Phyre2

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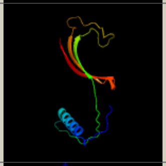
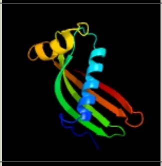
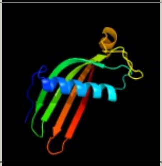
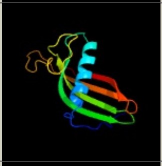
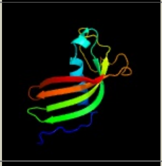
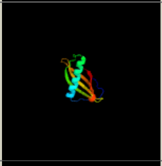
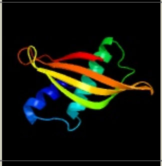
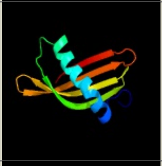
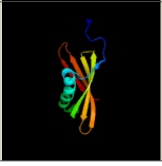
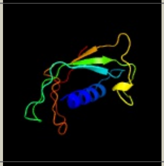
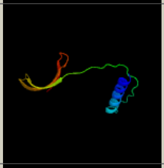
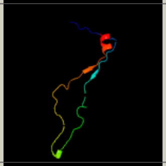
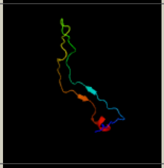
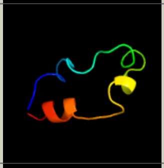
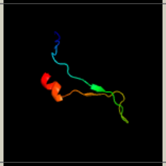
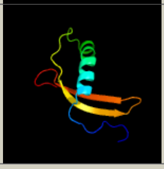
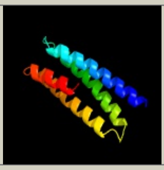
Description	Dangers_of_Intensive
Date	Sun Sep 7 17:29:03 BST 2014
Unique Job ID	093f1646326a5fe1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1roaa_	Alignment		100.0	56	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
2	d1r4ca_	Alignment		100.0	97	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
3	c2ch9A_	Alignment		100.0	33	**PDB header:**inhibitor **Chain:** A: **PDB Molecule:**cystatin f; **PDBTitle:** crystal structure of dimeric human cystatin f
4	d1cewi_	Alignment		100.0	44	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
5	c4it7C_	Alignment		100.0	27	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**cpi; **PDBTitle:** crystal structure of al-cpi
6	c3mwzA_	Alignment		100.0	25	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**sialostatin l2; **PDBTitle:** crystal structure of the selenomethionine derivative of the l 22,47,2 100 m mutant of sialostatin l2
7	c3l0rA_	Alignment		100.0	23	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**cystatin-2; **PDBTitle:** crystal structure of salivary cystatin from the soft tick ornithodoros2 moubata
8	c4lziA_	Alignment		99.9	24	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**multicystatin; **PDBTitle:** characterization of solanum tuberosum multicystatin and significance2 of core domains
9	c2l4vA_	Alignment		99.9	30	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**cystatin; **PDBTitle:** three dimensional structure of pineapple cystatin
10	c3imaD_	Alignment		99.8	30	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**cysteine proteinase inhibitor; **PDBTitle:** complex strcuture of tarocystatin and papain
11	d1eqka_	Alignment		99.8	23	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins

12	c2w9pC_	Alignment		99.8	20	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**multicystatin; **PDBTitle:** crystal structure of potato multicystatin
13	c4eycA_	Alignment		99.8	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cathelicidin antimicrobial peptide; **PDBTitle:** crystal structure of the cathelin-like domain of human cathelicidin2 ll-37 (hcld)
14	c3ul5C_	Alignment		99.7	25	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**canecystatin-1; **PDBTitle:** saccharum officinarum canecystatin-1 in space group c2221
15	d2b4cg1	Alignment		99.6	80	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core
16	d1stfi_	Alignment		99.5	24	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
17	c3j5mI_	Alignment		99.5	72	**PDB header:**viral protein/immune system **Chain:** I: **PDB Molecule:**bg505 sosip gp120; **PDBTitle:** cryo-em structure of the bg505 sosip.664 hiv-1 env trimer with 3 pgv042 fabs
18	c1ce4A_	Alignment		99.0	85	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (v3 loop of hiv-1 envelope protein); **PDBTitle:** conformational model for the consensus v3 loop of the2 envelope protein gp120 of hiv-1
19	c3ngbI_	Alignment		98.7	62	**PDB header:**viral protein/immune system **Chain:** I: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** crystal structure of broadly and potently neutralizing antibody vrc012 in complex with hiv-1 gp120
20	d1nb5i_	Alignment		98.6	24	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
21	d1kwia_	Alignment	not modelled	97.8	22	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cathelicidin motif
22	c4i3rG_	Alignment	not modelled	97.7	51	**PDB header:**viral protein/immune system **Chain:** G: **PDB Molecule:**outer domain of hiv-1 gp120 (ker2018 od4.2.2); **PDBTitle:** crystal structure of the outer domain of hiv-1 gp120 in complex with2 vrc-pg04 space group p3221
23	d2bo9b1	Alignment	not modelled	97.3	17	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Latexin-like
24	c2bo9B_	Alignment	not modelled	96.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**human latexin; **PDBTitle:** human carboxypeptidase a4 in complex with human latexin.
25	c3rjqA_	Alignment	not modelled	96.8	84	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**c186 gp120; **PDBTitle:** crystal structure of anti-hiv llama vhh antibody a12 in complex with2 c186 gp120
26	c3jwdA_	Alignment	not modelled	96.5	91	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 gp120 envelope glycoprotein; **PDBTitle:** structure of hiv-1 gp120 with gp41-interactive region: layered2 architecture and basis of conformational mobility
27	c3dnlB_	Alignment	not modelled	96.3	82	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hiv-1 envelope glycoprotein gp120; **PDBTitle:** molecular structure for the hiv-1 gp120 trimer in the b12-2 bound state
28	d2nxya1	Alignment	not modelled	96.3	79	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core

29	d1yymg1	Alignment	not modelled	95.9	64	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core
30	c4ccvA_	Alignment	not modelled	93.6	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**histidine-rich glycoprotein; **PDBTitle:** crystal structure of histidine-rich glycoprotein n2 domain2 reveals redox activity at an interdomain disulfide bridge:3 implications for the regulation of angiogenesis
31	c3mlwQ_	Alignment	not modelled	92.1	100	**PDB header:**immune system **Chain:** Q: **PDB Molecule:**hiv-1 gp120 third variable region (v3) crown; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 1006-15d in complex with an mn2 v3 peptide
32	c3ujiP_	Alignment	not modelled	92.0	100	**PDB header:**immune system **Chain:** P: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 2558 in complex with mn peptide
33	c3ujjP_	Alignment	not modelled	91.8	65	**PDB header:**immune system **Chain:** P: **PDB Molecule:**gp120; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 4025 in complex with con a2 peptide
34	c2b1aP_	Alignment	not modelled	89.2	75	**PDB header:**immune system **Chain:** P: **PDB Molecule:**ug1033 peptide of exterior membrane glycoprotein gp120; **PDBTitle:** crystal structure analysis of anti-hiv-1 v3 fab 2219 in complex with2 ug1033 peptide
35	c3mlwP_	Alignment	not modelled	88.5	100	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv-1 gp120 third variable region (v3) crown; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 1006-15d in complex with an mn2 v3 peptide
36	c2kxgA_	Alignment	not modelled	80.5	21	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**aspartic protease inhibitor; **PDBTitle:** the solution structure of the squash aspartic acid proteinase2 inhibitor (sqapi)
37	c2bf1A_	Alignment	not modelled	80.0	4	**PDB header:**virus protein **Chain:** A: **PDB Molecule:**exterior membrane glycoprotein gp120; **PDBTitle:** structure of an unliganded and fully-glycosylated siv gp1202 envelope glycoprotein
38	c1y4cA_	Alignment		73.1	12	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
39	c2zv4O_	Alignment	not modelled	58.4	17	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
40	c1acyP_	Alignment	not modelled	43.8	91	**PDB header:**complex(antibody/hiv-1 fragment) **Chain:** P: **PDB Molecule:**hiv-1 gp120 (mn isolate); **PDBTitle:** crystal structure of the principal neutralizing site of hiv-2 1
41	c3mlrP_	Alignment	not modelled	40.0	50	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv-1 gp120 third variable region (v3) crown; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 2557 in complex with a ny5 v32 peptide
42	c2w82C_	Alignment	not modelled	31.4	24	**PDB header:**replication inhibitor **Chain:** C: **PDB Molecule:**orf18; **PDBTitle:** the structure of arda
43	d1fcda3	Alignment	not modelled	29.7	25	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
44	c2e4wA_	Alignment	not modelled	18.0	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 3; **PDBTitle:** crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd
45	c3fewX_	Alignment	not modelled	17.4	21	**PDB header:**immune system **Chain:** X: **PDB Molecule:**colicin s4; **PDBTitle:** structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
46	c3mlvQ_	Alignment	not modelled	15.5	53	**PDB header:**immune system **Chain:** Q: **PDB Molecule:**hiv-1 gp120 third variable region (v3) crown; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 2557 in complex with an nof v32 peptide
