

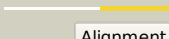
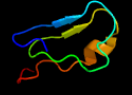
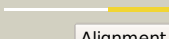

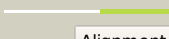
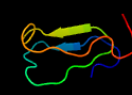
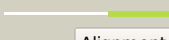






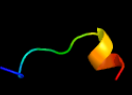



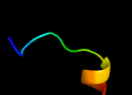


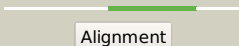



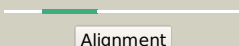

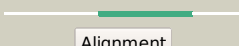
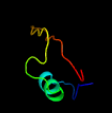
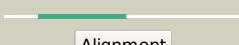

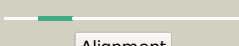

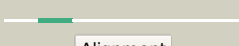




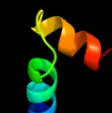


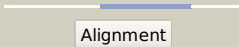
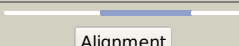
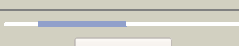

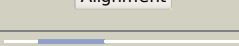
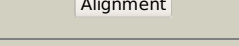
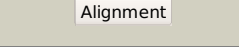


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1579c_(-)_1783316_1783630
Date	Fri Aug 2 13:30:17 BST 2019
Unique Job ID	ea01d8b1b2c38ef8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1tr8A_</a>	 Alignment		92.2	40	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein (mth177); <b>PDBTitle:</b> crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
2	<a href="#">c6riqP_</a>	 Alignment		73.5	31	<b>PDB header:</b> protein fibril <b>Chain:</b> P: <b>PDB Molecule:</b> minc; <b>PDBTitle:</b> mincd filament from pseudomonas aeruginosa
3	<a href="#">c4v02C_</a>	 Alignment		70.8	31	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> probable septum site-determining protein minc; <b>PDBTitle:</b> minc:mind cell division protein complex, aquifex aeolicus
4	<a href="#">c5xdmA_</a>	 Alignment		64.4	29	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> septum site-determining protein minc; <b>PDBTitle:</b> structure of the c-terminal domain of e. coli minc at 3.0 angstrom2 resolution
5	<a href="#">d1hf2a1</a>	 Alignment		64.3	26	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Cell-division inhibitor MinC, C-terminal domain <b>Family:</b> Cell-division inhibitor MinC, C-terminal domain
6	<a href="#">c5fjaQ_</a>	 Alignment		59.9	69	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7; <b>PDBTitle:</b> cryo-em structure of yeast rna polymerase iii at 4.7 a
7	<a href="#">c6cnbQ_</a>	 Alignment		56.6	69	<b>PDB header:</b> transcription/dna <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7,dna-directed <b>PDBTitle:</b> yeast rna polymerase iii initial transcribing complex
8	<a href="#">c6cncQ_</a>	 Alignment		56.6	69	<b>PDB header:</b> transcription/dna <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7,dna-directed <b>PDBTitle:</b> yeast rna polymerase iii open complex
9	<a href="#">c6cndQ_</a>	 Alignment		56.4	69	<b>PDB header:</b> transcription/dna <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7,dna-directed <b>PDBTitle:</b> yeast rna polymerase iii natural open complex (noc)
10	<a href="#">c6cnfQ_</a>	 Alignment		56.4	69	<b>PDB header:</b> transcription/dna <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7,dna-directed <b>PDBTitle:</b> yeast rna polymerase iii elongation complex
11	<a href="#">c5fj8Q_</a>	 Alignment		55.5	69	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7; <b>PDBTitle:</b> cryo-em structure of yeast rna polymerase iii elongation complex at 3.2 9 a

12	<a href="#">c1hf2A_</a>	 Alignment		53.1	26	<b>PDB header:</b> cell division protein <b>Chain:</b> A: <b>PDB Molecule:</b> septum site-determining protein minc; <b>PDBTitle:</b> crystal structure of the bacterial cell-division inhibitor minc from <i>2 t. maritima</i>
13	<a href="#">c5fj9Q_</a>	 Alignment		52.6	69	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7; <b>PDBTitle:</b> cryo-em structure of yeast apo rna polymerase iii at 4.6 a
14	<a href="#">d1v92a_</a>	 Alignment		44.9	32	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TAP-C domain-like
15	<a href="#">d1ou8a_</a>	 Alignment		43.8	29	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
16	<a href="#">d1k78a1</a>	 Alignment		41.7	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
17	<a href="#">d1msza_</a>	 Alignment		41.4	36	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
18	<a href="#">c1mszA_</a>	 Alignment		41.4	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein smubp-2; <b>PDBTitle:</b> solution structure of the r3h domain from human smubp-2
19	<a href="#">c3akqA_</a>	 Alignment		37.4	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted alpha l-arabinofuranosidase ii; <b>PDBTitle:</b> crystal structure of exo-1,5-alpha-l-arabinofuranosidase complexed2 with alpha-1,5-l-arabinofuranobiose
20	<a href="#">c2dzlA_</a>	 Alignment		30.0	42	<b>PDB header:</b> structural genomics unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein fam100b; <b>PDBTitle:</b> solution structure of the uba domain in human protein2 fam100b
21	<a href="#">c5zjlA_</a>	 Alignment	not modelled	29.1	58	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> der f 23 allergen; <b>PDBTitle:</b> crystal structure of the dust mite allergen der f 23 from <i>2 dermatophagoides farinae</i>
22	<a href="#">d1pdnc_</a>	 Alignment	not modelled	28.8	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
23	<a href="#">d1ou9a_</a>	 Alignment	not modelled	26.5	29	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
24	<a href="#">d1yfnal</a>	 Alignment	not modelled	25.3	24	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
25	<a href="#">c6paxA_</a>	 Alignment	not modelled	24.1	26	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
26	<a href="#">d2csba1</a>	 Alignment	not modelled	24.0	64	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
27	<a href="#">d1gg4a4</a>	 Alignment	not modelled	20.8	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
28	<a href="#">d2euca1</a>	 Alignment	not modelled	20.6	31	<b>Fold:</b> YfmB-like <b>Superfamily:</b> YfmB-like <b>Family:</b> YfmB-like
29	<a href="#">d1zszc1</a>	 Alignment	not modelled	20.1	26	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like

						<b>Family:</b> Stringent starvation protein B, SspB
30	<a href="#">d6paxa1</a>	Alignment	not modelled	18.3	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
31	<a href="#">c5gkeB_</a>	Alignment	not modelled	17.8	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease endoms; <b>PDBTitle:</b> structure of endoms-dsdna1 complex
32	<a href="#">c2cpmA_</a>	Alignment	not modelled	17.3	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sperm-associated antigen 7; <b>PDBTitle:</b> solution structure of the r3h domain of human sperm-2 associated antigen 7
33	<a href="#">d1ko7a1</a>	Alignment	not modelled	16.5	18	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> HPr kinase/phoshatase HprK N-terminal domain
34	<a href="#">c3csqC_</a>	Alignment	not modelled	15.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> morphogenesis protein 1; <b>PDBTitle:</b> crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
35	<a href="#">c5ho0A_</a>	Alignment	not modelled	15.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular arabinanase; <b>PDBTitle:</b> crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
36	<a href="#">d2hyec3</a>	Alignment	not modelled	14.3	15	<b>Fold:</b> Cullin homology domain <b>Superfamily:</b> Cullin homology domain <b>Family:</b> Cullin homology domain
37	<a href="#">c5u0pT_</a>	Alignment	not modelled	14.2	34	<b>PDB header:</b> transcription <b>Chain:</b> T: <b>PDB Molecule:</b> mediator complex subunit 20; <b>PDBTitle:</b> cryo-em structure of the transcriptional mediator
38	<a href="#">d1omza_</a>	Alignment	not modelled	13.6	7	<b>Fold:</b> Nucleotide-diphospho- sugar transferases <b>Superfamily:</b> Nucleotide-diphospho- sugar transferases <b>Family:</b> Exostosin
39	<a href="#">c3ixtC_</a>	Alignment	not modelled	13.5	60	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> fusion glycoprotein f1; <b>PDBTitle:</b> crystal structure of motavizumab fab bound to peptide epitope
40	<a href="#">c3ixtP_</a>	Alignment	not modelled	13.5	60	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> fusion glycoprotein f1; <b>PDBTitle:</b> crystal structure of motavizumab fab bound to peptide epitope
41	<a href="#">c3kstA_</a>	Alignment	not modelled	12.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-xylanase (np_811807.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.70 a resolution
42	<a href="#">d1tiha_</a>	Alignment	not modelled	12.0	33	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
43	<a href="#">c1u78A_</a>	Alignment	not modelled	11.2	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
44	<a href="#">c1omxB_</a>	Alignment	not modelled	11.2	6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4-n-acetylhexosaminyltransferase extl2; <b>PDBTitle:</b> crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
45	<a href="#">d1pjua2</a>	Alignment	not modelled	11.1	33	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
46	<a href="#">c2opwA_</a>	Alignment	not modelled	10.9	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phyhd1 protein; <b>PDBTitle:</b> crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
47	<a href="#">d1whra_</a>	Alignment	not modelled	10.6	36	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
48	<a href="#">c1fvyA_</a>	Alignment	not modelled	10.1	75	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone; <b>PDBTitle:</b> solution structure of the osteogenic 1-31 fragment of the2 human parathyroid hormone
49	<a href="#">c6eu1Q_</a>	Alignment	not modelled	10.1	50	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc7; <b>PDBTitle:</b> rna polymerase iii - open dna complex (oc-pol3)
50	<a href="#">c2k27A_</a>	Alignment	not modelled	9.8	28	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
51	<a href="#">c3bmzA_</a>	Alignment	not modelled	9.5	27	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> violacein biosynthetic enzyme vioe
52	<a href="#">c3zljC_</a>	Alignment	not modelled	9.1	55	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
53	<a href="#">c6cauA_</a>	Alignment	not modelled	9.0	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with ampnpn
54	<a href="#">d1ayaa_</a>	Alignment	not modelled	9.0	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
55	<a href="#">c5xtaC_</a>	Alignment	not modelled	8.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> virK protein; <b>PDBTitle:</b> crystal structure of lpg1832, a virk family protein from legionella2 pneumophila

56	<a href="#">c2ge9A</a>	Alignment	not modelled	8.4	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase btk; <b>PDBTitle:</b> solution structures of the sh2 domain of bruton's tyrosine2 kinase
57	<a href="#">c1wn4A</a>	Alignment	not modelled	8.3	67	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> vontr protein; <b>PDBTitle:</b> nmr structure of vontr
58	<a href="#">c3zljD</a>	Alignment	not modelled	8.2	55	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
59	<a href="#">c3tr7A</a>	Alignment	not modelled	8.2	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of a uracil-dna glycosylase (ung) from coxiella burnetii
60	<a href="#">c3lv4B</a>	Alignment	not modelled	8.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase xyia; <b>PDBTitle:</b> crystal structure of the glycoside hydrolase, family 43 xyia protein2 from bacillus licheniformis. northeast structural genomics consortium3 target bir14.
61	<a href="#">d1e8ca3</a>	Alignment	not modelled	7.9	6	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
62	<a href="#">d1moua</a>	Alignment	not modelled	7.8	32	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
63	<a href="#">d4sgbi</a>	Alignment	not modelled	7.7	21	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
64	<a href="#">c5eriD</a>	Alignment	not modelled	7.7	36	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> snon,snon; <b>PDBTitle:</b> crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro
65	<a href="#">c4ae4B</a>	Alignment	not modelled	7.6	35	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-associated protein 1; <b>PDBTitle:</b> the ubap1 subunit of escrt-i interacts with ubiquitin via a novel2 souba domain
66	<a href="#">d1s6ia1</a>	Alignment	not modelled	7.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MerB N-terminal domain-like
67	<a href="#">c1x6cA</a>	Alignment	not modelled	7.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase, non-receptor type <b>PDBTitle:</b> solution structures of the sh2 domain of human protein-2 tyrosine phosphatase shp-1
68	<a href="#">c5gtuB</a>	Alignment	not modelled	7.3	44	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tbc1 domain family member 5; <b>PDBTitle:</b> structural and mechanistic insights into regulation of the retromer2 coat by tbc1d5
69	<a href="#">c4zonB</a>	Alignment	not modelled	7.3	31	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> verruculogen synthase; <b>PDBTitle:</b> structure of ftmox1 with fumitremorgen b complex
70	<a href="#">d1fyba1</a>	Alignment	not modelled	7.1	36	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
71	<a href="#">d1z67a1</a>	Alignment	not modelled	7.0	16	<b>Fold:</b> YidB-like <b>Superfamily:</b> YidB-like <b>Family:</b> YidB-like
72	<a href="#">d1ldja3</a>	Alignment	not modelled	6.9	24	<b>Fold:</b> Cullin homology domain <b>Superfamily:</b> Cullin homology domain <b>Family:</b> Cullin homology domain
73	<a href="#">c5n6yD</a>	Alignment	not modelled	6.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein alpha chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
74	<a href="#">d1tlea2</a>	Alignment	not modelled	6.8	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Subtilase propeptides/inhibitors
75	<a href="#">c5ncrA</a>	Alignment	not modelled	6.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine phosphatase; <b>PDBTitle:</b> oh1 from the orf virus: a tyrosine phosphatase that displays distinct2 structural features and triple substrate specificity
76	<a href="#">c5vwwA</a>	Alignment	not modelled	6.6	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> structure of murc from pseudomonas aeruginosa
77	<a href="#">c5m0tA</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash; <b>PDBTitle:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash
78	<a href="#">c3eagA</a>	Alignment	not modelled	6.3	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
79	<a href="#">c1j6uA</a>	Alignment	not modelled	6.3	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
80	<a href="#">c2booA</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> the crystal structure of uracil-dna n-glycosylase (ung) from 2 deinococcus radiodurans.

81	<a href="#">c2mtpB_</a>	Alignment	not modelled	6.2	46	<b>PDB header:</b> protein binding/cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> the structure of filamin repeat 21 bound to integrin
82	<a href="#">d1oyvi_</a>	Alignment	not modelled	6.2	36	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
83	<a href="#">d1i3za_</a>	Alignment	not modelled	6.1	16	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
84	<a href="#">c2lseA_</a>	Alignment	not modelled	6.1	34	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> four helix bundle protein; <b>PDBTitle:</b> solution nmr structure of de novo designed four helix bundle protein,2 northeast structural genomics consortium (nsg) target or188
85	<a href="#">c4xc9B_</a>	Alignment	not modelled	6.1	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidase/hydroxylase; <b>PDBTitle:</b> crystal structure of apo hygx from streptomyces hygroscopicus
86	<a href="#">c6reqB_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (methylmalonyl-coa mutase); <b>PDBTitle:</b> methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
87	<a href="#">c2z5bB_</a>	Alignment	not modelled	5.9	56	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ylr021w; <b>PDBTitle:</b> crystal structure of a novel chaperone complex for yeast20s proteasome assembly
88	<a href="#">c3m6zA_</a>	Alignment	not modelled	5.9	64	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase v; <b>PDBTitle:</b> crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride
89	<a href="#">c5ermA_</a>	Alignment	not modelled	5.8	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fusiccoccadiene synthase; <b>PDBTitle:</b> crystal structure of cyclization domain of phomopsis amygdali2 fusiccoccadiene synthase complexed with magnesium ions and pamidronate
90	<a href="#">d1gyxa_</a>	Alignment	not modelled	5.8	7	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
91	<a href="#">c3mazA_</a>	Alignment	not modelled	5.8	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal-transducing adaptor protein 1; <b>PDBTitle:</b> crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntlal ptyr136 peptide
92	<a href="#">d1pjua1</a>	Alignment	not modelled	5.7	21	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
93	<a href="#">c2ci8A_</a>	Alignment	not modelled	5.7	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic protein nck1; <b>PDBTitle:</b> sh2 domain of human nck1 adaptor protein - uncomplexed
94	<a href="#">c4xbzB_</a>	Alignment	not modelled	5.6	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> evdo1; <b>PDBTitle:</b> crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
95	<a href="#">c1m8oA_</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> platelet integrin alfaiib subunit: cytoplasmic <b>PDBTitle:</b> platelet integrin alfaiib-beta3 cytoplasmic domain
96	<a href="#">c1s4wA_</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> nmr structure of the cytoplasmic domain of integrin aiib in2 dpc micelles
97	<a href="#">c1dpkA_</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib subunit; <b>PDBTitle:</b> solution structure of the cytoplasmic domain of the2 integrin alpha-iib subunit
98	<a href="#">c4jlrS_</a>	Alignment	not modelled	5.6	60	<b>PDB header:</b> immune system <b>Chain:</b> S: <b>PDB Molecule:</b> rsv_1isea designed scaffold; <b>PDBTitle:</b> crystal structure of a designed respiratory syncytial virus immunogen2 in complex with motavizumab
99	<a href="#">c5zm4B_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dioxygenase anda; <b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c