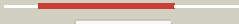



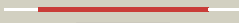






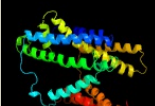












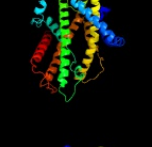

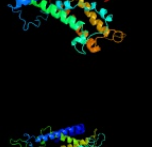
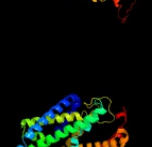
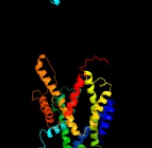

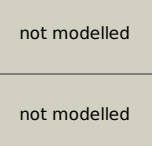


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3454 (- )_3875001_3876269
Date	Fri Aug 9 18:20:12 BST 2019
Unique Job ID	dc1303f5283fcee8

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ainB_</a>	 Alignment		99.8	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of betp with asymmetric protomers.
2	<a href="#">c3hfxA_</a>	 Alignment		99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
3	<a href="#">c2jlnA_</a>	 Alignment		99.8	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	<a href="#">c2w8aC_</a>	 Alignment		99.8	14	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
5	<a href="#">c5i6xA_</a>	 Alignment		99.2	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium-dependent serotonin transporter; <b>PDBTitle:</b> x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
6	<a href="#">c5nvaA_</a>	 Alignment		99.1	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sodium:solute symporter; <b>PDBTitle:</b> substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
7	<a href="#">c4m48A_</a>	 Alignment		99.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transporter; <b>PDBTitle:</b> x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
8	<a href="#">c2xq2A_</a>	 Alignment		98.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsgt
9	<a href="#">c6csfC_</a>	 Alignment		98.7	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> sodium/alanine symporter agcs; <b>PDBTitle:</b> crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
10	<a href="#">c3dh4A_</a>	 Alignment		98.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
11	<a href="#">c5m87A_</a>	 Alignment		98.6	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of eremococcus coleocola manganese transporter

12	<a href="#">d2a65a1</a>	Alignment		98.6	11	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
13	<a href="#">c4wgvC</a>	Alignment		98.4	11	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
14	<a href="#">c4wgvA</a>	Alignment		98.4	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
15	<a href="#">c4us3A</a>	Alignment		98.4	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transporter; <b>PDBTitle:</b> crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
16	<a href="#">c4djiA</a>	Alignment		98.1	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
17	<a href="#">c6nplA</a>	Alignment		98.1	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 12 (sodium/potassium/chloride) <b>PDBTitle:</b> cryo-em structure of nkcc1
18	<a href="#">c3giaA</a>	Alignment		98.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
19	<a href="#">c6irtB</a>	Alignment		97.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> large neutral amino acids transporter small subunit 1; <b>PDBTitle:</b> human lat1-4f2hc complex bound with bch
20	<a href="#">c6f2wA</a>	Alignment		97.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative amino acid/polyamine transport protein; <b>PDBTitle:</b> bacterial asc transporter crystal structure in open to in conformation
21	<a href="#">c6jmqA</a>	Alignment	not modelled	95.3	12	<b>PDB header:</b> membrane protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> large neutral amino acids transporter small subunit 1; <b>PDBTitle:</b> lat1-cd98hc complex bound to mem-108 fab
22	<a href="#">c5kteA</a>	Alignment	not modelled	94.4	14	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans mnth, an nramp-family2 transition metal transporter
23	<a href="#">c3lrcC</a>	Alignment	not modelled	91.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
24	<a href="#">c5oqtA</a>	Alignment	not modelled	88.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid transporter; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
25	<a href="#">c4yifD</a>	Alignment	not modelled	59.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase subunit a; <b>PDBTitle:</b> insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
26	<a href="#">d1e7la2</a>	Alignment	not modelled	59.3	22	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> Recombination endonuclease VII, N-terminal domain
27	<a href="#">c2kdxA</a>	Alignment	not modelled	51.9	19	<b>PDB header:</b> metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein <b>PDBTitle:</b> solution structure of hypa protein
28	<a href="#">d2atcb2</a>	Alignment	not modelled	51.6	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain <b>Family:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-

						terminal domain
29	<a href="#">d2dida1</a>	Alignment	not modelled	50.5	33	<b>Fold:</b> B-box zinc-binding domain <b>Superfamily:</b> B-box zinc-binding domain <b>Family:</b> B-box zinc-binding domain
30	<a href="#">c6genS</a>	Alignment	not modelled	49.6	19	<b>PDB header:</b> nuclear protein <b>Chain:</b> S: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 71; <b>PDBTitle:</b> chromatin remodeller-nucleosome complex at 4.5 a resolution.
31	<a href="#">c2csvA</a>	Alignment	not modelled	49.3	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tripartite motif protein 29; <b>PDBTitle:</b> solution structure of the zf-b_box type2 domain of human2 tripartite motif protein trim29 isoform alpha
32	<a href="#">c3lyrA</a>	Alignment	not modelled	49.1	20	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor coe1; <b>PDBTitle:</b> human early b-cell factor 1 (ebf1) dna-binding domain
33	<a href="#">c3zyqA</a>	Alignment	not modelled	48.1	20	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
34	<a href="#">c5lc5I</a>	Alignment	not modelled	48.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
35	<a href="#">c6qajB</a>	Alignment	not modelled	47.3	14	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> endolysin,transcription intermediary factor 1-beta; <b>PDBTitle:</b> structure of the tripartite motif of kap1/trim28
36	<a href="#">d2csva1</a>	Alignment	not modelled	46.1	18	<b>Fold:</b> B-box zinc-binding domain <b>Superfamily:</b> B-box zinc-binding domain <b>Family:</b> B-box zinc-binding domain
37	<a href="#">c1freA</a>	Alignment	not modelled	46.1	26	<b>PDB header:</b> zinc-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear factor xnf7; <b>PDBTitle:</b> xnf7 bbox, developmental protein, ph 7.5, 30 c, with zinc,2 nmr, 1 structure
38	<a href="#">c2qnfB</a>	Alignment	not modelled	44.0	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> recombination endonuclease vii; <b>PDBTitle:</b> crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
39	<a href="#">d1u5ka2</a>	Alignment	not modelled	44.0	24	<b>Fold:</b> ArfGap/RecO-like zinc finger <b>Superfamily:</b> ArfGap/RecO-like zinc finger <b>Family:</b> RecO C-terminal domain-like
40	<a href="#">c3goxB</a>	Alignment	not modelled	43.7	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> restriction endonuclease hpy99i; <b>PDBTitle:</b> crystal structure of the beta-beta-alpha-me type ii restriction2 endonuclease hpy99i in the absence of edta
41	<a href="#">d2fzcb2</a>	Alignment	not modelled	43.3	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain <b>Family:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
42	<a href="#">c5oqj4</a>	Alignment	not modelled	43.2	16	<b>PDB header:</b> transcription <b>Chain:</b> 4: <b>PDB Molecule:</b> rna polymerase ii transcription factor b subunit 4; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih
43	<a href="#">c2jtgA</a>	Alignment	not modelled	42.4	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> thap domain-containing protein 1; <b>PDBTitle:</b> solution structure of the thap-zinc finger of thap1
44	<a href="#">c2egmA</a>	Alignment	not modelled	42.1	22	<b>PDB header:</b> transcription/metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tripartite motif-containing protein 41; <b>PDBTitle:</b> solution structure of the zf-b_box domain from human2 tripartite motif protein 41
45	<a href="#">c2fugG</a>	Alignment	not modelled	41.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 9; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
46	<a href="#">d2fug91</a>	Alignment	not modelled	41.8	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
47	<a href="#">c2h3eB</a>	Alignment	not modelled	41.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate carbamoyltransferase regulatory chain; <b>PDBTitle:</b> structure of wild-type e. coli aspartate transcarbamoylase in the2 presence of n-phosphonacetyl-l-isoasparagine at 2.3a resolution
48	<a href="#">c2lv9A</a>	Alignment	not modelled	41.1	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase ml15; <b>PDBTitle:</b> solution nmr structure of the phd domain of human ml15, northeast2 structural genomics consortium target hr6512a
49	<a href="#">c6gcsI</a>	Alignment	not modelled	40.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> tyky subunit (nuim); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
50	<a href="#">c6nmiF</a>	Alignment	not modelled	39.2	21	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> general transcription factor iih subunit 3, p34; <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
51	<a href="#">c2yrgA</a>	Alignment	not modelled	39.2	34	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tripartite motif-containing protein 5; <b>PDBTitle:</b> solution structure of the b-box domain from tripartite2 motif-containing protein 5
52	<a href="#">c3py7A</a>	Alignment	not modelled	38.1	7	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,paxillin ld1,protein e6 <b>PDBTitle:</b> crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a

					resolution	
53	<a href="#">c3mlpE</a>	Alignment	not modelled	37.5	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> transcription factor coe1; <b>PDBTitle:</b> early b-cell factor 1 (ebf1) bound to dna
54	<a href="#">d1t61c1</a>	Alignment	not modelled	37.4	22	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Noncollagenous (NC1) domain of collagen IV
55	<a href="#">c2elvA</a>	Alignment	not modelled	37.1	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 6th c2h2 zinc finger of human2 zinc finger protein 406
56	<a href="#">c3mlpA</a>	Alignment	not modelled	36.4	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor coe1; <b>PDBTitle:</b> early b-cell factor 1 (ebf1) bound to dna
57	<a href="#">d2dlqa3</a>	Alignment	not modelled	35.7	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
58	<a href="#">c2yvrB</a>	Alignment	not modelled	35.2	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcription intermediary factor 1-beta; <b>PDBTitle:</b> crystal structure of ms1043
59	<a href="#">d1li1c1</a>	Alignment	not modelled	35.1	23	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Noncollagenous (NC1) domain of collagen IV
60	<a href="#">d1wewa</a>	Alignment	not modelled	33.7	26	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> PHD domain
61	<a href="#">d1pg5b2</a>	Alignment	not modelled	33.7	11	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain <b>Family:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
62	<a href="#">c2difA</a>	Alignment	not modelled	32.8	31	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tripartite motif protein 39; <b>PDBTitle:</b> one sequence two fold ? : miss fold of the zf-b-box domain2 from human tripartite motif protein 39
63	<a href="#">d2d8ra1</a>	Alignment	not modelled	32.4	25	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> THAP domain
64	<a href="#">c5ieaF</a>	Alignment	not modelled	32.0	24	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> tripartite motif-containing protein 5, serine-trna ligase <b>PDBTitle:</b> trim5 b-box2 and coiled-coil chimera
65	<a href="#">d1wema</a>	Alignment	not modelled	31.7	26	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> PHD domain
66	<a href="#">c2vdcl</a>	Alignment	not modelled	31.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
67	<a href="#">d2cs3a1</a>	Alignment	not modelled	31.1	22	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> Variant RING domain
68	<a href="#">c1pg5B</a>	Alignment	not modelled	31.0	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate carbamoyltransferase regulatory chain; <b>PDBTitle:</b> crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfobolus3 acidocaldarius
69	<a href="#">c5jpxA</a>	Alignment	not modelled	30.5	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase trim21; <b>PDBTitle:</b> solution structure of the trim21 b-box2 (b2)
70	<a href="#">c1z2qA</a>	Alignment	not modelled	30.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lm5-1; <b>PDBTitle:</b> high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
71	<a href="#">d1ma3a</a>	Alignment	not modelled	30.1	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
72	<a href="#">c5tbnA</a>	Alignment	not modelled	30.0	22	<b>PDB header:</b> transcription / structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 20; <b>PDBTitle:</b> solution nmr structure of phf20 phd domain in complex with a histone2 h3k4me2 peptide
73	<a href="#">c1u5kA</a>	Alignment	not modelled	29.8	24	<b>PDB header:</b> recombination,replication <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> recombinational repair protein reco
74	<a href="#">c3kdeC</a>	Alignment	not modelled	29.8	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transposable element p transposase; <b>PDBTitle:</b> crystal structure of the thap domain from d. melanogaster p-element2 transposase in complex with its natural dna binding site
75	<a href="#">c2rsdA</a>	Alignment	not modelled	29.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 sumo-protein ligase siz1; <b>PDBTitle:</b> solution structure of the plant homeodomain (phd) of the e3 sumo2 ligase siz1 from rice
76	<a href="#">d2yt9a1</a>	Alignment	not modelled	29.6	41	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
77	<a href="#">c5ikfA</a>	Alignment	not modelled	28.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> chromatin remodeling factor mit1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the mit1 nucleosome2 remodeler in complex with clr1
						<b>Fold:</b> C-type lectin-like

78	<a href="#">d1t61a1</a>	Alignment	not modelled	28.3	18	<b>Superfamily:</b> C-type lectin-like <b>Family:</b> Noncollagenous (NC1) domain of collagen IV
79	<a href="#">c2n95A</a>	Alignment	not modelled	28.2	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein hit1; <b>PDBTitle:</b> nmr structure of yeast hit1 protein zinc finger
80	<a href="#">c2co8A</a>	Alignment	not modelled	28.1	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nedd9 interacting protein with calponin homology <b>PDBTitle:</b> solution structures of the lim domain of human nedd92 interacting protein with calponin homology and lim domains
81	<a href="#">c2yqpA</a>	Alignment	not modelled	27.9	23	<b>PDB header:</b> gene regulation, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx59; <b>PDBTitle:</b> solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
82	<a href="#">c1a87A</a>	Alignment	not modelled	27.1	12	<b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n; <b>PDBTitle:</b> colicin n
83	<a href="#">d1a87a</a>	Alignment	not modelled	27.1	12	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
84	<a href="#">c1dvpA</a>	Alignment	not modelled	26.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine <b>PDBTitle:</b> crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
85	<a href="#">c2d8uA</a>	Alignment	not modelled	26.5	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin ligase trim63; <b>PDBTitle:</b> solution structure of the b-box domain of the human2 tripartite motif-containing 63 protein
86	<a href="#">c2l9zA</a>	Alignment	not modelled	26.3	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pr domain zinc finger protein 4; <b>PDBTitle:</b> zinc knuckle in prdm4
87	<a href="#">c3j2wS</a>	Alignment	not modelled	26.1	21	<b>PDB header:</b> virus <b>Chain:</b> S: <b>PDB Molecule:</b> glycoprotein e2; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya virus
88	<a href="#">c6ffyA</a>	Alignment	not modelled	25.7	12	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> vps10 domain-containing receptor sorcs2; <b>PDBTitle:</b> structure of the mouse sorcs2-ngf complex
89	<a href="#">c5tdwA</a>	Alignment	not modelled	25.6	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> set domain-containing protein 3; <b>PDBTitle:</b> set3 phd finger in complex with histone h3k4me3
90	<a href="#">c2hjhB</a>	Alignment	not modelled	25.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of the sir2 deacetylase
91	<a href="#">c2l0bA</a>	Alignment	not modelled	25.1	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase praja-1; <b>PDBTitle:</b> solution nmr structure of zinc finger domain of e3 ubiquitin-protein2 ligase praja-1 from homo sapiens, northeast structural genomics3 consortium (nesg) target hr4710b
92	<a href="#">c3g6jB</a>	Alignment	not modelled	24.9	10	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement c3 alpha chain; <b>PDBTitle:</b> c3b in complex with a c3b specific fab
93	<a href="#">c3mkrB</a>	Alignment	not modelled	24.3	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> crystal structure of yeast alpha/epsilon-cop subcomplex of the cop2 vesicular coat
94	<a href="#">c3q8dB</a>	Alignment	not modelled	24.3	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein reco; <b>PDBTitle:</b> e. coli reco complex with ssb c-terminus
95	<a href="#">d2adra2</a>	Alignment	not modelled	24.1	36	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
96	<a href="#">c5n7yC</a>	Alignment	not modelled	23.9	22	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> anti-sigma-g factor gin; <b>PDBTitle:</b> solution structure of b. subtilis sigma g inhibitor csfb
97	<a href="#">c6btmB</a>	Alignment	not modelled	23.7	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alternative complex iii subunit b; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
98	<a href="#">c2n94A</a>	Alignment	not modelled	23.5	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> box c/d snorna protein 1; <b>PDBTitle:</b> nmr structure of yeast bcd1 protein zinc finger
99	<a href="#">c3o70A</a>	Alignment	not modelled	23.2	29	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 13; <b>PDBTitle:</b> phd-type zinc finger of human phd finger protein 13
100	<a href="#">c1t60R</a>	Alignment	not modelled	22.9	23	<b>PDB header:</b> structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> type iv collagen; <b>PDBTitle:</b> crystal structure of type iv collagen nc1 domain from2 bovine lens capsule
101	<a href="#">c4heaO</a>	Alignment	not modelled	22.4	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 9; <b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus
102	<a href="#">c6blhG</a>	Alignment	not modelled	22.4	26	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> G: <b>PDB Molecule:</b> major surface glycoprotein g; <b>PDBTitle:</b> rsv g central conserved region bound to fab cb017.5
103	<a href="#">c2l03A</a>	Alignment	not modelled	22.3	26	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> ly-6/neurotoxin-like protein 1; <b>PDBTitle:</b> spatial structure of water-soluble lynx1



104	<a href="#">c3zq6A_</a>	Alignment	not modelled	22.2	27	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-6; <b>PDBTitle:</b> the novel de-long chain fatty acid function of human sirt6
105	<a href="#">c2ecvA_</a>	Alignment	not modelled	22.2	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tripartite motif-containing protein 5; <b>PDBTitle:</b> solution structure of the zinc finger, c3hc4 type (ring2 finger) domain of tripartite motif-containing protein 5
106	<a href="#">c2ywwA_</a>	Alignment	not modelled	21.8	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate carbamoyltransferase regulatory chain; <b>PDBTitle:</b> crystal structure of aspartate carbamoyltransferase2 regulatory chain from methanocaldococcus jannaschii
107	<a href="#">c1x4uA_</a>	Alignment	not modelled	21.7	22	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger, fyve domain containing 27 isoform b; <b>PDBTitle:</b> solution structure of the fyve domain from human fyve2 domain containing 27 isoform b protein
108	<a href="#">d1znfa_</a>	Alignment	not modelled	21.5	33	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
109	<a href="#">c1znfA_</a>	Alignment	not modelled	21.5	33	<b>PDB header:</b> zinc finger dna binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> 31st zinc finger from xfin; <b>PDBTitle:</b> three-dimensional solution structure of a single zinc finger dna-2 binding domain
110	<a href="#">c3wsxA_</a>	Alignment	not modelled	21.5	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sortilin-related receptor; <b>PDBTitle:</b> sorla vps10p domain in ligand-free form
111	<a href="#">c6bliF_</a>	Alignment	not modelled	21.2	24	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> F: <b>PDB Molecule:</b> major surface glycoprotein g; <b>PDBTitle:</b> rsv g peptide bound to fab cb002.5
112	<a href="#">d1yc5a1</a>	Alignment	not modelled	21.2	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
113	<a href="#">d1r5ya_</a>	Alignment	not modelled	21.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> tRNA-guanine transglycosylase <b>Family:</b> tRNA-guanine transglycosylase
114	<a href="#">c6bliI_</a>	Alignment	not modelled	21.1	24	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> I: <b>PDB Molecule:</b> major surface glycoprotein g; <b>PDBTitle:</b> rsv g peptide bound to fab cb002.5
115	<a href="#">c2junA_</a>	Alignment	not modelled	21.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> midline-1; <b>PDBTitle:</b> structure of the mid1 tandem b-boxes reveals an interaction2 reminiscent of intermolecular ring heterodimers
116	<a href="#">c3a44D_</a>	Alignment	not modelled	20.9	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase nickel incorporation protein hypa; <b>PDBTitle:</b> crystal structure of hypa in the dimeric form
117	<a href="#">c2k17A_</a>	Alignment	not modelled	20.5	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor tffiid subunit 3; <b>PDBTitle:</b> solution structure of the taf3 phd domain in complex with a2 h3k4me3 peptide
118	<a href="#">c4qf3A_</a>	Alignment	not modelled	20.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain adjacent to zinc finger domain protein 2b; <b>PDBTitle:</b> crystal structure of human baz2b phd zinc finger in the free form
119	<a href="#">c6o9lQ_</a>	Alignment	not modelled	20.4	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> Q: <b>PDB Molecule:</b> general transcription factor iie subunit 1; <b>PDBTitle:</b> human holo-pic in the closed state
120	<a href="#">d1paaa_</a>	Alignment	not modelled	20.4	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2