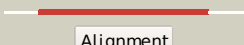

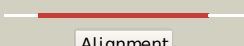

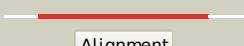

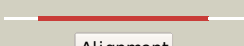


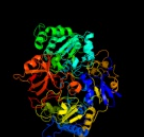








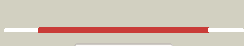















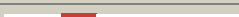
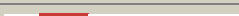

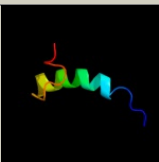



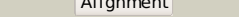
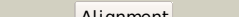
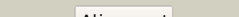






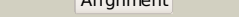
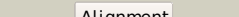






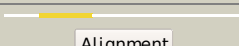

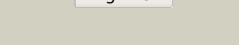
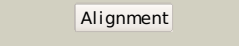

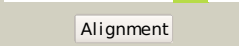
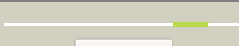

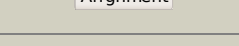
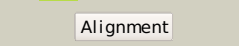

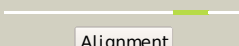

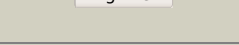

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tmoA_	 Alignment		100.0	53	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
2	c1h5nC_	 Alignment		100.0	50	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
3	c1eu1A_	 Alignment		100.0	49	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.
4	c1vlfQ_	 Alignment		100.0	27	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
5	c1y5iA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
6	c2e7zA_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
7	c2ivfA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
8	c1h0hA_	 Alignment		100.0	20	PDB header: dehydrogenase Chain: A: PDB Molecule: formate dehydrogenase (large subunit); PDBTitle: tungsten containing formate dehydrogenase from2 desulfovibrio gigas
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	c1kqgA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
11	c2nyaF_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli

12	clogyA	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
13	c2v45A	Alignment		100.0	21	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
14	d1tmoa2	Alignment		100.0	49	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
15	d1dmra2	Alignment		100.0	49	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	c2iv2X	Alignment		100.0	21	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
17	d1eu1a2	Alignment		100.0	47	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	c1g8iC	Alignment		100.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
19	d1vlfm2	Alignment		100.0	27	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	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
21	d1kqfa2	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
22	d2jioa2	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
23	d1h0ha2	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
24	d2iv2x2	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
25	d1ogya2	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	d1g8ka2	Alignment	not modelled	100.0	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
27	c2fugC	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-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	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

29	d1tmoa1	Alignment	not modelled	100.0	64	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
30	d1eu1a1	Alignment	not modelled	100.0	54	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
31	d1dmra1	Alignment	not modelled	100.0	51	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
32	d1vlfm1	Alignment	not modelled	100.0	32	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
33	d1kqfa1	Alignment	not modelled	100.0	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
34	d1h0ha1	Alignment	not modelled	100.0	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
35	d1y5ia1	Alignment	not modelled	100.0	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
36	d2jioa1	Alignment	not modelled	100.0	27	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
37	d1ogya1	Alignment	not modelled	99.9	23	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d1g8ka1	Alignment	not modelled	99.9	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
39	c2ki8A_	Alignment	not modelled	99.9	23	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
40	d2iv2x1	Alignment	not modelled	99.9	26	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
41	d2fug31	Alignment	not modelled	96.7	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
42	c2pjhb_	Alignment	not modelled	96.6	13	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
43	d1ozha1	Alignment	not modelled	96.4	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
44	d2ez9a1	Alignment	not modelled	96.4	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
45	d1e32a1	Alignment	not modelled	95.8	13	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
46	d1tk9a_	Alignment	not modelled	95.8	11	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
47	d1zpdal	Alignment	not modelled	95.7	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
48	c1cz5A_	Alignment	not modelled	95.6	20	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)
49	d2djia1	Alignment	not modelled	95.5	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
50	d1ovma1	Alignment	not modelled	95.3	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
51	d2ji7a1	Alignment	not modelled	95.2	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
52	d1x92a_	Alignment	not modelled	95.1	10	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
53	d2ihta1	Alignment	not modelled	95.1	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
54	d1cz5a1	Alignment	not modelled	95.0	22	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like

55	c3knzA	 Alignment	not modelled	94.5	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
56	c3k35D	 Alignment	not modelled	94.3	14	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
57	dlq6za1	 Alignment	not modelled	94.2	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
58	c2x3yA	 Alignment	not modelled	94.1	15	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
59	c3pkiF	 Alignment	not modelled	94.1	14	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
60	d1ybha1	 Alignment	not modelled	93.9	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
61	c2pq4B	 Alignment		93.7	29	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
62	c3hu2C	 Alignment	not modelled	93.4	12	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
63	cls3sA	 Alignment	not modelled	93.3	12	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
64	c3euaD	 Alignment	not modelled	92.0	14	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
65	d2b4ya1	 Alignment	not modelled	91.6	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
66	c3cvjB	 Alignment	not modelled	91.5	10	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
67	c3cf1C	 Alignment	not modelled	91.3	13	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
68	d1t9ba1	 Alignment	not modelled	90.8	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
69	d1ma3a	 Alignment	not modelled	90.7	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
70	c2yvaB	 Alignment	not modelled	90.6	11	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
71	c3jwpA	 Alignment	not modelled	89.3	9	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
72	c3fxaA	 Alignment	not modelled	89.3	16	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
73	cljxaA	 Alignment	not modelled	88.7	18	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
74	c2fyfO	 Alignment	not modelled	88.1	17	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
75	c3g68A	 Alignment	not modelled	88.0	8	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
76	d1s5pa	 Alignment	not modelled	87.8	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
77	d1m2ka	 Alignment	not modelled	87.8	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
78	c2a3nA	 Alignment	not modelled	87.8	15	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
79	c2e76D_	Alignment	not modelled	87.3	33	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
80	d1pvda1	Alignment	not modelled	87.2	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
81	d1yc5a1	Alignment	not modelled	87.0	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
82	c3etnD_	Alignment	not modelled	86.8	14	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
83	d1x94a_	Alignment	not modelled	86.3	10	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
84	c1p84E_	Alignment	not modelled	86.2	7	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
85	c2x7jA_	Alignment	not modelled	85.8	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
86	c1wlfa_	Alignment	not modelled	85.6	26	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
87	c3fkjA_	Alignment	not modelled	84.0	10	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
88	c2zj3A_	Alignment	not modelled	83.6	12	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
89	d1ylea1	Alignment	not modelled	82.8	33	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
90	d1moqa_	Alignment	not modelled	81.7	20	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
91	d1nria_	Alignment	not modelled	81.5	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
92	c1nriA_	Alignment	not modelled	81.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
93	c2vbiF_	Alignment	not modelled	81.1	15	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
94	c3glsC_	Alignment	not modelled	80.9	10	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
95	c3hbaA_	Alignment	not modelled	79.2	8	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
96	c2fyuE_	Alignment	not modelled	78.7	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
97	c2ev2B_	Alignment	not modelled	76.5	14	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyl cyclase rv1264, at ph 8.5
98	d1wlfa2	Alignment	not modelled	76.4	27	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
99	c2vbgB_	Alignment	not modelled	76.3	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
100	c1zpdA_	Alignment	not modelled	75.7	10	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
101	d1cr5a1	Alignment	not modelled	75.0	15	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
102	d1qcsa1	Alignment	not modelled	74.6	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like

103	c2yujA_		Alignment	not modelled	72.7	21	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
104	dljeoa_		Alignment	not modelled	72.6	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
105	c3lq1A_		Alignment	not modelled	71.6	10	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
106	dlm3sa_		Alignment	not modelled	71.5	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
107	c2djiA_		Alignment	not modelled	71.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
108	clzc1A_		Alignment	not modelled	69.1	20	PDB header: protein turnover Chain: A: PDB Molecule: ubiquitin fusion degradation protein 1; PDBTitle: ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
109	c2l66B_		Alignment	not modelled	67.3	17	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.
110	c3m7aA_		Alignment	not modelled	67.2	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 novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution
111	clovmC_		Alignment	not modelled	67.1	12	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
112	c3tbfA_		Alignment	not modelled	66.9	14	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate aminotransferase PDBTitle: c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
113	c2panF_		Alignment	not modelled	63.9	13	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
114	dlvima_		Alignment	not modelled	63.5	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
115	clqdnA_		Alignment	not modelled	62.2	14	PDB header: fusion protein Chain: A: PDB Molecule: protein (n-ethylmaleimide sensitive fusion PDBTitle: amino terminal domain of the n-ethylmaleimide sensitive2 fusion protein (nsf)
116	cly6uA_		Alignment	not modelled	61.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
117	clozhD_		Alignment	not modelled	60.2	14	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.
118	c2dwcB_		Alignment	not modelled	58.7	14	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
119	c3pjyB_		Alignment	not modelled	57.6	18	PDB header: transcription regulator Chain: B: PDB Molecule: hypothetical signal peptide protein; PDBTitle: crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
120	dlqlaa_		Alignment	not modelled	57.2	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators