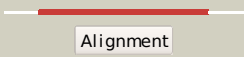

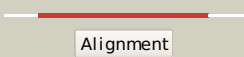

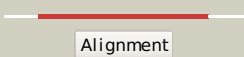

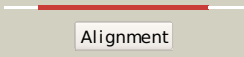

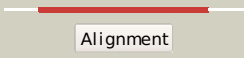

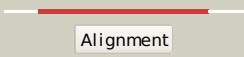

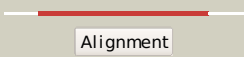

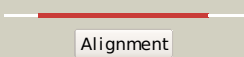

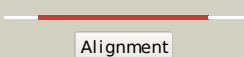

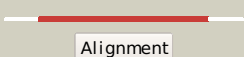

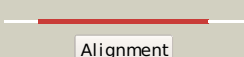










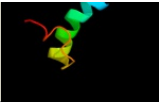
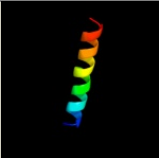
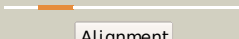
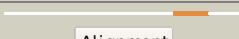


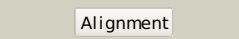
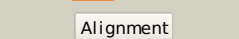




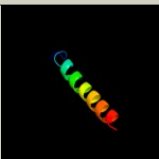
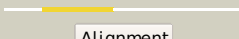
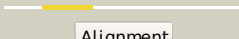

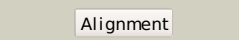
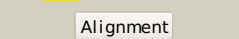

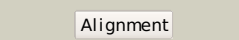
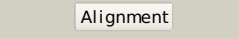
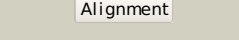

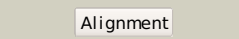




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1tmoA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> trimethylamine n-oxide reductase; <b>PDBTitle:</b> trimethylamine n-oxide reductase from shewanella massilia
2	<a href="#">c1y5iA_</a>	 Alignment		100.0	27	<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
3	<a href="#">c1h5nC_</a>	 Alignment		100.0	28	<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
4	<a href="#">c1kqgA_</a>	 Alignment		100.0	23	<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
5	<a href="#">c2e7zA_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> acetylene hydratase ahy; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
6	<a href="#">c1h0hA_</a>	 Alignment		100.0	21	<b>PDB header:</b> dehydrogenase <b>Chain:</b> A; <b>PDB Molecule:</b> formate dehydrogenase (large subunit); <b>PDBTitle:</b> tungsten containing formate dehydrogenase from2 desulfovibrio gigas
7	<a href="#">c1eu1A_</a>	 Alignment		100.0	28	<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.
8	<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-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
9	<a href="#">c2vpyE_</a>	 Alignment		100.0	29	<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)
10	<a href="#">c2ivfA_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoeum aromaticum
11	<a href="#">c2nyaF_</a>	 Alignment		100.0	22	<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

12	<a href="#">clogyA</a>	Alignment		100.0	21	<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
13	<a href="#">c2v45A</a>	Alignment		100.0	22	<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 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
14	<a href="#">c2iv2X</a>	Alignment		100.0	24	<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 h2 from e. coli
15	<a href="#">c1g8jC</a>	Alignment		100.0	18	<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
16	<a href="#">d1tmoa2</a>	Alignment		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
17	<a href="#">d1dmra2</a>	Alignment		100.0	25	<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="#">d1y5ia2</a>	Alignment		100.0	28	<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
19	<a href="#">d2jioa2</a>	Alignment		100.0	22	<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="#">d1kqfa2</a>	Alignment		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
21	<a href="#">d1vlfm2</a>	Alignment	not modelled	100.0	23	<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="#">d1eu1a2</a>	Alignment	not modelled	100.0	28	<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="#">d1h0ha2</a>	Alignment	not modelled	100.0	22	<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="#">d2iv2x2</a>	Alignment	not modelled	100.0	25	<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="#">d1logya2</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
26	<a href="#">d1g8ka2</a>	Alignment	not modelled	100.0	18	<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="#">c2fugC</a>	Alignment	not modelled	100.0	19	<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
28	<a href="#">d2fug32</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

29	<a href="#">d1kqfa1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
30	<a href="#">d1tmoa1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
31	<a href="#">d1dmra1</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
32	<a href="#">d1eula1</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
33	<a href="#">d1vlfm1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
34	<a href="#">d1h0ha1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
35	<a href="#">d2jioa1</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
36	<a href="#">d1g8ka1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
37	<a href="#">d1ogya1</a>	Alignment	not modelled	99.9	25	<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="#">d1y5ia1</a>	Alignment	not modelled	99.9	24	<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="#">d2iv2x1</a>	Alignment	not modelled	99.9	25	<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="#">c2ki8A_</a>	Alignment	not modelled	99.8	17	<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
41	<a href="#">d2fug31</a>	Alignment	not modelled	97.0	19	<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="#">c2pjhb_</a>	Alignment	not modelled	96.4	13	<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
43	<a href="#">d1ozha1</a>	Alignment	not modelled	96.0	19	<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
44	<a href="#">d1q6za1</a>	Alignment	not modelled	95.9	14	<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
45	<a href="#">d2ihta1</a>	Alignment	not modelled	95.9	14	<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
46	<a href="#">d2ez9a1</a>	Alignment	not modelled	95.8	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
47	<a href="#">d2ji7a1</a>	Alignment	not modelled	95.6	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
48	<a href="#">d1ybha1</a>	Alignment	not modelled	95.6	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
49	<a href="#">d1e32a1</a>	Alignment	not modelled	95.5	13	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
50	<a href="#">c1cz5A_</a>	Alignment	not modelled	94.7	13	<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)
51	<a href="#">d2djia1</a>	Alignment	not modelled	94.6	14	<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
52	<a href="#">d1cz5a1</a>	Alignment	not modelled	94.1	16	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
53	<a href="#">c1s3sa_</a>	Alignment	not modelled	93.0	13	<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
						<b>PDB header:</b> chaperone/oxidoreductase

54	<a href="#">c2pq4B_</a>	Alignment		92.9	31	<b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic nitrate reductase precursor; <b>PDBTitle:</b> nmr solution structure of napd in complex with napa1-352 signal peptide
55	<a href="#">c3hu2C_</a>	Alignment	not modelled	92.6	13	<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
56	<a href="#">d1t9ba1</a>	Alignment	not modelled	92.5	8	<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
57	<a href="#">c3k35D_</a>	Alignment	not modelled	92.4	17	<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
58	<a href="#">d1ovma1</a>	Alignment	not modelled	92.2	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
59	<a href="#">c3knzA_</a>	Alignment	not modelled	91.6	12	<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
60	<a href="#">c3pkiF_</a>	Alignment	not modelled	91.5	20	<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
61	<a href="#">d1x94a_</a>	Alignment	not modelled	91.3	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
62	<a href="#">c3jwpA_</a>	Alignment	not modelled	91.1	10	<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
63	<a href="#">c2e76D_</a>	Alignment		91.0	22	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome b6-f complex iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
64	<a href="#">c2x3yA_</a>	Alignment	not modelled	90.9	6	<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
65	<a href="#">c3fxaA_</a>	Alignment	not modelled	90.3	16	<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
66	<a href="#">d1tk9a_</a>	Alignment	not modelled	90.1	10	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
67	<a href="#">d1zpdal</a>	Alignment	not modelled	89.9	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
68	<a href="#">c3cf1C_</a>	Alignment	not modelled	89.5	11	<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
69	<a href="#">c3g68A_</a>	Alignment	not modelled	89.5	11	<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
70	<a href="#">d1ma3a_</a>	Alignment	not modelled	88.6	10	<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
71	<a href="#">c2dwcB_</a>	Alignment	not modelled	87.8	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 433aa long hypothetical phosphoribosylglycinamide formyl <b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
72	<a href="#">d2b4ya1</a>	Alignment	not modelled	87.7	7	<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
73	<a href="#">c1p84E_</a>	Alignment	not modelled	87.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex
74	<a href="#">c2yvaB_</a>	Alignment	not modelled	87.3	8	<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
75	<a href="#">c3etnD_</a>	Alignment	not modelled	87.0	13	<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 a resolution
76	<a href="#">c2a3nA_</a>	Alignment	not modelled	84.8	9	<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 a resolution

77	<a href="#">c2fyuO</a>	 Alignment	not modelled	84.3	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
78	<a href="#">d1ylea1</a>	 Alignment	not modelled	83.7	26	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> AstA-like
79	<a href="#">d1nria</a>	 Alignment	not modelled	83.2	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
80	<a href="#">c1nriA</a>	 Alignment	not modelled	83.2	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
81	<a href="#">d1x92a</a>	 Alignment	not modelled	83.2	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
82	<a href="#">c3euaD</a>	 Alignment	not modelled	82.8	13	<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) from2 bacillus subtilis at 1.90 a resolution
83	<a href="#">d1kja2</a>	 Alignment	not modelled	82.6	17	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
84	<a href="#">c1wfa</a>	 Alignment	not modelled	82.1	29	<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
85	<a href="#">d1yc5a1</a>	 Alignment	not modelled	80.9	7	<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="#">c2fyuE</a>	 Alignment		80.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
87	<a href="#">c2amlB</a>	 Alignment	not modelled	79.9	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
88	<a href="#">c2ji6B</a>	 Alignment	not modelled	79.4	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
89	<a href="#">d1m2ka</a>	 Alignment	not modelled	77.5	13	<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
90	<a href="#">d1moqa</a>	 Alignment	not modelled	77.5	23	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
91	<a href="#">c2x7jA</a>	 Alignment	not modelled	76.2	15	<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
92	<a href="#">d1wfa2</a>	 Alignment	not modelled	75.2	28	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
93	<a href="#">d1qcsa1</a>	 Alignment	not modelled	74.6	19	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
94	<a href="#">d1vima</a>	 Alignment	not modelled	74.0	10	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
95	<a href="#">d1s5pa</a>	 Alignment	not modelled	73.3	7	<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
96	<a href="#">c1kja</a>	 Alignment	not modelled	73.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase 2; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
97	<a href="#">d1cr5a1</a>	 Alignment	not modelled	71.1	13	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
98	<a href="#">c3q2oB</a>	 Alignment	not modelled	70.2	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
99	<a href="#">c1qdnA</a>	 Alignment	not modelled	69.8	16	<b>PDB header:</b> fusion protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (n-ethylmaleimide sensitive fusion <b>PDBTitle:</b> amino terminal domain of the n-ethylmaleimide sensitive2 fusion protein (nsf)
100	<a href="#">c2l66B</a>	 Alignment	not modelled	68.9	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, abrb family; <b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea. <b>PDB header:</b> isomerase



101	<a href="#">c3fkjA_</a>	Alignment	not modelled	66.5	15	<b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerases; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
102	<a href="#">c3m7aA_</a>	Alignment	not modelled	65.3	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution
103	<a href="#">c3iwfA_</a>	Alignment	not modelled	64.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
104	<a href="#">c1powA_</a>	Alignment	not modelled	60.8	16	<b>PDB header:</b> oxidoreductase(oxygen as acceptor) <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
105	<a href="#">c2ev2B_</a>	Alignment	not modelled	60.1	17	<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 adenyllyl cylcase rv1264, at ph 8.5
106	<a href="#">c3glsC_</a>	Alignment	not modelled	58.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-3, <b>PDBTitle:</b> crystal structure of human sirt3
107	<a href="#">d1mvfd_</a>	Alignment	not modelled	58.2	26	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Kis/PemI addition antidote
108	<a href="#">c3cvjB_</a>	Alignment	not modelled	57.6	10	<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
109	<a href="#">c3pjyB_</a>	Alignment	not modelled	55.8	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical signal peptide protein; <b>PDBTitle:</b> crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
110	<a href="#">d2vbu1</a>	Alignment	not modelled	54.9	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin kinase-like <b>Family:</b> CTP-dependent riboflavin kinase-like
111	<a href="#">c3orgA_</a>	Alignment	not modelled	54.1	14	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
112	<a href="#">c3shoA_</a>	Alignment	not modelled	53.2	13	<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 spharobacter2 thermophilus (sugar isomerase domain)
113	<a href="#">c3uvzB_</a>	Alignment	not modelled	52.8	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
114	<a href="#">c2djiA_</a>	Alignment	not modelled	52.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
115	<a href="#">c3fj1A_</a>	Alignment	not modelled	52.6	11	<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
116	<a href="#">d1b25a1</a>	Alignment	not modelled	51.9	14	<b>Fold:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Superfamily:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Family:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains
117	<a href="#">c3trjC_</a>	Alignment	not modelled	51.1	10	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
118	<a href="#">c1cr5B_</a>	Alignment	not modelled	50.5	13	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> sec18p (residues 22 - 210); <b>PDBTitle:</b> n-terminal domain of sec18p
119	<a href="#">c2decA_</a>	Alignment	not modelled	50.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 325aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
120	<a href="#">d1jeoa_</a>	Alignment	not modelled	49.7	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain