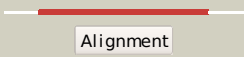

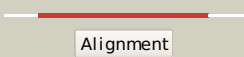

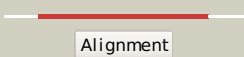
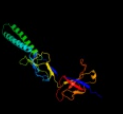
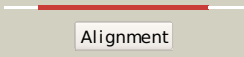

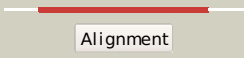

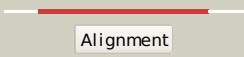
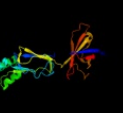
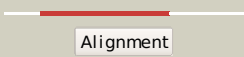

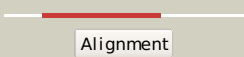
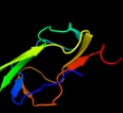
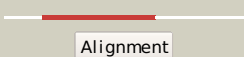
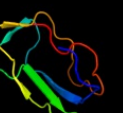
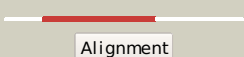

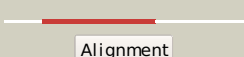

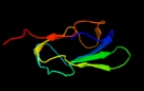

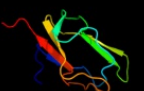
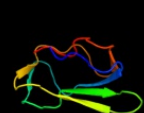







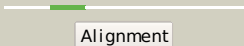

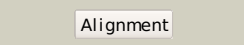
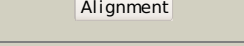
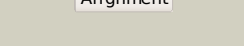
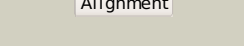
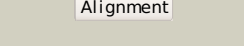
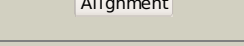
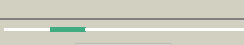
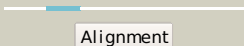
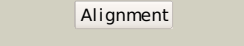
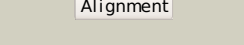
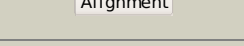

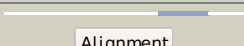
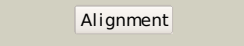
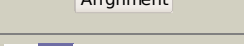






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f1mA_	 Alignment		100.0	25	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
2	c3fppB_	 Alignment		100.0	23	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
3	c3InnB_	 Alignment		100.0	22	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
4	c1t5eB_	 Alignment		99.9	22	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
5	d1vf7a_	 Alignment		99.9	20	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
6	c3h9lB_	 Alignment		99.9	15	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
7	c2k33A_	 Alignment		99.6	29	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
8	c2b8gA_	 Alignment		98.6	24	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)
9	d1o78a_	 Alignment		98.4	30	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
10	c2ejgD_	 Alignment		98.4	32	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
11	d1dcza_	 Alignment		98.4	31	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains

12	c2ejmA	Alignment		98.1	27	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
13	c2dn8A	Alignment		98.0	17	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
14	c2kccA	Alignment		98.0	16	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
15	c3n6rK	Alignment		97.9	31	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
16	d1qjoa	Alignment		97.9	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
17	d1k8ma	Alignment		97.8	27	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
18	d1y8ob1	Alignment		97.7	45	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
19	d1ghja	Alignment		97.7	22	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
20	d1laba	Alignment		97.7	55	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
21	c2q8iB	Alignment	not modelled	97.7	45	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
22	d1gjxa	Alignment	not modelled	97.4	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
23	c2dncA	Alignment	not modelled	97.4	29	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
24	c2l5tA	Alignment	not modelled	97.4	38	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
25	d1pmra	Alignment	not modelled	97.3	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
26	d1iyua	Alignment	not modelled	97.3	11	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
27	d1bdoa	Alignment	not modelled	97.2	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
28	c2dneA	Alignment	not modelled	96.9	22	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

29	d1glaf_	Alignment	not modelled	96.5	29	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
30	d1gprra_	Alignment	not modelled	96.4	26	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
31	d2pnrc1	Alignment	not modelled	96.4	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
32	d2gprra_	Alignment	not modelled	96.4	42	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
33	d1uoua3	Alignment	not modelled	96.4	25	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
34	d2f3ga_	Alignment	not modelled	96.3	35	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
35	c2qf7A_	Alignment	not modelled	96.1	28	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etl
36	d1brwa3	Alignment	not modelled	95.6	30	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
37	d2tpa3	Alignment	not modelled	95.6	18	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
38	c2dsjA_	Alignment	not modelled	95.5	31	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
39	c2jkuA_	Alignment	not modelled	94.8	21	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
40	c3h5qA_	Alignment	not modelled	94.8	32	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
41	c1otpa_	Alignment	not modelled	94.5	18	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
42	c2j0fC_	Alignment	not modelled	94.3	30	PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
43	c1brwB_	Alignment	not modelled	94.1	30	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
44	c2gu1A_	Alignment	not modelled	91.0	23	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
45	c2hsiB_	Alignment	not modelled	91.0	22	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
46	d1qwya_	Alignment	not modelled	89.1	22	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
47	c2aukA_	Alignment	not modelled	88.8	26	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
48	c3fmcC_	Alignment	not modelled	88.1	14	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
49	c2qj8B_	Alignment	not modelled	87.9	18	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
50	c3na6A_	Alignment	not modelled	87.5	21	PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
51	d1qpoa2	Alignment	not modelled	84.9	29	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
52	c2b44A_	Alignment	not modelled	83.6	22	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
53	d1e4u3	Alignment	not modelled	83.1	14	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-

53	d1o4uB2	Alignment	not modelled	83.1	14	like Family: NadC N-terminal domain-like
54	c3cdxB	Alignment	not modelled	82.9	12	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
55	c2xhaB	Alignment	not modelled	82.7	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)
56	c3nyyA	Alignment	not modelled	82.6	21	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
57	c3d4rE	Alignment	not modelled	82.2	21	PDB header: unknown function Chain: E: PDB Molecule: domain of unknown function from the pfam-b_34464 family; PDBTitle: crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
58	d1ci3m2	Alignment	not modelled	81.8	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
59	d1e2wa2	Alignment	not modelled	81.4	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
60	d1qapa2	Alignment	not modelled	78.1	10	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
61	c3it5B	Alignment	not modelled	77.1	19	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
62	c2xhcA	Alignment	not modelled	76.8	33	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
63	c2aujD	Alignment	not modelled	74.6	15	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
64	c3gnnA	Alignment	not modelled	68.6	8	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
65	c1o4uA	Alignment	not modelled	66.6	14	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
66	c1e2vB	Alignment	not modelled	64.3	38	PDB header: electron transport proteins Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
67	c1ctmA	Alignment	not modelled	64.0	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
68	c2jxmB	Alignment	not modelled	62.8	44	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
69	d1tu2b2	Alignment	not modelled	61.6	50	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
70	c1tu2B	Alignment	not modelled	61.2	50	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
71	c1q90A	Alignment	not modelled	59.8	38	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
72	c2jbmA	Alignment	not modelled	59.2	4	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
73	c3csqC	Alignment	not modelled	58.8	27	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
74	c1qapA	Alignment	not modelled	58.7	10	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
75	c3paiA	Alignment	not modelled	57.4	17	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

76	c2b7pA	 Alignment	not modelled	57.1	29	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
77	c3l0gD	 Alignment	not modelled	57.0	15	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
78	c2e75C	 Alignment	not modelled	56.6	44	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
79	c3tqvA	 Alignment	not modelled	56.3	16	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
80	c2edgA	 Alignment	not modelled	54.8	8	PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
81	d1onla	 Alignment	not modelled	54.8	16	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
82	c3iftA	 Alignment	not modelled	54.0	20	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.
83	c1qpoA	 Alignment	not modelled	53.7	24	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
84	c1x1oC	 Alignment	not modelled	51.0	9	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
85	c3mxuA	 Alignment	not modelled	47.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
86	d1hpca	 Alignment	not modelled	46.4	15	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
87	d1vf5c2	 Alignment	not modelled	43.7	44	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
88	c3a8iF	 Alignment	not modelled	38.1	24	PDB header: transferase/transport protein Chain: F: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
89	d1hcza2	 Alignment	not modelled	33.5	19	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
90	c3tbiB	 Alignment	not modelled	27.6	29	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
91	d1uwfa1	 Alignment	not modelled	26.9	27	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
92	d2je6i2	 Alignment	not modelled	25.2	28	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
93	c1zeqX	 Alignment	not modelled	24.8	12	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
94	d1h9ma2	 Alignment	not modelled	21.9	17	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
95	d1krha1	 Alignment	not modelled	19.0	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
96	c2ka7A	 Alignment	not modelled	18.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: nmr solution structure of tm0212 at 40 c
97	d1m56d	 Alignment	not modelled	17.8	24	Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV
98	d2bmwa1	 Alignment	not modelled	17.6	26	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
99	d1h9ma1	Alignment	not modelled	16.8	17	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain