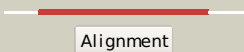

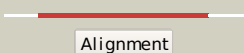

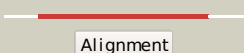

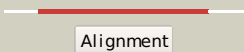

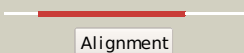
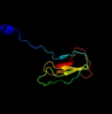
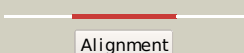

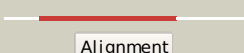

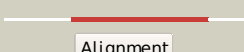

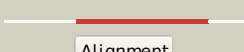
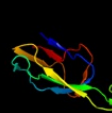
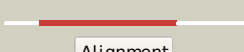

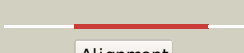
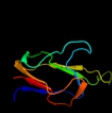


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1glaf_	 Alignment		100.0	98	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
2	d2f3ga_	 Alignment		100.0	100	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
3	d1gpaa_	 Alignment		100.0	43	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
4	d2gpaa_	 Alignment		100.0	36	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
5	c3n6rK_	 Alignment		97.4	26	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
6	c2b44A_	 Alignment		97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
7	d1qwya_	 Alignment		97.2	17	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
8	d1dcza_	 Alignment		97.0	28	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
9	c2ejgD_	 Alignment		96.8	24	PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
10	c2gu1A_	 Alignment		96.8	20	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
11	d1bdoa_	 Alignment		96.2	22	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains

12	d1o78a_	Alignment		96.2	32	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
13	d1vf7a_	Alignment		96.1	32	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
14	c2hsiB_	Alignment		95.9	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
15	c3nyyA_	Alignment		95.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
16	c2aukA_	Alignment		95.7	23	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
17	c2dn8A_	Alignment		95.7	22	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
18	c2ejmA_	Alignment		95.3	19	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotinyl domain form2 human acetyl coenzyme a carboxylase
19	c3fppB_	Alignment		95.2	20	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
20	c2b8gA_	Alignment		95.0	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
21	d1ci3m2	Alignment	not modelled	94.9	22	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
22	c1q90A_	Alignment	not modelled	94.6	23	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
23	c1e2vB_	Alignment	not modelled	94.4	23	PDB header: electron transport proteins Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
24	d1iyua_	Alignment	not modelled	94.2	16	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
25	d1uoua3	Alignment	not modelled	93.7	23	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
26	c2jxmB_	Alignment	not modelled	93.7	25	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
27	d1ghja_	Alignment	not modelled	93.1	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
28	d1qjoa_	Alignment	not modelled	93.0	15	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
						Fold: Barrel-sandwich hybrid

29	d1k8ma_	Alignment	not modelled	92.7	16	Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
30	c1t5eB_	Alignment	not modelled	92.7	28	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
31	c3h9iB_	Alignment	not modelled	92.4	23	PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli
32	c1tu2B_	Alignment	not modelled	92.3	30	PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
33	c3csqC_	Alignment	not modelled	92.1	23	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
34	c2q8iB_	Alignment	not modelled	91.7	18	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
35	c2l5tA_	Alignment	not modelled	91.1	16	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
36	d1gjxa_	Alignment	not modelled	91.1	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
37	d1brwa3	Alignment	not modelled	90.9	21	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
38	d1y8ob1	Alignment	not modelled	90.8	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
39	c2f1mA_	Alignment	not modelled	90.7	19	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
40	d1laba_	Alignment	not modelled	90.6	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
41	c1ctmA_	Alignment	not modelled	90.0	19	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
42	c3lnnB_	Alignment	not modelled	89.9	25	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
43	c2kccA_	Alignment	not modelled	89.3	15	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
44	d1e2wa2	Alignment	not modelled	88.7	29	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
45	d2tpta3	Alignment	not modelled	88.5	21	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
46	c2dncA_	Alignment	not modelled	86.9	23	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
47	c2k33A_	Alignment	not modelled	85.6	21	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
48	c2e75C_	Alignment	not modelled	84.3	33	PDB header: photosynthesis Chain: C: PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
49	d2pnrc1	Alignment	not modelled	83.5	20	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
50	c1brwB_	Alignment	not modelled	83.4	21	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
51	c2aujD_	Alignment	not modelled	83.2	20	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
52	c2dsjA_	Alignment	not modelled	83.1	25	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
53	c3h5qA_	Alignment	not modelled	82.8	17	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
						PDB header: transferase

54	c2j0fC_	Alignment	not modelled	82.0	25	Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
55	c1otpA_	Alignment	not modelled	81.9	21	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
56	c2qf7A_	Alignment	not modelled	78.0	18	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
57	d1pmra_	Alignment	not modelled	77.1	11	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
58	c3fmcC_	Alignment	not modelled	76.2	22	PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
59	d1kl9a2	Alignment	not modelled	75.1	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
60	c2dneA_	Alignment	not modelled	75.0	25	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
61	c3it5B_	Alignment	not modelled	71.0	20	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
62	c3a0jB_	Alignment	not modelled	70.4	24	PDB header: transcription Chain: B: PDB Molecule: cold shock protein; PDBTitle: crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
63	d2es2a1	Alignment	not modelled	69.2	36	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
64	d1q46a2	Alignment	not modelled	63.0	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
65	c3a8jF_	Alignment	not modelled	62.4	27	PDB header: transferase/transport protein Chain: F: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-hred complex
66	c2jkuA_	Alignment	not modelled	61.3	15	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
67	d1qpoa2	Alignment	not modelled	59.1	25	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
68	d1o4ua2	Alignment	not modelled	58.5	20	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
69	d1g6pa_	Alignment	not modelled	56.4	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
70	d2nn6h1	Alignment	not modelled	55.0	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
71	d1c9oa_	Alignment	not modelled	54.2	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
72	c2qj8B_	Alignment	not modelled	53.5	25	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
73	d1qapa2	Alignment	not modelled	53.0	20	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
74	d1at0a_	Alignment	not modelled	50.9	18	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Hedgehog C-terminal (Hog) autoprocessing domain
75	d1smxa_	Alignment	not modelled	50.0	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
76	c3mxuA_	Alignment	not modelled	46.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
77	d1onla_	Alignment	not modelled	45.8	37	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
78	c3gnnA_	Alignment	not modelled	44.9	30	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderia pseudomallei
						Fold: Barrel-sandwich hybrid

79	d1hpca_	Alignment	not modelled	44.7	26	Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
80	c1q46A_	Alignment	not modelled	43.8	10	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
81	c2hc8A_	Alignment	not modelled	43.5	25	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
82	c3na6A_	Alignment	not modelled	43.4	15	PDB header: hydrolase Chain: A: PDB Molecule: succinyl glutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
83	c2edgA_	Alignment	not modelled	41.7	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
84	c2khiA_	Alignment	not modelled	41.6	22	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
85	c3iftA_	Alignment	not modelled	41.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
86	c3tqvA_	Alignment	not modelled	40.6	15	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
87	d2je6i2	Alignment	not modelled	40.1	15	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
88	c3cdxB_	Alignment	not modelled	39.7	25	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
89	c1qapA_	Alignment	not modelled	39.6	20	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
90	c1yz6A_	Alignment	not modelled	39.3	22	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 alpha PDBTitle: crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
91	c3pajA_	Alignment	not modelled	38.3	10	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
92	d2ba0a1	Alignment	not modelled	37.4	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
93	c2xhaB_	Alignment	not modelled	37.2	33	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
94	c1x1oC_	Alignment	not modelled	35.9	35	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
95	c2eqsA_	Alignment	not modelled	35.7	25	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
96	c3l0gD_	Alignment	not modelled	34.6	10	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
97	c2ka7A_	Alignment	not modelled	34.3	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: nmr solution structure of tm0212 at 40 c
98	c1o4uA_	Alignment	not modelled	33.7	20	PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
99	c2b7pA_	Alignment	not modelled	33.6	20	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
100	d1h95a_	Alignment	not modelled	33.1	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
						PDB header: nucleic acid binding protein Chain: A: PDB Molecule: cold shock domain family protein;

101	c2kcmA	Alignment	not modelled	32.1	23	PDBTitle: solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
102	c1qpoA	Alignment	not modelled	31.7	25	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
103	d1hcza2	Alignment	not modelled	30.7	17	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
104	c2k5nA	Alignment	not modelled	30.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cold-shock protein; PDBTitle: solution nmr structure of the n-terminal domain of protein2 eca1580 from erwinia carotovora, northeast structural3 genomics consortium target ewr156a
105	d2dda1	Alignment	not modelled	30.4	33	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: PH0223-like
106	c2jbmA	Alignment	not modelled	29.8	20	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
107	d2z0sa1	Alignment	not modelled	29.4	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
108	d1mjca	Alignment	not modelled	28.9	30	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
109	c3ic8D	Alignment	not modelled	26.4	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized gst-like proteinprotein; PDBTitle: the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
110	c3camB	Alignment	not modelled	26.1	38	PDB header: gene regulation Chain: B: PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from neisseria2 meningitidis
111	c2khjA	Alignment	not modelled	25.7	18	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
112	c2xhcA	Alignment	not modelled	25.5	33	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
113	c2kxoA	Alignment	not modelled	23.8	15	PDB header: cell cycle Chain: A: PDB Molecule: cell division topological specificity factor; PDBTitle: solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
114	c2bh8B	Alignment	not modelled	23.1	32	PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11
115	c1q8kA	Alignment	not modelled	22.7	15	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 PDBTitle: solution structure of alpha subunit of human eif2
116	d1tu2b2	Alignment	not modelled	21.1	44	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
117	d2je6i1	Alignment	not modelled	20.5	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like