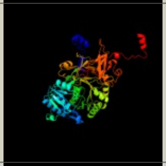
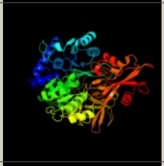
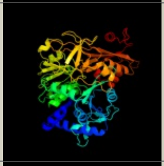
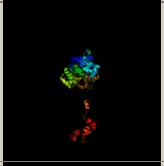
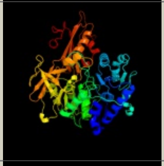
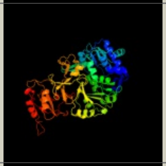
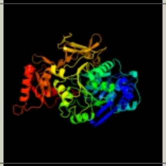
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77495
Date	Thu Jan 5 12:29:54 GMT 2012
Unique Job ID	ea2a3c3ac7b6bb48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pg4a_	Alignment		100.0	37	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
2	d1ry2a_	Alignment		100.0	39	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
3	c2vsqA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**surfactin synthetase subunit 3; **PDBTitle:** structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
4	c3etcB_	Alignment		100.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
5	d3cw9a1	Alignment		100.0	24	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
6	c3e7wA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
7	c3tsyA_	Alignment		100.0	17	**PDB header:**ligase, transferase **Chain:** A: **PDB Molecule:**fusion protein 4-coumarate--coa ligase 1, resveratrol **PDBTitle:** 4-coumaroyl-coa ligase::stilbene synthase fusion protein
8	d1mdba_	Alignment		100.0	21	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
9	c3eynB_	Alignment		100.0	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acyl-coenzyme a synthetase acsm2a; **PDBTitle:** crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
10	c3ni2A_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**4-coumarate:coa ligase; **PDBTitle:** crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
11	c3kxwA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila

12	c3gqwB_	Alignment		100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fatty acid amp ligase; **PDBTitle:** crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
13	c3iteB_	Alignment		100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
14	c2d1tA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferin 4-monooxygenase; **PDBTitle:** crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
15	c2v7bB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
16	d1amua_	Alignment		100.0	17	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
17	c1amuB_	Alignment		100.0	16	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
18	c3l8cA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
19	c3dhvA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
20	d1lcia_	Alignment		100.0	17	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
21	c3g7sA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
22	d1v25a_	Alignment	not modelled	100.0	16	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
23	c3iplB_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
24	c3nyrA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
25	c3o82B_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
26	c3o82A_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
27	c3ivrA_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative long-chain-fatty-acid coa ligase; **PDBTitle:** crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
						PDB header:ligase

28	c3e53A_	Alignment	not modelled	100.0	19	**Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28; **PDBTitle:** crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
29	c2y4oA_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak2 in complex with phenylacetyl adenylate
30	c2y27B_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
31	c3qovD_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
32	c3hguB_	Alignment	not modelled	100.0	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
33	c3laxA_	Alignment	not modelled	99.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
34	d2ayia1	Alignment	not modelled	74.2	27	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
35	c3smaD_	Alignment	not modelled	63.8	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
36	d2nyga1	Alignment	not modelled	58.9	30	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
37	c3e4fB_	Alignment	not modelled	53.4	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
38	d1pl8a2	Alignment	not modelled	52.4	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
39	d1piwa2	Alignment	not modelled	48.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
40	d1e3ja2	Alignment	not modelled	47.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
41	c3ippA_	Alignment	not modelled	44.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
42	c1uarA_	Alignment	not modelled	43.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
43	d1z7wa1	Alignment	not modelled	40.0	12	**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
44	d1zjca1	Alignment	not modelled	38.4	20	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
45	c2ywiA_	Alignment	not modelled	34.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
46	c3olhA_	Alignment	not modelled	33.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
47	d1kola2	Alignment	not modelled	33.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
48	c3pdiG_	Alignment	not modelled	28.6	14	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
49	d1udxa3	Alignment	not modelled	28.1	24	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
50	d1d1ta2	Alignment	not modelled	27.9	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
51	c3pc3A_	Alignment	not modelled	26.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
52	c3aaxB_	Alignment	not modelled	25.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
53	c3bcxA_	Alignment	not modelled	25.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase

54	d1ykfa2	Alignment	not modelled	24.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
55	d1vkma_	Alignment	not modelled	24.5	12	**Fold:**Indigoidine synthase A-like **Superfamily:**Indigoidine synthase A-like **Family:**Indigoidine synthase A-like
56	d1uufa2	Alignment	not modelled	24.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
57	d1nula_	Alignment	not modelled	24.3	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
58	d1e3ia2	Alignment	not modelled	23.8	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
59	c2k85A_	Alignment	not modelled	23.8	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** p190-a rhogap ff1 domain
60	c3nnkC_	Alignment	not modelled	22.6	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase; **PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
61	d1qz9a_	Alignment	not modelled	22.2	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
62	d1f20a1	Alignment	not modelled	22.2	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
63	d1v74a_	Alignment	not modelled	21.9	28	**Fold:**Colicin D/E5 nuclease domain **Superfamily:**Colicin D/E5 nuclease domain **Family:**Colicin D nuclease domain
64	d1ja1a1	Alignment	not modelled	21.7	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
65	d1iz0a2	Alignment	not modelled	21.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
66	d1jqba2	Alignment	not modelled	20.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
67	d1okga1	Alignment	not modelled	19.8	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
68	c1okgA_	Alignment	not modelled	19.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
69	d1p0fa2	Alignment	not modelled	19.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
70	d1uara2	Alignment	not modelled	19.2	17	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
71	d1jvba2	Alignment	not modelled	19.2	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
72	d1k92a1	Alignment	not modelled	17.5	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
73	d1ddga1	Alignment	not modelled	17.2	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
74	c2vrgA_	Alignment	not modelled	16.2	5	**PDB header:**transport **Chain:** A: **PDB Molecule:**multiple coagulation factor deficiency protein 2; **PDBTitle:** structure of human mcfd2
75	c2l66B_	Alignment	not modelled	16.1	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
76	d1w36b2	Alignment	not modelled	15.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
77	d1uaaa2	Alignment	not modelled	15.7	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
78	d1h2ba2	Alignment	not modelled	15.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
79	d1aisa1	Alignment	not modelled	15.0	24	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
						PDB header:transferase

80	c2jkzB_	Alignment	not modelled	14.9	6	**Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
81	c2zy3A_	Alignment	not modelled	14.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
82	d1y7la1	Alignment	not modelled	14.1	11	**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
83	d2fzwa2	Alignment	not modelled	14.0	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
84	d1a9xa4	Alignment	not modelled	14.0	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
85	d1wkva1	Alignment	not modelled	14.0	13	**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
86	d1fcja_	Alignment	not modelled	13.7	11	**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
87	d2ch1a1	Alignment	not modelled	13.2	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
88	d1a3xa3	Alignment	not modelled	13.2	13	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
89	d1liua3	Alignment	not modelled	13.2	20	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
90	d2jhfa2	Alignment	not modelled	13.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
91	d2c5sa1	Alignment	not modelled	12.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
92	d1u3wa2	Alignment	not modelled	12.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
93	c2wh7A_	Alignment	not modelled	12.7	73	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-phage associated; **PDBTitle:** the partial structure of a group a streptpcoccal phage-2 encoded tail fibre hyaluronate lyase hylp2
94	d1i1ga2	Alignment	not modelled	12.2	22	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
95	c1pzmB_	Alignment	not modelled	12.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
96	c1b74A_	Alignment	not modelled	12.1	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
97	d1cdoa2	Alignment	not modelled	12.0	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
98	c2diuA_	Alignment	not modelled	12.0	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0430 protein; **PDBTitle:** solution structure of the rrm domain of kiaa0430 protein
99	c1oftC_	Alignment	not modelled	11.9	29	**PDB header:**bacterial cell division inhibitor **Chain:** C: **PDB Molecule:**hypothetical protein pa3008; **PDBTitle:** crystal structure of sula from pseudomonas aeruginosa