Phyre2

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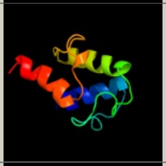
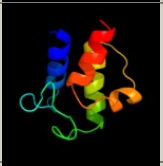
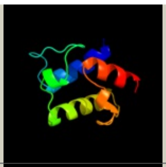
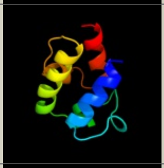
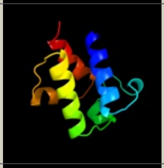
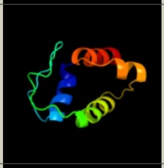
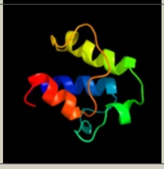
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t8ka_	Alignment		99.7	100	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
2	c2qnwA_	Alignment		99.7	51	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** toxoplasma gondii apicoplast-targeted acyl carrier protein
3	c2cnrA_	Alignment		99.7	42	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structural studies on the interaction of scfas acp with2 acps
4	c2fq2A_	Alignment		99.7	51	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
5	c2l3vA_	Alignment		99.7	62	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** nmr structure of acyl carrier protein from brucella melitensis
6	c3ejbC_	Alignment		99.7	100	**PDB header:**oxidoreductase/lipid transport **Chain:** C: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of p450bioi in complex with tetradecanoic2 acid ligated acyl carrier protein
7	d1klpa_	Alignment		99.6	34	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
8	c2dnwA_	Alignment		99.6	41	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
9	c2kwlA_	Alignment		99.6	45	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of acyl carrier protein from borrelia burgdorferi
10	c2ehtA_	Alignment		99.6	64	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
11	c1x3oA_	Alignment		99.6	59	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of the acyl carrier protein from thermus2 thermophilus hb8

12	c2fvfA_	Alignment		99.6	41	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structure of 10:0-acp (protein with docked fatty acid)
13	c2liuA_	Alignment		99.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cura; **PDBTitle:** nmr structure of holo-acpi domain from cura module from lyngbya2 majuscula
14	c2l4bA_	Alignment		99.6	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
15	d1vkua_	Alignment		99.6	34	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
16	c2kciA_	Alignment		99.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acyl carrier protein; **PDBTitle:** solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
17	d1f80d_	Alignment		99.5	54	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
18	c2l9fA_	Alignment		99.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
19	c2afdA_	Alignment		99.5	16	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**protein asl1650; **PDBTitle:** solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
20	c2kr5A_	Alignment		99.5	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase; **PDBTitle:** solution structure of an acyl carrier protein domain from fungal type2 i polyketide synthase
21	c2ju2A_	Alignment	not modelled	99.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase; **PDBTitle:** minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
22	d2af8a_	Alignment	not modelled	99.5	28	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
23	c3ce7A_	Alignment	not modelled	99.5	31	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochodrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochodrial acyl2 carrier protein, 59.m03510
24	d1dv5a_	Alignment	not modelled	99.5	22	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**apo-D-alanyl carrier protein
25	c2cgqA_	Alignment	not modelled	99.5	31	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**acyl carrier protein acpa; **PDBTitle:** a putative acyl carrier protein(rv0033) from mycobacterium2 tuberculosis
26	d1nq4a_	Alignment	not modelled	99.5	26	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
27	c3lmoA_	Alignment	not modelled	99.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**specialized acyl carrier protein; **PDBTitle:** crystal structure of specialized acyl carrier protein2 (rpa2022) from rhodopseudomonas palustris, northeast3 structural genomics consortium target rpr324
28	c2jqnA_	Alignment	not modelled	99.4	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3;

						PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine2 synthetase tycc
29	c2cq8A_	Alignment	not modelled	99.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** solution structure of rsgi ruh-033, a pp-binding domain of2 10-fthfdh from human cdna
30	d1or5a_	Alignment	not modelled	99.4	25	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
31	d2gdwa1	Alignment	not modelled	99.4	21	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Peptidyl carrier domain
32	c2roqA_	Alignment	not modelled	99.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**enterobactin synthetase component f; **PDBTitle:** solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f
33	d2jq4a1	Alignment	not modelled	99.3	21	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
34	c2jq4A_	Alignment	not modelled	99.3	21	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein atu2571; **PDBTitle:** complete resonance assignments and solution structure2 calculation of atc2521 (nesg id: att6) from agrobacterium3 tumefaciens
35	c2fq1A_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
36	c2vsqA_	Alignment	not modelled	99.2	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
37	d2pnga1	Alignment	not modelled	99.1	31	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
38	c2amwA_	Alignment	not modelled	97.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ne2163; **PDBTitle:** solution nmr structure of protein ne2163 from nitrosomonas europaea.2 northeast structural genomics consortium target net1.
39	c2lkiA_	Alignment	not modelled	97.8	26	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.
40	c3s8mA_	Alignment	not modelled	90.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
41	c2uv8C_	Alignment	not modelled	85.9	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha (fas2); **PDBTitle:** crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
42	c2uv9B_	Alignment	not modelled	59.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase alpha subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
43	c2vkzC_	Alignment	not modelled	58.8	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
44	d2gyc31	Alignment	not modelled	24.8	47	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
45	c1rqtA_	Alignment	not modelled	24.2	47	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
46	d1rqta_	Alignment	not modelled	24.2	47	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
47	c1rqtB_	Alignment	not modelled	24.2	47	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
48	c3k13A_	Alignment	not modelled	22.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
49	d1af7a1	Alignment	not modelled	17.8	9	**Fold:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Superfamily:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Family:**Chemotaxis receptor methyltransferase CheR, N-terminal domain
50	c3a2kB_	Alignment	not modelled	16.7	27	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase;

						PDBTitle: crystal structure of tils complexed with trna
51	d2c5ra1	Alignment	not modelled	16.6	23	**Fold:**Phage replication organizer domain **Superfamily:**Phage replication organizer domain **Family:**Phage replication organizer domain
52	d1wui1	Alignment	not modelled	14.3	17	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
53	d1dd4d_	Alignment	not modelled	14.2	29	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
54	d1jrma_	Alignment	not modelled	14.1	22	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
55	d2dt5a1	Alignment	not modelled	13.5	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
56	d1dd3a1	Alignment	not modelled	12.5	30	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
57	c1u9hB_	Alignment	not modelled	12.5	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of e(22)l(23)
58	d1iv3a_	Alignment	not modelled	11.5	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
59	d1q1va_	Alignment	not modelled	11.2	13	**Fold:**Another 3-helical bundle **Superfamily:**DEK C-terminal domain **Family:**DEK C-terminal domain
60	d1h99a1	Alignment	not modelled	10.9	19	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
61	c1unyA_	Alignment	not modelled	10.5	24	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
62	c3pvpA_	Alignment	not modelled	10.4	17	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
63	d1j1va_	Alignment	not modelled	10.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
64	d1ql3a_	Alignment	not modelled	9.8	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
65	c3m20A_	Alignment	not modelled	8.2	19	**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
66	d1nera_	Alignment	not modelled	8.2	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
67	c2fwtA_	Alignment	not modelled	8.0	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides
68	c3ketA_	Alignment	not modelled	7.9	24	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
69	c3mb2G_	Alignment	not modelled	7.9	14	**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
70	d1y7ea1	Alignment	not modelled	7.8	14	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
71	c3t5sA_	Alignment	not modelled	7.7	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor; **PDBTitle:** structure of macrophage migration inhibitory factor from giardia2 lamblia
72	d1bjpa_	Alignment	not modelled	7.6	23	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
73	d2rk5a1	Alignment	not modelled	7.4	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
74	c2kp6A_	Alignment	not modelled	7.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cv0237 from2

						chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
75	d2bw3a1	Alignment	not modelled	7.1	14	**Fold:**Hermes dimerisation domain **Superfamily:**Hermes dimerisation domain **Family:**Hermes dimerisation domain
76	c1dd3C_	Alignment	not modelled	6.9	38	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima
77	c1dd3D_	Alignment	not modelled	6.9	38	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima
78	c3ry0A_	Alignment	not modelled	6.8	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
79	c2kxoA_	Alignment	not modelled	6.8	8	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
80	d2gdga1	Alignment	not modelled	6.7	9	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
81	d1dd4c_	Alignment	not modelled	6.7	38	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
82	d1otfa_	Alignment	not modelled	6.7	23	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
83	d1gd0a_	Alignment	not modelled	6.6	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
84	c2op8A_	Alignment	not modelled	6.6	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
85	c3hrdF_	Alignment	not modelled	6.5	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
86	d1fima_	Alignment	not modelled	6.4	9	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
87	d1yh5a1	Alignment	not modelled	6.4	26	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
88	c2ormA_	Alignment	not modelled	6.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
89	d2r2za1	Alignment	not modelled	6.2	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
90	c3abfB_	Alignment	not modelled	6.2	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
91	d1c75a_	Alignment	not modelled	6.0	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
92	c1zunA_	Alignment	not modelled	5.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
93	d1u0ma2	Alignment	not modelled	5.9	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
94	c2xczA_	Alignment	not modelled	5.9	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein; **PDBTitle:** crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
95	d1wjua_	Alignment	not modelled	5.9	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
96	c1u9hA_	Alignment	not modelled	5.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of e(22)l(23)
97	d1hfoa_	Alignment	not modelled	5.7	9	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
98	d1w55a2	Alignment	not modelled	5.7	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
99	d1dpta_	Alignment	not modelled	5.7	9	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related