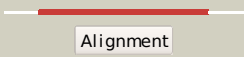
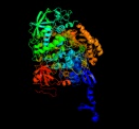
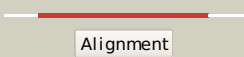

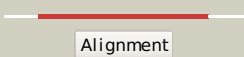

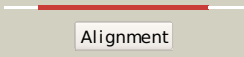

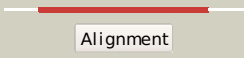

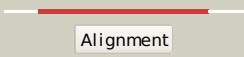

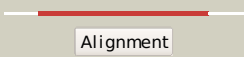

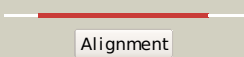

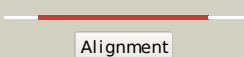

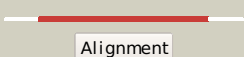

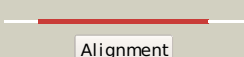







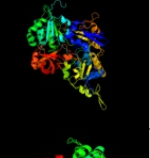


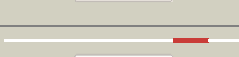
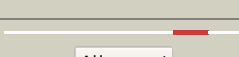
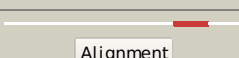


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1y5iA_</a>	 Alignment		100.0	79	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory nitrate reductase 1 alpha chain; <b>PDBTitle:</b> the crystal structure of the narghi mutant nari-k86a
2	<a href="#">d1y5ia2</a>	 Alignment		100.0	79	<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
3	<a href="#">c2ivfA_</a>	 Alignment		100.0	25	<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
4	<a href="#">c1kqgA_</a>	 Alignment		100.0	18	<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="#">c1h0hA_</a>	 Alignment		100.0	17	<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
6	<a href="#">c1vlfQ_</a>	 Alignment		100.0	23	<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
7	<a href="#">c2nyaF_</a>	 Alignment		100.0	17	<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
8	<a href="#">c1ogyA_</a>	 Alignment		100.0	20	<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
9	<a href="#">c1tmoA_</a>	 Alignment		100.0	23	<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
10	<a href="#">c1h5nC_</a>	 Alignment		100.0	26	<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
11	<a href="#">c1eu1A_</a>	 Alignment		100.0	26	<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.

12	<a href="#">c2e7zA</a>	Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahy; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
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 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
14	<a href="#">c2vpyE</a>	Alignment		100.0	27	<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)
15	<a href="#">c2iv2X</a>	Alignment		100.0	26	<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
16	<a href="#">d1h0ha2</a>	Alignment		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
17	<a href="#">d1kqfa2</a>	Alignment		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
18	<a href="#">c1g8iC</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
19	<a href="#">d1vlfm2</a>	Alignment		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
20	<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
21	<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
22	<a href="#">d1tmoa2</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
23	<a href="#">d1dmra2</a>	Alignment	not modelled	100.0	26	<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	26	<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="#">d1eu1a2</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
26	<a href="#">d1g8ka2</a>	Alignment	not modelled	100.0	20	<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	22	<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	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

29	<a href="#">dly5ia1</a>	 Alignment	not modelled	100.0	81	<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="#">dleu1a1</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
31	<a href="#">dlkqfa1</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
32	<a href="#">dlvlfm1</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
33	<a href="#">dltmoa1</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
34	<a href="#">dlh0ha1</a>	 Alignment	not modelled	99.9	15	<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="#">dldmra1</a>	 Alignment	not modelled	99.9	18	<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="#">d2jioa1</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
37	<a href="#">dlg8ka1</a>	 Alignment	not modelled	99.9	18	<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="#">dlogya1</a>	 Alignment	not modelled	99.9	18	<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	99.8	23	<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	99.7	19	<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="#">d2ihta1</a>	 Alignment	not modelled	97.0	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
42	<a href="#">c3etnD_</a>	 Alignment	not modelled	96.8	12	<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
43	<a href="#">d1tk9a_</a>	 Alignment	not modelled	96.7	9	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
44	<a href="#">c2yvaB_</a>	 Alignment	not modelled	96.7	9	<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
45	<a href="#">dlzoha1</a>	 Alignment	not modelled	96.6	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
46	<a href="#">d1x92a_</a>	 Alignment	not modelled	96.6	8	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
47	<a href="#">dlzpdal</a>	 Alignment	not modelled	96.2	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
48	<a href="#">c2pjhB_</a>	 Alignment	not modelled	96.1	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
49	<a href="#">c3euaD_</a>	 Alignment	not modelled	96.1	26	<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
50	<a href="#">dljeoa_</a>	 Alignment	not modelled	96.0	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
51	<a href="#">dlvima_</a>	 Alignment	not modelled	96.0	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
52	<a href="#">d2fug31</a>	 Alignment	not modelled	95.9	26	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
53	<a href="#">d2ez9a1</a>	 Alignment	not modelled	95.9	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

54	<a href="#">dlybha1</a>	Alignment	not modelled	95.9	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
55	<a href="#">dlq6za1</a>	Alignment	not modelled	95.8	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
56	<a href="#">d2djia1</a>	Alignment	not modelled	95.7	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
57	<a href="#">c2x3yA</a>	Alignment	not modelled	95.7	14	<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
58	<a href="#">d2ji7a1</a>	Alignment	not modelled	95.6	11	<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="#">c3fxaA</a>	Alignment	not modelled	95.4	11	<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
60	<a href="#">dllovma1</a>	Alignment	not modelled	95.4	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
61	<a href="#">c2a3nA</a>	Alignment	not modelled	94.8	24	<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
62	<a href="#">c3fkjA</a>	Alignment	not modelled	94.6	14	<b>PDB header:</b> isomerase <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
63	<a href="#">clcz5A</a>	Alignment	not modelled	94.6	18	<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)
64	<a href="#">dlm3sa</a>	Alignment	not modelled	94.4	11	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
65	<a href="#">dle32a1</a>	Alignment	not modelled	94.4	15	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
66	<a href="#">c3cvjB</a>	Alignment	not modelled	94.3	15	<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
67	<a href="#">dlnria</a>	Alignment	not modelled	94.2	11	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
68	<a href="#">clnriA</a>	Alignment	not modelled	94.2	11	<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
69	<a href="#">c3k35D</a>	Alignment	not modelled	93.9	10	<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
70	<a href="#">c3shoA</a>	Alignment	not modelled	93.8	19	<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)
71	<a href="#">dlm2ka</a>	Alignment	not modelled	93.5	21	<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="#">dlcz5a1</a>	Alignment	not modelled	93.5	18	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
73	<a href="#">dlx94a</a>	Alignment	not modelled	93.5	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
74	<a href="#">c3pkiF</a>	Alignment	not modelled	93.1	11	<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
75	<a href="#">dl1t9ba1</a>	Alignment	not modelled	92.8	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
76	<a href="#">c3hu2C</a>	Alignment	not modelled	92.7	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 n-d1 r86a mutant in complex with atpgs
77	<a href="#">d2b4ya1</a>	Alignment	not modelled	92.5	11	<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
78	<a href="#">dlpvda1</a>	Alignment	not modelled	92.3	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
79	<a href="#">c3knzA</a>	Alignment	not modelled	91.9	21	<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

80	<a href="#">d1ma3a_</a>	Alignment	not modelled	91.3	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
81	<a href="#">c1s3sa_</a>	Alignment	not modelled	90.7	15	<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
82	<a href="#">d1yc5a1</a>	Alignment	not modelled	90.5	15	<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
83	<a href="#">c3cf1C_</a>	Alignment	not modelled	90.1	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
84	<a href="#">c1ozhD_</a>	Alignment	not modelled	89.4	9	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acetolactate synthase, catabolic; <b>PDBTitle:</b> the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
85	<a href="#">c3jwpA_</a>	Alignment	not modelled	89.3	12	<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
86	<a href="#">c3trjC_</a>	Alignment	not modelled	88.5	12	<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
87	<a href="#">c2dwcB_</a>	Alignment	not modelled	88.2	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
88	<a href="#">c2vbgB_</a>	Alignment	not modelled	87.8	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain alpha-ketoacid decarboxylase; <b>PDBTitle:</b> the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
89	<a href="#">c2pgnA_</a>	Alignment	not modelled	87.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexane-1,2-dione hydrolase (cdh); <b>PDBTitle:</b> the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
90	<a href="#">d1s5pa_</a>	Alignment	not modelled	87.5	20	<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
91	<a href="#">c2vbiF_</a>	Alignment	not modelled	87.2	12	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
92	<a href="#">c2xhzC_</a>	Alignment	not modelled	85.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
93	<a href="#">c2ji6B_</a>	Alignment	not modelled	84.6	12	<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
94	<a href="#">c1zpdA_</a>	Alignment	not modelled	83.4	14	<b>PDB header:</b> alcohol fermentation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> pyruvate decarboxylase from zymomonas mobilis
95	<a href="#">c2zj3A_</a>	Alignment	not modelled	83.2	17	<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
96	<a href="#">c1ovmC_</a>	Alignment	not modelled	82.9	9	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> indole-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
97	<a href="#">c1wifA_</a>	Alignment	not modelled	82.9	15	<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
98	<a href="#">c3g68A_</a>	Alignment	not modelled	82.0	17	<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
99	<a href="#">d1ylea1</a>	Alignment	not modelled	81.4	24	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> AstA-like
100	<a href="#">c2q27B_</a>	Alignment	not modelled	81.3	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> crystal structure of oxalyl-coa decarboxylase from escherichia coli
101	<a href="#">c2djiA_</a>	Alignment	not modelled	80.1	15	<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
102	<a href="#">c2amlB_</a>	Alignment	not modelled	79.1	21	<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
103	<a href="#">c2panF_</a>	Alignment	not modelled	79.0	11	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> glyoxylate carboligase; <b>PDBTitle:</b> crystal structure of e. coli glyoxylate carboligase



104	<a href="#">c3hbaA_</a>	 Alignment	not modelled	76.7	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 (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
105	<a href="#">c1powA_</a>	 Alignment	not modelled	76.5	14	<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
106	<a href="#">c3fj1A_</a>	 Alignment	not modelled	74.4	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
107	<a href="#">d1x9ia_</a>	 Alignment	not modelled	74.0	11	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
108	<a href="#">d1wlfa2</a>	 Alignment	not modelled	73.0	15	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
109	<a href="#">c1yi1A_</a>	 Alignment	not modelled	70.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
110	<a href="#">c2l66B_</a>	 Alignment	not modelled	69.1	14	<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.
111	<a href="#">c1kjjA_</a>	 Alignment	not modelled	68.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase 2; <b>PDBTitle:</b> crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
112	<a href="#">c2x7jA_</a>	 Alignment	not modelled	68.0	11	<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
113	<a href="#">c2ag1A_</a>	 Alignment	not modelled	66.5	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> benzaldehyde lyase; <b>PDBTitle:</b> crystal structure of benzaldehyde lyase (bal)- semet
114	<a href="#">d1kjqA2</a>	 Alignment	not modelled	66.3	13	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
115	<a href="#">c2nxwB_</a>	 Alignment	not modelled	64.5	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phenyl-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasillense
116	<a href="#">c1upaC_</a>	 Alignment	not modelled	63.0	15	<b>PDB header:</b> synthase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxyethylarginine synthase; <b>PDBTitle:</b> carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
117	<a href="#">c3iwfA_</a>	 Alignment	not modelled	62.8	8	<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
118	<a href="#">c3glsC_</a>	 Alignment	not modelled	62.6	16	<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
119	<a href="#">c3k5lB_</a>	 Alignment	not modelled	61.2	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl-aminimidazole carboxylase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminimidazole ribonucleotide
120	<a href="#">c3orqA_</a>	 Alignment	not modelled	60.5	11	<b>PDB header:</b> ligase, biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminimidazole synthetase from2 staphylococcus aureus complexed with adp