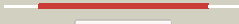



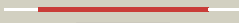





















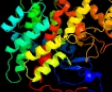






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1131_(gltA1)_1256137_1257318
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	a2de23e4edafb24a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3hwkE_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> methylcitrate synthase; <b>PDBTitle:</b> crystal structure of methylcitrate synthase from mycobacterium2 tuberculosis
2	<a href="#">c2h12C_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> structure of acetobacter aceti citrate synthase complexed with2 oxaloacetate and carboxymethyldehia coenzyme a (cmx)
3	<a href="#">c3msuA_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> crystal structure of citrate synthase from francisella tularensis
4	<a href="#">d1a59a_</a>	 Alignment		100.0	59	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
5	<a href="#">d1k3pa_</a>	 Alignment		100.0	28	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
6	<a href="#">d1ioma_</a>	 Alignment		100.0	41	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
7	<a href="#">d1aj8a_</a>	 Alignment		100.0	40	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
8	<a href="#">c1vgpA_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 373aa long hypothetical citrate synthase; <b>PDBTitle:</b> crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
9	<a href="#">c2ibpB_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> crystal structure of citrate synthase from pyrobaculum aerophilum
10	<a href="#">c6abxA_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> crystal structure of citrate synthase (msed_1522) from metallospiraera2 sedula in complex with citrate
11	<a href="#">c1vgmB_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 378aa long hypothetical citrate synthase; <b>PDBTitle:</b> crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7

12	<a href="#">c2c6xA_</a>	Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrate synthase 1; <b>PDBTitle:</b> structure of bacillus subtilis citrate synthase
13	<a href="#">d1csHA_</a>	Alignment		100.0	23	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
14	<a href="#">c2r26C_</a>	Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum
15	<a href="#">d1o7xA_</a>	Alignment		100.0	35	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
16	<a href="#">d2ctsa_</a>	Alignment		100.0	23	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
17	<a href="#">d1csca_</a>	Alignment		100.0	24	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
18	<a href="#">c3tqgA_</a>	Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-methylcitrate synthase; <b>PDBTitle:</b> structure of the 2-methylcitrate synthase (prpc) from coxiella2 burnetii
19	<a href="#">c3o8jH_</a>	Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> 2-methylcitrate synthase; <b>PDBTitle:</b> crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
20	<a href="#">c2p2wA_</a>	Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> crystal structure of citrate synthase from thermotoga maritima msb8
21	<a href="#">c4tvmA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> structure of citrate synthase from mycobacterium tuberculosis
22	<a href="#">c5uqqD_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-methylcitrate synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of 2-methylcitrate synthase from aspergillus2 fumigatus
23	<a href="#">c4xgHA_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> x-ray crystal structure of citrate synthase from burkholderia2 thailandensis
24	<a href="#">c6hxpA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> citryl-coa lyase; <b>PDBTitle:</b> structure of citryl-coa lyase from hydrogenobacter thermophilus
25	<a href="#">c6hxjB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate lyase alpha-subunit; <b>PDBTitle:</b> structure of atp citrate lyase from chlorobium limicola in complex2 with citrate and coenzyme a.
26	<a href="#">c6hxiD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa ligase (adp-forming) subunit alpha; <b>PDBTitle:</b> structure of atp citrate lyase from methanotrux soehngeni in complex2 with citrate and coenzyme a
27	<a href="#">c6hxoH_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> atp-citrate lyase alpha-subunit; <b>PDBTitle:</b> structure of the citryl-coa lyase core module of chlorobium limicola2 atp citrate lyase (space group p21)
28	<a href="#">c6hxiD_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> structure of the citryl-coa lyase core module of human

						atp citrate2 lyase in complex with citrate and coash (space group p21)
29	<a href="#">c6qfbB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> structure of the human atp citrate lyase holoenzyme in complex with2 citrate, coenzyme a and mg.adp
30	<a href="#">c6hxoE</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> atp-citrate lyase alpha-subunit; <b>PDBTitle:</b> structure of the citryl-coa lyase core module of chlorobium limicola2 atp citrate lyase (space group p21)
31	<a href="#">c3zeyl</a>	Alignment	not modelled	55.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> I; <b>PDB Molecule:</b> 40s ribosomal protein s15, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
32	<a href="#">c3j38P</a>	Alignment	not modelled	52.6	29	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> 40s ribosomal protein s15, isoform a; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
33	<a href="#">c2xzmS</a>	Alignment	not modelled	49.7	27	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> rps15e; <b>PDBTitle:</b> 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
34	<a href="#">c3j20T</a>	Alignment	not modelled	46.8	43	<b>PDB header:</b> ribosome <b>Chain:</b> T; <b>PDB Molecule:</b> 30s ribosomal protein s19p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
35	<a href="#">c5xyiP</a>	Alignment	not modelled	38.9	38	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> ribosomal protein s19, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
36	<a href="#">c3if8B</a>	Alignment	not modelled	34.8	15	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> protein zwilch homolog; <b>PDBTitle:</b> crystal structure of zwilch, a member of the rzz kinetochore complex
37	<a href="#">c5xxuP</a>	Alignment	not modelled	32.6	29	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> ribosomal protein us19; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
38	<a href="#">c4ay8B</a>	Alignment	not modelled	30.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methylcobalamin\; coenzyme m methyltransferase; <b>PDBTitle:</b> semet-derivative of a methyltransferase from m. mazei
39	<a href="#">c1jpkA</a>	Alignment	not modelled	23.8	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
40	<a href="#">d1poib</a>	Alignment	not modelled	23.8	18	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase beta subunit-like
41	<a href="#">c2ly8A</a>	Alignment	not modelled	22.3	20	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> budding yeast chaperone scm3; <b>PDBTitle:</b> the budding yeast chaperone scm3 recognizes the partially unfolded2 dimer of the centromere-specific cse4/h4 histone variant
42	<a href="#">d1r3sa</a>	Alignment	not modelled	19.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
43	<a href="#">c5n02B</a>	Alignment	not modelled	18.6	16	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> glutaconate coa-transferase family, subunit b; <b>PDBTitle:</b> crystal structure of the decarboxylase aiba/aibb c56s variant
44	<a href="#">d2huec1</a>	Alignment	not modelled	18.1	14	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
45	<a href="#">c3cyvA</a>	Alignment	not modelled	14.9	19	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from2 shigella flexneri: new insights into its catalytic3 mechanism
46	<a href="#">c1rr2A</a>	Alignment	not modelled	14.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
47	<a href="#">c6co6B</a>	Alignment	not modelled	14.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> probable coa-transferase beta subunit; <b>PDBTitle:</b> crystal structure of rhodococcus jostii rha1 ipdab
48	<a href="#">d1kx5b</a>	Alignment	not modelled	14.7	14	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
49	<a href="#">c2nx9B</a>	Alignment	not modelled	13.7	12	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
50	<a href="#">d1mtyb</a>	Alignment	not modelled	13.3	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
51	<a href="#">c4y0cB</a>	Alignment	not modelled	12.2	10	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> clp protease-related protein at4g12060, chloroplastic; <b>PDBTitle:</b> the structure of arabidopsis clpt2
52	<a href="#">d1id3b</a>	Alignment	not modelled	12.1	12	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
53	<a href="#">c2infB</a>	Alignment	not modelled	11.1	11	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from

						bacillus2 subtilis
54	<a href="#">c3j20S_</a>	Alignment	not modelled	10.7	16	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 30s ribosomal protein s17e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
55	<a href="#">c5xxuR_</a>	Alignment	not modelled	10.6	24	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> ribosomal protein es17; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
56	<a href="#">c3o30L_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 40s ribosomal protein s15; <b>PDBTitle:</b> yeast 80s ribosome. this entry consists of the 40s subunit of the2 second 80s in the asymmetric unit.
57	<a href="#">d1khda2</a>	Alignment	not modelled	10.2	26	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
58	<a href="#">c2l5aA_</a>	Alignment	not modelled	10.0	20	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h3-like centromeric protein cse4, protein scm3, <b>PDBTitle:</b> structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
59	<a href="#">c2l0cA_</a>	Alignment	not modelled	9.5	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> solution nmr structure of protein sty4237 (residues 36-120) from2 salmonella enterica, northeast structural genomics consortium target3 slr115
60	<a href="#">c1j9zB_</a>	Alignment	not modelled	9.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-cytochrome p450 reductase; <b>PDBTitle:</b> cypor-w677g
61	<a href="#">c5t59D_</a>	Alignment	not modelled	8.6	17	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> klla0f02343p; <b>PDBTitle:</b> structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
62	<a href="#">d1mhyb_</a>	Alignment	not modelled	8.1	21	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
63	<a href="#">c3ajvD_</a>	Alignment	not modelled	7.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> trna-splicing endonuclease; <b>PDBTitle:</b> splicing endonuclease from aeropyrum pernix
64	<a href="#">d1hiod_</a>	Alignment	not modelled	7.8	25	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
65	<a href="#">c5foeA_</a>	Alignment	not modelled	7.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-fucose protein o-fucosyltransferase 2,thrombospondin-1; <b>PDBTitle:</b> crystal structure of the c. elegans protein o-fucosyltransferase 22 (cepofut2) double mutant (r298k-r299k) in complex with gdp and the3 human tsr1 from thrombospondin 1
66	<a href="#">c3j3aR_</a>	Alignment	not modelled	7.4	24	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 40s ribosomal protein s17; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
67	<a href="#">c5dizB_</a>	Alignment	not modelled	7.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proteinaceous rnase p 2; <b>PDBTitle:</b> crystal structure of nuclear proteinaceous rnase p 2 (prop2) from a.2 thaliana
68	<a href="#">c3t5qA_</a>	Alignment	not modelled	6.9	17	<b>PDB header:</b> viral protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> 3a structure of lassa virus nucleoprotein in complex with ssrna
69	<a href="#">d1mula_</a>	Alignment	not modelled	6.7	16	<b>Fold:</b> IHF-like DNA-binding proteins <b>Superfamily:</b> IHF-like DNA-binding proteins <b>Family:</b> Prokaryotic DNA-binding protein
70	<a href="#">c1fctA_</a>	Alignment	not modelled	6.5	100	<b>PDB header:</b> transit peptide <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin chloroplastic transit peptide <b>PDBTitle:</b> nmr structures of ferredoxin chloroplastic transit peptide2 from chlamydomonas reinhardtii promoted by3 trifluoroethanol in aqueous solution
71	<a href="#">d1orna_</a>	Alignment	not modelled	6.5	11	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
72	<a href="#">c6efvA_</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [nadph] flavoprotein alpha-component; <b>PDBTitle:</b> the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
73	<a href="#">c3dzoA_</a>	Alignment	not modelled	6.4	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhoptry kinase domain; <b>PDBTitle:</b> crystal structure of a rhoptry kinase from toxoplasma gondii
74	<a href="#">c4gyxA_</a>	Alignment	not modelled	6.4	56	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
75	<a href="#">c4gyxB_</a>	Alignment	not modelled	6.4	56	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
76	<a href="#">c4e2i3_</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> hydrolase/dna binding protein <b>Chain:</b> 3: <b>PDB Molecule:</b> dna polymerase alpha subunit b; <b>PDBTitle:</b> the complex structure of the sv40 helicase large t antigen and p682 subunit of dna polymerase alpha-primase

77	<a href="#">c2kebA</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase subunit alpha b; <b>PDBTitle:</b> nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
78	<a href="#">c3tkaA</a>	Alignment	not modelled	6.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase h; <b>PDBTitle:</b> crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
79	<a href="#">d1b8za</a>	Alignment	not modelled	6.3	38	<b>Fold:</b> IHF-like DNA-binding proteins <b>Superfamily:</b> IHF-like DNA-binding proteins <b>Family:</b> Prokaryotic DNA-bending protein
80	<a href="#">d2nx2a1</a>	Alignment	not modelled	6.3	18	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> YpsA-like
81	<a href="#">c5f4tA</a>	Alignment	not modelled	6.2	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> izumo sperm-egg fusion protein 1; <b>PDBTitle:</b> crystal structure of the human sperm izumo1 residues 22-254
82	<a href="#">c6nmiE</a>	Alignment	not modelled	6.2	16	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> general transcription factor iih subunit 2, p44; <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
83	<a href="#">c4gyxC</a>	Alignment	not modelled	6.1	56	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
84	<a href="#">d1uoua2</a>	Alignment	not modelled	6.0	15	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
85	<a href="#">d1e29a</a>	Alignment	not modelled	5.9	11	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
86	<a href="#">c4dmtC</a>	Alignment	not modelled	5.9	56	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
87	<a href="#">c4dmtB</a>	Alignment	not modelled	5.9	56	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
88	<a href="#">c4dmtA</a>	Alignment	not modelled	5.9	56	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
89	<a href="#">c6hemA</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 25; <b>PDBTitle:</b> structure of the c-terminal domain of usp25 (748-1048)
90	<a href="#">c4ga5H</a>	Alignment	not modelled	5.8	11	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> putative thymidine phosphorylase; <b>PDBTitle:</b> crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
91	<a href="#">d1fhea1</a>	Alignment	not modelled	5.8	10	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
92	<a href="#">c6conF</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> coa-transferase subunit beta; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis ipdab
93	<a href="#">d2csba3</a>	Alignment	not modelled	5.7	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
94	<a href="#">c2v53D</a>	Alignment	not modelled	5.7	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
95	<a href="#">c2v53B</a>	Alignment	not modelled	5.7	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
96	<a href="#">c2v53C</a>	Alignment	not modelled	5.7	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
97	<a href="#">c4exqA</a>	Alignment	not modelled	5.7	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
98	<a href="#">d2pbla1</a>	Alignment	not modelled	5.7	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
99	<a href="#">c1tllA</a>	Alignment	not modelled	5.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide synthase, brain; <b>PDBTitle:</b> crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.