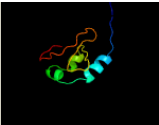
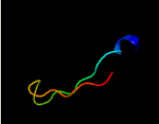

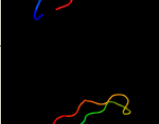


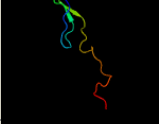
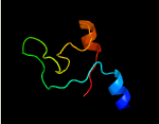
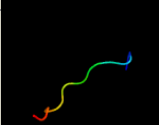


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2674 (-) _2990716_2991126
Date	Wed Aug 7 12:50:32 BST 2019
Unique Job ID	307a37ab7af3646d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2k8dA_</a>	Alignment		100.0	57	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msrb; <b>PDBTitle:</b> solution structure of a zinc-binding methionine sulfoxide reductase
2	<a href="#">c3cezA_</a>	Alignment		100.0	49	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase; <b>PDBTitle:</b> crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
3	<a href="#">c3e0mB_</a>	Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra/msrb <b>PDBTitle:</b> crystal structure of fusion protein of msra and msrb
4	<a href="#">d1l1da_</a>	Alignment		100.0	41	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> SelR domain
5	<a href="#">c5fa9B_</a>	Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra; <b>PDBTitle:</b> bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
6	<a href="#">c3hcbJ_</a>	Alignment		100.0	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase; <b>PDBTitle:</b> structure of msrb from xanthomonas campestris (oxidized2 form)
7	<a href="#">d1xm0a1</a>	Alignment		100.0	44	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> SelR domain
8	<a href="#">c2l1uA_</a>	Alignment		100.0	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase b2, mitochondrial; <b>PDBTitle:</b> structure-functional analysis of mammalian msrb2 protein
9	<a href="#">c2kaoA_</a>	Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase b1; <b>PDBTitle:</b> structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
10	<a href="#">c4v30A_</a>	Alignment		94.2	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cereblon isoform 4; <b>PDBTitle:</b> cereblon isoform 4 from magnetospirillum gryphiswaldense in2 complex with lenalidomide
11	<a href="#">c5hj0C_</a>	Alignment		93.8	21	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> kinetochore protein mis18; <b>PDBTitle:</b> crystal structure of mis18 'yippee-like' domain

12	<a href="#">c6b5bA</a>	Alignment		60.8	29	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 1e; <b>PDBTitle:</b> cryo-em structure of the naip5-nlrc4-flagellin inflammasome
13	<a href="#">d1v7mh1</a>	Alignment		43.7	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
14	<a href="#">d1aj7h1</a>	Alignment		42.9	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
15	<a href="#">d1gafh1</a>	Alignment		41.5	9	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
16	<a href="#">d1pfta</a>	Alignment		40.6	18	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
17	<a href="#">d1dl6a</a>	Alignment		40.2	18	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
18	<a href="#">c6cceD</a>	Alignment		37.1	18	<b>PDB header:</b> transcription/dna/antibiotic <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis rna polymerase2 transcription initiation complex with inhibitor kanglemycin a
19	<a href="#">d1smyd</a>	Alignment		36.4	33	<b>Fold:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Superfamily:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Family:</b> RNA-polymerase beta-prime
20	<a href="#">d1vera</a>	Alignment		36.1	20	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
21	<a href="#">d2raxa1</a>	Alignment	not modelled	36.0	15	<b>Fold:</b> Inhibitor of apoptosis (IAP) repeat <b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat <b>Family:</b> Inhibitor of apoptosis (IAP) repeat
22	<a href="#">c4mngE</a>	Alignment	not modelled	34.0	33	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> tra@ protein,tra@ protein, ti antigen cd3-associated <b>PDBTitle:</b> structure of the dp10.7 tcr with cd1d-sulfatide
23	<a href="#">d1j8hd1</a>	Alignment	not modelled	33.8	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
24	<a href="#">c4g7oN</a>	Alignment	not modelled	32.5	31	<b>PDB header:</b> transcription, transferase/dna <b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of thermus thermophilus transcription initiation2 complex containing 2 nt of rna
25	<a href="#">d1h8ba</a>	Alignment	not modelled	32.2	18	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
26	<a href="#">c2w4rB</a>	Alignment	not modelled	31.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase dhx58; <b>PDBTitle:</b> crystal structure of the regulatory domain of human Igp2
27	<a href="#">c3qqcA</a>	Alignment	not modelled	30.5	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit b, dna-directed rna <b>PDBTitle:</b> crystal structure of archaeal spt4/5 bound to the rnap clamp domain
28	<a href="#">c3h0gl</a>	Alignment	not modelled	30.3	18	<b>PDB header:</b> transcription <b>Chain:</b> I: <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb9; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe

29	<a href="#">d1b88a_</a>	Alignment	not modelled	29.9	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
30	<a href="#">d1ggbh1</a>	Alignment	not modelled	29.8	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
31	<a href="#">d1mim1</a>	Alignment	not modelled	29.4	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
32	<a href="#">c6oanD_</a>	Alignment	not modelled	28.6	19	<b>PDB header:</b> cell invasion <b>Chain:</b> D: <b>PDB Molecule:</b> antibody 053054 single chain variable fragment; <b>PDBTitle:</b> structure of dbp in complex with human neutralizing antibody 053054
33	<a href="#">c2o5iD_</a>	Alignment	not modelled	28.6	33	<b>PDB header:</b> transferase/dna-rna hybrid <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase elongation2 complex
34	<a href="#">c3facE_</a>	Alignment	not modelled	28.2	17	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides protein2 rsp_2168. northeast structural genomics target rhr83.
35	<a href="#">c3w0fA_</a>	Alignment	not modelled	28.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease 8-like 3; <b>PDBTitle:</b> crystal structure of mouse endonuclease viii-like 3 (mneil3)
36	<a href="#">c6dcfD_</a>	Alignment	not modelled	28.0	33	<b>PDB header:</b> transcription/dna/antibiotic <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rifampicin-resistant rna polymerase and bound3 to kanglemycin a
37	<a href="#">d1nakh1</a>	Alignment	not modelled	27.9	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
38	<a href="#">c5x22D_</a>	Alignment	not modelled	26.9	31	<b>PDB header:</b> transferase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of thermus thermophilus transcription initiation2 complex with gpa and cmpcpp
39	<a href="#">c3k7aM_</a>	Alignment	not modelled	26.2	21	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> crystal structure of an rna polymerase ii-tfiib complex
40	<a href="#">d1ynjd1</a>	Alignment	not modelled	25.7	31	<b>Fold:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Superfamily:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Family:</b> RNA-polymerase beta-prime
41	<a href="#">c4c2mX_</a>	Alignment	not modelled	25.4	15	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa12; <b>PDBTitle:</b> structure of rna polymerase i at 2.8 a resolution
42	<a href="#">c5xcqB_</a>	Alignment	not modelled	25.3	25	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> vi-sarah(m24c) chimera; <b>PDBTitle:</b> crystal structure of p20.1 fv-clasp fragment with its antigen peptide
43	<a href="#">c3i0yC_</a>	Alignment	not modelled	25.3	12	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
44	<a href="#">d1dfb1</a>	Alignment	not modelled	25.1	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
45	<a href="#">c4llgJ_</a>	Alignment	not modelled	24.7	33	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure analysis of the e.coli holoenzyme/gp2 complex
46	<a href="#">c2znwB_</a>	Alignment	not modelled	24.3	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> scfv10; <b>PDBTitle:</b> crystal structure of scfv10 in complex with hen egg lysozyme
47	<a href="#">c4wqsD_</a>	Alignment	not modelled	24.3	33	<b>PDB header:</b> transferase/dna/rna <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> thermus thermophilus rna polymerase backtracked complex
48	<a href="#">c1ua6H_</a>	Alignment	not modelled	24.2	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ig vh,anti-lysozyme; <b>PDBTitle:</b> crystal structure of hyhel-10 fv mutant sfsf complexed with2 hen egg white lysozyme complex
49	<a href="#">d2i27n1</a>	Alignment	not modelled	23.9	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
50	<a href="#">d1jnlh1</a>	Alignment	not modelled	23.7	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
51	<a href="#">c2zkr2_</a>	Alignment	not modelled	23.5	30	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 2: <b>PDB Molecule:</b> 60s ribosomal protein l37e; <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
52	<a href="#">c4c57C_</a>	Alignment	not modelled	23.3	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nanobody; <b>PDBTitle:</b> structure of gak kinase in complex with a nanobody
53	<a href="#">c2ybaA_</a>	Alignment	not modelled	23.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> archaemetzincin;

53	<a href="#">c2n1qA</a>	Alignment	not modelled	23.2	33	<b>PDBTitle:</b> crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution <b>PDB header:</b> transferase/dna-rna hybrid
54	<a href="#">c2o5jN</a>	Alignment	not modelled	23.2	33	<b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> crystal structure of the t. thermophilus rnap polymerase elongation2 complex with the ntp substrate analog
55	<a href="#">c5c6wH</a>	Alignment	not modelled	23.1	22	<b>PDB header:</b> immune system <b>Chain:</b> H: <b>PDB Molecule:</b> protein ighv1-69-2,ig lambda chain v-ii region nig-84; <b>PDBTitle:</b> anti-cxcl13 scfv - e10
56	<a href="#">c5tw1D</a>	Alignment	not modelled	22.7	33	<b>PDB header:</b> transcription activator/transferase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
57	<a href="#">c1ic4H</a>	Alignment	not modelled	22.4	10	<b>PDB header:</b> protein binding/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> igg1 fab chain h; <b>PDBTitle:</b> crystal structure of hyhel-10 fv mutant(hd32a)-hen lysozyme2 complex
58	<a href="#">d2dktA2</a>	Alignment	not modelled	22.4	31	<b>Fold:</b> Zinc hairpin stack <b>Superfamily:</b> Zinc hairpin stack <b>Family:</b> Zinc hairpin stack
59	<a href="#">c1i3qL</a>	Alignment	not modelled	22.3	14	<b>PDB header:</b> transcription <b>Chain:</b> I: <b>PDB Molecule:</b> dna-directed rna polymerase ii 14.2kd <b>PDBTitle:</b> rna polymerase ii crystal form i at 3.1 a resolution
60	<a href="#">c4iqcD</a>	Alignment	not modelled	21.9	33	<b>PDB header:</b> transcription, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> x-ray crystal structure of escherichia coli sigma70 holoenzyme
61	<a href="#">c1dzbB</a>	Alignment	not modelled	21.8	22	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> scfv fragment 1f9; <b>PDBTitle:</b> crystal structure of phage library-derived single-chain fv fragment2 1f9 in complex with turkey egg-white lysozyme
62	<a href="#">c1qokA</a>	Alignment	not modelled	21.6	26	<b>PDB header:</b> immunoglobulin <b>Chain:</b> A: <b>PDB Molecule:</b> mfe-23 recombinant antibody fragment; <b>PDBTitle:</b> mfe-23 an anti-carcinoembryonic antigen single-chain fv antibody
63	<a href="#">c1s1iY</a>	Alignment	not modelled	21.6	38	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l37-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
64	<a href="#">c5yudA</a>	Alignment	not modelled	21.4	26	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 1e; <b>PDBTitle:</b> flagellin derivative in complex with the nlr protein naip5
65	<a href="#">c2dqeH</a>	Alignment	not modelled	21.4	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ig vh,anti-lysozyme; <b>PDBTitle:</b> crystal structure of hyhel-10 fv mutant (hy53a) complexed2 with hen egg lysozyme
66	<a href="#">d1q9wb1</a>	Alignment	not modelled	21.3	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
67	<a href="#">d3dggA1</a>	Alignment	not modelled	21.3	26	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
68	<a href="#">d1n7ml1</a>	Alignment	not modelled	21.2	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
69	<a href="#">d1xx6a2</a>	Alignment	not modelled	21.1	32	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Type II thymidine kinase zinc finger
70	<a href="#">d1beca1</a>	Alignment	not modelled	21.1	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
71	<a href="#">c2dqcH</a>	Alignment	not modelled	20.9	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ig vh,anti-lysozyme; <b>PDBTitle:</b> crystal structure of hyhel-10 fv mutant(hy33f) complexed2 with hen egg lysozyme
72	<a href="#">c2gkiA</a>	Alignment	not modelled	20.8	26	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> nuclease; <b>PDBTitle:</b> heavy and light chain variable single domains of an anti-dna binding2 antibody hydrolyze both double- and single-stranded dnas without3 sequence specificity
73	<a href="#">c2jsoA</a>	Alignment	not modelled	20.7	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> polymyxin resistance protein pmrd; <b>PDBTitle:</b> antimicrobial resistance protein
74	<a href="#">d1w72l1</a>	Alignment	not modelled	20.7	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
75	<a href="#">c3j3bj</a>	Alignment	not modelled	20.5	29	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 60s ribosomal protein l11; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
76	<a href="#">c1nqbC</a>	Alignment	not modelled	20.4	26	<b>PDB header:</b> immunoglobulin <b>Chain:</b> C: <b>PDB Molecule:</b> single-chain antibody fragment; <b>PDBTitle:</b> trivalent antibody fragment
77	<a href="#">d1ospl1</a>	Alignment	not modelled	20.3	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
78	<a href="#">c6ehxB</a>	Alignment	not modelled	19.7	22	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> scfv advance: increasing our knowledge of antibody <b>PDBTitle:</b> scfv advance: increasing our knowledge of antibody

						structural space to2 enable faster and better decision making in drug discovery
79	<a href="#">c3iydD_</a>	Alignment	not modelled	19.7	33	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta; <b>PDBTitle:</b> three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
80	<a href="#">d2oslb1</a>	Alignment	not modelled	19.2	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
81	<a href="#">c5iy9M_</a>	Alignment	not modelled	19.1	18	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> human holo-pic in the initial transcribing state (no iis)
82	<a href="#">d1dl7h_</a>	Alignment	not modelled	19.1	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
83	<a href="#">c5xcuA_</a>	Alignment	not modelled	19.1	8	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> vh(s112c)-sarah chimera,vh(s112c)-sarah chimera; <b>PDBTitle:</b> crystal structure of 12ca5 fv-clasp fragment with its antigen peptide
84	<a href="#">c4f9pD_</a>	Alignment	not modelled	19.0	29	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> 103.2 anti-btn3a1 antibody fragment; <b>PDBTitle:</b> crystal structure of the human btn3a1 ectodomain in complex with the2 103.2 single chain antibody
85	<a href="#">d1nbyb1</a>	Alignment	not modelled	19.0	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
86	<a href="#">d1ndmb1</a>	Alignment	not modelled	19.0	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
87	<a href="#">d1bbjb1</a>	Alignment	not modelled	18.9	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
88	<a href="#">d3c6la1</a>	Alignment	not modelled	18.9	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
89	<a href="#">d1sm3h1</a>	Alignment	not modelled	18.9	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
90	<a href="#">c5jvvA_</a>	Alignment	not modelled	18.7	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,3-glucosyltransferase; <b>PDBTitle:</b> crystal structure and characterization an elongating gh family 162 beta-1,3-glucosyltransferase
91	<a href="#">c4xsxj_</a>	Alignment	not modelled	18.6	33	<b>PDB header:</b> transcription/antibiotic <b>Chain:</b> J: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of cbr 703 bound to escherichia coli rna polymerase2 holoenzyme
92	<a href="#">d1q9rb1</a>	Alignment	not modelled	18.6	7	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
93	<a href="#">d1igfl1</a>	Alignment	not modelled	18.6	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
94	<a href="#">d1nj9b1</a>	Alignment	not modelled	18.5	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
95	<a href="#">c2dqjH_</a>	Alignment	not modelled	18.5	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ig vh,anti-lysozyme; <b>PDBTitle:</b> crystal structure of hyhel-10 fv (wild-type) complexed with2 hen egg lysozyme at 1.8a resolution
96	<a href="#">c2dqjH_</a>	Alignment	not modelled	18.5	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ig vh,anti-lysozyme; <b>PDBTitle:</b> crystal structure of hyhel-10 fv mutant (ly50a) complexed2 with hen egg lysozyme
97	<a href="#">c1j1pH_</a>	Alignment	not modelled	18.5	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ig vh,anti-lysozyme; <b>PDBTitle:</b> crystal structure of hyhel-10 fv mutant ls91a complexed2 with hen egg white lysozyme
98	<a href="#">c3a6cH_</a>	Alignment	not modelled	18.5	10	<b>PDB header:</b> immune system/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ig vh, anti-lysozyme; <b>PDBTitle:</b> crystal structure of hyhel-10 fv mutant ln92d complexed with hen egg2 white lysozyme
99	<a href="#">d1j1ph_</a>	Alignment	not modelled	18.5	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)