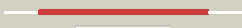
















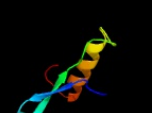

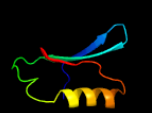


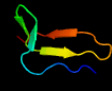


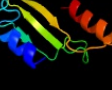



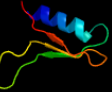



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1321_(-)_1484285_1484965
Date	Wed Jul 31 22:05:42 BST 2019
Unique Job ID	5e8fb648db8b32c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5gkeB_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease endoms; <b>PDBTitle:</b> structure of endoms-dsdna1 complex
2	<a href="#">c2vldA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease nucs; <b>PDBTitle:</b> crystal structure of a repair endonuclease from pyrococcus abyssi
3	<a href="#">d1y88a2</a>	 Alignment		96.8	12	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> MRR-like
4	<a href="#">c3fovA_</a>	 Alignment		96.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0102 protein rpa0323; <b>PDBTitle:</b> crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
5	<a href="#">c1y88A_</a>	 Alignment		96.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1548; <b>PDBTitle:</b> crystal structure of protein of unknown function af1548
6	<a href="#">d1xmx_</a>	 Alignment		95.7	13	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Hypothetical protein VC1899
7	<a href="#">c5zyuA_</a>	 Alignment		95.0	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial genome maintenance exonuclease 1; <b>PDBTitle:</b> the crytal struture of humanmgme1 with single strand dna2
8	<a href="#">c4ic1D_</a>	 Alignment		94.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of sso0001
9	<a href="#">c4onbA_</a>	 Alignment		93.8	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated exonuclease, cas4 family; <b>PDBTitle:</b> crystal structure of crispr-associated exonuclease (cas4 family) from2 pyrobaculum calidifontis jcm 11548
10	<a href="#">c3u4qA_</a>	 Alignment		93.3	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent helicase/nuclease subunit a; <b>PDBTitle:</b> structure of addab-dna complex at 2.8 angstroms
11	<a href="#">c3h1tA_</a>	 Alignment		93.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type i site-specific restriction-modification <b>PDBTitle:</b> the fragment structure of a putative hsdR subunit of a type2 i restriction enzyme from vibrio vulnificus yj016

12	<a href="#">c3dnxA</a>	Alignment		92.9	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein spo1766; <b>PDBTitle:</b> spo1766 protein of unknown function from silicibacter pomeroyi.
13	<a href="#">c4oc8A</a>	Alignment		91.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> restriction endonuclease aspghi; <b>PDBTitle:</b> dna modification-dependent restriction endonuclease aspghi
14	<a href="#">c1w36E</a>	Alignment		88.7	26	<b>PDB header:</b> recombination <b>Chain:</b> E; <b>PDB Molecule:</b> exodeoxyribonuclease v beta chain; <b>PDBTitle:</b> recbcd:dna complex
15	<a href="#">c2eo0A</a>	Alignment		88.6	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein st1444; <b>PDBTitle:</b> crystal structure of holliday junction resolvase st1444
16	<a href="#">d1gefa</a>	Alignment		83.8	24	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Hjc-like
17	<a href="#">c2wj0B</a>	Alignment		83.5	34	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> archaeal hjc; <b>PDBTitle:</b> crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
18	<a href="#">d1hh1a</a>	Alignment		83.0	23	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Hjc-like
19	<a href="#">c4qbnA</a>	Alignment		79.6	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nuclease; <b>PDBTitle:</b> vrr_nuc domain
20	<a href="#">d1ob8a</a>	Alignment		79.4	29	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Hjc-like
21	<a href="#">d1w36b3</a>	Alignment	not modelled	78.8	26	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
22	<a href="#">c5eaxB</a>	Alignment	not modelled	77.3	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> dna replication atp-dependent helicase/nuclease dna2; <b>PDBTitle:</b> crystal structure of dna2 in complex with an ssdna
23	<a href="#">c4dapA</a>	Alignment	not modelled	76.1	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> sugar fermentation stimulation protein a; <b>PDBTitle:</b> the structure of escherichia coli sfsa
24	<a href="#">c3r3pB</a>	Alignment	not modelled	66.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> mobile intron protein; <b>PDBTitle:</b> homing endonuclease i-bth0305i catalytic domain
25	<a href="#">d2inba1</a>	Alignment	not modelled	65.4	26	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> XisH-like
26	<a href="#">c3u44B</a>	Alignment	not modelled	64.6	26	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> atp-dependent helicase/deoxyribonuclease subunit b; <b>PDBTitle:</b> crystal structure of addab-dna complex
27	<a href="#">c6hz9N</a>	Alignment	not modelled	62.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> N; <b>PDB Molecule:</b> protein mcrC; <b>PDBTitle:</b> structure of mcrbc without dna binding domains (class 5)
28	<a href="#">c4qbaA</a>	Alignment	not modelled	62.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nuclease; <b>PDBTitle:</b> vrr_nuc domain
						<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> sugar fermentation stimulation protein

29	<a href="#">c4davA</a>	Alignment	not modelled	60.7	22	homolog; <b>PDBTitle:</b> the structure of pyrococcus furiosus sfsa in complex with dna
30	<a href="#">c2w00B</a>	Alignment	not modelled	59.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> hsdr; <b>PDBTitle:</b> crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme in complex with atp
31	<a href="#">d1rxxa</a>	Alignment	not modelled	59.0	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Arginine deiminase
32	<a href="#">c6h2jB</a>	Alignment	not modelled	56.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> type i restriction enzyme r protein; <b>PDBTitle:</b> crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme with the c-terminal domain
33	<a href="#">d2okfa1</a>	Alignment	not modelled	56.4	21	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> XisH-like
34	<a href="#">c3frmF</a>	Alignment	not modelled	55.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F; <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown conserved protein from2 staphylococcus epidermidis atcc 12228.
35	<a href="#">c8jdwA</a>	Alignment	not modelled	54.2	8	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (l-arginine:glycine amidinotransferase); <b>PDBTitle:</b> crystal structure of human l-arginine:glycine amidinotransferase in2 complex with l-alanine
36	<a href="#">c4e4jj</a>	Alignment	not modelled	51.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> J; <b>PDB Molecule:</b> arginine deiminase; <b>PDBTitle:</b> crystal structure of arginine deiminase from mycoplasma penetrans
37	<a href="#">d1jdwa</a>	Alignment	not modelled	50.8	8	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Amidinotransferase
38	<a href="#">c1jdwA</a>	Alignment	not modelled	50.8	8	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> l-arginine\glycine amidinotransferase; <b>PDBTitle:</b> crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
39	<a href="#">c4bofA</a>	Alignment	not modelled	50.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> arginine deiminase; <b>PDBTitle:</b> crystal structure of arginine deiminase from group a streptococcus
40	<a href="#">d1s9ra</a>	Alignment	not modelled	50.3	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Arginine deiminase
41	<a href="#">c5zrtB</a>	Alignment	not modelled	49.6	7	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> upf0587 protein c1orf123; <b>PDBTitle:</b> crystal structure of human c1orf123 protein
42	<a href="#">c5wpiB</a>	Alignment	not modelled	48.3	5	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> hsva; <b>PDBTitle:</b> the virulence-associated protein hsva from the fire blight pathogen2 erwinia amylovora is a polyamine amidinotransferase
43	<a href="#">d1bwda</a>	Alignment	not modelled	41.9	15	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Amidinotransferase
44	<a href="#">c1zczA</a>	Alignment	not modelled	35.7	20	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
45	<a href="#">c3p42D</a>	Alignment	not modelled	34.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
46	<a href="#">c2kgyA</a>	Alignment	not modelled	34.3	40	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> possible exported protein; <b>PDBTitle:</b> solution structure of rv0603 protein from mycobacterium2 tuberculosis h37rv
47	<a href="#">c2w74B</a>	Alignment	not modelled	34.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> type i restriction enzyme ecor124ii r protein; <b>PDBTitle:</b> mutant (k220r) of the hsdR subunit of the ecor124i2 restriction enzyme in complex with atp
48	<a href="#">c3m7aA</a>	Alignment	not modelled	33.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of saro_0823 (yp_496102.1) a protein of unknown2 function from novosphingobium aromaticivorans dsm 12444 at 1.22 a3 resolution
49	<a href="#">d1zcz2</a>	Alignment	not modelled	32.9	20	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
50	<a href="#">d2pyta1</a>	Alignment	not modelled	31.7	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> EutQ-like
51	<a href="#">d1zsoa1</a>	Alignment	not modelled	31.4	11	<b>Fold:</b> MAL13P1.257-like <b>Superfamily:</b> MAL13P1.257-like <b>Family:</b> MAL13P1.257-like
52	<a href="#">d1pkxa2</a>	Alignment	not modelled	30.4	18	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
53	<a href="#">c3l0aA</a>	Alignment	not modelled	29.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative exonuclease; <b>PDBTitle:</b> crystal structure of putative exonuclease

						(rer070207002219) from2 eubacterium rectale at 2.19 a resolution
54	<a href="#">c4f0qC</a>	Alignment	not modelled	28.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> restriction endonuclease; <b>PDBTitle:</b> mspji restriction endonuclease - p21 form
55	<a href="#">c3gg6A</a>	Alignment	not modelled	26.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 18; <b>PDBTitle:</b> crystal structure of the nudix domain of human nudt18
56	<a href="#">c2dnrA</a>	Alignment	not modelled	26.4	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> synaptojanin-1; <b>PDBTitle:</b> solution structure of rna binding domain in synaptojanin 1
57	<a href="#">d1h70a</a>	Alignment	not modelled	25.9	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Dimethylarginine dimethylaminohydrolase DDAH
58	<a href="#">c2rfpA</a>	Alignment	not modelled	25.5	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ntp pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
59	<a href="#">c4v194</a>	Alignment	not modelled	24.5	55	<b>PDB header:</b> ribosome <b>Chain:</b> 4: <b>PDB Molecule:</b> mitoribosomal protein bl31m, mrpl55; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
60	<a href="#">c3pjyB</a>	Alignment	not modelled	24.0	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical signal peptide protein; <b>PDBTitle:</b> crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
61	<a href="#">c3j21P</a>	Alignment	not modelled	23.5	24	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 50s ribosomal protein l18e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
62	<a href="#">d1ufwa</a>	Alignment	not modelled	23.2	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
63	<a href="#">d2bvca1</a>	Alignment	not modelled	22.4	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Glutamine synthetase, N-terminal domain <b>Family:</b> Glutamine synthetase, N-terminal domain
64	<a href="#">c1thzA</a>	Alignment	not modelled	22.3	12	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
65	<a href="#">d1f52a1</a>	Alignment	not modelled	21.8	7	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Glutamine synthetase, N-terminal domain <b>Family:</b> Glutamine synthetase, N-terminal domain
66	<a href="#">d1g8ma2</a>	Alignment	not modelled	21.7	11	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
67	<a href="#">c2zkro</a>	Alignment	not modelled	21.1	28	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> O: <b>PDB Molecule:</b> rna expansion segment es30; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
68	<a href="#">c3iz5R</a>	Alignment	not modelled	20.5	32	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 60s ribosomal protein l18 (l18e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
69	<a href="#">c3j3bQ</a>	Alignment	not modelled	20.5	28	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l18; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
70	<a href="#">c4kyxA</a>	Alignment	not modelled	20.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribose pyrophosphatase mutt; <b>PDBTitle:</b> crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
71	<a href="#">c3zf7I</a>	Alignment	not modelled	19.1	36	<b>PDB header:</b> ribosome <b>Chain:</b> l: <b>PDB Molecule:</b> 60s ribosomal protein l18; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
72	<a href="#">c3hrlA</a>	Alignment	not modelled	18.4	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease-like protein; <b>PDBTitle:</b> crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
73	<a href="#">c4a1aN</a>	Alignment	not modelled	18.0	32	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> rpl18; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 3.
74	<a href="#">c2b5dX</a>	Alignment	not modelled	17.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
75	<a href="#">c3j39Q</a>	Alignment	not modelled	17.7	28	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l18; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
76	<a href="#">d1k2ea</a>	Alignment	not modelled	17.6	12	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MuT-like
77	<a href="#">d2phla1</a>	Alignment	not modelled	16.3	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
78	<a href="#">c4qc8A</a>	Alignment	not modelled	16.2	33	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> vp2; <b>PDBTitle:</b> structural annotation of pathogenic bovine parvovirus-1

79	<a href="#">c3fcmA</a>	Alignment	not modelled	16.0	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a nudix hydrolase from clostridium perfringens
80	<a href="#">c4b6aQ</a>	Alignment	not modelled	15.9	36	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l18-b; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
81	<a href="#">d2rnrbl</a>	Alignment	not modelled	15.5	21	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> TFIIH domain
82	<a href="#">d1f3va</a>	Alignment	not modelled	15.2	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> TRADD, N-terminal domain <b>Family:</b> TRADD, N-terminal domain
83	<a href="#">c5ovqL</a>	Alignment	not modelled	14.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> peroxiredoxin; <b>PDBTitle:</b> crystal structure of the peroxiredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
84	<a href="#">c5ikfB</a>	Alignment	not modelled	14.7	40	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cryptic loci regulator protein 1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the mit1 nucleosome2 remodeler in complex with clr1
85	<a href="#">d1irya</a>	Alignment	not modelled	14.5	16	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
86	<a href="#">c3h4rA</a>	Alignment	not modelled	14.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease 8; <b>PDBTitle:</b> crystal structure of e. coli rece exonuclease
87	<a href="#">d1m0da</a>	Alignment	not modelled	14.4	19	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Endonuclease I (Holliday junction resolvase)
88	<a href="#">c4ehiB</a>	Alignment	not modelled	13.9	19	<b>PDB header:</b> hydrolase,transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
89	<a href="#">d2oyza1</a>	Alignment	not modelled	13.9	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> VPA0057-like
90	<a href="#">d2cyua1</a>	Alignment	not modelled	13.8	32	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
91	<a href="#">d1rpya</a>	Alignment	not modelled	13.6	13	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
92	<a href="#">c3eo6B</a>	Alignment	not modelled	13.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of unknown function (duf1255); <b>PDBTitle:</b> crystal structure of protein of unknown function (duf1255) (afe_2634)2 from acidithiobacillus ferrooxidans ncbi8455 at 0.97 a resolution
93	<a href="#">c3kieF</a>	Alignment	not modelled	13.1	33	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> capsid protein vp1; <b>PDBTitle:</b> crystal structure of adeno-associated virus serotype 3b
94	<a href="#">c2rrkA</a>	Alignment	not modelled	13.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of the e. coli orf135 protein
95	<a href="#">c4ce4l</a>	Alignment	not modelled	12.9	17	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
96	<a href="#">c4a1oB</a>	Alignment	not modelled	12.7	28	<b>PDB header:</b> transferase-hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
97	<a href="#">d1lp3a</a>	Alignment	not modelled	12.5	33	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> ssDNA viruses <b>Family:</b> Parvoviridae-like VP
98	<a href="#">d3euqa</a>	Alignment	not modelled	12.3	23	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
99	<a href="#">d1jkna</a>	Alignment	not modelled	12.3	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like