





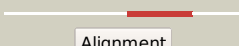

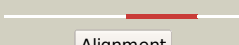

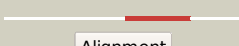













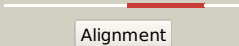



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3693 (-) _4134904_4136226
Date	Fri Aug 9 18:20:38 BST 2019
Unique Job ID	2cbcc3f872ce0553

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4fx5A_</a>	 Alignment		98.8	17	<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="#">d1jeyb2</a>	 Alignment		98.5	13	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Ku80 subunit N-terminal domain
3	<a href="#">c6nmIE_</a>	 Alignment		98.4	9	<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
4	<a href="#">c5oqj6_</a>	 Alignment		98.4	8	<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
5	<a href="#">c6fpzA_</a>	 Alignment		98.4	8	<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
6	<a href="#">c4b4tW_</a>	 Alignment		98.3	8	<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
7	<a href="#">c6o9I6_</a>	 Alignment		98.3	8	<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
8	<a href="#">d1yvra2</a>	 Alignment		98.2	14	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> RoRNP C-terminal domain-like
9	<a href="#">c3ibsA_</a>	 Alignment		98.2	13	<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
10	<a href="#">c4rckB_</a>	 Alignment		98.2	13	<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
11	<a href="#">c2nvoA_</a>	 Alignment		98.1	15	<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

12	<a href="#">c4wfgA</a>	 Alignment		98.1	7	<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
13	<a href="#">c2x5nA</a>	 Alignment		98.1	10	<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
14	<a href="#">d1jeva2</a>	 Alignment		97.9	10	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Ku70 subunit N-terminal domain
15	<a href="#">c5a8jA</a>	 Alignment		97.9	14	<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 sulfobolus acidocaldarius
16	<a href="#">c2x31F</a>	 Alignment		97.9	21	<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
17	<a href="#">c2i6sA</a>	 Alignment		97.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement c2a fragment; <b>PDBTitle:</b> complement component c2a
18	<a href="#">c1jevB</a>	 Alignment		97.8	10	<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
19	<a href="#">c5iy70</a>	 Alignment		97.8	10	<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
20	<a href="#">c2iueA</a>	 Alignment		97.7	9	<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
21	<a href="#">c1rs0A</a>	 Alignment	not modelled	97.7	10	<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)
22	<a href="#">c5gjqW</a>	 Alignment	not modelled	97.6	9	<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="#">c2ok5A</a>	 Alignment	not modelled	97.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement factor b; <b>PDBTitle:</b> human complement factor b
24	<a href="#">c3jbrF</a>	 Alignment	not modelled	97.6	14	<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
25	<a href="#">c5gjvF</a>	 Alignment	not modelled	97.5	16	<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
26	<a href="#">c4okuA</a>	 Alignment	not modelled	97.5	8	<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
27	<a href="#">c4hqnb</a>	 Alignment	not modelled	97.5	15	<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
28	<a href="#">c3n2nG</a>	 Alignment	not modelled	97.2	15	<b>PDB header:</b> toxin receptor <b>Chain:</b> C: <b>PDB Molecule:</b> anthrax toxin receptor 1;

28	<a href="#">c3fznc</a>	Alignment	not modelled	97.2	10	<b>PDBTitle:</b> the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain <b>PDB header:</b> cell adhesion
29	<a href="#">c5e6rA</a>	Alignment	not modelled	97.2	11	<b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-I; <b>PDBTitle:</b> structures of leukocyte integrin alb2: the ai domain, the headpiece,2 and the pocket for the internal ligand
30	<a href="#">d2ok5a1</a>	Alignment	not modelled	97.1	14	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
31	<a href="#">c4cnbA</a>	Alignment	not modelled	97.0	9	<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
32	<a href="#">c2xggB</a>	Alignment	not modelled	96.9	8	<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
33	<a href="#">c2b2xB</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> vla1 rdelta1 i-domain complexed with a quadruple mutant of the aqc22 fab
34	<a href="#">d1shux</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
35	<a href="#">c1l9mB</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> protein-glutamine glutamyltransferase e3; <b>PDBTitle:</b> three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
36	<a href="#">d1pd0a3</a>	Alignment	not modelled	96.3	9	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Trunk domain of Sec23/24
37	<a href="#">c1yvra</a>	Alignment	not modelled	96.3	14	<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
38	<a href="#">c3txaA</a>	Alignment	not modelled	95.8	13	<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
39	<a href="#">d1v7pc</a>	Alignment	not modelled	95.5	13	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
40	<a href="#">c6djpB</a>	Alignment	not modelled	95.4	11	<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
41	<a href="#">d1w8oa1</a>	Alignment	not modelled	95.4	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
42	<a href="#">d1n3ya</a>	Alignment	not modelled	95.2	12	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
43	<a href="#">c6bxjA</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> chimera protein of integrin beta-3 and integrin alpha-I; <b>PDBTitle:</b> structure of a single-chain beta3 integrin
44	<a href="#">c4hqfA</a>	Alignment	not modelled	94.9	15	<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
45	<a href="#">d1vja3</a>	Alignment	not modelled	94.8	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
46	<a href="#">c4fxkB</a>	Alignment	not modelled	94.8	17	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> complement c4-a alpha chain; <b>PDBTitle:</b> human complement c4
47	<a href="#">d1g0da3</a>	Alignment	not modelled	94.6	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
48	<a href="#">d1mf7a</a>	Alignment	not modelled	94.4	11	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
49	<a href="#">d1ex0a3</a>	Alignment	not modelled	94.3	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
50	<a href="#">c6bxfA</a>	Alignment	not modelled	94.0	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> chimera protein of integrin beta-3 and integrin alpha-I; <b>PDBTitle:</b> crystal structure of an extended b3 integrin I33
51	<a href="#">c4u48A</a>	Alignment	not modelled	93.9	22	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> putative inner membrane lipoprotein; <b>PDBTitle:</b> crystal structure of salmonella alpha-2-macroglobulin
52	<a href="#">c2kl6A</a>	Alignment	not modelled	93.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
53	<a href="#">d1pt6a</a>	Alignment	not modelled	93.5	14	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
54	<a href="#">d1q0pa</a>	Alignment	not modelled	93.4	13	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain

55	<a href="#">c1g0dA_</a>	Alignment	not modelled	93.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> crystal structure of red sea bream transglutaminase
56	<a href="#">c3ragA_</a>	Alignment	not modelled	93.3	15	<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
57	<a href="#">d1mjna_</a>	Alignment	not modelled	92.9	12	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
58	<a href="#">c2xzza_</a>	Alignment	not modelled	92.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase k; <b>PDBTitle:</b> crystal structure of the human transglutaminase 1 beta-barrel domain
59	<a href="#">c4rtdA_</a>	Alignment	not modelled	92.4	22	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized lipoprotein yfhm; <b>PDBTitle:</b> escherichia coli alpha-2-macroglobulin activated by porcine elastase
60	<a href="#">c3tw0D_</a>	Alignment	not modelled	92.3	15	<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
61	<a href="#">d1tyeb2</a>	Alignment	not modelled	92.1	17	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
62	<a href="#">c4ihkA_</a>	Alignment	not modelled	92.0	13	<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
63	<a href="#">d2q3za3</a>	Alignment	not modelled	91.9	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
64	<a href="#">c2e6jA_</a>	Alignment	not modelled	91.8	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hydin protein; <b>PDBTitle:</b> solution structure of the c-terminal papd-like domain from2 human hydin protein
65	<a href="#">c4acqA_</a>	Alignment	not modelled	91.7	16	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-2-macroglobulin; <b>PDBTitle:</b> alpha-2 macroglobulin
66	<a href="#">c5y58E_</a>	Alignment	not modelled	91.7	13	<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
67	<a href="#">d1ijba_</a>	Alignment	not modelled	91.3	11	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
68	<a href="#">c1jeqA_</a>	Alignment	not modelled	91.3	10	<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="#">d1ck4a_</a>	Alignment	not modelled	90.9	17	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
70	<a href="#">c3hs0B_</a>	Alignment	not modelled	90.5	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> cobra venom factor (cvf) in complex with human factor b
71	<a href="#">d2q3za2</a>	Alignment	not modelled	90.4	9	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
72	<a href="#">c1f13A_</a>	Alignment	not modelled	90.3	10	<b>PDB header:</b> coagulation factor <b>Chain:</b> A: <b>PDB Molecule:</b> cellular coagulation factor xiii zymogen; <b>PDBTitle:</b> recombinant human cellular coagulation factor xiii
73	<a href="#">c2ys4A_</a>	Alignment	not modelled	89.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hydrocephalus-inducing protein homolog; <b>PDBTitle:</b> solution structure of the n-terminal papd-like domain of2 hydin protein from human
74	<a href="#">c6i2xB_</a>	Alignment	not modelled	89.8	13	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> structure of complement c5 in complex with small molecule inhibitor2 and cvf
75	<a href="#">c3gxbB_</a>	Alignment	not modelled	89.7	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
76	<a href="#">c1kv3F_</a>	Alignment	not modelled	89.7	14	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> human tissue transglutaminase in gdp bound form
77	<a href="#">c2qsvA_</a>	Alignment	not modelled	89.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
78	<a href="#">c3v4pB_</a>	Alignment	not modelled	89.5	17	<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
79	<a href="#">d1u0oc1</a>	Alignment	not modelled	89.4	10	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
80	<a href="#">c2a74B_</a>	Alignment	not modelled	89.3	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement component c3c; <b>PDBTitle:</b> human complement component c3c
81	<a href="#">c3fcuB_</a>	Alignment	not modelled	89.1	16	<b>PDB header:</b> cell adhesion/blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3;

81	<a href="#">c3t0B_</a>	Alignment	not modelled	89.1	10	<b>PDBTitle:</b> structure of headpiece of integrin aiibb3 in open conformation
82	<a href="#">c4acqC_</a>	Alignment	not modelled	89.0	19	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> alpha-2-macroglobulin; <b>PDBTitle:</b> alpha-2 macroglobulin
83	<a href="#">c3g6jB_</a>	Alignment	not modelled	88.6	17	<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
84	<a href="#">d1atza_</a>	Alignment	not modelled	87.1	16	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
85	<a href="#">c2a73B_</a>	Alignment	not modelled	86.9	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement c3; <b>PDBTitle:</b> human complement component c3
86	<a href="#">c4zo9B_</a>	Alignment	not modelled	85.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lin1840 protein; <b>PDBTitle:</b> crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
87	<a href="#">c4um9D_</a>	Alignment	not modelled	85.3	17	<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
88	<a href="#">c3qbtH_</a>	Alignment	not modelled	84.8	8	<b>PDB header:</b> protein transport/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1; <b>PDBTitle:</b> crystal structure of ocr1 540-678 in complex with rab8a:gppnhp
89	<a href="#">d1vjia2</a>	Alignment	not modelled	84.2	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
90	<a href="#">c5jp0A_</a>	Alignment	not modelled	83.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase bogh3b; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh3b with bound glucose
91	<a href="#">c3ay2A_</a>	Alignment	not modelled	83.0	18	<b>PDB header:</b> antitumor protein, antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid modified azurin protein; <b>PDBTitle:</b> crystal structure of neisserial azurin
92	<a href="#">c3rfrI_</a>	Alignment	not modelled	83.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> pmob; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
93	<a href="#">c3cu7A_</a>	Alignment	not modelled	81.8	10	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> complement c5; <b>PDBTitle:</b> human complement component 5
94	<a href="#">c3vi3D_</a>	Alignment	not modelled	80.8	18	<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)
95	<a href="#">c5z87B_</a>	Alignment	not modelled	80.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> emgh1; <b>PDBTitle:</b> structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus
96	<a href="#">c5z9sB_</a>	Alignment	not modelled	78.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 3 protein; <b>PDBTitle:</b> functional and structural characterization of a beta-glucosidase2 involved in saponin metabolism from intestinal bacteria
97	<a href="#">c3isyA_</a>	Alignment	not modelled	78.4	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular proteinase inhibitor; <b>PDBTitle:</b> crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
98	<a href="#">c2l0dA_</a>	Alignment	not modelled	78.1	6	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein; <b>PDBTitle:</b> solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
99	<a href="#">d1g0da2</a>	Alignment	not modelled	77.9	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
100	<a href="#">c2kutA_</a>	Alignment	not modelled	77.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
101	<a href="#">c4oleD_</a>	Alignment	not modelled	76.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> next to brca1 gene 1 protein; <b>PDBTitle:</b> crystal structure of a neighbor of brca1 gene 1 (nbr1) from homo2 sapiens at 2.52 a resolution
102	<a href="#">c3zz1A_</a>	Alignment	not modelled	76.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-d-glucoside glucohydrolase; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from hypocrea jecorina at 2.1a resolution.
103	<a href="#">c2x41A_</a>	Alignment	not modelled	75.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
104	<a href="#">c3qisA_</a>	Alignment	not modelled	74.5	10	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1; <b>PDBTitle:</b> recognition of the f&h motif by the lowe syndrome protein ocr1
105	<a href="#">c5wabD_</a>	Alignment	not modelled	74.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative beta-glucosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
106	<a href="#">c3u48A_</a>	Alignment	not modelled	74.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> jmb19063; <b>PDBTitle:</b> from soil to structure: a novel dimeric family 3-beta-glucosidase2 isolated from compost using metagenomic analysis

107	<a href="#">c3pvmB_</a>	Alignment	not modelled	74.0	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> structure of complement c5 in complex with cvf
108	<a href="#">d1ex0a2</a>	Alignment	not modelled	72.8	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
109	<a href="#">c5y59B_</a>	Alignment	not modelled	71.6	11	<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
110	<a href="#">d3es6b1</a>	Alignment	not modelled	70.4	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> SVA-like
111	<a href="#">c1u8cB_</a>	Alignment	not modelled	70.2	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
112	<a href="#">c5wabC_</a>	Alignment	not modelled	70.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative beta-glucosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
113	<a href="#">c4i3gB_</a>	Alignment	not modelled	70.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
114	<a href="#">c6q7jB_</a>	Alignment	not modelled	70.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-1,4-beta-xylosidase xlnD; <b>PDBTitle:</b> gh3 exo-beta-xylosidase (xlnD) in complex with xylobiose aziridine2 activity based probe
115	<a href="#">c4a5wA_</a>	Alignment	not modelled	69.9	11	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> complement c5; <b>PDBTitle:</b> crystal structure of c5b6
116	<a href="#">d2ccwa1</a>	Alignment	not modelled	69.9	13	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
117	<a href="#">c2b39B_</a>	Alignment	not modelled	69.0	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> c3; <b>PDBTitle:</b> structure of mammalian c3 with an intact thioester at 3a resolution
118	<a href="#">d1cuoa_</a>	Alignment	not modelled	68.8	10	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
119	<a href="#">c2h47C_</a>	Alignment	not modelled	66.0	15	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> azurin; <b>PDBTitle:</b> crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
120	<a href="#">c6abhG_</a>	Alignment	not modelled	65.3	13	<b>PDB header:</b> luminescent protein <b>Chain:</b> G: <b>PDB Molecule:</b> red-bioluminescence eliciting luciferase; <b>PDBTitle:</b> structure of a natural red emitting luciferase from phrixothrix hirtus2 (p1 crystal form)