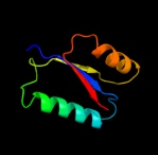
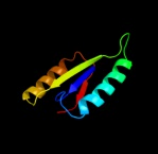


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mk3L_	 Alignment		100.0	91	PDB header: transferase Chain: L: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase; PDBTitle: crystal structure of lumazine synthase from salmonella typhimurium lt2
2	d1rvv1_	 Alignment		100.0	53	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
3	d1nqua_	 Alignment		100.0	50	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
4	d1c2ya_	 Alignment		100.0	50	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
5	d1c41a_	 Alignment		100.0	43	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
6	d1kz1a_	 Alignment		100.0	38	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
7	d1ejba_	 Alignment		100.0	35	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
8	d1di0a_	 Alignment		100.0	32	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
9	c2f59B_	 Alignment		100.0	40	PDB header: transferase Chain: B: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
10	c2obxH_	 Alignment		100.0	32	PDB header: transferase Chain: H: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh2 from mesorhizobium loti (gene ml17281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
11	c1w19E_	 Alignment		100.0	45	PDB header: transferase Chain: E: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase; PDBTitle: lumazine synthase from mycobacterium tuberculosis bound to 2 3-(1,3,7-trihydro-9-d-ribityl-2,6,8-purinetrione-7-yl)3 propane 1-phosphate

12	c2b99A_	Alignment		97.7	25	PDB header: transferase Chain: A: PDB Molecule: riboflavin synthase; PDBTitle: crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
13	c3lftA_	Alignment		94.9	16	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
14	c2qh8A_	Alignment		92.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
15	c3h5oB_	Alignment		90.9	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
16	c3kkeA_	Alignment		90.7	13	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
17	dlguda_	Alignment		90.6	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
18	dlgcaa_	Alignment		89.3	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
19	c3ksmA_	Alignment		88.1	13	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system, periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
20	c3ma0A_	Alignment		87.8	9	PDB header: sugar binding protein Chain: A: PDB Molecule: d-xylose-binding periplasmic protein; PDBTitle: closed liganded crystal structure of xylose binding protein from2 escherichia coli
21	c3bi1A_	Alignment	not modelled	87.6	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable laci-family transcriptional regulator; PDBTitle: crystal structure of a probable laci family transcriptional2 regulator from corynebacterium glutamicum
22	c3l6uA_	Alignment	not modelled	86.6	14	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system periplasmic PDBTitle: crystal structure of abc-type sugar transport system,2 periplasmic component from exigubacterium sibiricum
23	c3o74A_	Alignment	not modelled	86.1	8	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
24	c2fn9A_	Alignment	not modelled	86.0	24	PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form
25	c3hchwB_	Alignment	not modelled	85.8	13	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
26	c3o1hB_	Alignment	not modelled	84.8	17	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
27	d8abpa_	Alignment	not modelled	83.8	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
						PDB header: transcription regulator

28	c3brqA	Alignment	not modelled	82.8	13	Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
29	c3e3mA	Alignment	not modelled	82.6	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a lacI family transcriptional2 regulator from silicibacter pomeroyi
30	c3mizB	Alignment	not modelled	82.4	14	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator protein, lacI PDBTitle: crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
31	c3c3kA	Alignment	not modelled	82.2	12	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
32	c3ctpB	Alignment	not modelled	81.9	10	PDB header: transcription regulator Chain: B: PDB Molecule: periplasmic binding protein/lacI transcriptional regulator; PDBTitle: crystal structure of periplasmic binding protein/lacI transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
33	c2qu7B	Alignment	not modelled	81.6	11	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
34	d2dria	Alignment	not modelled	80.9	19	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
35	c2vk2A	Alignment	not modelled	80.7	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
36	c3d8uA	Alignment	not modelled	79.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
37	d2fvya1	Alignment	not modelled	76.6	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
38	d1byka	Alignment	not modelled	76.4	18	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
39	d1dbqa	Alignment	not modelled	75.6	8	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
40	d1y5ea1	Alignment	not modelled	74.8	19	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
41	c3gv0A	Alignment	not modelled	74.1	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
42	c2o20H	Alignment	not modelled	71.7	11	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
43	d1tjya	Alignment	not modelled	71.5	24	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
44	c2rjoA	Alignment	not modelled	71.0	14	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
45	c3egcF	Alignment	not modelled	70.6	11	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative ribose operon repressor; PDBTitle: crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
46	c3k9cA	Alignment	not modelled	70.1	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family protein; PDBTitle: crystal structure of lacI transcriptional regulator from rhodococcus2 species.
47	c3l49D	Alignment	not modelled	69.7	13	PDB header: transport protein Chain: D: PDB Molecule: abc sugar (ribose) transporter, periplasmic PDBTitle: crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
48	d2nzug1	Alignment	not modelled	68.6	18	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
49	c3clkB	Alignment	not modelled	67.8	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
50	c3jy6B	Alignment	not modelled	67.8	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI transcriptional regulator from lactobacillus2 brevis
51	c2h0aA	Alignment	not modelled	67.4	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
52	c2iksA	Alignment	not modelled	66.5	9	PDB header: transcription Chain: A: PDB Molecule: dna-binding transcriptional dual regulator; PDBTitle: crystal structure of n-terminal truncated dna-binding

						transcriptional2 dual regulator from escherichia coli k12
53	d1uuya_	Alignment	not modelled	65.8	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
54	c3e61A_	Alignment	not modelled	65.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional repressor of ribose operon; PDBTitle: crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
55	c3bblA_	Alignment	not modelled	64.9	11	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of laci family; PDBTitle: crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
56	c2fqxA_	Alignment	not modelled	64.5	18	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
57	c3rota_	Alignment	not modelled	63.2	17	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
58	d2f7wa1	Alignment	not modelled	62.5	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
59	c3cs3A_	Alignment	not modelled	61.4	18	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, laci family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
60	c2ioyB_	Alignment	not modelled	61.3	17	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
61	d1tfA_	Alignment	not modelled	59.9	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
62	d1jyea_	Alignment	not modelled	59.1	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
63	c1jyeA_	Alignment	not modelled	59.1	10	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
64	c3huuC_	Alignment	not modelled	58.7	14	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
65	c2x7xA_	Alignment	not modelled	58.1	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
66	c3qk7C_	Alignment	not modelled	56.9	18	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
67	d1jlja_	Alignment	not modelled	55.2	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
68	c3lq1A_	Alignment	not modelled	53.1	28	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
69	c3k4hA_	Alignment	not modelled	48.6	9	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
70	c2is8A_	Alignment	not modelled	48.2	18	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
71	d2csua3	Alignment	not modelled	48.1	20	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
72	c2w7tA_	Alignment	not modelled	46.4	18	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
73	c2csuB_	Alignment	not modelled	46.3	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
74	c3g1wB_	Alignment	not modelled	45.9	13	PDB header: transport protein Chain: B: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
75	d1di6a_	Alignment	not modelled	45.6	11	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
76	c2nu9E_	Alignment	not modelled	45.1	21	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
						PDB header: transferase

77	c2jlaD	Alignment	not modelled	43.2	33	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
78	d2nu7b1	Alignment	not modelled	42.8	21	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
79	c3gybB	Alignment	not modelled	42.4	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulators (laci-family) PDBTitle: crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
80	d2a5la1	Alignment	not modelled	42.3	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
81	c2qvcC	Alignment	not modelled	42.2	12	PDB header: transport protein Chain: C: PDB Molecule: sugar abc transporter, periplasmic sugar-binding PDBTitle: crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
82	c2dzaA	Alignment	not modelled	42.0	41	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
83	c3c5yD	Alignment	not modelled	41.6	24	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
84	d1mkza	Alignment	not modelled	41.5	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
85	c3dbiA	Alignment	not modelled	41.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, laci family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (laci2 family) from escherichia coli complexed with phosphate
86	c2rgyA	Alignment	not modelled	38.6	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
87	c3g85A	Alignment	not modelled	38.2	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
88	d2nqra3	Alignment	not modelled	36.6	24	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
89	d1u11a	Alignment	not modelled	36.3	16	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
90	d1o2da	Alignment	not modelled	36.1	15	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
91	d1b43a2	Alignment	not modelled	35.2	28	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
92	d1rxwa2	Alignment	not modelled	34.4	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
93	d2pjua1	Alignment	not modelled	34.0	19	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
94	c2fw9A	Alignment	not modelled	32.9	16	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
95	c3jvdA	Alignment	not modelled	32.8	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
96	d7reqa2	Alignment	not modelled	31.8	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
97	d4pgaa	Alignment	not modelled	31.7	32	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
98	c3lp6D	Alignment	not modelled	31.4	21	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
99	c3kk1A	Alignment	not modelled	31.2	20	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
100	d1vlja	Alignment	not modelled	31.1	28	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
						PDB header: transport protein

101	c3brsA_	Alignment	not modelled	30.8	15	Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
102	c3orsD_	Alignment	not modelled	30.1	15	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
103	c2y5sA_	Alignment	not modelled	29.8	33	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
104	c3s99A_	Alignment	not modelled	29.6	8	PDB header: lipid binding protein Chain: A: PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
105	c3oryA_	Alignment	not modelled	28.8	27	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
106	d2jgra1	Alignment	not modelled	28.3	25	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
107	c2ywxA_	Alignment	not modelled	27.9	29	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
108	c1b43A_	Alignment	not modelled	27.9	31	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
109	c2hmcA_	Alignment	not modelled	27.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
110	d1ofux_	Alignment	not modelled	27.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Bacterial cell division inhibitor SulA
111	c2x7jA_	Alignment	not modelled	26.0	25	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
112	d1jx6a_	Alignment	not modelled	25.3	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
113	c2r94B_	Alignment	not modelled	25.2	18	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
114	c1dl5A_	Alignment	not modelled	24.9	27	PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase
115	c2zkiH_	Alignment	not modelled	24.0	8	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
116	c1oftC_	Alignment	not modelled	23.9	17	PDB header: bacterial cell division inhibitor Chain: C: PDB Molecule: hypothetical protein pa3008; PDBTitle: crystal structure of sula from pseudomonas aeruginosa
117	c3hs3A_	Alignment	not modelled	23.5	14	PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
118	d1o7ja_	Alignment	not modelled	23.4	32	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
119	d1a77a2	Alignment	not modelled	22.6	29	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
120	c3okfA_	Alignment	not modelled	22.5	24	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae