



























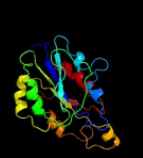
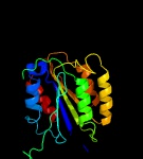



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0959_(-)_1071259_1073277
Date	Fri Jul 26 01:50:55 BST 2019
Unique Job ID	fb15ae28318628c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4fx5A_</a>	 Alignment		99.9	19	<b>PDB header:</b> blood clotting <b>Chain:</b> A; <b>PDB Molecule:</b> von willebrand factor type a; <b>PDBTitle:</b> von willebrand factor type a from catenulispora acidiphila
2	<a href="#">c5a8jA_</a>	 Alignment		99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> vwa2; <b>PDBTitle:</b> crystal structure of the arnb paralog vwa2 from2 sulfolobus acidocaldarius
3	<a href="#">c6fpzA_</a>	 Alignment		99.9	19	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> inter-alpha-trypsin inhibitor heavy chain h1; <b>PDBTitle:</b> inter-alpha-inhibitor heavy chain 1, d298a
4	<a href="#">c6o9l6_</a>	 Alignment		99.8	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> 6; <b>PDB Molecule:</b> general transcription factor iih subunit 2; <b>PDBTitle:</b> human holo-pic in the closed state
5	<a href="#">c6nmiE_</a>	 Alignment		99.8	16	<b>PDB header:</b> transcription <b>Chain:</b> E; <b>PDB Molecule:</b> general transcription factor iih subunit 2, p44; <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
6	<a href="#">c3ibsA_</a>	 Alignment		99.8	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein batb; <b>PDBTitle:</b> crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
7	<a href="#">c4rckB_</a>	 Alignment		99.8	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical membrane spanning protein; <b>PDBTitle:</b> crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri
8	<a href="#">c5iy70_</a>	 Alignment		99.8	15	<b>PDB header:</b> transcription, transferase/dna <b>Chain:</b> 0; <b>PDB Molecule:</b> general transcription factor iih subunit 2; <b>PDBTitle:</b> human holo-pic in the open state
9	<a href="#">c3ibrF_</a>	 Alignment		99.8	22	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> voltage-dependent calcium channel subunit alpha-2/delta-1; <b>PDBTitle:</b> cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
10	<a href="#">c4wfgA_</a>	 Alignment		99.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> suppressor of stem-loop protein 1; <b>PDBTitle:</b> crystal structure of tfiih subunit
11	<a href="#">c2x5nA_</a>	 Alignment		99.7	15	<b>PDB header:</b> nuclear protein <b>Chain:</b> A; <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn10; <b>PDBTitle:</b> crystal structure of the sprpn10 vwa domain

12	<a href="#">c5oqj6_</a>	Alignment		99.7	14	<b>PDB header:</b> transcription <b>Chain:</b> 6: <b>PDB Molecule:</b> suppressor of stem-loop protein 1; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih
13	<a href="#">c4b4tW_</a>	Alignment		99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> W: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn10; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
14	<a href="#">d2ok5a1</a>	Alignment		99.7	15	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
15	<a href="#">c5gjfF_</a>	Alignment		99.7	19	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent calcium channel subunit alpha-2/delta-1; <b>PDBTitle:</b> structure of the mammalian voltage-gated calcium channel cav1.12 complex at near atomic resolution
16	<a href="#">c1rs0A_</a>	Alignment		99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement factor b; <b>PDBTitle:</b> crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
17	<a href="#">c2ok5A_</a>	Alignment		99.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement factor b; <b>PDBTitle:</b> human complement factor b
18	<a href="#">c2x31F_</a>	Alignment		99.7	19	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> magnesium-chelatase 60 kda subunit; <b>PDBTitle:</b> modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
19	<a href="#">d1pd0a3</a>	Alignment		99.6	16	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Trunk domain of Sec23/24
20	<a href="#">c3txaA_</a>	Alignment		99.6	23	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
21	<a href="#">c4hqnb_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> sporozoite surface protein 2; <b>PDBTitle:</b> crystal structure of manganese-loaded plasmodium vivax trap protein
22	<a href="#">c5gjqW_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> W: <b>PDB Molecule:</b> 26s proteasome non-atpase regulatory subunit 4; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
23	<a href="#">d1jeyb2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Ku80 subunit N-terminal domain
24	<a href="#">c2i6sA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement c2a fragment; <b>PDBTitle:</b> complement component c2a
25	<a href="#">d1jeya2</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Ku70 subunit N-terminal domain
26	<a href="#">c3tw0D_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
27	<a href="#">c2iueA_</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> pactolus i-domain; <b>PDBTitle:</b> pactolus i-domain: functional switching of the rossmann2 fold
28	<a href="#">d1q0pa_</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain

29	<a href="#">c3n2nC</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> toxin receptor <b>Chain:</b> C: <b>PDB Molecule:</b> anthrax toxin receptor 1; <b>PDBTitle:</b> the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
30	<a href="#">d1shux</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
31	<a href="#">c2b2xB</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> vla1 rdelta i-domain complexed with a quadruple mutant of the agc22 fab
32	<a href="#">d1yvra2</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> RoRNP C-terminal domain-like
33	<a href="#">c4hqfA</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> thrombospondin-related anonymous protein, trap; <b>PDBTitle:</b> crystal structure of plasmodium falciparum trap, i4 form
34	<a href="#">d1ijba</a>	Alignment	not modelled	99.5	9	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
35	<a href="#">c2nvoA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ro sixty-related protein, rsr; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans ro (rsr) protein
36	<a href="#">c4cnbA</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> proximal thread matrix protein 1; <b>PDBTitle:</b> structure of proximal thread matrix protein 1 (ptmp1) from the2 mussel byssus - crystal form 2
37	<a href="#">c3gxbB</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> von willebrand factor; <b>PDBTitle:</b> crystal structure of vwf a2 domain
38	<a href="#">d1atza</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
39	<a href="#">d1u0oc1</a>	Alignment	not modelled	99.4	10	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
40	<a href="#">c5e6rA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-l; <b>PDBTitle:</b> structures of leukocyte integrin alb2: the ai domain, the headpiece,2 and the pocket for the internal ligand
41	<a href="#">c4okuA</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> micronemal protein mic2; <b>PDBTitle:</b> structure of toxoplasma gondii promic2
42	<a href="#">d1n3ya</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
43	<a href="#">c2xggB</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> microneme protein 2; <b>PDBTitle:</b> structure of toxoplasma gondii micronemal protein 2 a_i2 domain
44	<a href="#">d1v7pc</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
45	<a href="#">c1jeyB</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> ku80; <b>PDBTitle:</b> crystal structure of the ku heterodimer bound to dna
46	<a href="#">c4ihkA</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha3(vi); <b>PDBTitle:</b> crystal structure of the collagen vi alpha3 n5 domain r1061q
47	<a href="#">d1pt6a</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
48	<a href="#">d1ck4a</a>	Alignment	not modelled	99.2	16	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
49	<a href="#">d1mf7a</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
50	<a href="#">c3egxB</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein transport protein sec24a; <b>PDBTitle:</b> crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22b and bound to the transport3 signal sequence of the snare protein bet1
51	<a href="#">d1mjna</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
52	<a href="#">d1tyeb2</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
53	<a href="#">c1pd0A</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec24; <b>PDBTitle:</b> crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
54	<a href="#">c3eg9B</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> sec24 related gene family, member d; <b>PDBTitle:</b> crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
						<b>PDB header:</b> protein transport

55	<a href="#">c3eh2B_</a>	Alignment	not modelled	98.9	13	<b>Chain:</b> B: <b>PDB Molecule:</b> protein transport protein sec24c; <b>PDBTitle:</b> crystal structure of the human copii-coat protein sec24c
56	<a href="#">c6nmiF_</a>	Alignment	not modelled	98.9	19	<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
57	<a href="#">c6djpB_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-8; <b>PDBTitle:</b> integrin alpha-v beta-8 in complex with the fabs 8b8 and 68
58	<a href="#">c1m2oA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> protein transport/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec23; <b>PDBTitle:</b> crystal structure of the sec23-sar1 complex
59	<a href="#">c4um9D_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> integrin beta-6; <b>PDBTitle:</b> crystal structure of alpha v beta 6 with peptide
60	<a href="#">c6bxjA_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of integrin beta-3 and integrin alpha-l; <b>PDBTitle:</b> structure of a single-chain beta3 integrin
61	<a href="#">c1m2vB_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein transport protein sec24; <b>PDBTitle:</b> crystal structure of the yeast sec23/24 heterodimer
62	<a href="#">c3eg9A_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec23a; <b>PDBTitle:</b> crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
63	<a href="#">c3fcuB_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> cell adhesion/blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> structure of headpiece of integrin aiibb3 in open conformation
64	<a href="#">c3vi3D_</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> cell adhesion/immune system <b>Chain:</b> D: <b>PDB Molecule:</b> integrin beta-1; <b>PDBTitle:</b> crystal structure of alpha5beta1 integrin headpiece (ligand-free form)
65	<a href="#">c6bxfA_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of integrin beta-3 and integrin alpha-l; <b>PDBTitle:</b> crystal structure of an extended b3 integrin I33
66	<a href="#">d2qtva3</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Trunk domain of Sec23/24
67	<a href="#">c3v4pB_</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-7; <b>PDBTitle:</b> crystal structure of a4b7 headpiece complexed with fab act-1
68	<a href="#">c1jeqA_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ku70; <b>PDBTitle:</b> crystal structure of the ku heterodimer
69	<a href="#">c5y58E_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> atp-dependent dna helicase ii subunit 1; <b>PDBTitle:</b> crystal structure of ku70/80 and tlc1
70	<a href="#">c1yvrA_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 60-kda ss-a/ro ribonucleoprotein; <b>PDBTitle:</b> ro autoantigen
71	<a href="#">c1u8cB_</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> a novel adaptation of the integrin psi domain revealed from its2 crystal structure
72	<a href="#">c3ragA_</a>	Alignment	not modelled	98.4	20	<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 aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
73	<a href="#">c4pn7A_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of the tfiih p34 n-terminal domain
74	<a href="#">c5y59B_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent dna helicase ii subunit 2; <b>PDBTitle:</b> crystal structure of ku80 and sir4
75	<a href="#">c5y58D_</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent dna helicase ii subunit 2; <b>PDBTitle:</b> crystal structure of ku70/80 and tlc1
76	<a href="#">c3k71G_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> G: <b>PDB Molecule:</b> integrin alpha-x; <b>PDBTitle:</b> structure of integrin alphax beta2 ectodomain
77	<a href="#">c5iy63_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> transcription, transferase/dna <b>Chain:</b> 3: <b>PDB Molecule:</b> general transcription factor iih subunit 3; <b>PDBTitle:</b> human holo-pic in the closed state
78	<a href="#">c5oqj4_</a>	Alignment	not modelled	98.2	14	<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
79	<a href="#">c3ijeB_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> crystal structure of the complete integrin alphavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment
80	<a href="#">c3k6sB_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-2; <b>PDBTitle:</b> structure of integrin alphaxbeta2 ectodomain
81	<a href="#">c4cgkA_</a>	Alignment	not modelled	97.3	7	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> secreted 45 kda protein; <b>PDBTitle:</b> crystal structure of the essential protein pcsb from streptococcus2 pneumoniae

82	<a href="#">c5jxA</a>	Alignment	not modelled	97.3	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
83	<a href="#">c3wolB</a>	Alignment	not modelled	96.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl aminopeptidase bii; <b>PDBTitle:</b> crystal structure of the dap bii dipeptide complex i
84	<a href="#">c1ciiA</a>	Alignment	not modelled	96.2	10	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
85	<a href="#">c5ew5C</a>	Alignment	not modelled	95.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
86	<a href="#">c1c1gA</a>	Alignment	not modelled	94.9	8	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> tropomyosin; <b>PDBTitle:</b> crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
87	<a href="#">c1bf5A</a>	Alignment	not modelled	94.5	9	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription 1- <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
88	<a href="#">c3ojaB</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
89	<a href="#">c3ojaA</a>	Alignment	not modelled	94.4	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich immune molecule 1; <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
90	<a href="#">c1bg1A</a>	Alignment	not modelled	93.1	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
91	<a href="#">c3cwgA</a>	Alignment	not modelled	92.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment
92	<a href="#">c6f1tX</a>	Alignment	not modelled	92.5	12	<b>PDB header:</b> motor protein <b>Chain:</b> X: <b>PDB Molecule:</b> bicd family-like cargo adapter 1,bicd family-like cargo <b>PDBTitle:</b> cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
93	<a href="#">c1yvlB</a>	Alignment	not modelled	92.4	7	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
94	<a href="#">c6o7xa</a>	Alignment	not modelled	91.7	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
95	<a href="#">c6gaoC</a>	Alignment	not modelled	91.0	12	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail and body
96	<a href="#">c4xa3A</a>	Alignment	not modelled	90.0	8	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp7-myh7(1361-1425)-eb1 chimera protein; <b>PDBTitle:</b> crystal structure of the coiled-coil surrounding skip 2 of myh7
97	<a href="#">c5jxA</a>	Alignment	not modelled	89.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
98	<a href="#">c6gvwD</a>	Alignment	not modelled	87.4	17	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> brisc and brca1-a complex member 1; <b>PDBTitle:</b> crystal structure of the brca1-a complex
99	<a href="#">c6ewyA</a>	Alignment	not modelled	86.9	10	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan endopeptidase ripa; <b>PDBTitle:</b> ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
100	<a href="#">c1f5nA</a>	Alignment	not modelled	86.8	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced guanylate-binding protein 1; <b>PDBTitle:</b> human guanylate binding protein-1 in complex with the gtp analogue,2 gmppnp.
101	<a href="#">c2oevA</a>	Alignment	not modelled	86.3	10	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 6-interacting protein; <b>PDBTitle:</b> crystal structure of alix/aip1
102	<a href="#">c1jchC</a>	Alignment	not modelled	86.0	10	<b>PDB header:</b> ribosome inhibitor, hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin e3; <b>PDBTitle:</b> crystal structure of colicin e3 in complex with its immunity protein
103	<a href="#">c1g8xB</a>	Alignment	not modelled	85.8	12	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin ii heavy chain fused to alpha-actinin 3; <b>PDBTitle:</b> structure of a genetically engineered molecular motor
104	<a href="#">c5xg2A</a>	Alignment	not modelled	85.4	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of a coiled-coil segment (residues 345-468 and 694-2 814) of pyrococcus yayanosii smc
105	<a href="#">c6gapB</a>	Alignment	not modelled	85.1	7	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t3d reovirus sigma1 coiled coil tail and body
106	<a href="#">c3ghgl</a>	Alignment	not modelled	84.7	12	<b>PDB header:</b> blood clotting <b>Chain:</b> I: <b>PDB Molecule:</b> fibrinogen gamma chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
						<b>PDB header:</b> toxin

107	<a href="#">c6ogdB_</a>	Alignment	not modelled	84.0	10	<b>Chain:</b> B; <b>PDB Molecule:</b> toxin subunit yena2; <b>PDBTitle:</b> cryo-em structure of yentca in its prepore state
108	<a href="#">c1deqF_</a>	Alignment	not modelled	83.4	5	<b>PDB header:</b> blood clotting <b>Chain:</b> F; <b>PDB Molecule:</b> fibrinogen (gamma chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
109	<a href="#">c5cwsJ_</a>	Alignment	not modelled	83.3	7	<b>PDB header:</b> protein transport <b>Chain:</b> J; <b>PDB Molecule:</b> nucleoporin nup49; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
110	<a href="#">c3vkgB_</a>	Alignment	not modelled	82.9	15	<b>PDB header:</b> motor protein <b>Chain:</b> B; <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein motor domain
111	<a href="#">d1jsca3</a>	Alignment	not modelled	82.4	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
112	<a href="#">c3wuqA_</a>	Alignment	not modelled	81.1	10	<b>PDB header:</b> motor protein <b>Chain:</b> A; <b>PDB Molecule:</b> cytoplasmic dynein 1 heavy chain 1; <b>PDBTitle:</b> structure of the entire stalk region of the dynein motor domain
113	<a href="#">c5wjbA_</a>	Alignment	not modelled	80.4	14	<b>PDB header:</b> actin/dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> capsid assembly scaffolding protein,myosin-7; <b>PDBTitle:</b> crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7
114	<a href="#">c4cg4D_</a>	Alignment	not modelled	80.4	12	<b>PDB header:</b> actin-binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> pyrin; <b>PDBTitle:</b> crystal structure of the chs-b30.2 domains of trim20
115	<a href="#">c2efrB_</a>	Alignment	not modelled	79.7	11	<b>PDB header:</b> contractile protein <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
116	<a href="#">c6f1tx_</a>	Alignment	not modelled	78.8	6	<b>PDB header:</b> motor protein <b>Chain:</b> X; <b>PDB Molecule:</b> bicd family-like cargo adapter 1,bicd family-like cargo <b>PDBTitle:</b> cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
117	<a href="#">c5yixA_</a>	Alignment	not modelled	78.6	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> caulobacter crescentus gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
118	<a href="#">c5nmoA_</a>	Alignment	not modelled	78.4	9	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> chromosome partition protein smc,chromosome partition <b>PDBTitle:</b> structure of the bacillus subtilis smc joint domain
119	<a href="#">c5dfzD_</a>	Alignment	not modelled	77.7	10	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
120	<a href="#">c1ei3E_</a>	Alignment	not modelled	77.5	10	<b>PDB header:</b> blood clotting <b>Chain:</b> E; <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen