







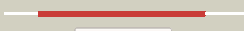













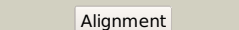

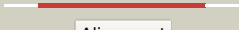








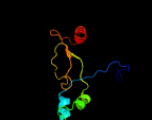






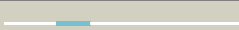





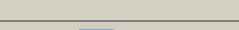
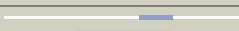


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3378c (- )_3792538_3793428
Date	Fri Aug 9 18:20:04 BST 2019
Unique Job ID	c1b424aefddd301e

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4cmxB_</a>	 Alignment		100.0	100	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> rv3378c; <b>PDBTitle:</b> crystal structure of rv3378c
2	<a href="#">c6acsA_</a>	 Alignment		98.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)-) <b>PDBTitle:</b> poly-cis-prenyltransferase
3	<a href="#">c4h8eA_</a>	 Alignment		98.6	13	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthase; <b>PDBTitle:</b> structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
4	<a href="#">c2vg2C_</a>	 Alignment		98.5	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthetase; <b>PDBTitle:</b> rv2361 with ipp
5	<a href="#">c5hc7A_</a>	 Alignment		98.5	14	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> prenyltransferase for protein; <b>PDBTitle:</b> crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thiolo-isopentenylidiphosphate
6	<a href="#">c5hxpA_</a>	 Alignment		98.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> (2z,6z)-farnesyl diphosphate synthase, chloroplastic; <b>PDBTitle:</b> crystal structure of z,z-farnesyl diphosphate synthase (d71m, e75a and2 h103y mutants) complexed with ipp
7	<a href="#">c4q9mA_</a>	 Alignment		98.4	16	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> isoprenyl transferase; <b>PDBTitle:</b> crystal structure of upps in complex with fpp and an allosteric2 inhibitor
8	<a href="#">d1f75a_</a>	 Alignment		98.3	16	<b>Fold:</b> Undecaprenyl diphosphate synthase <b>Superfamily:</b> Undecaprenyl diphosphate synthase <b>Family:</b> Undecaprenyl diphosphate synthase
9	<a href="#">d1ueha_</a>	 Alignment		98.3	17	<b>Fold:</b> Undecaprenyl diphosphate synthase <b>Superfamily:</b> Undecaprenyl diphosphate synthase <b>Family:</b> Undecaprenyl diphosphate synthase
10	<a href="#">c3ugsB_</a>	 Alignment		98.3	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
11	<a href="#">c1jp3A_</a>	 Alignment		98.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthase; <b>PDBTitle:</b> structure of e.coli undecaprenyl pyrophosphate synthase

12	<a href="#">c2d2rA_</a>	 Alignment		98.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
13	<a href="#">c2vfwB_</a>	 Alignment		98.1	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain z-isoprenyl diphosphate synthetase; <b>PDBTitle:</b> rv1086 native
14	<a href="#">c5xk9F_</a>	 Alignment		97.7	18	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> undecaprenyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of isosquilavandulyl diphosphate synthase from2 streptomyces sp. strain cnh-189 in complex with gsp and dmapp
15	<a href="#">c5gukA_</a>	 Alignment		97.1	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclolavandulyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of apo form of cyclolavandulyl diphosphate synthase2 (clds) from streptomyces sp. cl190
16	<a href="#">d1jhfa1</a>	 Alignment		68.7	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
17	<a href="#">c6jcnB_</a>	 Alignment		58.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrodolichyl diphosphate synthase complex subunit nus1; <b>PDBTitle:</b> yeast dehydrodolichyl diphosphate synthase complex subunit nus1
18	<a href="#">c4kviA_</a>	 Alignment		45.1	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid alpha-oxidase; <b>PDBTitle:</b> crystal structure of oryza sativa fatty acid alpha-dioxygenase with2 hydrogen peroxide
19	<a href="#">c5iq5A_</a>	 Alignment		44.4	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> macro domain; <b>PDBTitle:</b> nmr solution structure of mayaro virus macro domain
20	<a href="#">c2kmuA_</a>	 Alignment		38.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase q4; <b>PDBTitle:</b> recq14 amino-terminal domain
21	<a href="#">d1k8ba_</a>	 Alignment	not modelled	37.9	19	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Translation initiation factor 2 beta, aIF2beta, N-terminal domain <b>Family:</b> Translation initiation factor 2 beta, aIF2beta, N-terminal domain
22	<a href="#">d1xo1a2</a>	 Alignment	not modelled	31.9	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
23	<a href="#">d1qwga_</a>	 Alignment	not modelled	30.7	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
24	<a href="#">c6b1zA_</a>	 Alignment	not modelled	30.7	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from elizabethkingia2 anophelis
25	<a href="#">c2e9hA_</a>	 Alignment	not modelled	30.2	30	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
26	<a href="#">c5hr4J_</a>	 Alignment	not modelled	26.9	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> J: <b>PDB Molecule:</b> mmei; <b>PDBTitle:</b> structure of type iii restriction-modification enzyme mmei in complex2 with dna has implications for engineering of new specificities
27	<a href="#">c3ff4A_</a>	 Alignment	not modelled	26.5	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein chu_1412
28	<a href="#">d1cvua1</a>	 Alignment	not modelled	25.7	10	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Myeloperoxidase-like

29	<a href="#">c1ddxA</a>	Alignment	not modelled	25.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (prostaglandin h2 synthase-2); <b>PDBTitle:</b> crystal structure of a mixture of arachidonic acid and prostaglandin2 bound to the cyclooxygenase active site of cox-2: prostaglandin3 structure
30	<a href="#">c5bthA</a>	Alignment	not modelled	24.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> decapping nuclease rail1; <b>PDBTitle:</b> crystal structure of candida albicans rail1
31	<a href="#">c1oheA</a>	Alignment	not modelled	24.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cdc14b2 phosphatase; <b>PDBTitle:</b> structure of cdc14b phosphatase with a peptide ligand
32	<a href="#">c1pggB</a>	Alignment	not modelled	23.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> prostaglandin h2 synthase-1; <b>PDBTitle:</b> prostaglandin h2 synthase-1 complexed with 1-(4-iodobenzoyl)-5-2 methoxy-2-methylindole-3-acetic acid (iodoindomethacin), trans model
33	<a href="#">c1ht8B</a>	Alignment	not modelled	23.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> prostaglandin h2 synthase-1; <b>PDBTitle:</b> the 2.7 angstrom resolution model of ovine cox-1 complexed with2 alclofenac
34	<a href="#">d1bdga2</a>	Alignment	not modelled	22.9	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
35	<a href="#">c3pghD</a>	Alignment	not modelled	22.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> cyclooxygenase-2; <b>PDBTitle:</b> cyclooxygenase-2 (prostaglandin synthase-2) complexed with a non-2 selective inhibitor, flurbiprofen
36	<a href="#">c6md3F</a>	Alignment	not modelled	22.4	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rrp44p homologue; <b>PDBTitle:</b> structure of t. brucei rrp44 pin domain
37	<a href="#">d1q4ga1</a>	Alignment	not modelled	22.1	17	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Myeloperoxidase-like
38	<a href="#">c1ig8A</a>	Alignment	not modelled	21.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase pii; <b>PDBTitle:</b> crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
39	<a href="#">c4zwwA</a>	Alignment	not modelled	21.0	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of human rhodopsin, mouse s-arrestin, and <b>PDBTitle:</b> crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
40	<a href="#">c3gebC</a>	Alignment	not modelled	20.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> eyes absent homolog 2; <b>PDBTitle:</b> crystal structure of edeya2
41	<a href="#">c2oyuP</a>	Alignment	not modelled	20.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> prostaglandin g/h synthase 1; <b>PDBTitle:</b> indomethacin-(s)-alpha-ethyl-ethanolamide bound to cyclooxygenase-1
42	<a href="#">d2bgxa1</a>	Alignment	not modelled	20.4	37	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> Peptidoglycan binding domain, PGBD
43	<a href="#">c5uqyB</a>	Alignment	not modelled	20.1	20	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> envelope glycoprotein gp2; <b>PDBTitle:</b> crystal structure of marburg virus gp in complex with the human2 survivor antibody mr78
44	<a href="#">c6d6rK</a>	Alignment	not modelled	19.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> exosome complex exonuclease rrp44; <b>PDBTitle:</b> human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
45	<a href="#">d2npta1</a>	Alignment	not modelled	19.3	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
46	<a href="#">c6ajjA</a>	Alignment	not modelled	19.1	26	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
47	<a href="#">c1jpeA</a>	Alignment	not modelled	18.6	20	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> dsbd-alpha; <b>PDBTitle:</b> crystal structure of dsbd-alpha; the n-terminal domain of2 dsbd
48	<a href="#">d1ig8a2</a>	Alignment	not modelled	18.5	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
49	<a href="#">d1iuKa</a>	Alignment	not modelled	18.4	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
50	<a href="#">c2of5A</a>	Alignment	not modelled	18.3	21	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> death domain-containing protein cradd; <b>PDBTitle:</b> oligomeric death domain complex
51	<a href="#">c4pv6E</a>	Alignment	not modelled	18.1	19	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> n-terminal acetyltransferase complex subunit [ard1]; <b>PDBTitle:</b> crystal structure analysis of ard1 from thermoplasma volcanium
52	<a href="#">c4zwwC</a>	Alignment	not modelled	17.5	26	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> chimera protein of human rhodopsin, mouse s-arrestin, and <b>PDBTitle:</b> crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
53	<a href="#">d2qtva4</a>	Alignment	not modelled	17.3	27	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> C-terminal, gelsolin-like domain of Sec23/24 <b>Family:</b> C-terminal, gelsolin-like domain of Sec23/24

54	<a href="#">d1uqa_</a>	Alignment	not modelled	17.2	12	<b>Fold:</b> Glycerol-3-phosphate (1)-acyltransferase <b>Superfamily:</b> Glycerol-3-phosphate (1)-acyltransferase <b>Family:</b> Glycerol-3-phosphate (1)-acyltransferase
55	<a href="#">d1u83a_</a>	Alignment	not modelled	17.2	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
56	<a href="#">c1u83A_</a>	Alignment	not modelled	17.2	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphosulfolactate synthase; <b>PDBTitle:</b> psl synthase from bacillus subtilis
57	<a href="#">c4p9eA_</a>	Alignment	not modelled	16.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form
58	<a href="#">c3a10C_</a>	Alignment	not modelled	16.7	16	<b>PDB header:</b> ligase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c,linker, <b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
59	<a href="#">d1l6pa_</a>	Alignment	not modelled	16.6	20	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha) <b>Family:</b> Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha)
60	<a href="#">c3zddA_</a>	Alignment	not modelled	16.2	17	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein xni; <b>PDBTitle:</b> structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
61	<a href="#">c3j6vj_</a>	Alignment	not modelled	15.3	30	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 28s ribosomal protein s10, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
62	<a href="#">c2x7bA_</a>	Alignment	not modelled	15.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase sso0209; <b>PDBTitle:</b> crystal structure of the n-terminal acetylase ard1 from2 sulfolobus solfataricus p2
63	<a href="#">d1l0oc_</a>	Alignment	not modelled	14.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
64	<a href="#">c1l0c_</a>	Alignment	not modelled	14.9	20	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> sigma factor; <b>PDBTitle:</b> crystal structure of the bacillus stearotherophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
65	<a href="#">c2fb6A_</a>	Alignment	not modelled	14.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> structure of conserved protein of unknown function bt1422 from2 bacteroides thetaiotaomicron
66	<a href="#">c4bqeA_</a>	Alignment	not modelled	14.5	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucan phosphorylase 2,4-glucan phosphorylase; <b>PDBTitle:</b> arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2)
67	<a href="#">c2mxtA_</a>	Alignment	not modelled	14.5	13	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein q; <b>PDBTitle:</b> nmr structure of the acidic domain of syncrip (hnrnpq)
68	<a href="#">d2bcqa2</a>	Alignment	not modelled	13.9	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> PsbU/PolX domain-like <b>Family:</b> DNA polymerase beta-like, second domain
69	<a href="#">d1o98a1</a>	Alignment	not modelled	13.8	18	<b>Fold:</b> 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain <b>Superfamily:</b> 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain <b>Family:</b> 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
70	<a href="#">c5y26A_</a>	Alignment	not modelled	13.6	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase epsilon subunit d; <b>PDBTitle:</b> crystal structure of native dpb4-dpb3
71	<a href="#">c4f0qC_</a>	Alignment	not modelled	13.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> restriction endonuclease; <b>PDBTitle:</b> mspji restriction endonuclease - p21 form
72	<a href="#">c4f0qA_</a>	Alignment	not modelled	13.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> restriction endonuclease; <b>PDBTitle:</b> mspji restriction endonuclease - p21 form
73	<a href="#">c3d7iB_</a>	Alignment	not modelled	13.4	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family protein; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
74	<a href="#">c2a5wC_</a>	Alignment	not modelled	13.2	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfite reductase, desulfoviridin-type subunit gamma <b>PDBTitle:</b> crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
75	<a href="#">c2k0rA_</a>	Alignment	not modelled	13.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbd; <b>PDBTitle:</b> solution structure of the c103s mutant of the n-terminal2 domain of dsbd from neisseria meningitidis
76	<a href="#">c5kzoA_</a>	Alignment	not modelled	13.0	44	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1; <b>PDBTitle:</b> notch1 transmembrane and associated juxtamembrane segment
77	<a href="#">c6c95B_</a>	Alignment	not modelled	12.7	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-alpha-acetyltransferase 10; <b>PDBTitle:</b> the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk <b>Fold:</b> DNA/RNA-binding 3-helical bundle

78	<a href="#">d1stza1</a>	Alignment	not modelled	12.7	15	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
79	<a href="#">c3jsoA_</a>	Alignment	not modelled	12.4	31	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> classic protein with a new twist: crystal structure of a lexa2 repressor dna complex
80	<a href="#">d1ygha_</a>	Alignment	not modelled	12.2	9	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
81	<a href="#">d2icwg1</a>	Alignment	not modelled	11.9	23	<b>Fold:</b> Superantigen MAM <b>Superfamily:</b> Superantigen MAM <b>Family:</b> Superantigen MAM
82	<a href="#">c2jpmA_</a>	Alignment	not modelled	11.5	15	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit beta; <b>PDBTitle:</b> lactococcin g-b in tfe
83	<a href="#">c3qbuD_</a>	Alignment	not modelled	11.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative peptidoglycan deactelyase (hp0310) from2 helicobacter pylori
84	<a href="#">c2n6vA_</a>	Alignment	not modelled	11.4	25	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> astexin3; <b>PDBTitle:</b> solution study of astexin3
85	<a href="#">c1yx3A_</a>	Alignment	not modelled	11.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein dsrc; <b>PDBTitle:</b> nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
86	<a href="#">c4giwB_</a>	Alignment	not modelled	11.3	24	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> run and sh3 domain-containing protein 1; <b>PDBTitle:</b> crystal structure of the run domain of human nesca
87	<a href="#">c4im4F_</a>	Alignment	not modelled	11.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> endoglucanase e; <b>PDBTitle:</b> multifunctional cellulase, xylanase, mannanase
88	<a href="#">c3wo6A_</a>	Alignment	not modelled	10.9	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> membrane protein insertase yidc 2; <b>PDBTitle:</b> crystal structure of yidc from bacillus halodurans (form i)
89	<a href="#">d2iw0a1</a>	Alignment	not modelled	10.8	15	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> NodB-like polysaccharide deacetylase
90	<a href="#">c4e5gB_</a>	Alignment	not modelled	10.8	20	<b>PDB header:</b> viral protein, transcription <b>Chain:</b> B; <b>PDB Molecule:</b> polymerase protein pa; <b>PDBTitle:</b> crystal structure of avian influenza virus pan bound to compound 2
91	<a href="#">c4oc8A_</a>	Alignment	not modelled	10.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> restriction endonuclease aspbhi; <b>PDBTitle:</b> dna modification-dependent restriction endonuclease aspbhi
92	<a href="#">c2jpkA_</a>	Alignment	not modelled	10.7	15	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit beta; <b>PDBTitle:</b> lactococcin g-b in dpc
93	<a href="#">c4griB_</a>	Alignment	not modelled	10.6	18	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of a glutamyl-trna synthetase glurs from borrelia2 burgdorferi bound to glutamic acid and zinc
94	<a href="#">c4hhsA_</a>	Alignment	not modelled	10.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-dioxygenase; <b>PDBTitle:</b> crystal structure of fatty acid alpha-dioxygenase (arabidopsis2 thaliana)
95	<a href="#">c5ccuA_</a>	Alignment	not modelled	10.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative secreted endoglycosylceramidase; <b>PDBTitle:</b> crystal structure of endoglycoceramidase i from rhodococ-cus equi
96	<a href="#">c3gqeA_</a>	Alignment	not modelled	10.5	13	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> non-structural protein 3; <b>PDBTitle:</b> crystal structure of macro domain of venezuelan equine encephalitis2 virus
97	<a href="#">c6mzdC_</a>	Alignment	not modelled	10.4	18	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 3; <b>PDBTitle:</b> human tfiid lobe a canonical
98	<a href="#">c2m8fA_</a>	Alignment	not modelled	10.3	25	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> astexin3; <b>PDBTitle:</b> structure of lasso peptide astexin3
99	<a href="#">c1kbiB_</a>	Alignment	not modelled	10.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> cytochrome b2; <b>PDBTitle:</b> crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme