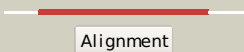

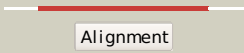







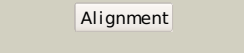

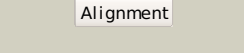

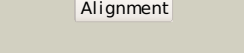



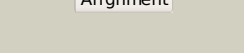

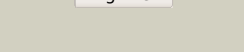



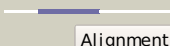
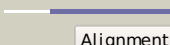
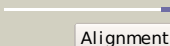
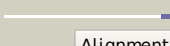

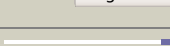
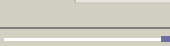


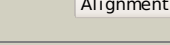






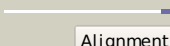
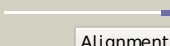
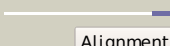


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nbaa_	 Alignment		100.0	25	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
2	c2fq1A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: isochorismatase; PDBTitle: crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
3	c3kl2K_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase from streptomyces2 avermitilis
4	c3irvA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: cysteine hydrolase; PDBTitle: crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
5	d1nf9a_	 Alignment		100.0	24	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
6	d1j2ra_	 Alignment		100.0	28	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
7	c3oqpA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bx_e_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
8	c3oqpB_	 Alignment		100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bx_e_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
9	c3hu5B_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
10	c3mcwA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
11	c3ot4F_	 Alignment		100.0	21	PDB header: hydrolase Chain: F: PDB Molecule: putative isochorismatase; PDBTitle: structure and catalytic mechanism of bordetella bronchiseptica nif

12	c3hb7G_	Alignment		100.0	26	PDB header: hydrolase Chain: G: PDB Molecule: isochorismatase hydrolase; PDBTitle: the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
13	c2wtaA_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: acinetobacter baumannii nicotinamidase pyrazinamidase
14	c3eefA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: n-carbamoylsarcosine amidase related protein; PDBTitle: crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
15	c3r2jC_	Alignment		100.0	26	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta-hydrolase-like protein; PDBTitle: crystal structure of pnc1 from l. infantum in complex with nicotinate
16	d1m5a_	Alignment		100.0	26	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
17	c3lqvA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: putative isochorismatase hydrolase; PDBTitle: crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica
18	c3o93A_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
19	c2a67C_	Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein
20	c3gbcA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: pyrazinamidase/nicotinamidase pncA; PDBTitle: determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
21	c2h0rD_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: nicotinamidase; PDBTitle: structure of the yeast nicotinamidase pnc1p
22	d1yaca_	Alignment	not modelled	100.0	17	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
23	c1yzvA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: hypothetical protein from trypanosoma cruzi
24	c2b34C_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: mar1 ribonuclease; PDBTitle: structure of mar1 ribonuclease from caenorhabditis elegans
25	d1x9ga_	Alignment	not modelled	100.0	16	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
26	d1cmwa2	Alignment	not modelled	89.7	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
27	c3g8rA_	Alignment	not modelled	74.8	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
28	c1xuzA_	Alignment	not modelled	71.9	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siaC; PDBTitle: crystal structure analysis of sialic acid synthase

						(neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
29	c2ihnA	Alignment	not modelled	64.3	5	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
30	d1tfa2	Alignment	not modelled	64.1	2	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
31	d2zdra2	Alignment	not modelled	62.2	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
32	d1vla2	Alignment	not modelled	53.7	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
33	c1ddzA	Alignment	not modelled	47.7	14	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
34	d1a9xa3	Alignment	not modelled	46.8	13	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
35	d4pfka	Alignment	not modelled	46.1	16	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
36	c1vliA	Alignment	not modelled	44.1	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
37	c1z2iA	Alignment	not modelled	37.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
38	c2nwqA	Alignment	not modelled	35.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
39	d1tyza	Alignment	not modelled	34.8	17	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
40	d1xrha	Alignment	not modelled	33.0	14	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
41	d1f2da	Alignment	not modelled	32.8	15	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
42	c1vbiA	Alignment	not modelled	31.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: type 2 malate/lactate dehydrogenase; PDBTitle: crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
43	d1xsea	Alignment	not modelled	30.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
44	c3uoeB	Alignment	not modelled	29.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from sinorhizobium meliloti
45	d1gz6a	Alignment	not modelled	28.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	d1rfma	Alignment	not modelled	28.4	20	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
47	d1pfka	Alignment	not modelled	27.8	18	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
48	d1nxua	Alignment	not modelled	27.3	14	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
49	c2b4qB	Alignment	not modelled	26.9	10	PDB header: oxidoreductase Chain: B: PDB Molecule: rhannolipids biosynthesis 3-oxoacyl-[acyl- PDBTitle: pseudomonas aeruginosa rhlg/nadp active-site complex
50	d1qsga	Alignment	not modelled	26.5	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
51	c2ptgA	Alignment	not modelled	25.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acyl carrier reductase; PDBTitle: crystal structure of eimeria tenella enoyl reductase
52	c3ijrF	Alignment	not modelled	24.7	7	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+ PDB header: oxidoreductase

53	c2nm0B_	Alignment	not modelled	24.1	13	Chain: B: PDB Molecule: probable 3-oxacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
54	c1v9nA_	Alignment	not modelled	23.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structure of malate dehydrogenase from pyrococcus horikoshii ot3
55	d1mxia_	Alignment	not modelled	23.7	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
56	c2g8yB_	Alignment	not modelled	23.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
57	d1xp8a1_	Alignment	not modelled	23.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
58	d1j0aa_	Alignment	not modelled	23.5	17	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
59	d1xqla_	Alignment	not modelled	23.2	7	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
60	c3eywA_	Alignment	not modelled	22.8	20	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
61	c2rgoA_	Alignment	not modelled	22.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
62	c3toxG_	Alignment	not modelled	22.1	13	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
63	c3fkjA_	Alignment	not modelled	22.0	12	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerases; PDBTitle: crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
64	c3nugA_	Alignment	not modelled	21.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
65	c1zxxA_	Alignment	not modelled	21.6	21	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
66	c2ha8A_	Alignment	not modelled	21.4	12	PDB header: rna binding protein Chain: A: PDB Molecule: tar (hiv-1) rna loop binding protein; PDBTitle: methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
67	d1o0ea_	Alignment	not modelled	20.8	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c3euaD_	Alignment	not modelled	20.8	11	PDB header: isomerase Chain: D: PDB Molecule: putative fructose-aminoacid-6-phosphate deglycase; PDBTitle: crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
69	d1ddza2_	Alignment	not modelled	20.8	9	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
70	c3rd5A_	Alignment	not modelled	20.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: mypaa.01249.c; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
71	d1lulua_	Alignment	not modelled	19.9	3	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	d1ddza1_	Alignment	not modelled	19.9	16	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
73	d1nlfa_	Alignment	not modelled	19.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
74	c3iccA_	Alignment	not modelled	19.5	7	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 3-oxoacyl-(acyl carrier protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
75	c3i0pA_	Alignment	not modelled	19.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from entamoeba histolytica
76	c3grkE_	Alignment	not modelled	19.3	10	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis

77	c1wtjB_	 Alignment	not modelled	19.3	22	PDB header: oxidoreductase Chain: B: PDB Molecule: ureidoglycolate dehydrogenase; PDBTitle: crystal structure of delta1-piperidine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
78	c1cmwA_	 Alignment	not modelled	19.0	13	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
79	c3g68A_	 Alignment	not modelled	18.9	16	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
80	d1k2wa_	 Alignment	not modelled	17.9	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
81	c3tfoD_	 Alignment	not modelled	17.6	13	PDB header: oxidoreductase Chain: D: PDB Molecule: putative 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
82	c1f8sA_	 Alignment	not modelled	17.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
83	d1mg5a_	 Alignment	not modelled	17.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	c2cfcB_	 Alignment	not modelled	17.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-(r)-hydroxypropyl-com dehydrogenase; PDBTitle: structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
85	d1xg5a_	 Alignment	not modelled	16.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
86	c3o8oB_	 Alignment	not modelled	16.9	25	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
87	c3llvA_	 Alignment	not modelled	16.4	5	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphate-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphate-related protein from archaeoglobus fulgidus to3 1.7a
88	c3fwzA_	 Alignment	not modelled	16.1	15	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
89	c3kvoB_	 Alignment	not modelled	16.0	10	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxysteroid dehydrogenase-like protein 2; PDBTitle: crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdl2)
90	c3lasA_	 Alignment	not modelled	15.9	13	PDB header: lyase Chain: A: PDB Molecule: putative carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
91	c2zroA_	 Alignment	not modelled	15.7	13	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
92	c3i1jB_	 Alignment	not modelled	15.6	23	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain PDBTitle: structure of a putative short chain dehydrogenase from2 pseudomonas syringae
93	c3v2hB_	 Alignment	not modelled	15.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: d-beta-hydroxybutyrate dehydrogenase; PDBTitle: the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
94	c2pd6D_	 Alignment	not modelled	15.4	7	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
95	c3ek2D_	 Alignment	not modelled	15.1	10	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of enoyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
96	c3rkrC_	 Alignment	not modelled	15.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain oxidoreductase; PDBTitle: crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
97	c3m1aF_	 Alignment	not modelled	14.8	7	PDB header: oxidoreductase Chain: F: PDB Molecule: putative dehydrogenase; PDBTitle: the crystal structure of a short-chain dehydrogenase from2 streptomyces avermitilis to2a
98	c3nklA_	 Alignment	not modelled	14.5	7	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase; PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
99	d1t9ha2	 Alignment	not modelled	14.4	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins