














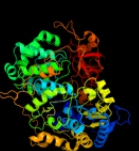








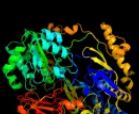
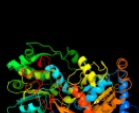






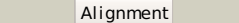
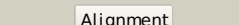
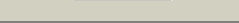



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nyaF_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
2	c1ogyA_	 Alignment		100.0	68	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
3	c1kqgA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
4	c1h0hA_	 Alignment		100.0	22	PDB header: dehydrogenase Chain: A: PDB Molecule: formate dehydrogenase (large subunit); PDBTitle: tungsten containing formate dehydrogenase from2 desulfovibrio gigas
5	c2v45A_	 Alignment		100.0	41	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
6	c1y5iA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
7	c2ivfA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
8	c2e7zA_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
9	c2vpyE_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor, 2 pentachlorophenol (pcp)
10	c2iv2X_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
11	c1tmoA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia

12	c1h5nC	Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsio reductase; PDBTitle: dmsio reductase modified by the presence of dms and air
13	c1g8jC	Alignment		100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
14	c1eu1A	Alignment		100.0	17	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.
15	d1ogya2	Alignment		100.0	69	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
16	c1vlfO	Alignment		100.0	19	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
17	d1kqfa2	Alignment		100.0	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
18	d1h0ha2	Alignment		100.0	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
19	d2jioa2	Alignment		100.0	40	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
20	d1y5ia2	Alignment		100.0	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
21	d2iv2x2	Alignment	not modelled	100.0	25	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
22	d1g8ka2	Alignment	not modelled	100.0	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
23	d1tmoa2	Alignment	not modelled	100.0	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
24	d1dmra2	Alignment	not modelled	100.0	16	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
25	d1vlfm2	Alignment	not modelled	100.0	19	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
26	d1eu1a2	Alignment	not modelled	100.0	16	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
27	c2fugC	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: nahd-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
28	d2fug32	Alignment	not modelled	100.0	22	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3

29	d2jioa1	Alignment	not modelled	100.0	48	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
30	d1h0ha1	Alignment	not modelled	100.0	33	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
31	dlogya1	Alignment	not modelled	100.0	64	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
32	d1kqfa1	Alignment	not modelled	100.0	27	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
33	d1g8ka1	Alignment	not modelled	99.9	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
34	d1dmra1	Alignment	not modelled	99.9	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
35	d1eu1a1	Alignment	not modelled	99.9	23	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
36	d1tmoa1	Alignment	not modelled	99.9	27	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
37	d1vlfm1	Alignment	not modelled	99.9	26	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d2iv2x1	Alignment	not modelled	99.9	30	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
39	d1y5ia1	Alignment	not modelled	99.9	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
40	c2ki8A_	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
41	c2pq4B_	Alignment		97.2	100	PDB header: chaperone/oxidoreductase Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide
42	c3etnD_	Alignment	not modelled	96.7	12	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
43	d1tk9a_	Alignment	not modelled	96.2	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
44	d2ji7a1	Alignment	not modelled	95.9	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
45	c2yvaB_	Alignment	not modelled	95.9	13	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
46	d1ozha1	Alignment	not modelled	95.8	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
47	d2fug31	Alignment	not modelled	95.8	32	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
48	d1x92a_	Alignment	not modelled	95.6	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
49	d2ihta1	Alignment	not modelled	95.6	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
50	d1ybha1	Alignment	not modelled	95.5	8	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
51	c3euaD_	Alignment	not modelled	95.3	10	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
52	c2pjhb_	Alignment	not modelled	95.3	21	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex

53	c1cz5A	Alignment	not modelled	94.6	15	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
54	c2x3yA	Alignment	not modelled	94.5	9	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
55	d1m3sa	Alignment	not modelled	94.1	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
56	d1q6za1	Alignment	not modelled	94.1	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
57	d1jeoa	Alignment	not modelled	94.1	18	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
58	c3k35D	Alignment	not modelled	93.9	13	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
59	d1x94a	Alignment	not modelled	93.9	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
60	c3pkiF	Alignment	not modelled	93.8	10	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
61	d2ez9a1	Alignment	not modelled	93.8	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
62	d1vima	Alignment	not modelled	92.9	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
63	d1e32a1	Alignment	not modelled	92.8	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
64	d1zpdal	Alignment	not modelled	92.5	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
65	d1cz5a1	Alignment	not modelled	92.4	18	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
66	d1ovma1	Alignment	not modelled	92.1	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
67	d1m2ka	Alignment	not modelled	92.0	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
68	c2a3nA	Alignment	not modelled	91.8	10	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
69	d1ma3a	Alignment	not modelled	91.8	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
70	c3shoA	Alignment	not modelled	91.5	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from spheraerobacter2 thermophilus (sugar isomerase domain)
71	d2djia1	Alignment	not modelled	91.0	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
72	c3trjC	Alignment	not modelled	90.6	11	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
73	d2b4ya1	Alignment	not modelled	90.3	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
74	d1yc5a1	Alignment	not modelled	90.3	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
75	c3fkjA	Alignment	not modelled	90.2	11	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerases; PDBTitle: crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
76	c2e76D	Alignment	not modelled	89.8	29	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
77	c1s3sA	Alignment	not modelled	88.1	20	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
78	c3lqlA	Alignment	not modelled	87.5	7	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
79	c1ozhD_	 Alignment	not modelled	86.9	12	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.
80	c3jwpA_	 Alignment	not modelled	86.6	7	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
81	d1t9ba1	 Alignment	not modelled	85.7	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
82	c2xhzC_	 Alignment	not modelled	85.5	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
83	c2x7jA_	 Alignment	not modelled	83.9	8	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
84	c3cf1C_	 Alignment	not modelled	83.4	20	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
85	c1wlfA_	 Alignment	not modelled	83.3	30	PDB header: protein transport Chain: A: PDB Molecule: peroxisome biogenesis factor 1; PDBTitle: structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
86	c1p84E_	 Alignment	not modelled	83.0	13	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
87	c3hu2C_	 Alignment	not modelled	82.8	20	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
88	c2fynO_	 Alignment	not modelled	82.8	35	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
89	d1ylea1	 Alignment	not modelled	80.1	22	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
90	c1jscA_	 Alignment	not modelled	80.0	11	PDB header: lyase Chain: A: PDB Molecule: acetohydroxy-acid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
91	d1s5pa_	 Alignment	not modelled	79.5	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
92	c3fxaA_	 Alignment	not modelled	78.9	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
93	c2ji6B_	 Alignment	not modelled	78.7	5	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
94	d1wlfa2	 Alignment	not modelled	77.2	30	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
95	c2puwA_	 Alignment	not modelled	76.8	9	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
96	c3knzA_	 Alignment	not modelled	75.4	11	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
97	c1yi1A_	 Alignment	not modelled	75.4	8	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
98	c2zj3A_	 Alignment	not modelled	75.2	12	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
99	d1pvdal	 Alignment	not modelled	75.1	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
100	c3fj1A_	 Alignment	not modelled	74.8	9	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
101	c1t9dB_	Alignment	not modelled	74.2	13	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

102	c3g68A	Alignment	not modelled	73.2	10	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from <i>Clostridium difficile</i> 630 at 1.80 Å resolution
103	c2fyuE	Alignment	not modelled	73.0	14	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
104	c3cvjB	Alignment	not modelled	72.6	12	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from <i>Bacillus halodurans</i> C-125 at 2.00 Å resolution
105	c1zpdA	Alignment	not modelled	71.5	11	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from <i>Zymomonas mobilis</i>
106	c2vbiF	Alignment	not modelled	71.3	16	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from <i>Acetobacter pasteurianus</i>
107	c2ag1A	Alignment	not modelled	69.9	11	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
108	c3glsC	Alignment	not modelled	69.3	9	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3; PDBTitle: crystal structure of human sirt3
109	c2dwcB	Alignment	not modelled	62.6	16	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl transferase from <i>Pyrococcus horikoshii</i> OT3 complexed with adp
110	c3cf4G	Alignment	not modelled	62.3	8	PDB header: oxidoreductase Chain: G: PDB Molecule: acetyl-coa decarboxylase/synthase epsilon subunit; PDBTitle: structure of the codh component of the <i>M. barkeri</i> acds complex
111	c2panF	Alignment	not modelled	60.9	11	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of <i>E. coli</i> glyoxylate carboligase
112	c2l66B	Alignment	not modelled	59.5	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, abrb family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
113	c2pgnA	Alignment	not modelled	57.3	9	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
114	c2vbgB	Alignment	not modelled	57.2	10	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 <i>Lactococcus lactis</i> with 2r-1-3 hydroxyethyl-deazathdp
115	c3f2hA	Alignment	not modelled	56.9	15	PDB header: lyase Chain: A: PDB Molecule: alkylmercury lyase; PDBTitle: crystal structure of the mercury-bound form of merB mutant2 c160s, the organomercurial lyase involved in a bacterial3 mercury resistance system
116	d1mvfd	Alignment	not modelled	56.6	26	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/PemI addiction antidote
117	c2amlB	Alignment	not modelled	56.2	14	PDB header: transferase Chain: B: PDB Molecule: sis domain protein; PDBTitle: crystal structure of lmo0035 protein (46906266) from <i>Listeria monocytogenes</i> 4b f2365 at 1.50 Å resolution
118	d1s6la2	Alignment	not modelled	55.8	15	Fold: NosL/MerB-like Superfamily: NosL/MerB-like Family: MerB-like
119	d2nx2a1	Alignment	not modelled	55.7	15	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like
120	c3m7aA	Alignment	not modelled	54.5	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from <i>Novosphingobium aromaticivorans</i> DSM3 12444 at 1.22 Å resolution