Phyre²

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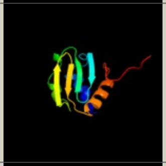
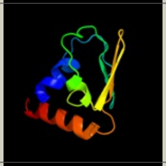
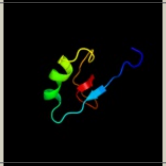
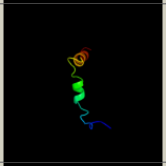
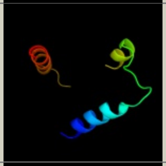
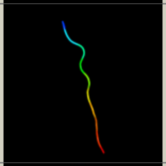
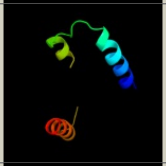
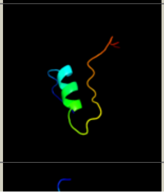
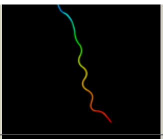
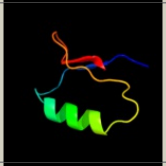
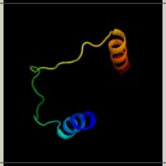
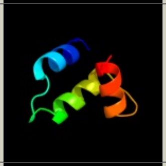
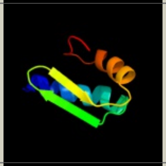
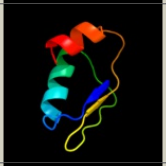
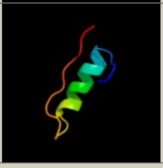
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		100.0	16	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	c3ipjB_	Alignment		99.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, iiabc component; **PDBTitle:** the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
3	c1ibaA_	Alignment		99.9	34	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures
4	d3bp8c1	Alignment		99.8	35	**Fold:**Homing endonuclease-like **Superfamily:**Glucose permease domain IIB **Family:**Glucose permease domain IIB
5	d1i1ga2	Alignment		50.5	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
6	c2voyB_	Alignment		42.4	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
7	d1ciia1	Alignment		39.1	8	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
8	d2cyya2	Alignment		37.3	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
9	c3t2lA_	Alignment		33.5	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**putative cell adhesion protein; **PDBTitle:** crystal structure of a putative cell adhesion protein (bf1858) from2 bacteroides fragilis nctc 9343 at 2.33 a resolution
10	d1rh1a2	Alignment		29.0	21	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
11	c2pjmA_	Alignment		28.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii

12	c3sy6A_	Alignment		27.4	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbrial protein bf1861; **PDBTitle:** crystal structure of a fimbrial protein bf1861 [bacteroides fragilis2 nctc 9343] (bf1861) from bacteroides fragilis nctc 9343 at 1.90 a3 resolution
13	d2cfxa2	Alignment		26.8	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
14	d1cola_	Alignment		26.7	17	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
15	d2gola1	Alignment		25.8	28	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
16	c1vbkA_	Alignment		23.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
17	c1a0oH_	Alignment		23.2	14	**PDB header:**chemotaxis **Chain:** H: **PDB Molecule:**chea; **PDBTitle:** chey-binding domain of chea in complex with chey
18	d1ffgb_	Alignment		23.1	17	**Fold:**Ferredoxin-like **Superfamily:**CheY-binding domain of CheA **Family:**CheY-binding domain of CheA
19	c2djwF_	Alignment		23.0	17	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
20	c3ibwA_	Alignment		22.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
21	c1lkzB_	Alignment	not modelled	19.8	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
22	c2xv4S_	Alignment	not modelled	19.7	14	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc3; **PDBTitle:** structure of human rpc62 (partial)
23	c2e1aD_	Alignment	not modelled	19.3	8	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
24	c2pmuD_	Alignment	not modelled	19.0	16	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
25	c2i88A_	Alignment	not modelled	18.5	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**colicin-e1; **PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1
26	c3ksiA_	Alignment	not modelled	18.5	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
27	c2zbcH_	Alignment	not modelled	17.2	14	**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.
28	c2c5sA_	Alignment	not modelled	16.7	13	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2

						modifying enzyme containing the predicted rna-binding3 thump domain
29	c3l7oB_	Alignment	not modelled	14.8	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
30	d1l6na1	Alignment	not modelled	14.6	29	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
31	d1gxqa_	Alignment	not modelled	14.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
32	d1t4za_	Alignment	not modelled	13.0	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
33	c2hqnA_	Alignment	not modelled	12.8	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
34	d2cfua2	Alignment	not modelled	12.6	11	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
35	c3kwmC_	Alignment	not modelled	12.5	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
36	c1oy8A_	Alignment	not modelled	12.3	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
37	c3ufiA_	Alignment	not modelled	12.3	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**hypothetical protein bacova_04980; **PDBTitle:** crystal structure of a hypothetical protein2 bacova_04980(zp_02067969.1) from bacteroides ovatus atcc 8483 at 2.183 a resolution
38	d1mwza_	Alignment	not modelled	12.0	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
39	c1m6yA_	Alignment	not modelled	12.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
40	c2dbbA_	Alignment	not modelled	12.0	17	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
41	c1lk5C_	Alignment	not modelled	11.4	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
42	d1fpoa2	Alignment	not modelled	11.1	10	**Fold:**Open three-helical up-and-down bundle **Superfamily:**HSC20 (HSCB), C-terminal oligomerisation domain **Family:**HSC20 (HSCB), C-terminal oligomerisation domain
43	c2cfuA_	Alignment	not modelled	11.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
44	d1uj4a2	Alignment	not modelled	10.5	28	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
45	d1vbka2	Alignment	not modelled	10.5	10	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
46	c3hheA_	Alignment	not modelled	10.3	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
47	d2c5sa2	Alignment	not modelled	10.0	12	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
48	d2cg4a2	Alignment	not modelled	10.0	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
49	c1uj6A_	Alignment	not modelled	9.8	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
50	d1kgsa1	Alignment	not modelled	9.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
51	c2f8mB_	Alignment	not modelled	9.6	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
52	d2prra1	Alignment	not modelled	9.0	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
53	d1ilea1	Alignment	not modelled	8.8	12	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I

						aminoacyl-tRNA synthetases
54	d2ff4a1	Alignment	not modelled	8.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
55	d1qm4a1	Alignment	not modelled	8.3	12	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
56	d1ry9a_	Alignment	not modelled	8.2	15	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
57	d1ciya1	Alignment	not modelled	8.1	29	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
58	c3zqsB_	Alignment	not modelled	8.1	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase fancl; **PDBTitle:** human fancl central domain
59	d2bgwa1	Alignment	not modelled	7.9	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
60	d1ivsa2	Alignment	not modelled	7.7	22	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
61	d1ji6a1	Alignment	not modelled	7.7	36	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
62	d1kona_	Alignment	not modelled	7.7	9	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
63	d1fzda_	Alignment	not modelled	7.4	17	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
64	d1qupa2	Alignment	not modelled	7.4	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
65	c2j61B_	Alignment	not modelled	7.4	26	**PDB header:**lectin **Chain:** B: **PDB Molecule:**ficolin-2; **PDBTitle:** l-ficolin complexed to n-acetylglucosamine (forme c)
66	c2kscA_	Alignment	not modelled	7.3	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
67	c2janD_	Alignment	not modelled	7.1	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
68	d1ffya1	Alignment	not modelled	7.0	12	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
69	c3n0uB_	Alignment	not modelled	6.9	21	**PDB header:**hydrolase, lyase **Chain:** B: **PDB Molecule:**probable n-glycosylase/dna lyase; **PDBTitle:** crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
70	d1iq0a3	Alignment	not modelled	6.9	9	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain **Family:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
71	c2kyzA_	Alignment	not modelled	6.8	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
72	d1wi9a_	Alignment	not modelled	6.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
73	c2ifoA_	Alignment	not modelled	6.7	25	**PDB header:**virus **Chain:** A: **PDB Molecule:**inovirus; **PDBTitle:** model-building studies of inovirus: genetic variations on a2 geometric theme
74	c2i9sA_	Alignment	not modelled	6.7	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mesoderm development candidate 2; **PDBTitle:** the solution structure of the core of mesoderm development2 (mesd).
75	d1ngka_	Alignment	not modelled	6.6	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
76	d1o8ba2	Alignment	not modelled	6.6	24	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
77	d1m0sa2	Alignment	not modelled	6.6	10	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
78	c3mahA_	Alignment	not modelled	6.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
						Fold: Fibrinogen C-terminal domain-like

79	d1lwub1	Alignment	not modelled	6.5	13	**Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
80	d2o3aa1	Alignment	not modelled	6.5	27	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
81	d1tama_	Alignment	not modelled	6.5	27	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
82	d1m1ha2	Alignment	not modelled	6.5	13	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
83	c2kddB_	Alignment	not modelled	6.4	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**borealin; **PDBTitle:** solution structure of the conserved c-terminal dimerization2 domain of borealin
84	d1jkva_	Alignment	not modelled	6.4	5	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
85	d1m1jc1	Alignment	not modelled	6.3	30	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
86	d1s69a_	Alignment	not modelled	6.3	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
87	d1rzsa_	Alignment	not modelled	6.3	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
88	d1lk5a2	Alignment	not modelled	6.2	19	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
89	c3aq8A_	Alignment	not modelled	6.2	22	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
90	c3ofgA_	Alignment	not modelled	6.2	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**boca/mesd chaperone for ywtd beta-propeller-egf protein 1; **PDBTitle:** structured domain of caenorhabditis elegans bmy-1
91	c2e1cA_	Alignment	not modelled	6.2	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
92	d1hiwa_	Alignment	not modelled	6.1	29	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
93	c3ofeB_	Alignment	not modelled	6.1	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**ldlr chaperone boca; **PDBTitle:** structured domain of drosophila melanogaster boca p41 2 2 crystal form
94	c1m0sA_	Alignment	not modelled	6.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
95	c3dxsX_	Alignment	not modelled	5.9	26	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
96	c1ph4A_	Alignment	not modelled	5.9	21	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggttttggcg
97	c1jb7A_	Alignment	not modelled	5.9	21	**PDB header:**dna-binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
98	d1vr6a1	Alignment	not modelled	5.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
99	c1vcnA_	Alignment	not modelled	5.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion