



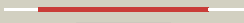




















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ab0a1	 Alignment		100.0	100	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
2	c3ot1B_	 Alignment		100.0	42	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
3	d1p5fa_	 Alignment		100.0	39	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
4	c3ewnA_	 Alignment		100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
5	c3nooB_	 Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
6	c3cneD_	 Alignment		100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
7	c3fseB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
8	d1g2ia_	 Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
9	c3mgkA_	 Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: intracellular protease/amidase related enzyme PDBTitle: crystal structure of probable protease/amidase from2 clostridium acetobutylicum atcc 824
10	c3bhnA_	 Alignment		100.0	17	PDB header: unknown function Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution
11	c3uk7B_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d

12	dloi4a1	Alignment		100.0	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
13	c3graA	Alignment		100.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
14	c2vrnA	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: protease i; PDBTitle: the structure of the stress response protein dr1199 from2 deinococcus radiodurans: a member of the dj-1 superfamily
15	c3er6D	Alignment		100.0	12	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative transcriptional regulator protein; PDBTitle: crystal structure of a putative transcriptional regulator2 protein from2 vibrio parahaemolyticus
16	c3efeC	Alignment		100.0	20	PDB header: chaperone Chain: C: PDB Molecule: thij/pfpi family protein; PDBTitle: the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
17	c3f5dA	Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from2 bacillus subtilis
18	d2fexa1	Alignment		100.0	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
19	d1u9ca	Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
20	c3kklA	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
21	dlsy7a1	Alignment	not modelled	100.0	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
22	c1sy7B	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
23	d1qvwa	Alignment	not modelled	100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
24	c3n7tA	Alignment	not modelled	100.0	20	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
25	d1vhqa	Alignment	not modelled	100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
26	d1n57a	Alignment	not modelled	100.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
27	c3l3bA	Alignment	not modelled	99.9	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
28	d1p80a1	Alignment	not modelled	99.9	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
						PDB header: oxidoreductase

29	c1p81A	Alignment	not modelled	99.5	13	Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
30	d1t3ta2	Alignment	not modelled	98.7	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
31	c3ej6D	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: neurospora crassa catalase-3 crystal structure
32	c3d54D	Alignment	not modelled	98.3	18	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: stucture of purlqs from thermotoga maritima
33	d1q7ra	Alignment	not modelled	97.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
34	d2nv0a1	Alignment	not modelled	97.9	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	c2iufA	Alignment	not modelled	97.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the structures of penicillium vitale catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole
36	c2issF	Alignment	not modelled	97.8	19	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
37	d1ka9h	Alignment	not modelled	97.7	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
38	d1o1ya	Alignment	not modelled	97.5	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	c3l7nA	Alignment	not modelled	97.4	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
40	c2ywjA	Alignment	not modelled	97.3	16	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
41	d1jvna2	Alignment	not modelled	97.2	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
42	c1t3ta	Alignment	not modelled	97.1	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
43	d1gpma2	Alignment	not modelled	96.8	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
44	c2ywdA	Alignment	not modelled	96.7	17	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
45	d1k9vf	Alignment	not modelled	96.6	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
46	c3l83A	Alignment	not modelled	96.5	14	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
47	d2abwa1	Alignment	not modelled	96.4	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
48	d1wl8a1	Alignment	not modelled	96.4	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
49	c3r74B	Alignment	not modelled	96.4	20	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
50	c1keeH	Alignment	not modelled	96.1	18	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
51	d2a9va1	Alignment	not modelled	95.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
52	d1a9xb2	Alignment	not modelled	95.6	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
53	c3fijD	Alignment	not modelled	95.5	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
54	d1qdlb	Alignment	not modelled	95.3	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
55	d1ilqb	Alignment	not modelled	95.2	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

56	c1jvnB_	<div><div></div></div> Alignment	not modelled	94.6	14	PDB header: transferase Chain: B; PDB Molecule: bifunctional histidine biosynthesis protein hshf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
57	dli7qb_	<div><div></div></div> Alignment	not modelled	93.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
58	d1d4aa_	<div><div></div></div> Alignment	not modelled	93.8	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
59	c3l4eA_	<div><div></div></div> Alignment	not modelled	93.2	16	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
60	c2vpiA_	<div><div></div></div> Alignment	not modelled	93.1	14	PDB header: ligase Chain: A; PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
61	c2ad5B_	<div><div></div></div> Alignment	not modelled	91.6	22	PDB header: ligase Chain: B; PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
62	d1fyea_	<div><div></div></div> Alignment	not modelled	90.7	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
63	d1s1ma1	<div><div></div></div> Alignment	not modelled	90.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
64	c3nvaB_	<div><div></div></div> Alignment	not modelled	90.7	13	PDB header: ligase Chain: B; PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
65	c2w7tA_	<div><div></div></div> Alignment	not modelled	90.4	15	PDB header: ligase Chain: A; PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
66	d2ghra1	<div><div></div></div> Alignment	not modelled	89.2	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
67	d1vcoa1	<div><div></div></div> Alignment	not modelled	89.2	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
68	c1vcnA_	<div><div></div></div> Alignment	not modelled	88.3	20	PDB header: ligase Chain: A; PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
69	c3klbA_	<div><div></div></div> Alignment	not modelled	86.5	16	PDB header: flavoprotein Chain: A; PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
70	c3en0A_	<div><div></div></div> Alignment	not modelled	85.4	17	PDB header: hydrolase Chain: A; PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
71	c2ywcC_	<div><div></div></div> Alignment	not modelled	85.0	25	PDB header: ligase Chain: C; PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
72	c3uowB_	<div><div></div></div> Alignment	not modelled	84.5	21	PDB header: ligase Chain: B; PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
73	c2ax3A_	<div><div></div></div> Alignment	not modelled	84.5	12	PDB header: transferase Chain: A; PDB Molecule: hypothetical protein tm0922; PDBTitle: crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
74	c3ragA_	<div><div></div></div> Alignment	not modelled	81.7	15	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
75	d2a5la1	<div><div></div></div> Alignment	not modelled	80.0	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
76	d1dxqa_	<div><div></div></div> Alignment	not modelled	79.6	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
77	c2v4uA_	<div><div></div></div> Alignment	not modelled	79.3	15	PDB header: ligase Chain: A; PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
78	d1vmea1	<div><div></div></div> Alignment	not modelled	79.1	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
79	c3okfA_	<div><div></div></div> Alignment	not modelled	78.2	14	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
80	d1ycga1	<div><div></div></div> Alignment	not modelled	76.6	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
		<div><div></div></div>				Fold: vWA-like

81	d1jeyb2	Alignment	not modelled	76.2	12	Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
82	d1qlda	Alignment	not modelled	76.0	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
83	c3b6iB	Alignment	not modelled	75.6	19	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
84	c1gpmD	Alignment	not modelled	75.5	15	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
85	c2h2wA	Alignment	not modelled	75.2	19	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
86	c2dg2D	Alignment	not modelled	73.2	13	PDB header: protein binding Chain: D: PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding2 protein
87	d2ax3a2	Alignment	not modelled	69.2	12	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
88	c3ezxA	Alignment	not modelled	67.6	15	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
89	c3tqiB	Alignment	not modelled	67.0	20	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
90	c1y80A	Alignment	not modelled	63.6	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
91	d1e5da1	Alignment	not modelled	61.8	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
92	d2qwxal	Alignment	not modelled	59.8	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
93	c3edoA	Alignment	not modelled	59.6	19	PDB header: flavoprotein Chain: A: PDB Molecule: putative trp repressor binding protein; PDBTitle: crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
94	c2zkiH	Alignment	not modelled	56.2	18	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)
95	c1l9xA	Alignment	not modelled	54.9	18	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
96	d1l9xa	Alignment	not modelled	54.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
97	d1ccwa	Alignment	not modelled	54.3	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
98	d3bula2	Alignment	not modelled	53.4	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
99	c2vx0B	Alignment	not modelled	50.3	13	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
100	d1iowa1	Alignment	not modelled	50.1	29	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
101	c3d3kD	Alignment	not modelled	47.2	10	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
102	c3fniA	Alignment	not modelled	46.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
103	d1kwga3	Alignment	not modelled	45.6	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: A4 beta-galactosidase middle domain
104	d1g5qa	Alignment	not modelled	45.3	17	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
105	d1fmfa	Alignment	not modelled	44.9	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
106	c2dlnA	Alignment	not modelled	39.4	23	PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-

					alanine2 ligase at 2.3 angstroms resolution
107	c3d3jA_	Alignment	not modelled	39.2	10 PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
108	c1bmtB_	Alignment	not modelled	33.5	14 PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
109	c2zktB_	Alignment	not modelled	31.9	15 PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
110	d1u0ta_	Alignment	not modelled	31.5	23 Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
111	c2i2xD_	Alignment	not modelled	30.9	16 PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
112	c2r47C_	Alignment	not modelled	27.7	26 PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein mth_862; PDBTitle: crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
113	c3k1tA_	Alignment	not modelled	26.8	14 PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase gsha; PDBTitle: crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
114	d1mkza_	Alignment	not modelled	25.8	17 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
115	c3g05B_	Alignment	not modelled	25.4	25 PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg
116	d2h80a1	Alignment	not modelled	24.3	33 Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
117	d7reqa2	Alignment	not modelled	23.8	9 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
118	c2iyaB_	Alignment	not modelled	21.3	19 PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering