Phyre2

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Description	P0A7F9
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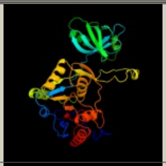
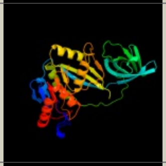
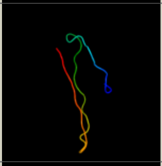
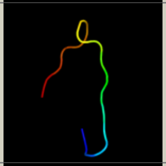
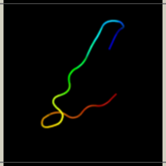
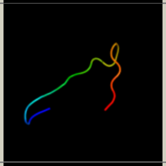
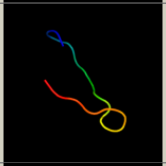
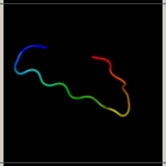
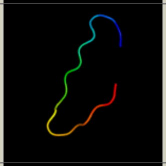
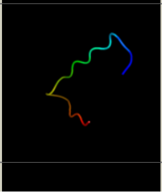
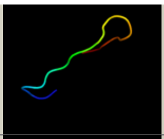
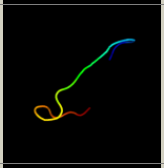
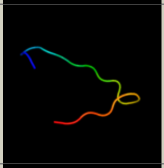
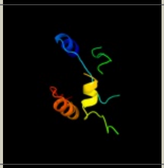
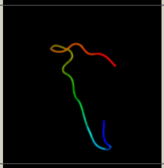
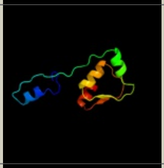
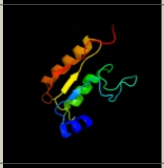
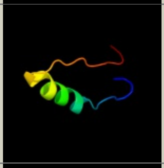
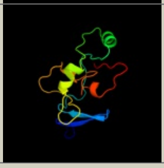
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yy3A_	Alignment		100.0	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
2	d1wdia_	Alignment		100.0	48	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
3	d1vkya_	Alignment		100.0	46	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
4	d1jr7a_	Alignment		88.5	20	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Gab protein (hypothetical protein YgaT)
5	c3ms5A_	Alignment		86.1	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase; **PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
6	d1ds1a_	Alignment		84.7	56	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
7	c2og5A_	Alignment		83.4	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
8	c2wbqA_	Alignment		81.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
9	d1oiha_	Alignment		81.2	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
10	d1otja_	Alignment		79.3	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
11	c3r1jB_	Alignment		77.2	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form

12	c3pvjB_	Alignment		76.1	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
13	c3eatX_	Alignment		74.8	22	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb; **PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
14	d1y0za_	Alignment		69.3	33	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
15	d1qyia_	Alignment		63.7	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
16	d1nx4a_	Alignment		61.9	50	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
17	c3p9zA_	Alignment		47.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**uroporphyrinogen iii cosynthase (hemd); **PDBTitle:** crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
18	c2nuxB_	Alignment		47.4	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
19	d1hg3a_	Alignment		44.7	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
20	c2hc9A_	Alignment		44.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
21	d1a3xa1	Alignment	not modelled	44.5	11	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
22	c3ny0D_	Alignment	not modelled	43.2	14	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**urease accessory protein uree; **PDBTitle:** crystal structure of uree from helicobacter pylori (ni2+ bound form)
23	c3pihA_	Alignment	not modelled	42.8	32	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
24	d1ttja_	Alignment	not modelled	40.1	45	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
25	c2h6rG_	Alignment	not modelled	40.0	19	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
26	d1jr2a_	Alignment	not modelled	38.6	20	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
27	c1jr2A_	Alignment	not modelled	38.6	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
28	d1n55a_	Alignment	not modelled	37.4	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
29	c2vf7B_	Alignment	not modelled	37.2	39	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans

30	d1mo0a_	Alignment	not modelled	37.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
31	d1pkla1	Alignment	not modelled	35.5	15	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
32	d1w0ma_	Alignment	not modelled	35.5	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
33	d2ebfx2	Alignment	not modelled	34.9	10	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
34	d1wjja_	Alignment	not modelled	34.6	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
35	d2evra2	Alignment	not modelled	34.5	28	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
36	d1sw3a_	Alignment	not modelled	33.4	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
37	c2dp3A_	Alignment	not modelled	32.9	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
38	c1pklB_	Alignment	not modelled	32.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
39	d1wd7a_	Alignment	not modelled	31.0	18	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
40	d2b8ea1	Alignment	not modelled	30.1	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
41	c3fkkA_	Alignment	not modelled	29.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
42	c1yyaA_	Alignment	not modelled	29.4	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
43	d1omha_	Alignment	not modelled	28.7	31	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
44	d1neya_	Alignment	not modelled	28.6	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
45	c3kxqB_	Alignment	not modelled	28.4	45	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
46	c3i5aA_	Alignment	not modelled	28.2	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
47	c3hvbB_	Alignment	not modelled	28.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
48	c3l6tB_	Alignment	not modelled	28.2	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mobilization protein trai; **PDBTitle:** crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain
49	d1b9ba_	Alignment	not modelled	28.1	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
50	c3d8tB_	Alignment	not modelled	28.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** thermus thermophilus uroporphyrinogen iii synthase
51	d1diha1	Alignment	not modelled	27.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	c2x7jA_	Alignment	not modelled	26.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
53	d1r2ra_	Alignment	not modelled	26.7	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
54	d1suxa_	Alignment	not modelled	26.6	42	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
55	d1o7ia_	Alignment	not modelled	26.2	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
56	d1kv5a_	Alignment	not modelled	25.8	45	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM)

						Family: Triosephosphate isomerase (TIM)
57	c1nl3B_	Alignment	not modelled	25.8	31	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase seca 1 subunit; **PDBTitle:** crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
58	d1xnea_	Alignment	not modelled	24.4	33	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
59	d1w3ia_	Alignment	not modelled	23.7	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
60	c1ayeA_	Alignment	not modelled	23.4	16	**PDB header:**serine protease **Chain:** A: **PDB Molecule:**procarboxypeptidase a2; **PDBTitle:** human procarboxypeptidase a2
61	c3m9yB_	Alignment	not modelled	22.5	35	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
62	c3civA_	Alignment	not modelled	22.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase; **PDBTitle:** crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
63	c2gm2A_	Alignment	not modelled	21.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
64	c3ijpA_	Alignment	not modelled	21.7	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
65	c2jgqB_	Alignment	not modelled	21.6	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
66	c3shoA_	Alignment	not modelled	20.7	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
67	c3dinB_	Alignment	not modelled	20.5	25	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
68	d1jmca1	Alignment	not modelled	20.5	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
69	d1m6ja_	Alignment	not modelled	20.5	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
70	c2boaB_	Alignment	not modelled	20.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxypeptidase a4; **PDBTitle:** human procarboxypeptidase a4.
71	d2g50a1	Alignment	not modelled	20.4	8	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
72	c2k50A_	Alignment	not modelled	20.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
73	d1ntga_	Alignment	not modelled	19.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
74	c3bi8A_	Alignment	not modelled	19.9	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
75	d1o5xa_	Alignment	not modelled	19.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
76	c1drwA_	Alignment	not modelled	19.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
77	d1hl2a_	Alignment	not modelled	19.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
78	c2eo2A_	Alignment	not modelled	18.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**adult male hypothalamus cdna, riken full-length **PDBTitle:** solution structure of the insertion region (510-573) of2 fthfs domain from mouse methylenetetrahydrofolate3 dehydrogenase (nadp+ dependent) 1-like protein
79	c3s6dA_	Alignment	not modelled	18.3	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative triosephosphate isomerase; **PDBTitle:** crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
80	c3lerA_	Alignment	not modelled	18.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
81	c1ynxA_	Alignment	not modelled	18.0	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication factor-a protein 1; **PDBTitle:** solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)
						PDB header:isomerase

82	c3krsB_	Alignment	not modelled	17.9	32	**Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
83	c3gvgA_	Alignment	not modelled	17.6	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
84	c2zpmA_	Alignment	not modelled	16.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
85	d1o1xa_	Alignment	not modelled	16.8	25	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
86	c3th6B_	Alignment	not modelled	16.8	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
87	c2ygrD_	Alignment	not modelled	16.7	36	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
88	c3pl0B_	Alignment	not modelled	16.2	25	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
89	d1trea_	Alignment	not modelled	16.2	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
90	c3ahxC_	Alignment	not modelled	16.1	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
91	d1p4da_	Alignment	not modelled	16.0	28	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
92	d1aw1a_	Alignment	not modelled	15.8	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
93	d1wcga1	Alignment	not modelled	15.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
94	d1owfa_	Alignment	not modelled	15.6	22	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
95	c3hv9A_	Alignment	not modelled	15.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
96	c3e96B_	Alignment	not modelled	15.4	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
97	d1s04a_	Alignment	not modelled	15.4	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
98	c2iyeC_	Alignment	not modelled	15.3	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**copper-transporting atpase; **PDBTitle:** structure of catalytic cpx-atpase domain copb-b
99	d1o5ka_	Alignment	not modelled	14.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase