











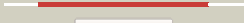

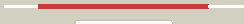

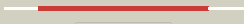





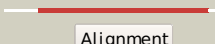

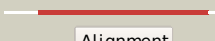

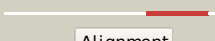

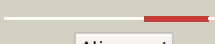




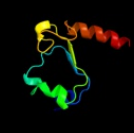


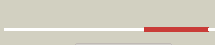




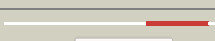



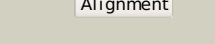
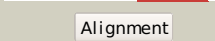


Detailed template information



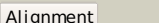



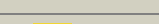
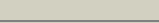
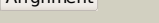

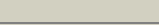
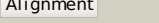
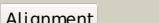


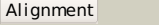


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s5pa_	 Alignment		100.0	97	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
2	d1m2ka_	 Alignment		100.0	40	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
3	c3jwpA_	 Alignment		100.0	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein sir2 homologue; PDBTitle: crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
4	d1j8fa_	 Alignment		100.0	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
5	c2hjhb_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase
6	d1yc5a1	 Alignment		100.0	31	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
7	c3qlsC_	 Alignment		100.0	26	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
8	d2b4ya1	 Alignment		100.0	37	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
9	d1q1aa_	 Alignment		100.0	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
10	c1q14A_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: hst2 protein; PDBTitle: structure and autoregulation of the yeast hst2 homolog of sir2
11	c3k35D_	 Alignment		100.0	27	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6

12	c3pkiF_	 <div>Alignment</div>		100.0	26	PDB header: hydrolase Chain: F; PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
13	dlma3a_	 <div>Alignment</div>		100.0	35	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
14	d2ji7a1	 <div>Alignment</div>		97.2	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
15	d2djia1	 <div>Alignment</div>		97.2	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
16	d2ez9a1	 <div>Alignment</div>		97.0	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
17	d1ybha1	 <div>Alignment</div>		97.0	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
18	d1ozha1	 <div>Alignment</div>		96.8	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
19	d1t9ba1	 <div>Alignment</div>		96.8	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
20	d2ihta1	 <div>Alignment</div>		96.7	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
21	c2ivfA_	 <div>Alignment</div>	not modelled	96.4	13	PDB header: oxidoreductase Chain: A; PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
22	d1h0ha2	 <div>Alignment</div>	not modelled	96.4	14	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
23	c2vpyE_	 <div>Alignment</div>	not modelled	96.4	14	PDB header: oxidoreductase Chain: E; PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor, 2 pentachlorophenol (pcp)
24	c1powA_	 <div>Alignment</div>	not modelled	96.3	13	PDB header: oxidoreductase(oxygen as acceptor) Chain: A; PDB Molecule: pyruvate oxidase; PDBTitle: the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
25	c3lq1A_	 <div>Alignment</div>	not modelled	96.0	6	PDB header: transferase Chain: A; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- PDBTitle: crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
26	d1q6za1	 <div>Alignment</div>	not modelled	96.0	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
27	c2djiA_	 <div>Alignment</div>	not modelled	96.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad PDB header: lyase

28	c2ji6B_	Alignment	not modelled	96.0	16	Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
29	c2x7jA_	Alignment	not modelled	95.9	13	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
30	c1h0hA_	Alignment	not modelled	95.9	14	PDB header: dehydrogenase Chain: A: PDB Molecule: formate dehydrogenase (large subunit); PDBTitle: tungsten containing formate dehydrogenase from2 desulfovibrio gigas
31	c1h5nC_	Alignment	not modelled	95.8	10	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
32	c1yi1A_	Alignment	not modelled	95.6	9	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
33	c2e7zA_	Alignment	not modelled	95.6	12	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
34	c2q27B_	Alignment	not modelled	95.6	18	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
35	c1ozhD_	Alignment	not modelled	95.4	19	PDB header: lyase Chain: D: PDB Molecule: acetolactate synthase, catabolic; PDBTitle: the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
36	c2panF_	Alignment	not modelled	95.4	20	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
37	c3eyaE_	Alignment	not modelled	95.4	14	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
38	d3clsd2	Alignment	not modelled	95.3	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
39	c2iv2X_	Alignment	not modelled	95.3	13	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
40	d1y5ia2	Alignment	not modelled	95.3	17	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
41	c1efpC_	Alignment	not modelled	95.2	25	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans
42	d1kqfa2	Alignment	not modelled	95.2	7	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
43	c1t9dB_	Alignment	not modelled	95.2	17	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
44	d2iv2x2	Alignment	not modelled	95.1	13	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
45	d1vlfm2	Alignment	not modelled	95.1	12	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
46	c2pgnA_	Alignment	not modelled	95.1	16	PDB header: hydrolase Chain: A: PDB Molecule: cyclohexane-1,2-dione hydrolase (cdh); PDBTitle: the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
47	c1vlfQ_	Alignment	not modelled	94.9	11	PDB header: oxidoreductase Chain: Q: PDB Molecule: pyrogallol hydroxytransferase large subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
48	d1dmra2	Alignment	not modelled	94.9	10	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
49	c2v45A_	Alignment	not modelled	94.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: 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
50	c3shoA_	Alignment	not modelled	94.7	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
51	d1efpa2	Alignment	not modelled	94.6	25	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit

52	d1efva2	Alignment	not modelled	94.6	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
53	c1y5iA_	Alignment	not modelled	94.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
54	c2nyaF_	Alignment	not modelled	94.5	7	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
55	d1ogya2	Alignment	not modelled	94.5	9	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
56	c1kqgA_	Alignment	not modelled	94.3	7	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
57	d1ovma1	Alignment	not modelled	94.3	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
58	c2jlaD_	Alignment	not modelled	94.3	8	PDB header: transferase Chain: D: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
59	c1ogyA_	Alignment	not modelled	94.2	9	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
60	c2khzB_	Alignment	not modelled	94.2	16	PDB header: nuclear protein Chain: B: PDB Molecule: c-myc-responsive protein rcl; PDBTitle: solution structure of rcl
61	d2jioa2	Alignment	not modelled	94.2	11	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
62	d1d4oa_	Alignment	not modelled	94.1	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
63	c1tmoA_	Alignment	not modelled	94.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
64	c1pt9B_	Alignment	not modelled	93.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
65	c1jscA_	Alignment	not modelled	93.6	17	PDB header: lyase Chain: A: PDB Molecule: acetoxyhydroxy-acid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetoxyhydroxyacid synthase: a target for herbicidal3 inhibitors
66	d1zpdal	Alignment	not modelled	93.6	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
67	c1upaC_	Alignment	not modelled	93.2	7	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
68	d1pvdal	Alignment	not modelled	93.2	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
69	c2ag1A_	Alignment	not modelled	93.0	12	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
70	d1tmoa2	Alignment	not modelled	92.9	11	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
71	d1tk9a_	Alignment	not modelled	92.0	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
72	d1pnoa_	Alignment	not modelled	91.9	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
73	c1ovmC_	Alignment	not modelled	90.9	27	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
74	c2v3wC_	Alignment	not modelled	90.4	13	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase2 variant I461a from pseudomonas putida
75	c3dnfB_	Alignment	not modelled	89.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
76	c2x3yA_	Alignment	not modelled	89.7	17	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
						Fold: Formate dehydrogenase/DMSO reductase, domains 1-3

77	d1g8ka2	Alignment	not modelled	89.5	13	Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
78	c2vbiF_	Alignment	not modelled	89.2	12	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
79	d1m3sa_	Alignment	not modelled	88.8	19	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
80	d1vima_	Alignment	not modelled	88.5	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
81	d1x94a_	Alignment	not modelled	88.4	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
82	d1x92a_	Alignment	not modelled	88.3	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
83	c2xhzC_	Alignment	not modelled	87.9	15	PDB header: isomerase Chain: C: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
84	c3trjC_	Alignment	not modelled	87.7	20	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
85	c1zpdA_	Alignment	not modelled	87.6	14	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
86	d1eu1a2	Alignment	not modelled	87.5	10	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
87	c3cf4G_	Alignment	not modelled	86.6	15	PDB header: oxidoreductase Chain: G: PDB Molecule: acetyl-coa decarboxylase/synthase epsilon subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
88	c1g8jC_	Alignment	not modelled	86.2	11	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
89	d1jeoa_	Alignment	not modelled	85.8	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
90	c2yvaB_	Alignment	not modelled	85.6	18	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
91	c2bruC_	Alignment	not modelled	85.4	24	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
92	c1s24A_	Alignment	not modelled	85.2	23	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans
93	d1s24a_	Alignment	not modelled	85.2	23	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
94	c3cvjB_	Alignment	not modelled	84.7	21	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
95	c2lqcA_	Alignment	not modelled	84.6	10	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
96	c3ke8A_	Alignment	not modelled	84.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate PDBTitle: crystal structure of isph:hmbpp-complex
97	c3fxaA_	Alignment	not modelled	83.8	18	PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
98	c2vbgB_	Alignment	not modelled	83.0	18	PDB header: lyase Chain: B: PDB Molecule: branched-chain alpha-ketoacid decarboxylase; PDBTitle: the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
99	d4rxna_	Alignment	not modelled	81.8	14	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
100	c3hbaA_	Alignment	not modelled	81.7	23	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
101	c2w93A_	Alignment	not modelled	81.2	20	PDB header: lyase Chain: A: PDB Molecule: pyruvate decarboxylase isozyme 1; PDBTitle: crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide

102	c1eu1A	 Alignment	not modelled	81.1	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethyl sulfoxide reductase; PDBTitle: the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
103	c1nr1A	 Alignment	not modelled	80.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
104	d1nr1a	 Alignment	not modelled	80.6	21	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
105	c1yuzB	 Alignment	not modelled	80.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
106	c3a44D	 Alignment	not modelled	79.5	6	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
107	d1brfa	 Alignment	not modelled	78.7	17	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
108	d1lt1a	 Alignment	not modelled	78.5	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA replication initiator (cdc21/cdc54) N-terminal domain
109	c2kdxA	 Alignment	not modelled	78.3	15	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
110	c3etnD	 Alignment	not modelled	75.4	19	PDB header: isomerase Chain: D: PDB Molecule: putative phosphosugar isomerase involved in capsule PDBTitle: crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
111	d1qcva	 Alignment	not modelled	75.2	12	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
112	c2zj3A	 Alignment	not modelled	75.2	21	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
113	c3c2qA	 Alignment	not modelled	73.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
114	c2puwA	 Alignment	not modelled	73.6	18	PDB header: transferase Chain: A: PDB Molecule: isomerase domain of glutamine-fructose-6-phosphate PDBTitle: the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
115	c3euaD	 Alignment	not modelled	73.0	18	PDB header: isomerase Chain: D: PDB Molecule: putative fructose-aminoacid-6-phosphate deglycase; PDBTitle: crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
116	c2a3nA	 Alignment	not modelled	72.5	14	PDB header: sugar binding protein Chain: A: PDB Molecule: putative glucosamine-fructose-6-phosphate aminotransferase; PDBTitle: crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
117	d2dsxa1	 Alignment	not modelled	71.8	15	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
118	d1x9ia	 Alignment	not modelled	71.6	17	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
119	d1dx8a	 Alignment	not modelled	70.7	16	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
120	c1lt1E	 Alignment	not modelled	70.1	18	PDB header: replication Chain: E: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: the dodecamer structure of mcm from archaean m.2 thermoautotrophicum