

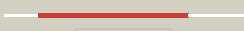
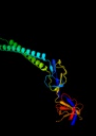

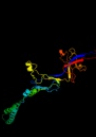

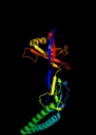

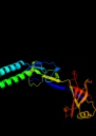








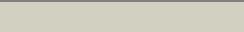


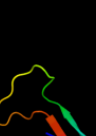
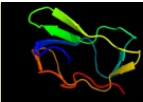




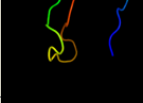
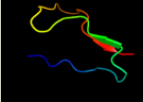
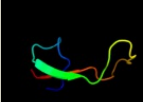
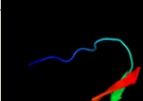


Phyre2

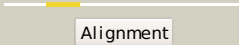
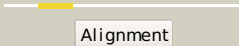
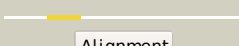
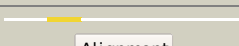
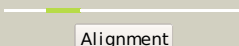
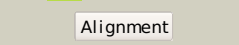
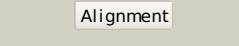
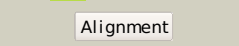
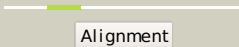
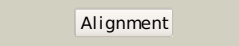
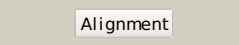




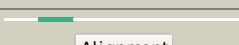

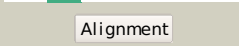


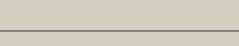
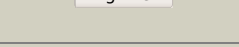
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Description	P37636
Date	Thu Jan 5 11:56:08 GMT 2012
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h9iB_	 Alignment		100.0	20	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
2	c2f1mA_	 Alignment		99.9	57	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
3	c3fppB_	 Alignment		99.9	24	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
4	d1vf7a_	 Alignment		99.9	50	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
5	c1t5eB_	 Alignment		99.9	50	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
6	c3lnnB_	 Alignment		99.9	24	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
7	c2k33A_	 Alignment		98.9	31	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		97.0	19	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	d1dcza_	 Alignment		96.8	28	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
10	c2ejgD_	 Alignment		96.8	20	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	d1o78a_	 Alignment		96.6	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains

12	c3n6rK_	Alignment		96.6	14	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
13	c2dn8A_	Alignment		96.5	20	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	c2l5tA_	Alignment		96.5	38	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
15	c2ejmA_	Alignment		96.5	35	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
16	c2kccA_	Alignment		96.4	19	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
17	d1bdoa_	Alignment		96.4	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
18	d1iyua_	Alignment		96.4	24	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
19	d1ghja_	Alignment		96.2	29	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
20	d1k8ma_	Alignment		95.9	24	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
21	d1qlaf_	Alignment	not modelled	95.9	33	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
22	d2gprr_	Alignment	not modelled	95.8	25	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
23	d2f3ga_	Alignment	not modelled	95.7	33	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
24	d1qjoa_	Alignment	not modelled	95.6	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
25	c2qf7A_	Alignment	not modelled	95.5	21	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
26	d1y8ob1	Alignment	not modelled	95.3	27	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
27	d1gprr_	Alignment	not modelled	95.3	31	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
28	d1laba_	Alignment	not modelled	95.1	29	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
29	d1qjxa_	Alignment	not modelled	95.1	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains

30	d2pnrc1	Alignment	not modelled	94.9	27	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
31	c2q8iB	Alignment	not modelled	94.6	25	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
32	d2tpta3	Alignment	not modelled	94.6	21	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
33	d1pmra	Alignment	not modelled	94.5	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
34	d1uoua3	Alignment	not modelled	94.4	14	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
35	d1brwa3	Alignment	not modelled	94.3	28	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
36	c2dncA	Alignment	not modelled	94.1	22	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
37	c1otpa	Alignment	not modelled	93.6	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
38	c2dneA	Alignment	not modelled	93.3	18	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
39	c2dsiA	Alignment	not modelled	92.1	27	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
40	c2jkuA	Alignment	not modelled	91.5	23	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
41	c3h5qA	Alignment	not modelled	91.1	40	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
42	c2j0fC	Alignment	not modelled	91.1	14	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	91.1	29	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
44	c3fmcC	Alignment	not modelled	88.6	10	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
45	c2gu1A	Alignment	not modelled	88.1	15	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
46	c2qj8B	Alignment	not modelled	87.5	21	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
47	c2hsiB	Alignment	not modelled	87.2	19	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
48	c2aukA	Alignment	not modelled	85.2	25	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
49	d1qwya	Alignment	not modelled	84.1	24	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
50	c3cdxB	Alignment	not modelled	78.2	16	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
51	c3na6A	Alignment	not modelled	77.2	18	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
52	c2b44A	Alignment	not modelled	75.4	24	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form