47	c3mlvP_	Alignment	not modelled	15.5	53	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv-1 gp120 third variable region (v3) crown; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 2557 in complex with an nof v32 peptide
48	c3oqtP_	Alignment	not modelled	14.7	21	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
49	c3p3wC_	Alignment	not modelled	13.8	23	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**glutamate receptor 3; **PDBTitle:** structure of a dimeric glua3 n-terminal domain (ntd) at 4.2 a2 resolution
50	c3monF_	Alignment	not modelled	13.6	23	**PDB header:**sweet-tasting protein **Chain:** F: **PDB Molecule:**monellin; **PDBTitle:** crystal structures of two intensely sweet proteins
51	d1wkaa1	Alignment	not modelled	12.5	30	**Fold:**ValRS/IleRS/LeuRS editing domain **Superfamily:**ValRS/IleRS/LeuRS editing domain **Family:**ValRS/IleRS/LeuRS editing domain
						PDB header:flavoprotein

52	c2vxaL_	Alignment	not modelled	11.8	29	**Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
53	c3onrI_	Alignment	not modelled	11.3	17	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
54	c2hlqA_	Alignment	not modelled	11.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bone morphogenetic protein receptor type-2; **PDBTitle:** crystal structure of the extracellular domain of the type2 ii bmp receptor
55	c3j20F_	Alignment	not modelled	10.6	10	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**30s ribosomal protein s5p; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
56	d2ux9a1	Alignment	not modelled	10.5	27	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
57	c4uqqD_	Alignment	not modelled	9.1	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**glutamate receptor ionotropic, kainate 2; **PDBTitle:** electron density map of gluk2 desensitized state in2 complex with 2s,4r-4-methylglutamate
58	c4f11A_	Alignment	not modelled	7.9	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**gamma-aminobutyric acid type b receptor subunit 2; **PDBTitle:** crystal structure of the extracellular domain of human gaba(b)2 receptor gbr2
59	d2o9ux1	Alignment	not modelled	7.6	23	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Monellin
60	c3sajB_	Alignment	not modelled	7.6	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate receptor 1; **PDBTitle:** crystal structure of glutamate receptor glua1 amino terminal domain
61	d1ntga_	Alignment	not modelled	7.4	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
62	c3heiF_	Alignment	not modelled	7.3	27	**PDB header:**transferase/signaling protein **Chain:** F: **PDB Molecule:**ephrin-a1; **PDBTitle:** ligand recognition by a-class eph receptors: crystal structures of the2 epha2 ligand-binding domain and the epha2/ephrin-a1 complex
63	c1rrqA_	Alignment	not modelled	6.9	36	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
64	c1zzaA_	Alignment	not modelled	6.8	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
65	d1t1ra3	Alignment	not modelled	6.7	57	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	d2nqda1	Alignment	not modelled	6.6	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ICP-like **Family:**ICP-like
67	d2p3ra1	Alignment	not modelled	6.5	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
68	c2qzvB_	Alignment	not modelled	6.4	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**major vault protein; **PDBTitle:** draft crystal structure of the vault shell at 9 angstroms2 resolution
69	d1mn4a_	Alignment	not modelled	6.4	25	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**DNA-binding domain from NDT80
70	d1vdda_	Alignment	not modelled	6.3	14	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
71	d1iyka1	Alignment	not modelled	6.3	9	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
72	c3om1A_	Alignment	not modelled	6.3	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor gluk5 (ka2); **PDBTitle:** crystal structure of the gluk5 (ka2) atd dimer at 1.7 angstrom2 resolution
73	c4kzzC_	Alignment	not modelled	6.2	20	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**40s ribosomal protein s2; **PDBTitle:** rabbit 40s ribosomal subunit in complex with mrna, initiator trna and2 eif1a
74	d1dx5i1	Alignment	not modelled	6.2	29	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
75	c3qwmA_	Alignment	not modelled	6.1	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**iq motif and sec7 domain-containing protein 1; **PDBTitle:** crystal structure of gep100, the plextrin homology domain of iq motif2 and sec7 domain-containing protein 1 isoform a
76	d1wlta1	Alignment	not modelled	6.1	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
						PDB header:translation

77	c2kkmA_	Alignment	not modelled	6.0	16	**Chain:** A: **PDB Molecule:**translation machinery-associated protein 16; **PDBTitle:** solution nmr structure of yeast protein yor252w [residues2 38-178]: northeast structural genomics consortium target3 yt654
78	d1m5ha2	Alignment	not modelled	5.9	23	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
79	c3kg2A_	Alignment	not modelled	5.9	8	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
80	d1iica1	Alignment	not modelled	5.8	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
81	c2xzmE_	Alignment	not modelled	5.8	19	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein s5 containing protein; **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
82	c1upiA_	Alignment	not modelled	5.7	26	**PDB header:**epimerase **Chain:** A: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** mycobacterium tuberculosis rmlc epimerase (rv3465)
83	c3h6hB_	Alignment	not modelled	5.7	17	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2; **PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form
84	d1zc6a1	Alignment	not modelled	5.7	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
85	c3zeyP_	Alignment	not modelled	5.6	13	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein s2, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
86	c3pz6F_	Alignment	not modelled	5.6	20	**PDB header:**ligase **Chain:** F: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** the crystal structure of glleurs-cp1
87	d2bvya1	Alignment	not modelled	5.5	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
88	c2lmkA_	Alignment	not modelled	5.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**exocrine gland-secreting peptide 1; **PDBTitle:** solution structure of mouse pheromone esp1
89	c4e1jA_	Alignment	not modelled	5.5	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
90	d2j5la1	Alignment	not modelled	5.4	28	**Fold:**Apical membrane antigen 1 **Superfamily:**Apical membrane antigen 1 **Family:**Apical membrane antigen 1
91	c2j5lA_	Alignment	not modelled	5.4	28	**PDB header:**immune system **Chain:** A: **PDB Molecule:**apical membrane antigen 1; **PDBTitle:** structure of a plasmodium falciparum apical membrane2 antigen 1-fab f8.12.19 complex
92	d1jb3a_	Alignment	not modelled	5.4	8	**Fold:**OB-fold **Superfamily:**TIMP-like **Family:**The laminin-binding domain of agrin
93	d1dzra_	Alignment	not modelled	5.3	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
94	c2wfdB_	Alignment	not modelled	5.3	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**leucyl-trna synthetase, cytoplasmic; **PDBTitle:** structure of the human cytosolic leucyl-trna synthetase2 editing domain
95	c1m5hF_	Alignment	not modelled	5.2	23	**PDB header:**transferase **Chain:** F: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin **PDBTitle:** formylmethanofuran:tetrahydromethanopterin2 formyltransferase from archaeoglobus fulgidus
96	c2ysaA_	Alignment	not modelled	5.2	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6; **PDBTitle:** solution structure of the zinc finger cchc domain from the2 human retinoblastoma-binding protein 6 (retinoblastoma-3 binding q protein 1, rbq-1)
97	c2fwvA_	Alignment	not modelled	5.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mtubf_01000852; **PDBTitle:** crystal structure of rv0813
98	c1vddC_	Alignment	not modelled	5.2	13	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
99	d1gr0a2	Alignment	not modelled	5.2	19	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like