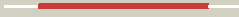























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1151c_(-)_1278909_1279622
Date	Wed Jul 31 22:05:23 BST 2019
Unique Job ID	57222149695bf52f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m2ka_	 Alignment		100.0	46	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
2	c3jwpA_	 Alignment		100.0	30	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
3	d1j8fa_	 Alignment		100.0	28	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
4	d1yc5a1	 Alignment		100.0	34	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
5	c5btrB_	 Alignment		100.0	28	PDB header: hydrolase/substrate Chain: B: PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of sirt1 in complex with resveratrol and an amc-2 containing peptide
6	c5oj7A_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacetylase; sirtuin-4 PDBTitle: sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
7	d2b4ya1	 Alignment		100.0	40	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
8	c2hjhB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase
9	d1s5pa_	 Alignment		100.0	39	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
10	c3glsC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
11	c4iaoB_	 Alignment		100.0	24	PDB header: hydrolase/transcription Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of sir2 c543s mutant in complex with sid domain of2 sir4

12	c4i5iA_	Alignment		100.0	27	PDB header: hydrolase Chain: A; PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of the sirt1 catalytic domain bound to nad and an2 ex527 analog
13	d1ma3a_	Alignment		100.0	37	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
14	d1q1aa_	Alignment		100.0	29	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
15	c5o10B_	Alignment		100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: putative silent information regulator 2,putative silent PDBTitle: structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide
16	c3zg6A_	Alignment		100.0	28	PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: nad-dependent protein deacetylase sirtuin-6; PDBTitle: the novel de-long chain fatty acid function of human sirt6
17	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
18	c3pkIF_	Alignment		100.0	29	PDB header: hydrolase Chain: F; PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
19	c3k35D_	Alignment		100.0	28	PDB header: hydrolase Chain: D; PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
20	c5fyqB_	Alignment		100.0	25	PDB header: hydrolase Chain: B; PDB Molecule: nad-dependent protein deacetylase sirtuin-2; PDBTitle: sirt2 in complex with a 13-mer trifluoroacetylated ran peptide
21	c5a3aA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A; PDB Molecule: sir2 family protein; PDBTitle: crystal structure of the adp-ribosylating sirtuin (sirtm)2 from streptococcus pyogenes (apo form)
22	d2ji7a1	Alignment	not modelled	97.4	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
23	c5o12D_	Alignment	not modelled	97.4	23	PDB header: flavoprotein Chain: D; PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
24	d1ybha1	Alignment	not modelled	97.3	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
25	d2djia1	Alignment	not modelled	97.2	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
26	d2ez9a1	Alignment	not modelled	97.1	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
27	c4l2iA_	Alignment	not modelled	97.1	22	PDB header: electron transport Chain: A; PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
28	d1t9ba1	Alignment	not modelled	96.9	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain

29	d2ihta1	Alignment	not modelled	96.9	7	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
30	d1ozha1	Alignment	not modelled	96.8	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
31	c6fahE	Alignment	not modelled	96.6	20	PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
32	c1yi1A	Alignment	not modelled	96.5	15	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonyleurea herbicide, tribenuron methyl
33	c1powA	Alignment	not modelled	96.5	21	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
34	c2j6B	Alignment	not modelled	96.5	12	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with 3-deaza-2 thdp and oxalyl-coa
35	c3lq1A	Alignment	not modelled	96.4	13	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
36	c2djiA	Alignment	not modelled	96.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
37	c2x7jA	Alignment	not modelled	96.1	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
38	d1q6za1	Alignment	not modelled	96.0	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
39	d3clsd2	Alignment	not modelled	95.9	20	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
40	c2q27B	Alignment	not modelled	95.9	24	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
41	c3clrD	Alignment	not modelled	95.7	19	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein subunit alpha; PDBTitle: crystal structure of the r236a etf mutant from m. methylotrophus
42	c1efpC	Alignment	not modelled	95.5	19	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans
43	c2panF	Alignment	not modelled	95.5	18	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
44	d1efva2	Alignment	not modelled	95.5	20	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
45	c5ahkB	Alignment	not modelled	95.5	21	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
46	c2pgnA	Alignment	not modelled	95.5	23	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	c1efvA	Alignment	not modelled	95.4	20	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein; PDBTitle: three-dimensional structure of human electron transfer2 flavoprotein to 2.1 a resolution
48	c1ozhD	Alignment	not modelled	95.4	13	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.
49	d1efpa2	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
50	c5ow0A	Alignment	not modelled	95.3	23	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein, alpha subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
51	c4rjB	Alignment	not modelled	95.2	10	PDB header: lyase Chain: B: PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
52	c1t9dB	Alignment	not modelled	95.2	18	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in complex with a2 sulfonyleurea herbicide, metsulfuron methyl

53	c3eyaE	Alignment	not modelled	95.2	18	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
54	c3ey9B	Alignment	not modelled	95.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic activation of the2 peripheral membrane enzyme pyruvate oxidase from escherichia coli
55	c2vpyE	Alignment	not modelled	94.8	19	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
56	c2jlaD	Alignment	not modelled	94.6	12	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
57	c1upaC	Alignment	not modelled	94.6	7	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
58	d1h0ha2	Alignment	not modelled	94.2	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
59	c1jscA	Alignment	not modelled	94.2	16	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
60	c2ivfA	Alignment	not modelled	94.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
61	c2ag1A	Alignment	not modelled	93.6	15	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
62	c1h5nC	Alignment	not modelled	93.4	20	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
63	c6cz7C	Alignment	not modelled	93.2	15	PDB header: oxidoreductase Chain: C: PDB Molecule: arra; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
64	d1ovma1	Alignment	not modelled	93.1	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
65	c2e7zA	Alignment	not modelled	93.1	15	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
66	c3shoA	Alignment	not modelled	93.0	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from spbaerobacter2 thermophilus (sugar isomerase domain)
67	d1zpdA1	Alignment	not modelled	92.9	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
68	d1tk9a	Alignment	not modelled	92.9	9	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
69	c1h0hA	Alignment	not modelled	92.8	17	PDB header: electron transport Chain: A: PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from desulfovibrio gigas
70	c4o9uB	Alignment	not modelled	92.3	25	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
71	c4q9dA	Alignment	not modelled	92.2	23	PDB header: lyase Chain: A: PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
72	d1kqfa2	Alignment	not modelled	91.9	23	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
73	c2v45A	Alignment	not modelled	91.8	15	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
74	d2iv2x2	Alignment	not modelled	91.8	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
75	d1pvdA1	Alignment	not modelled	91.6	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
76	c5ch7E	Alignment	not modelled	91.6	11	PDB header: oxidoreductase Chain: E: PDB Molecule: dmsO reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps PDB header: oxidoreductase

77	c2iv2X_	Alignment	not modelled	91.5	15	Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
78	c5fywW_	Alignment	not modelled	91.5	16	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
79	c1pt9B_	Alignment	not modelled	91.1	20	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
80	d1d4oa_	Alignment	not modelled	91.1	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
81	c2v3wC_	Alignment	not modelled	91.0	19	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant I461a2 from pseudomonas putida
82	d1vlfm2	Alignment	not modelled	91.0	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
83	c2vbiF_	Alignment	not modelled	90.9	21	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter pasteurianus
84	d1x94a_	Alignment	not modelled	90.8	20	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
85	c1ovmC_	Alignment	not modelled	90.6	24	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
86	c5by2A_	Alignment	not modelled	90.6	18	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
87	c1vlfQ_	Alignment	not modelled	90.5	9	PDB header: oxidoreductase Chain: Q: PDB Molecule: pyrogallol hydroxytransferase large subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
88	d1dmra2	Alignment	not modelled	90.4	20	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
89	d1y5ia2	Alignment	not modelled	90.4	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
90	c1kqgA_	Alignment	not modelled	90.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
91	c1ogyA_	Alignment	not modelled	89.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
92	c5oqmW_	Alignment	not modelled	89.8	14	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
93	c2nyaF_	Alignment	not modelled	89.7	13	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
94	c4jemA_	Alignment	not modelled	89.7	15	PDB header: hydrolase Chain: A: PDB Molecule: cmp/hydroxymethyl cmp hydrolase; PDBTitle: crystal structure of milb complexed with cytidine 5'-monophosphate
95	c5fmfR_	Alignment	not modelled	89.7	14	PDB header: transcription Chain: R: PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
96	d1m3sa_	Alignment	not modelled	89.3	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
97	c2xhzC_	Alignment	not modelled	89.2	12	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
98	d1ogya2	Alignment	not modelled	88.9	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
99	d2jioa2	Alignment	not modelled	88.9	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
100	d1vima_	Alignment	not modelled	88.8	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
101	c1tmoA_	Alignment	not modelled	88.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
						PDB header: alcohol fermentation

102	c1zpdA_	Alignment	not modelled	88.6	13	Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
103	c2x3yA_	Alignment	not modelled	88.5	15	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
104	d1pnoa_	Alignment	not modelled	87.7	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
105	c4ivnB_	Alignment	not modelled	87.4	19	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
106	c1y5iA_	Alignment	not modelled	87.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
107	d1jeoa_	Alignment	not modelled	86.7	12	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
108	c6gcsA_	Alignment	not modelled	86.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
109	d1tmoa2	Alignment	not modelled	86.1	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
110	c5t5mB_	Alignment	not modelled	85.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdb; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from 2 methanothermobacter wolfeii, trigonal form at 2.5 a.
111	c2yvaB_	Alignment	not modelled	85.0	12	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
112	c3fxaA_	Alignment	not modelled	84.6	13	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
113	d1x92a_	Alignment	not modelled	84.5	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
114	c5iy9Q_	Alignment	not modelled	84.3	17	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
115	c6o9lQ_	Alignment	not modelled	83.8	9	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
116	c3trjC_	Alignment	not modelled	83.2	14	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
117	c2vbgB_	Alignment	not modelled	83.2	14	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
118	c1nr1A_	Alignment	not modelled	83.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from 2 haemophilus influenzae
119	d1nr1a_	Alignment	not modelled	83.1	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
120	c3dnfB_	Alignment	not modelled	83.1	12	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