53	d1qpoa2	 Alignment	not modelled	73.9	22	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
54	c3d4rE_	 Alignment	not modelled	73.9	14	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
55	c2xhaB_	 Alignment	not modelled	73.5	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	d1o4ua2	 Alignment	not modelled	70.5	21	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
57	c3it5B_	 Alignment	not modelled	69.4	13	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
58	d1ci3m2	 Alignment	not modelled	68.4	31	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
59	c2aujD_	 Alignment	not modelled	68.4	28	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
60	c3nyyA_	 Alignment	not modelled	68.3	32	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
61	d1e2wa2	 Alignment	not modelled	67.7	25	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
62	d1qapa2	 Alignment	not modelled	67.6	11	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
63	c2xhcA_	 Alignment	not modelled	65.7	33	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
64	c3csqC_	 Alignment	not modelled	56.3	33	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
65	c1e2vB_	 Alignment	not modelled	52.4	28	PDB header: electron transport proteins Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
66	c3gnnA_	 Alignment	not modelled	50.9	16	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
67	c1o4uA_	 Alignment	not modelled	47.1	21	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
68	c3a8jF_	 Alignment	not modelled	46.8	22	PDB header: transferase/transport protein Chain: F: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
69	c1ctmA_	 Alignment	not modelled	45.8	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
70	c2jxmB_	 Alignment	not modelled	45.5	31	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
71	c1qapA_	 Alignment	not modelled	44.4	11	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
72	c3pajA_	 Alignment	not modelled	42.2	16	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
73	c1tu2B_	 Alignment	not modelled	41.7	38	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
74	c3iftA_	 Alignment	not modelled	41.5	16	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.
75	c2edgA_	 Alignment	not modelled	39.7	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse

						glycine
76	d1onla_	Alignment	not modelled	39.2	16	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
77	d1tu2b2	Alignment	not modelled	37.1	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
78	c3mxuA_	Alignment	not modelled	33.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
79	d1hpca_	Alignment	not modelled	32.4	16	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
80	c2zpmA_	Alignment	not modelled	28.6	60	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b
81	c2b7pA_	Alignment	not modelled	28.0	10	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
82	d1udxa3	Alignment	not modelled	27.7	26	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
83	d1hcza2	Alignment	not modelled	27.7	19	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
84	c3tbiB_	Alignment	not modelled	27.4	36	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
85	c1qpoA_	Alignment	not modelled	25.5	19	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
86	d2je6i2	Alignment	not modelled	25.2	17	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
87	c1x1oC_	Alignment	not modelled	25.0	19	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
88	c3l0gD_	Alignment	not modelled	24.4	13	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
89	c1q90A_	Alignment	not modelled	24.3	11	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
90	c2v4hA_	Alignment	not modelled	24.3	13	PDB header: transcription Chain: A: PDB Molecule: nf-kappa-b essential modulator; PDBTitle: nemo cc2-lz domain - 1d5 darpin complex
91	c2e75C_	Alignment	not modelled	22.1	11	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
92	c2j5uB_	Alignment	not modelled	21.1	38	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
93	c2dfuB_	Alignment	not modelled	20.7	29	PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
94	c1wzoC_	Alignment	not modelled	18.5	29	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
95	d1uwfa1	Alignment	not modelled	17.9	9	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
96	d1nkqa_	Alignment	not modelled	17.9	25	Fold: FAH Superfamily: FAH Family: FAH
97	c3lzkC_	Alignment	not modelled	17.7	22	PDB header: hydrolase Chain: C: PDB Molecule: fumarylacetoacetate hydrolase family protein; PDBTitle: the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
98	d1sawa_	Alignment	not modelled	17.3	21	Fold: FAH Superfamily: FAH Family: FAH
99	d1umua_	Alignment	not modelled	17.0	27	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: LexA-related