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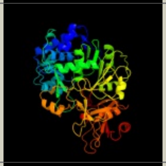
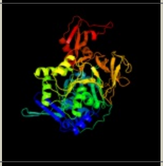
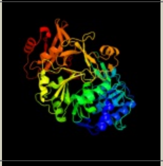
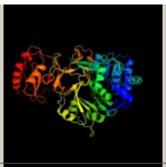
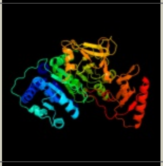
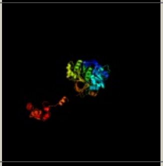
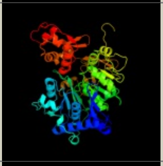
Description	P31552
Date	Thu Jan 5 11:48:13 GMT 2012
Unique Job ID	712358dac4fbf122

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pg4a_	Alignment		100.0	23	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
2	d1ry2a_	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
3	c2vsqA_	Alignment		100.0	22	**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	d3cw9a1	Alignment		100.0	24	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
5	d1mdba_	Alignment		100.0	21	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
6	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
7	c3eynB_	Alignment		100.0	22	**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
8	c3ni2A_	Alignment		100.0	27	**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
9	c3e7wA_	Alignment		100.0	21	**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
10	d1amua_	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
11	c2d1tA_	Alignment		100.0	21	**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

12	c3iteB_	Alignment		100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
13	c1amuB_	Alignment		100.0	18	**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
14	d1lcia_	Alignment		100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
15	c2v7bB_	Alignment		100.0	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
16	c3gqwB_	Alignment		100.0	19	**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
17	c3tsyA_	Alignment		100.0	24	**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
18	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
19	d1v25a_	Alignment		100.0	24	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
20	c3dhvA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
21	c3l8cA_	Alignment	not modelled	100.0	16	**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
22	c3nyrA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
23	c3iplB_	Alignment	not modelled	100.0	23	**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	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
25	c3o82B_	Alignment	not modelled	100.0	21	**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	21	**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	24	**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

28	c3e53A_	Alignment	not modelled	100.0	22	**PDB header:**ligase **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	14	**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	12	**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	14	**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	99.6	12	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
33	c3laxA_	Alignment	not modelled	99.6	12	**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	82.8	20	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
35	d1pl8a2	Alignment	not modelled	68.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
36	c3smaD_	Alignment	not modelled	62.3	23	**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
37	c3ippA_	Alignment	not modelled	52.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
38	d1piwa2	Alignment	not modelled	51.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
39	c1uarA_	Alignment	not modelled	49.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
40	d1ykfa2	Alignment	not modelled	49.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
41	d2nyga1	Alignment	not modelled	47.7	23	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
42	c3e4fB_	Alignment	not modelled	47.3	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
43	d1rjwa2	Alignment	not modelled	44.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
44	d1llua2	Alignment	not modelled	42.9	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
45	d1iz0a2	Alignment	not modelled	42.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
46	c3olhA_	Alignment	not modelled	39.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
47	c1vs3B_	Alignment	not modelled	37.0	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trna pseudouridine synthase a; **PDBTitle:** crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
48	c3bcxA_	Alignment	not modelled	36.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
49	c2ywiA_	Alignment	not modelled	34.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
50	d1jvba2	Alignment	not modelled	34.3	3	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
51	d1e3ja2	Alignment	not modelled	33.8	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
52	d1z7wa1	Alignment	not modelled	33.5	16	**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
53	d1i1ga2	Alignment	not modelled	33.3	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain

54	d1f06a2	Alignment	not modelled	33.0	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
55	d1d1ta2	Alignment	not modelled	32.7	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
56	d1kola2	Alignment	not modelled	32.7	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
57	d1uaaa2	Alignment	not modelled	27.8	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
58	d1zjca1	Alignment	not modelled	27.6	12	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
59	c2zy3A_	Alignment	not modelled	27.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
60	c3aaxB_	Alignment	not modelled	25.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
61	d1e3ia2	Alignment	not modelled	24.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
62	d1uara2	Alignment	not modelled	24.1	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
63	d1uufa2	Alignment	not modelled	22.5	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
64	d1qora2	Alignment	not modelled	22.4	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
65	d1jqba2	Alignment	not modelled	21.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
66	d1p0fa2	Alignment	not modelled	21.5	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
67	d1yb5a2	Alignment	not modelled	20.5	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
68	c2zbcH_	Alignment	not modelled	20.3	17	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
69	d2idba2	Alignment	not modelled	20.0	13	**Fold:**UbiD C-terminal domain-like **Superfamily:**UbiD C-terminal domain-like **Family:**UbiD C-terminal domain-like
70	c2jkzB_	Alignment	not modelled	19.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
71	c1c4kA_	Alignment	not modelled	19.1	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase); **PDBTitle:** ornithine decarboxylase mutant (gly121tyr)
72	c3s99A_	Alignment	not modelled	19.1	8	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**basic membrane lipoprotein; **PDBTitle:** crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
73	d2cfxa2	Alignment	not modelled	19.0	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
74	d1okga1	Alignment	not modelled	18.4	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
75	c2gn0A_	Alignment	not modelled	17.1	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine dehydratase catabolic; **PDBTitle:** crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
76	d2fzwa2	Alignment	not modelled	16.9	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
77	d2cg4a2	Alignment	not modelled	16.7	6	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
78	d1nula_	Alignment	not modelled	16.5	4	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
						PDB header:lyase

79	c1ydnA_	Alignment	not modelled	16.4	13	**Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
80	d1ja1a1	Alignment	not modelled	16.2	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
81	c2djwF_	Alignment	not modelled	15.7	22	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
82	d1f20a1	Alignment	not modelled	15.6	11	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
83	c2e1aD_	Alignment	not modelled	15.5	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
84	d1udxa3	Alignment	not modelled	15.2	25	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
85	c3hzuA_	Alignment	not modelled	15.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
86	c3n75E_	Alignment	not modelled	15.1	10	**PDB header:**lyase **Chain:** E: **PDB Molecule:**lysine decarboxylase, inducible; **PDBTitle:** x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
87	c3hjtB_	Alignment	not modelled	15.1	9	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
88	c1yj7A_	Alignment	not modelled	14.0	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
89	c1okgA_	Alignment	not modelled	13.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
90	c1e0cA_	Alignment	not modelled	13.5	16	**PDB header:**sulfurtransferase **Chain:** A: **PDB Molecule:**sulfurtransferase; **PDBTitle:** sulfurtransferase from azotobacter vinelandii
91	c2jwlB_	Alignment	not modelled	13.4	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
92	c3iauA_	Alignment	not modelled	13.4	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine deaminase; **PDBTitle:** the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
93	d1l9xa_	Alignment	not modelled	13.4	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
94	c1l9xA_	Alignment	not modelled	13.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
95	d1pwha_	Alignment	not modelled	13.4	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
96	d2jhfa2	Alignment	not modelled	13.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
97	d1u3wa2	Alignment	not modelled	12.7	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
98	d1liua3	Alignment	not modelled	12.4	17	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
99	d1wkva1	Alignment	not modelled	12.4	10	**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