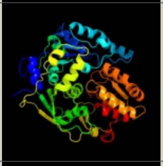
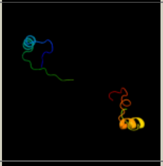
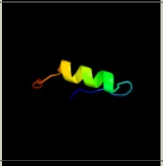
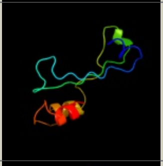
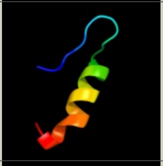
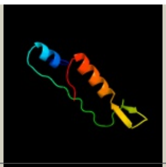
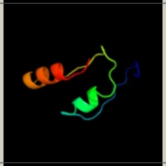
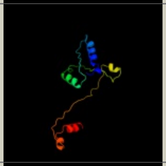
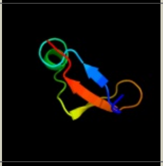
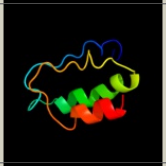
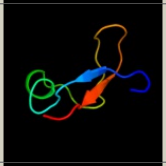
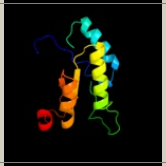
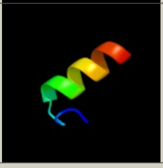
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A6A6
Date	Thu Jan 5 11:02:42 GMT 2012
Unique Job ID	409f84e5e971f966

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1acoa2	Alignment		100.0	25	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
2	d1l5ja3	Alignment		100.0	25	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
3	d2b3ya2	Alignment		100.0	25	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
4	c2b3yB_	Alignment		100.0	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
5	c5acnA_	Alignment		100.0	25	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
6	c1l5jB_	Alignment		100.0	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aconitate hydratase 2; **PDBTitle:** crystal structure of e. coli aconitase b.
7	c3bolB_	Alignment		69.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
8	d3bofa2	Alignment		61.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
9	c3iz5Q_	Alignment		40.4	12	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
10	d1lt7a_	Alignment		31.1	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
11	d1umya_	Alignment		28.3	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase

12	c1ni5A_	Alignment		26.9	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
13	c2o2qA_	Alignment		21.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
14	c2e21A_	Alignment		20.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
15	c3io1B_	Alignment		19.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
16	c1pt1B_	Alignment		19.9	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
17	d1ml4a2	Alignment		19.4	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
18	d1ppya_	Alignment		19.4	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
19	d1o60a_	Alignment		19.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
20	c2oxlA_	Alignment		18.6	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hypothetical protein ymgb; **PDBTitle:** structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
21	c3fseB_	Alignment	not modelled	17.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
22	c2zkrn_	Alignment	not modelled	17.6	18	**PDB header:**ribosomal protein/rna **Chain:** N: **PDB Molecule:**rna expansion segment es27; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
23	c2xivA_	Alignment	not modelled	17.6	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
24	c2c45F_	Alignment	not modelled	15.8	28	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase
25	c2gp4A_	Alignment	not modelled	15.6	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
26	d1ejba_	Alignment	not modelled	14.9	21	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
27	c2duwA_	Alignment	not modelled	14.0	26	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
						PDB header:dna replication

28	c2w9mB_	Alignment	not modelled	13.6	20	**Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
29	c4a1aM_	Alignment	not modelled	13.5	20	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l5; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
30	c1htrP_	Alignment	not modelled	13.3	19	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
31	c3izcQ_	Alignment	not modelled	13.0	18	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein rpl5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
32	d1oi4a1	Alignment	not modelled	12.0	30	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
33	c2jz2A_	Alignment	not modelled	11.5	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
34	d1rvv1_	Alignment	not modelled	11.4	15	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
35	c3uk7B_	Alignment	not modelled	11.3	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
36	d1c0aa2	Alignment	not modelled	10.9	27	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
37	c2ebbA_	Alignment	not modelled	10.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
38	c3hazA_	Alignment	not modelled	10.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
39	c2jzfA_	Alignment	not modelled	10.3	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** nmr conformer closest to the mean coordinates of the domain 513-651 of2 the sars-cov nonstructural protein nsp3
40	d2ga5a1	Alignment	not modelled	9.7	29	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
41	c3zquA_	Alignment	not modelled	9.6	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
42	d1obra_	Alignment	not modelled	9.5	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Carboxypeptidase T
43	c2fgxA_	Alignment	not modelled	9.5	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
44	c2x24B_	Alignment	not modelled	9.5	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** bovine acc2 ct domain in complex with inhibitor
45	c1xovA_	Alignment	not modelled	9.5	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ply protein; **PDBTitle:** the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
46	d1skye2	Alignment	not modelled	9.3	8	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
47	d1d3va_	Alignment	not modelled	8.9	28	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
48	c3m1rF_	Alignment	not modelled	8.9	28	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**formimidoylglutamase; **PDBTitle:** the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
49	d1woha_	Alignment	not modelled	8.8	28	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
50	c3h8aF_	Alignment	not modelled	8.7	17	**PDB header:**lyase/protein binding **Chain:** F: **PDB Molecule:**rnase e; **PDBTitle:** crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
51	c2yb1A_	Alignment	not modelled	8.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
52	d1v8ba2	Alignment	not modelled	8.6	21	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like

						Family:S-adenosylhomocystein hydrolase
53	d1sqda2	Alignment	not modelled	8.5	25	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
54	d2gp4a2	Alignment	not modelled	8.5	19	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**IvD/EDD N-terminal domain-like
55	c3h8aE_	Alignment	not modelled	8.2	18	**PDB header:**lyase/protein binding **Chain:** E: **PDB Molecule:**rnase e; **PDBTitle:** crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
56	c3qpbB_	Alignment	not modelled	8.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
57	d1c41a_	Alignment	not modelled	8.0	17	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
58	d1tska_	Alignment	not modelled	8.0	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
59	c2ejbA_	Alignment	not modelled	7.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
60	d1ru0a_	Alignment	not modelled	7.8	15	**Fold:**DCoH-like **Superfamily:**PCD-like **Family:**PCD-like
61	c2k89A_	Alignment	not modelled	7.8	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phospholipase a-2-activating protein; **PDBTitle:** solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
62	d2z06a1	Alignment	not modelled	7.7	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TTHA0625-like
63	d1iuka_	Alignment	not modelled	7.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
64	c3pbiA_	Alignment	not modelled	7.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
65	c2wwaJ_	Alignment	not modelled	7.5	21	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
66	d2evra2	Alignment	not modelled	7.3	17	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
67	d1w44a_	Alignment	not modelled	7.1	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
68	c3cdxB_	Alignment	not modelled	7.1	57	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
69	c3cmwA_	Alignment	not modelled	7.1	18	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
70	d2fqla1	Alignment	not modelled	7.1	29	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
71	d1li4a2	Alignment	not modelled	7.0	21	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
72	d2hs5a1	Alignment	not modelled	7.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
73	d1ew4a_	Alignment	not modelled	7.0	21	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
74	d1awda_	Alignment	not modelled	7.0	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
75	c1od4C_	Alignment	not modelled	6.9	8	**PDB header:**ligase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** acetyl-coa carboxylase carboxyltransferase domain
76	c1x0uB_	Alignment	not modelled	6.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical methylmalonyl-coa decarboxylase alpha subunit; **PDBTitle:** crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
77	c3f3bA_	Alignment	not modelled	6.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage-like element pbsx protein xkdh; **PDBTitle:** structure of the phage-like element pbsx protein xkdh from2 bacillus subtilus. northeast structural genomics3 consortium target sr352.

78	c3jtoE_	Alignment	not modelled	6.8	21	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**adapter protein meca 2; **PDBTitle:** crystal structure of the c-terminal domain of ypbh
79	c3mk3L_	Alignment	not modelled	6.8	15	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** crystal structure of lumazine synthase from salmonella typhimurium lt2
80	d2ac7a1	Alignment	not modelled	6.7	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
81	c3a2kB_	Alignment	not modelled	6.7	18	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
82	d1sp8a2	Alignment	not modelled	6.7	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
83	d1sbza_	Alignment	not modelled	6.7	18	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
84	d2aeba1	Alignment	not modelled	6.5	28	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
85	c2v6uB_	Alignment	not modelled	6.5	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pterin-4a-carbinolamine dehydratase; **PDBTitle:** high resolution crystal structure of pterin-4a-2 carbinolamine dehydratase from toxoplasma gondii
86	c3gt2A_	Alignment	not modelled	6.5	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
87	d1ni5a1	Alignment	not modelled	6.4	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
88	d1ws6a1	Alignment	not modelled	6.3	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
89	c2crcA_	Alignment	not modelled	6.1	83	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin conjugating enzyme 7 interacting **PDBTitle:** solution structure of the zf-ranbp domain of the protein2 hbv associated factor
90	d1usma_	Alignment	not modelled	6.0	18	**Fold:**DCoH-like **Superfamily:**PCD-like **Family:**PCD-like
91	c2vs1A_	Alignment	not modelled	5.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780; **PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
92	c2kmfA_	Alignment	not modelled	5.9	31	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kda protein; **PDBTitle:** solution structure of psb27 from cyanobacterial photosystem2 ii
93	d1wdva_	Alignment	not modelled	5.9	10	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
94	d2ceva_	Alignment	not modelled	5.9	28	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
95	c2nvgA_	Alignment	not modelled	5.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
96	c2vroB_	Alignment	not modelled	5.8	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
97	c1hvwA_	Alignment	not modelled	5.7	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-atracotoxin-hv1a; **PDBTitle:** hairpinless mutant of omega-atracotoxin-hv1a
98	d1hvwa_	Alignment	not modelled	5.7	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
99	d2a7sa1	Alignment	not modelled	5.7	8	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain