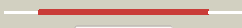





























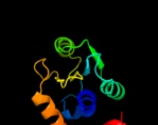


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0C0V7
Date	Tue Jul 17 17:05:08 BST 2012
Unique Job ID	c896433374b5eb81

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pdkB_	 Alignment		100.0	68	PDB header: isomerase Chain: B; PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
2	c1wqaB_	 Alignment		100.0	34	PDB header: isomerase Chain: B; PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
3	c2f71A_	 Alignment		100.0	30	PDB header: isomerase Chain: A; PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfobolus tokodaii2 phosphomannomutase/phosphoglucomutase
4	c3i3wB_	 Alignment		100.0	38	PDB header: isomerase Chain: B; PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
5	c3c04A_	 Alignment		100.0	26	PDB header: isomerase Chain: A; PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
6	c3uw2A_	 Alignment		100.0	25	PDB header: isomerase Chain: A; PDB Molecule: phosphoglucomutase/phosphomannomutase family protein; PDBTitle: x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_i1489)from burkholderia thailandensis
7	c1tuoA_	 Alignment		100.0	25	PDB header: biosynthetic protein Chain: A; PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
8	c2fuvB_	 Alignment		100.0	19	PDB header: isomerase Chain: B; PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium.
9	c1c4gB_	 Alignment		100.0	21	PDB header: transferase Chain: B; PDB Molecule: protein (alpha-d-glucose 1-phosphate PDBTitle: phosphoglucomutase vanadate based transition state analog2 complex
10	c2z0fA_	 Alignment		100.0	20	PDB header: isomerase Chain: A; PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
11	c1kfiA_	 Alignment		100.0	21	PDB header: isomerase Chain: A; PDB Molecule: phosphoglucomutase 1; PDBTitle: crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium

12	c2dkdA	Alignment		100.0	24	PDB header: isomerase Chain: A: PDB Molecule: phosphoacetylglucosamine mutase; PDBTitle: crystal structure of n-acetylglucosamine-phosphate mutase, 2 a member of the alpha-d-phosphohexomutase superfamily, in 3 the product complex
13	d1p5dx1	Alignment		100.0	31	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
14	d1kfia1	Alignment		100.0	22	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
15	d3pmga1	Alignment		100.0	24	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
16	d1p5dx3	Alignment		99.9	15	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
17	d3pmga3	Alignment		99.9	14	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
18	d1p5dx2	Alignment		99.9	30	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
19	d1kfia3	Alignment		99.9	19	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
20	d3pmga2	Alignment		99.8	30	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
21	d1kfia2	Alignment	not modelled	99.8	27	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
22	d1p5dx4	Alignment	not modelled	99.7	25	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
23	d1wjwa	Alignment	not modelled	99.5	30	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
24	d1kfia4	Alignment	not modelled	95.9	20	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
25	d3pmga4	Alignment	not modelled	95.8	17	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
26	d1nn4a	Alignment	not modelled	92.8	27	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
27	c3he8A	Alignment	not modelled	91.8	23	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate 2 isomerase b
28	c3s5pA	Alignment	not modelled	91.6	21	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpi b from giardia2 lamblia
29	c3k7pA	Alignment	not modelled	88.4	25	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from 2 trypanosoma cruzi.

30	c3m1pA	Alignment	not modelled	87.7	25	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with alllose-6-phosphate
31	d3bula2	Alignment	not modelled	82.6	12	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
32	d2vvpA1	Alignment	not modelled	81.9	28	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
33	c4em8A	Alignment	not modelled	77.7	33	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
34	c2yxB	Alignment	not modelled	72.5	13	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
35	c2ppwA	Alignment	not modelled	71.4	12	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
36	d1ccwa	Alignment	not modelled	66.2	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
37	c1k98A	Alignment	not modelled	65.9	14	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
38	c4amuB	Alignment	not modelled	65.7	16	PDB header: transferase Chain: B: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: structure of ornithine carbamoyltransferase from mycoplasma2 penetrans with a p321 space group
39	d1dxha2	Alignment	not modelled	65.0	16	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
40	d1o1xa	Alignment	not modelled	64.5	21	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
41	c3nvtA	Alignment	not modelled	60.5	14	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
42	d1e5da1	Alignment	not modelled	58.8	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
43	c3c5yD	Alignment	not modelled	57.7	15	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
44	c3hlyA	Alignment	not modelled	54.4	19	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
45	c3qd5B	Alignment	not modelled	54.3	27	PDB header: isomerase Chain: B: PDB Molecule: putative ribose-5-phosphate isomerase; PDBTitle: crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
46	d1a9xa4	Alignment	not modelled	52.8	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
47	d1xk7a1	Alignment	not modelled	52.2	19	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
48	c2i2xD	Alignment	not modelled	52.2	13	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
49	c3qayC	Alignment	not modelled	52.0	15	PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd27l endolysin targeting clostridia difficile
50	c3abfB	Alignment	not modelled	52.0	12	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
51	d1duvg2	Alignment	not modelled	50.0	11	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
52	c3onoA	Alignment	not modelled	49.9	10	PDB header: isomerase Chain: A: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
53	c3fniA	Alignment	not modelled	49.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
54	c1xa3B	Alignment	not modelled	49.5	19	PDB header: transferase Chain: B: PDB Molecule: crotonobetainyl-coa:carnitine coa-transferase;

						PDBTitle: crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
55	dlycga1	Alignment	not modelled	49.1	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
56	c1y80A_	Alignment	not modelled	48.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
57	d1xrsb1	Alignment	not modelled	48.2	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
58	d1ml4a2	Alignment	not modelled	46.5	22	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
59	c3d64A_	Alignment	not modelled	45.9	18	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
60	d1bjpa_	Alignment	not modelled	41.3	15	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
61	c2x4kB_	Alignment	not modelled	40.4	24	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
62	c3k6qB_	Alignment	not modelled	39.1	13	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
63	c2eiuE_	Alignment	not modelled	38.7	30	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: hypothetical protein aq_1627; PDBTitle: crystal structure of a putative protein (aq1627) from aquifex aeolicus
64	c2ohiB_	Alignment	not modelled	38.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
65	c1keeH_	Alignment	not modelled	38.3	17	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
66	c1a4iB_	Alignment	not modelled	38.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
67	c1d4fD_	Alignment	not modelled	37.6	16	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
68	d1fmfa_	Alignment	not modelled	36.8	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
69	c2ormA_	Alignment	not modelled	36.4	18	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
70	d1otfa_	Alignment	not modelled	36.4	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
71	d1b26a1	Alignment	not modelled	35.4	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
72	c1v8bA_	Alignment	not modelled	35.4	24	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
73	c2g04B_	Alignment	not modelled	34.3	19	PDB header: isomerase Chain: B: PDB Molecule: probable fatty-acid-coa racemase far; PDBTitle: crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
74	c1ortD_	Alignment	not modelled	33.6	16	PDB header: transferase Chain: D: PDB Molecule: ornithine transcarbamoylase; PDBTitle: ornithine transcarbamoylase from pseudomonas aeruginosa
75	d1k1ga_	Alignment	not modelled	33.4	24	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
76	c3ry0A_	Alignment	not modelled	33.3	18	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
77	c3mb2G_	Alignment	not modelled	32.7	18	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
78	c3qqzA_	Alignment	not modelled	32.1	5	PDB header: metal binding protein Chain: A: PDB Molecule: putative uncharacterized protein yjik; PDBTitle: crystal structure of the c-terminal domain of the yjik protein from2 escherichia coli cft073
79	c1hmtB_	Alignment	not modelled	31.5	11	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase;

79	c10mb_	Alignment	not modelled	31.5	11	PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of 2 the b12-binding domains of methionine synthase PDB header: transferase
80	c3ezxA_	Alignment	not modelled	31.5	11	Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
81	d7reqa2	Alignment	not modelled	31.4	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
82	d1x74a1	Alignment	not modelled	31.1	30	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
83	d2bl5a1	Alignment	not modelled	30.9	24	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
84	c2op8A_	Alignment	not modelled	30.8	29	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
85	c3n58D_	Alignment	not modelled	29.1	21	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinease; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
86	d1b1ca_	Alignment	not modelled	28.9	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
87	c3sz8D_	Alignment	not modelled	28.8	9	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
88	c1xrsB_	Alignment	not modelled	28.5	13	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
89	c3nolA_	Alignment	not modelled	28.0	24	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
90	c1luaA_	Alignment	not modelled	27.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
91	c3m20A_	Alignment	not modelled	26.7	18	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
92	c3a9gA_	Alignment	not modelled	26.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pqq-dependent sugar dehydrogenase apo-form
93	c2pfsA_	Alignment	not modelled	24.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
94	d1ekxa2	Alignment	not modelled	24.7	16	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
95	c2zkiH_	Alignment	not modelled	24.6	22	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
96	c3ntaA_	Alignment	not modelled	24.2	9	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
97	c3eglC_	Alignment	not modelled	23.5	14	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: degv family protein; PDBTitle: crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
98	c3icrA_	Alignment	not modelled	23.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
99	c3ne8A_	Alignment	not modelled	22.7	13	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
100	c4ed9A_	Alignment	not modelled	22.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: caib/baif family protein; PDBTitle: crystal structure of a caib/baif family protein from brucella suis
101	c2yh5A_	Alignment	not modelled	21.7	9	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
102	d1vlva2	Alignment	not modelled	21.0	21	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
103	c1vlvA_	Alignment	not modelled	21.0	20	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
						Fold: Toprim domain

104	d1t6t1_	Alignment	not modelled	20.9	26	Superfamily: Toprim domain Family: Toprim domain
105	d2vjma1	Alignment	not modelled	20.9	22	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
106	d1d9ea_	Alignment	not modelled	20.6	5	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase