href="#">d1c0aa2</a>	Alignment	not modelled	33.3	21	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
66	<a href="#">c2nyxB</a>	Alignment	not modelled	33.2	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory protein, rv1404; <b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis
67	<a href="#">c5hcdD</a>	Alignment	not modelled	31.4	45	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> rhhipcephalus microplus raci2; <b>PDBTitle:</b> ternary complex of human complement c5 with ornithodoros moubata omci2 and rhhipcephalus microplus raci2
68	<a href="#">c3oopA</a>	Alignment	not modelled	31.3	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
69	<a href="#">c2fxaB</a>	Alignment	not modelled	31.1	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protease production regulatory protein hpr; <b>PDBTitle:</b> structure of the protease production regulatory protein hpr from2 bacillus subtilis.
70	<a href="#">d1nh8a1</a>	Alignment	not modelled	31.0	24	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
71	<a href="#">c3cjnA</a>	Alignment	not modelled	30.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
72	<a href="#">c1zhvA</a>	Alignment	not modelled	30.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0741; <b>PDBTitle:</b> x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
73	<a href="#">c3bj6B</a>	Alignment	not modelled	30.3	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
74	<a href="#">c2nnnB</a>	Alignment	not modelled	30.3	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
75	<a href="#">c3nrvc</a>	Alignment	not modelled	30.3	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family); <b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
76	<a href="#">c2rdpA</a>	Alignment	not modelled	30.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 steaerotherophilus
77	<a href="#">c2qwwB</a>	Alignment	not modelled	30.0	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
78	<a href="#">c2o8rA</a>	Alignment	not modelled	28.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyphosphate kinase; <b>PDBTitle:</b> crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
79	<a href="#">d1r1ga</a>	Alignment	not modelled	27.9	71	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
						<b>PDB header:</b> toxin

80	<a href="#">c1r1gB_</a>	Alignment	not modelled	27.9	71	<b>Chain:</b> B: <b>PDB Molecule:</b> neurotoxin bmk37; <b>PDBTitle:</b> crystal structure of the scorpion toxin bmbktx1
81	<a href="#">c1r1gA_</a>	Alignment	not modelled	27.9	71	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> neurotoxin bmk37; <b>PDBTitle:</b> crystal structure of the scorpion toxin bmbktx1
82	<a href="#">d1lnwa_</a>	Alignment	not modelled	27.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
83	<a href="#">c3g3zA_</a>	Alignment	not modelled	27.1	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
84	<a href="#">c2fizC_</a>	Alignment	not modelled	26.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cis-3-chloroacrylic acid dehalogenase; <b>PDBTitle:</b> the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
85	<a href="#">d1zhva2</a>	Alignment	not modelled	26.7	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Atu0741-like
86	<a href="#">c5hccD_</a>	Alignment	not modelled	26.7	57	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> dermacentor andersoni raci3; <b>PDBTitle:</b> ternary complex of human complement c5 with ornithodoros moubata omci2 and dermacentor andersoni raci3.
87	<a href="#">c3w9zA_</a>	Alignment	not modelled	25.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
88	<a href="#">c5dleD_</a>	Alignment	not modelled	25.8	38	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, fructose-specific iabc component; <b>PDBTitle:</b> crystal structure from a domain (thr161-f265) from fructose-specific2 iabc component (pts system) from borrelia burgdorferi
89	<a href="#">d2r48a1</a>	Alignment	not modelled	25.8	38	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
90	<a href="#">d1ub3a_</a>	Alignment	not modelled	25.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
91	<a href="#">c3k0IA_</a>	Alignment	not modelled	25.1	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
92	<a href="#">c5un8B_</a>	Alignment	not modelled	25.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein o-glcnacase; <b>PDBTitle:</b> crystal structure of human o-glcnacase in complex with glycopeptide2 p53
93	<a href="#">d2etha1</a>	Alignment	not modelled	24.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
94	<a href="#">d1xp3a1</a>	Alignment	not modelled	23.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV
95	<a href="#">d1olta_</a>	Alignment	not modelled	23.8	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Oxygen-independent coproporphyrinogen III oxidase HemN
96	<a href="#">c5e1xA_</a>	Alignment	not modelled	23.8	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the organohalide sensing rdhr-cbdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form
97	<a href="#">d2frha1</a>	Alignment	not modelled	23.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
98	<a href="#">c2gxgA_</a>	Alignment	not modelled	23.4	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
99	<a href="#">c4w8yA_</a>	Alignment	not modelled	23.3	32	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr2; <b>PDBTitle:</b> structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
100	<a href="#">d2bv6a1</a>	Alignment	not modelled	23.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
101	<a href="#">c2m1zA_</a>	Alignment	not modelled	23.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0427 protein; <b>PDBTitle:</b> solution structure of uncharacterized protein lmo0427
102	<a href="#">d2r4qa1</a>	Alignment	not modelled	22.7	21	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
103	<a href="#">c3t7vA_</a>	Alignment	not modelled	22.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylornithine synthase pylb; <b>PDBTitle:</b> crystal structure of methylornithine synthase (pylb)
104	<a href="#">c5dckA_</a>	Alignment	not modelled	22.6	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid c-terminal domain; <b>PDBTitle:</b> crystal structure of fiv capsid c-terminal domain
105	<a href="#">d1t95a3</a>	Alignment	not modelled	22.3	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
						<b>PDB header:</b> transferase

106	<a href="#">c4jxdA_</a>	Alignment	not modelled	21.8	25	<b>Chain:</b> A; <b>PDB Molecule:</b> fructose-like phosphotransferase enzyme iib component 3; <b>PDBTitle:</b> crystal structure of predicted fructose specific iib from escherichia2 coli
107	<a href="#">c5jvoA_</a>	Alignment	not modelled	21.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor from the pathogenic2 bacterium corynebacterium pseudotuberculosis
108	<a href="#">c2kyrA_</a>	Alignment	not modelled	21.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> fructose-like phosphotransferase enzyme iib component 1; <b>PDBTitle:</b> solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
109	<a href="#">d1kkha2</a>	Alignment	not modelled	21.2	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Mevalonate kinase
110	<a href="#">d1a8oa_</a>	Alignment	not modelled	20.7	33	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Retrovirus capsid dimerization domain-like <b>Family:</b> Retrovirus capsid protein C-terminal domain
111	<a href="#">c4ayaA_</a>	Alignment	not modelled	20.4	8	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> dna-binding protein inhibitor id-2; <b>PDBTitle:</b> crystal structure of id2 hlh homodimer at 2.1a resolution