

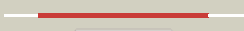





















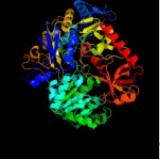



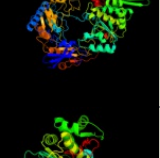
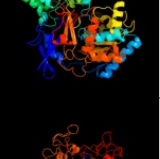
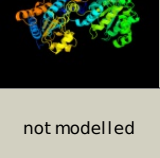

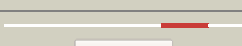
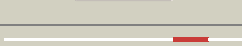
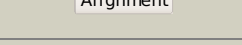
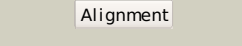

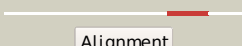

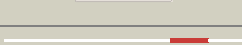
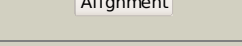
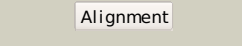

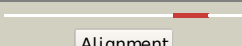
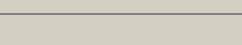
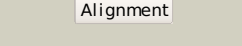
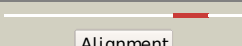

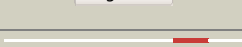
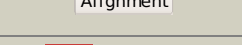
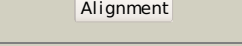


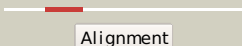
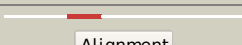

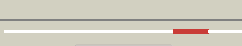


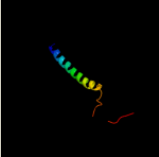






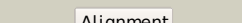




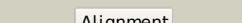

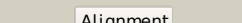




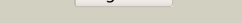
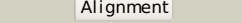
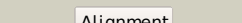

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tmoA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
2	c1y5iA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
3	c1h5nC_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
4	c1kqgA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
5	c1h0hA_	 Alignment		100.0	23	PDB header: dehydrogenase Chain: A: PDB Molecule: formate dehydrogenase (large subunit); PDBTitle: tungsten containing formate dehydrogenase from2 desulfovibrio gigas
6	c2e7zA_	 Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
7	c1eu1A_	 Alignment		100.0	32	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.
8	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
9	c2vpyE_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
10	c2ivfA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoeum aromaticum
11	c2nyaF_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli

12	c2v45A	Alignment		100.0	22	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
13	c1ogyA	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
14	c2iv2X	Alignment		100.0	24	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
15	c1g8jC	Alignment		100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
16	d1tmoa2	Alignment		100.0	26	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
17	d1y5ia2	Alignment		100.0	30	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	d1dmra2	Alignment		100.0	28	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	21	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	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
21	d1eu1a2	Alignment	not modelled	100.0	29	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	d1vlfm2	Alignment	not modelled	100.0	26	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	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
24	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
25	d1logya2	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
26	d1g8ka2	Alignment	not modelled	100.0	18	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	18	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	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

29	dltmoa1		Alignment	not modelled	100.0	36	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
30	dlkqfa1		Alignment	not modelled	100.0	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
31	didmra1		Alignment	not modelled	100.0	41	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
32	dleula1		Alignment	not modelled	100.0	42	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
33	dlvlfm1		Alignment	not modelled	100.0	38	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
34	dlh0ha1		Alignment	not modelled	100.0	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
35	d2jioa1		Alignment	not modelled	100.0	26	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
36	dlg8ka1		Alignment	not modelled	99.9	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
37	dlogya1		Alignment	not modelled	99.9	25	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
38	dly5ia1		Alignment	not modelled	99.9	25	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
39	d2iv2x1		Alignment	not modelled	99.9	25	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
40	c2ki8A_		Alignment	not modelled	99.9	17	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	d2fug31		Alignment	not modelled	96.9	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
42	c2pjhb_		Alignment	not modelled	96.4	9	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
43	dle32a1		Alignment	not modelled	95.4	9	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
44	dlq6za1		Alignment	not modelled	95.1	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
45	c1cz5A_		Alignment	not modelled	94.8	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)
46	d2ihta1		Alignment	not modelled	94.5	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
47	dlözha1		Alignment	not modelled	94.2	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
48	c3k35D_		Alignment	not modelled	94.1	17	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
49	c3pkif_		Alignment	not modelled	94.0	17	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
50	dlcz5a1		Alignment	not modelled	94.0	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
51	dlybha1		Alignment	not modelled	94.0	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
52	cls3sa_		Alignment	not modelled	93.4	8	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
53	dlx94a_		Alignment	not modelled	93.4	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
							PDB header: chaperone/oxidoreductase

54	c2pq4B_	Alignment		93.3	32	Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide
55	c3jwpA_	Alignment	not modelled	93.3	16	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
56	d2ez9a1	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
57	d1tk9a_	Alignment	not modelled	93.0	9	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
58	c2x3yA_	Alignment	not modelled	92.9	6	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
59	c3hu2C_	Alignment	not modelled	92.9	9	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
60	c2e76D_	Alignment		92.4	14	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
61	d1x92a_	Alignment	not modelled	92.0	12	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
62	d2djia1	Alignment	not modelled	91.6	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
63	d2b4ya1	Alignment	not modelled	91.4	7	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
64	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
65	c3knzA_	Alignment	not modelled	90.7	14	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
66	c3cf1C_	Alignment	not modelled	90.5	7	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
67	c3fxaA_	Alignment	not modelled	90.2	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
68	c1p84E_	Alignment	not modelled	89.8	8	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
69	c3etnD_	Alignment	not modelled	89.0	15	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
70	d1m2ka_	Alignment	not modelled	89.0	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
71	c2yvaB_	Alignment	not modelled	88.7	10	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
72	d1yc5a1	Alignment	not modelled	88.7	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
73	c3euaD_	Alignment	not modelled	88.5	12	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
74	c2dwcB_	Alignment	not modelled	86.5	13	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
75	c2fynO_	Alignment	not modelled	86.3	28	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
76	c1wlfa_	Alignment	not modelled	86.0	33	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

77	dlzpdal	Alignment	not modelled	83.1	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
78	dlwifa2	Alignment	not modelled	81.9	32	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
79	dls5pa	Alignment	not modelled	81.1	7	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
80	dlylea1	Alignment	not modelled	80.6	22	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
81	c3g68A	Alignment	not modelled	80.2	12	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
82	c2fyuE	Alignment		80.0	10	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
83	c1kjaA	Alignment	not modelled	79.8	14	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycnamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
84	d1kja2	Alignment	not modelled	78.2	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
85	d1ovma1	Alignment	not modelled	78.2	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
86	d1qcsa1	Alignment	not modelled	74.8	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
87	c1nriA	Alignment	not modelled	74.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
88	d1nria	Alignment	not modelled	74.2	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
89	d2ji7a1	Alignment	not modelled	73.5	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
90	d1cr5a1	Alignment	not modelled	69.4	15	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
91	c3cvjB	Alignment	not modelled	67.3	12	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
92	d1pvdal	Alignment	not modelled	66.8	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
93	c2zj3A	Alignment	not modelled	65.9	16	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
94	c3q2oB	Alignment	not modelled	65.6	16	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
95	c1jxaA	Alignment	not modelled	65.1	19	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
96	c3m7aA	Alignment	not modelled	65.0	43	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 dsm312444 at 1.22 a resolution
97	d1moqa	Alignment	not modelled	63.7	20	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
98	c3orqA	Alignment	not modelled	62.1	21	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
99	c3glsC	Alignment	not modelled	59.2	16	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
100	d1mvfd	Alignment	not modelled	57.5	26	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/Peml addiction antidote
101	c2l66B	Alignment	not modelled	57.3	26	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.

102	c2a3nA_	 Alignment	not modelled	56.3	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
103	c1qdnA_	 Alignment	not modelled	54.9	15	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)
104	d2vbua1	 Alignment	not modelled	54.5	21	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
105	c3pjyB_	 Alignment	not modelled	54.5	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
106	dlvima_	 Alignment	not modelled	54.3	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
107	c1y6uA_	 Alignment	not modelled	52.6	35	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
108	c2a8vA_	 Alignment	not modelled	52.2	13	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
109	d1m3sa_	 Alignment	not modelled	51.3	11	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
110	d1t9ba1	 Alignment	not modelled	50.7	29	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
111	c3shoA_	 Alignment	not modelled	49.4	9	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)
112	c1cr5B_	 Alignment	not modelled	48.5	15	PDB header: endocytosis/exocytosis Chain: B: PDB Molecule: sec18p (residues 22 - 210); PDBTitle: n-terminal domain of sec18p
113	c2ev2B_	 Alignment	not modelled	47.3	16	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
114	d1jeoa_	 Alignment	not modelled	46.7	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
115	d2b78a1	 Alignment	not modelled	46.6	12	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
116	c3trjC_	 Alignment	not modelled	46.3	10	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
117	c3iwfA_	 Alignment	not modelled	45.7	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
118	c2amlB_	 Alignment	not modelled	45.6	12	PDB header: transferase Chain: B: PDB Molecule: sis domain protein; PDBTitle: crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
119	d1ueba3	 Alignment	not modelled	44.9	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
120	d2grea1	 Alignment	not modelled	43.5	23	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Aminopeptidase/glucanase lid domain Family: Aminopeptidase/glucanase lid domain