Phyre2

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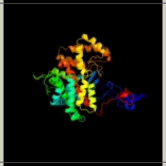
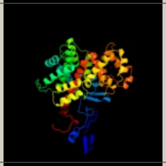
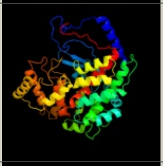
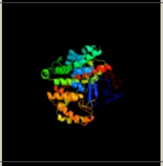
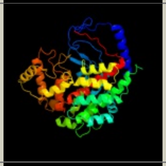
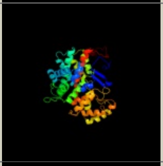
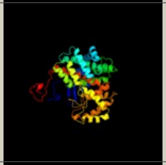
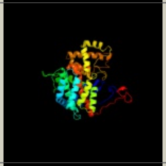
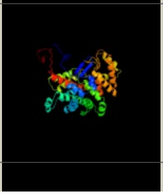
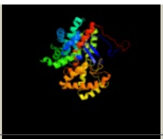
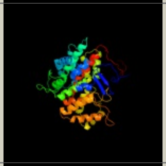
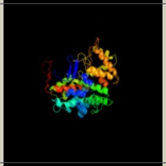
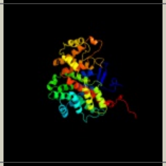
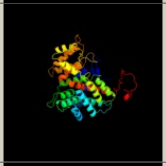
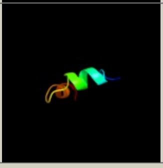
Description	P0ABH7
Date	Thu Jan 5 11:15:31 GMT 2012
Unique Job ID	e88f551d9979ec12

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k3pa_	Alignment		100.0	100	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
2	c2h12C_	Alignment		100.0	65	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyldethia coenzyme a (cmx)
3	c3msuA_	Alignment		100.0	52	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from francisella tularensis
4	d1csha_	Alignment		100.0	26	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
5	c2ibpB_	Alignment		100.0	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from pyrobaculum aerophilum
6	d1csca_	Alignment		100.0	25	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
7	d2ctsa_	Alignment		100.0	25	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
8	d1ioma_	Alignment		100.0	33	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
9	d1aj8a_	Alignment		100.0	35	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
10	c1vgmB_	Alignment		100.0	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**378aa long hypothetical citrate synthase; **PDBTitle:** crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
11	c1vgpA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**373aa long hypothetical citrate synthase; **PDBTitle:** crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7

12	c2r26C_	Alignment		100.0	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum
13	c3hwkE_	Alignment		100.0	28	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methylcitrate synthase; **PDBTitle:** crystal structure of methylcitrate synthase from2 mycobacterium tuberculosis
14	d1a59a_	Alignment		100.0	32	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
15	d1o7xa_	Alignment		100.0	33	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
16	c2p2wA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from thermotoga maritima msb8
17	c3tqgA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-methylcitrate synthase; **PDBTitle:** structure of the 2-methylcitrate synthase (prpc) from coxiella2 burnetii
18	c2c6xA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase 1; **PDBTitle:** structure of bacillus subtilis citrate synthase
19	c3o8jH_	Alignment		100.0	31	**PDB header:**transferase **Chain:** H: **PDB Molecule:**2-methylcitrate synthase; **PDBTitle:** crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
20	c2xzmS_	Alignment		49.8	27	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rps15e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
21	d1khda2	Alignment	not modelled	38.9	23	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
22	d1b8za_	Alignment	not modelled	29.5	30	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
23	d1mula_	Alignment	not modelled	25.7	15	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
24	d2o97b1	Alignment	not modelled	21.6	30	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
25	c2l0cA_	Alignment	not modelled	19.6	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** solution nmr structure of protein sty4237 (residues 36-120) from2 salmonella enterica, northeast structural genomics consortium target3 slr115
26	d1p71a_	Alignment	not modelled	19.2	30	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
27	d2elca2	Alignment	not modelled	15.5	22	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
						Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain

28	d1uoua2	Alignment	not modelled	15.4	17	**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
29	d1poib_	Alignment	not modelled	15.2	9	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
30	d1huua_	Alignment	not modelled	14.6	24	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
31	c3fcgB_	Alignment	not modelled	14.5	12	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
32	c2r9qD_	Alignment	not modelled	14.3	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**2'-deoxycytidine 5'-triphosphate deaminase; **PDBTitle:** crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
33	d1owfa_	Alignment	not modelled	14.0	35	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
34	d2prra1	Alignment	not modelled	13.9	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
35	c3f10A_	Alignment	not modelled	13.3	16	**PDB header:**hydrolase, lyase **Chain:** A: **PDB Molecule:**8-oxoguanine-dna-glycosylase; **PDBTitle:** crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine
36	d1owfb_	Alignment	not modelled	13.0	22	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
37	c3mesB_	Alignment	not modelled	12.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
38	d3bzka5	Alignment	not modelled	12.4	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
39	d1brwa2	Alignment	not modelled	12.4	15	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
40	c3if8B_	Alignment	not modelled	12.0	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**protein zwilch homolog; **PDBTitle:** crystal structure of zwilch, a member of the rzz kinetochore complex
41	d2fuka1	Alignment	not modelled	11.8	9	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
42	c2np2B_	Alignment	not modelled	11.1	17	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**hbb; **PDBTitle:** hbb-dna complex
43	c3c4iA_	Alignment	not modelled	10.5	35	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein hu homolog; **PDBTitle:** crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
44	c2xzmV_	Alignment	not modelled	10.4	29	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**rps17e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
45	c2ixsB_	Alignment	not modelled	10.4	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sdai restriction endonuclease; **PDBTitle:** structure of sdai restriction endonuclease
46	c3izbQ_	Alignment	not modelled	10.3	21	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein rps17 (s17e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
47	d2oyoa1	Alignment	not modelled	10.3	13	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
48	c3kgkA_	Alignment	not modelled	10.2	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd; **PDBTitle:** crystal structure of arsd
49	c3cw1D_	Alignment	not modelled	10.1	20	**PDB header:**splicing **Chain:** D: **PDB Molecule:**small nuclear ribonucleoprotein sm d3; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
50	c3c5iD_	Alignment	not modelled	10.0	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of plasmodium knowlesi choline kinase, pkh_134520
51	c2nx9B_	Alignment	not modelled	9.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
52	c3c65A_	Alignment	not modelled	9.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c;

52	c3c65A_	Alignment	not modelled	9.8	10	**PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain
53	c3ajvD_	Alignment	not modelled	9.7	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** splicing endonuclease from aeropyrum pernix
54	c3ktbD_	Alignment	not modelled	9.4	31	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
55	c2yzjB_	Alignment	not modelled	8.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**167aa long hypothetical dutpase; **PDBTitle:** crystal structure of dctp deaminase from sulfolobus tokodaii
56	d2g9ha2	Alignment	not modelled	8.8	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
57	d1es0a2	Alignment	not modelled	8.7	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
58	c2iifA_	Alignment	not modelled	8.5	27	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
59	d1uvqa2	Alignment	not modelled	8.3	25	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
60	d2tpta2	Alignment	not modelled	8.2	15	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
61	c1fctA_	Alignment	not modelled	8.1	43	**PDB header:**transit peptide **Chain:** A: **PDB Molecule:**ferredoxin chloroplastic transit peptide **PDBTitle:** nmr structures of ferredoxin chloroplastic transit peptide2 from chlamydomonas reinhardtii promoted by3 trifluoroethanol in aqueous solution
62	d1fnga2	Alignment	not modelled	8.0	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
63	c2rilA_	Alignment	not modelled	8.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
64	d1wg8a1	Alignment	not modelled	7.7	19	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
65	d1iaka2	Alignment	not modelled	7.6	25	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
66	d2p24a2	Alignment	not modelled	7.6	25	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
67	c3t07D_	Alignment	not modelled	7.4	31	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
68	d1r3sa_	Alignment	not modelled	7.2	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
69	d2nx2a1	Alignment	not modelled	7.1	16	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**YpsA-like
70	c2okdB_	Alignment	not modelled	7.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** high resolution crystal structures of vaccinia virus dutpase
71	d3er7a1	Alignment	not modelled	7.0	24	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Exig0174-like
72	d1mtyb_	Alignment	not modelled	7.0	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
73	d1kbla2	Alignment	not modelled	6.8	33	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
74	d1pkha_	Alignment	not modelled	6.8	25	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
75	c1v8gB_	Alignment	not modelled	6.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
76	c2f4nA_	Alignment	not modelled	6.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mj1651; **PDBTitle:** crystal structure of protein mj1651 from methanococcus2 jannaschii dsm 2661, pfam duf62
77	c3dzoA_	Alignment	not modelled	6.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhoptry kinase domain; **PDBTitle:** crystal structure of a rhoptry kinase from toxoplasma

						gondii
78	d1e6yb1	Alignment	not modelled	6.2	17	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
79	d1klua2	Alignment	not modelled	6.2	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
80	d1xs1a_	Alignment	not modelled	6.2	26	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
81	c2kebA_	Alignment	not modelled	6.1	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
82	c2qxxA_	Alignment	not modelled	6.1	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** bifunctional dctp deaminase: dutpase from mycobacterium tuberculosis2 in complex with dttp
83	c3eeqB_	Alignment	not modelled	5.9	35	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cobalamin biosynthesis protein g **PDBTitle:** crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
84	c2rf4A_	Alignment	not modelled	5.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
85	c2xsdC_	Alignment	not modelled	5.8	12	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**pou domain, class 3, transcription factor 1; **PDBTitle:** crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
86	d3eeqa2	Alignment	not modelled	5.8	35	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
87	d1j93a_	Alignment	not modelled	5.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
88	c3iz6Q_	Alignment	not modelled	5.7	32	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein s17 (s17e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
89	c3ieyA_	Alignment	not modelled	5.7	36	**PDB header:**hydrolase/rna binding protein **Chain:** A: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** crystal structure of the functional nanoarchaeum equitans trna2 splicing endonuclease
90	d2paga1	Alignment	not modelled	5.7	18	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
91	c3k2gA_	Alignment	not modelled	5.6	10	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
92	d1sq8a_	Alignment	not modelled	5.6	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
93	c2bazA_	Alignment	not modelled	5.6	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu20020; **PDBTitle:** structure of yoss, a putative dutpase from bacillus subtilis
94	d1muja2	Alignment	not modelled	5.5	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
95	d1vm7a_	Alignment	not modelled	5.4	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
96	c2fugC_	Alignment	not modelled	5.4	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
97	c2cv8A_	Alignment	not modelled	5.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** crystal structure of trna-intron endonuclease from2 sulfolobus tokodaii
98	c1rr2A_	Alignment	not modelled	5.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
99	c2o0tB_	Alignment	not modelled	5.3	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation