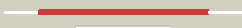























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1442_(bisC)_1619797_1622097
Date	Wed Jul 31 22:05:55 BST 2019
Unique Job ID	a79332dafa78170f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1tmoA_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylamine n-oxide reductase; <b>PDBTitle:</b> trimethylamine n-oxide reductase from shewanella massilia
2	<a href="#">c1h5nC_</a>	 Alignment		100.0	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dmsO reductase; <b>PDBTitle:</b> dmsO reductase modified by the presence of dms and air
3	<a href="#">c1eu1A_</a>	 Alignment		100.0	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase; <b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
4	<a href="#">c1vlfQ_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> pyrogallol hydroxytransferase large subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
5	<a href="#">c5ch7E_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> dmsO reductase family type ii enzyme, molybdopterin <b>PDBTitle:</b> crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
6	<a href="#">c1y5iA_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory nitrate reductase 1 alpha chain; <b>PDBTitle:</b> the crystal structure of the narghi mutant nari-k86a
7	<a href="#">c2e7zA_</a>	 Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahy; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
8	<a href="#">c1h0hA_</a>	 Alignment		100.0	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase subunit alpha; <b>PDBTitle:</b> tungsten containing formate dehydrogenase from desulfovibrio gigas
9	<a href="#">c1kqgA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, major subunit; <b>PDBTitle:</b> formate dehydrogenase n from e. coli
10	<a href="#">c2vpyE_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> thiosulfate reductase; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
11	<a href="#">c2ivfA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum

12	<a href="#">c6cz7C_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> arra; <b>PDBTitle:</b> the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
13	<a href="#">c2v45A_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from 3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
14	<a href="#">c2nyaF_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
15	<a href="#">c1ogyA_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
16	<a href="#">c2iv2X_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X; <b>PDB Molecule:</b> formate dehydrogenase h; <b>PDBTitle:</b> reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
17	<a href="#">d1tmoa2</a>	Alignment		100.0	35	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
18	<a href="#">c4aayE_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> araoa; <b>PDBTitle:</b> crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
19	<a href="#">d1dmra2</a>	Alignment		100.0	40	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
20	<a href="#">c1g8jC_</a>	Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> arsenite oxidase; <b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
21	<a href="#">d1eu1a2</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
22	<a href="#">d1vlfm2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
23	<a href="#">d2jioa2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
24	<a href="#">d1kqfa2</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
25	<a href="#">d1y5ia2</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
26	<a href="#">d2iv2x2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
27	<a href="#">d1h0ha2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
28	<a href="#">d1ogya2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3

29	<a href="#">d1g8ka2</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
30	<a href="#">c6btmB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alternative complex iii subunit b; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
31	<a href="#">c6f0kB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> fe-s-cluster-containing hydrogenase; <b>PDBTitle:</b> alternative complex iii
32	<a href="#">c2fugC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 3; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
33	<a href="#">c6gcsA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 75-kda protein (nuam); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
34	<a href="#">c5t5mB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdb; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, trigonal form at 2.5 a.
35	<a href="#">c5lnk3</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 3: <b>PDB Molecule:</b> mitochondrial complex i, 75 kda subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
36	<a href="#">d2fug32</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
37	<a href="#">d1eu1a1</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
38	<a href="#">d1dmra1</a>	Alignment	not modelled	100.0	45	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
39	<a href="#">d1tmoa1</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
40	<a href="#">d1vlfm1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
41	<a href="#">d1kqfa1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
42	<a href="#">d1h0ha1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
43	<a href="#">d2jioa1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
44	<a href="#">d1g8ka1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
45	<a href="#">d1ogya1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
46	<a href="#">d1y5ia1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
47	<a href="#">d2iv2x1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
48	<a href="#">c5t5iL</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdd; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
49	<a href="#">c2ki8A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase, <b>PDBTitle:</b> solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
50	<a href="#">d2fug31</a>	Alignment	not modelled	97.2	30	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
51	<a href="#">c2pjhB</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> strctural model of the p97 n domain- npl4 ubd complex
52	<a href="#">c4ga5H</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> putative thymidine phosphorylase; <b>PDBTitle:</b> crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
53	<a href="#">c3knzA</a>	Alignment	not modelled	96.1	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar binding protein; <b>PDBTitle:</b> crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution

54	<a href="#">c3euaD</a>	Alignment	not modelled	96.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative fructose-aminoacid-6-phosphate deglycase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (bsu32610) from <i>Bacillus subtilis</i> at 1.90 Å resolution
55	<a href="#">c5e7pA</a>	Alignment	not modelled	95.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msmeG_0858 (uniprot a0qqs4), a aaa atpase.
56	<a href="#">c5ifwB</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
57	<a href="#">d2ez9a1</a>	Alignment	not modelled	95.6	10	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
58	<a href="#">d1e32a1</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
59	<a href="#">c5cupB</a>	Alignment	not modelled	95.5	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate propanoyltransferase; <b>PDBTitle:</b> structure of rhodospseudomonas palustris pdul - phosphate bound form
60	<a href="#">d1ozha1</a>	Alignment	not modelled	95.4	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
61	<a href="#">c3k35D</a>	Alignment	not modelled	95.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> crystal structure of human sirt6
62	<a href="#">c1cz5A</a>	Alignment	not modelled	95.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
63	<a href="#">d2ihta1</a>	Alignment	not modelled	95.1	13	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
64	<a href="#">c3etnD</a>	Alignment	not modelled	95.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative phosphosugar isomerase involved in capsule <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 Å resolution
65	<a href="#">c3pkiF</a>	Alignment	not modelled	95.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> human sirt6 crystal structure in complex with adp ribose
66	<a href="#">d2djia1</a>	Alignment	not modelled	94.7	6	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
67	<a href="#">c6opcF</a>	Alignment	not modelled	94.6	26	<b>PDB header:</b> motor protein <b>Chain:</b> F: <b>PDB Molecule:</b> cell division control protein 48; <b>PDBTitle:</b> cdc48 hexamer in a complex with substrate and shp1(ubx domain)
68	<a href="#">c3zq6A</a>	Alignment	not modelled	94.6	27	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-6; <b>PDBTitle:</b> the novel de-long chain fatty acid function of human sirt6
69	<a href="#">d1cz5a1</a>	Alignment	not modelled	94.5	14	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
70	<a href="#">c3cf2B</a>	Alignment	not modelled	94.5	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/amp-pnp
71	<a href="#">d1m2ka</a>	Alignment	not modelled	94.3	19	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
72	<a href="#">c2a3nA</a>	Alignment	not modelled	94.2	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glucosamine-fructose-6-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 Å resolution
73	<a href="#">c5oj7A</a>	Alignment	not modelled	94.2	3	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacylase; <b>PDBTitle:</b> sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
74	<a href="#">d2b4ya1</a>	Alignment	not modelled	94.2	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
75	<a href="#">d1x94a</a>	Alignment	not modelled	94.1	11	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
76	<a href="#">c1s3sA</a>	Alignment	not modelled	94.1	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter) <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
77	<a href="#">c3fkjA</a>	Alignment	not modelled	94.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 Å resolution
78	<a href="#">d1q6za1</a>	Alignment	not modelled	94.0	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain

79	<a href="#">d1ma3a_</a>	Alignment	not modelled	94.0	14	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
80	<a href="#">d1ybha1</a>	Alignment	not modelled	93.8	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
81	<a href="#">c3jwpA_</a>	Alignment	not modelled	93.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein sir2 homologue; <b>PDBTitle:</b> crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
82	<a href="#">d1x92a_</a>	Alignment	not modelled	93.4	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
83	<a href="#">c3g68A_</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
84	<a href="#">d2ji7a1</a>	Alignment	not modelled	93.1	12	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
85	<a href="#">d1yc5a1</a>	Alignment	not modelled	93.0	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
86	<a href="#">c3hu2C_</a>	Alignment	not modelled	92.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
87	<a href="#">d1s5pa_</a>	Alignment	not modelled	91.5	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
88	<a href="#">c3fxaA_</a>	Alignment	not modelled	91.4	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
89	<a href="#">c3hbaA_</a>	Alignment	not modelled	91.3	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
90	<a href="#">d1tk9a_</a>	Alignment	not modelled	91.2	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
91	<a href="#">c3cvjB_</a>	Alignment	not modelled	91.1	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
92	<a href="#">c2zj3A_</a>	Alignment	not modelled	91.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate <b>PDBTitle:</b> isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
93	<a href="#">c3cf1C_</a>	Alignment	not modelled	90.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
94	<a href="#">c1jxaA_</a>	Alignment	not modelled	89.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate synthase; <b>PDBTitle:</b> glucosamine 6-phosphate synthase with glucose 6-phosphate
95	<a href="#">d1ovma1</a>	Alignment	not modelled	89.2	9	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
96	<a href="#">c2x3yA_</a>	Alignment	not modelled	88.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of gmha from burkholderia pseudomallei
97	<a href="#">c1nr1A_</a>	Alignment	not modelled	88.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hi0754; <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
98	<a href="#">d1nr1a_</a>	Alignment	not modelled	88.5	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
99	<a href="#">d1zpdal</a>	Alignment	not modelled	87.0	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
100	<a href="#">d1m3sa_</a>	Alignment	not modelled	87.0	18	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
101	<a href="#">d1t9ba1</a>	Alignment	not modelled	86.9	9	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
102	<a href="#">d1moqa_</a>	Alignment	not modelled	86.2	18	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
103	<a href="#">c2x7jA_</a>	Alignment	not modelled	86.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene <b>PDBTitle:</b> structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
104	<a href="#">c1wlfA_</a>	Alignment	not modelled	84.4	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisome biogenesis factor 1; <b>PDBTitle:</b> structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain



105	<a href="#">c2yvaB_</a>	Alignment	not modelled	84.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dnaa initiator-associating protein diaa; <b>PDBTitle:</b> crystal structure of escherichia coli diaa
106	<a href="#">c5g4gF_</a>	Alignment	not modelled	83.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> structure of the atpgs-bound vat complex
107	<a href="#">c4ivnB_</a>	Alignment	not modelled	82.2	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the vibrio vulnificus nanr protein complexed with manna-6p
108	<a href="#">d1wlfA2</a>	Alignment	not modelled	81.9	19	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
109	<a href="#">d1qcsa1</a>	Alignment	not modelled	81.0	14	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
110	<a href="#">c5udfB_</a>	Alignment	not modelled	81.0	24	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system transmembrane protein lole; <b>PDBTitle:</b> structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lole from acinetobacter baumannii
111	<a href="#">d1vima_</a>	Alignment	not modelled	80.7	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
112	<a href="#">d1ylea1</a>	Alignment	not modelled	80.7	22	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> Asta-like
113	<a href="#">c2ev2B_</a>	Alignment	not modelled	78.2	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> structure of rv1264n, the regulatory domain of the mycobacterial2 adenyl cyclase rv1264, at ph 8.5
114	<a href="#">d1jeoa_</a>	Alignment	not modelled	77.8	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
115	<a href="#">c4rjB_</a>	Alignment	not modelled	77.5	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
116	<a href="#">c4s12C_</a>	Alignment	not modelled	77.2	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetylmuramic acid 6-phosphate etherase; <b>PDBTitle:</b> 1.55 angstrom crystal structure of n-acetylmuramic acid 6-phosphate2 etherase from yersinia enterocolitica.
117	<a href="#">c2amB_</a>	Alignment	not modelled	76.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
118	<a href="#">c3shoA_</a>	Alignment	not modelled	76.1	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rpir family; <b>PDBTitle:</b> crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
119	<a href="#">c4s1wA_</a>	Alignment	not modelled	76.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--fructose-6-phosphate aminotransferase <b>PDBTitle:</b> structure of a putative glutamine--fructose-6-phosphate2 aminotransferase from staphylococcus aureus subsp. aureus mu50
120	<a href="#">c3fj1A_</a>	Alignment	not modelled	75.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution