

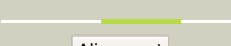
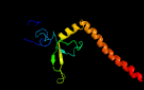

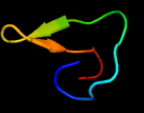

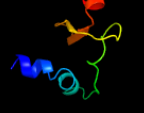





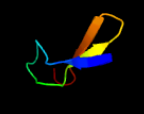



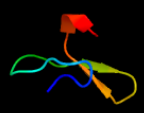


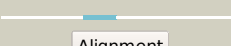




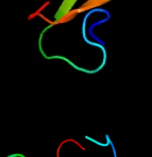
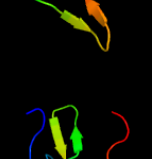
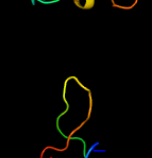
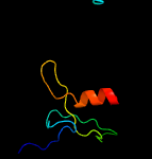

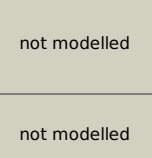


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2802c_(-)_3110790_3111833
Date	Wed Aug 7 12:50:46 BST 2019
Unique Job ID	b38a1bfe73f80894

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2owaB_</a>	 Alignment		69.5	26	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> arfgap-like finger domain containing protein; <b>PDBTitle:</b> crystal structure of putative gtpase activating protein for2 adp ribosylation factor from cryptosporidium parvum3 (cgd5_1040)
2	<a href="#">c6ro4G_</a>	 Alignment		69.1	14	<b>PDB header:</b> translocase <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair protein complementing xp-a cells; <b>PDBTitle:</b> structure of the core tfiih-xpa-dna complex
3	<a href="#">d2cuqa1</a>	 Alignment		53.8	30	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
4	<a href="#">d1dcqa2</a>	 Alignment		49.0	16	<b>Fold:</b> ArfGap/RecO-like zinc finger <b>Superfamily:</b> ArfGap/RecO-like zinc finger <b>Family:</b> Pyk2-associated protein beta ARF-GAP domain
5	<a href="#">c3d00A_</a>	 Alignment		49.0	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit e; <b>PDBTitle:</b> crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
6	<a href="#">c2b0oF_</a>	 Alignment		48.8	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> uplc1; <b>PDBTitle:</b> crystal structure of uplc1 gap domain
7	<a href="#">c1nuiA_</a>	 Alignment		47.8	25	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase/helicase; <b>PDBTitle:</b> crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
8	<a href="#">c5gjqZ_</a>	 Alignment		41.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> Z: <b>PDB Molecule:</b> 26s proteasome non-atpase regulatory subunit 2; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
9	<a href="#">c1x68A_</a>	 Alignment		41.5	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fhl5 protein; <b>PDBTitle:</b> solution structures of the c-terminal lim domain of human2 fhl5 protein
10	<a href="#">c3lvrE_</a>	 Alignment		36.8	23	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> arf-gap with sh3 domain, ank repeat and ph domain- <b>PDBTitle:</b> the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
11	<a href="#">c1dcqA_</a>	 Alignment		36.0	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pyk2-associated protein beta; <b>PDBTitle:</b> crystal structure of the arf-gap domain and ankyrin repeats of2 papbeta.

12	<a href="#">d1u5ka2</a>	Alignment		36.0	28	<b>Fold:</b> ArfGap/RecO-like zinc finger <b>Superfamily:</b> ArfGap/RecO-like zinc finger <b>Family:</b> RecO C-terminal domain-like
13	<a href="#">c3fehA</a>	Alignment		34.0	30	<b>PDB header:</b> hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> centaurin-alpha-1; <b>PDBTitle:</b> crystal structure of full length centaurin alpha-1
14	<a href="#">c1u5kA</a>	Alignment		32.9	29	<b>PDB header:</b> recombination,replication <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> recombinational repair protein reco
15	<a href="#">c6mifA</a>	Alignment		32.7	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> lim and senescent cell antigen-like-containing domain <b>PDBTitle:</b> lim5 domain of pinch1 protein
16	<a href="#">c1v6gA</a>	Alignment		32.7	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> actin binding lim protein 2; <b>PDBTitle:</b> solution structure of the lim domain of the human actin2 binding lim protein 2
17	<a href="#">c4gndC</a>	Alignment		32.2	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> histone-lysine n-methyltransferase nsd3; <b>PDBTitle:</b> crystal structure of nsd3 tandem phd5-c5hch domains
18	<a href="#">c2dloA</a>	Alignment		31.5	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> thyroid receptor-interacting protein 6; <b>PDBTitle:</b> solution structure of the second lim domain of human2 thyroid receptor-interacting protein 6
19	<a href="#">d2g45a1</a>	Alignment		29.9	29	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> Zf-UBP
20	<a href="#">c3o47A</a>	Alignment		29.3	22	<b>PDB header:</b> hydrolase, hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor gtpase-activating protein 1, adp- <b>PDBTitle:</b> crystal structure of arfgap1-arf1 fusion protein
21	<a href="#">c2iqjB</a>	Alignment	not modelled	28.5	26	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> stromal membrane-associated protein 1-like; <b>PDBTitle:</b> crystal structure of the gap domain of smap1l (loc64744) stromal2 membrane-associated protein 1-like
22	<a href="#">c1x64A</a>	Alignment	not modelled	28.2	24	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-actinin-2 associated lim protein; <b>PDBTitle:</b> solution structure of the lim domain of alpha-actinin-2 associated lim protein
23	<a href="#">c2mbvA</a>	Alignment	not modelled	27.1	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of lim domain transcription factor lmo4 (77- <b>PDBTitle:</b> lmo4-lim2 in complex with deaf1 (404-418)
24	<a href="#">c5us5B</a>	Alignment	not modelled	27.1	17	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> upf0297 protein ef_1202; <b>PDBTitle:</b> solution structure of the ireb homodimer
25	<a href="#">c1nypA</a>	Alignment	not modelled	27.0	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> pinch protein; <b>PDBTitle:</b> 4th lim domain of pinch protein
26	<a href="#">c2darA</a>	Alignment	not modelled	26.7	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pdz and lim domain protein 5; <b>PDBTitle:</b> solution structure of first lim domain of enigma-like pdz2 and lim domains protein
27	<a href="#">c5w54A</a>	Alignment	not modelled	26.0	42	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> stress response peptide-2; <b>PDBTitle:</b> cytokine-like stress response peptide-2 in manduca sexta
28	<a href="#">c2curA</a>	Alignment	not modelled	25.7	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> skeletal muscle lim-protein 1; <b>PDBTitle:</b> solution structure of skeletal muscle lim-protein 1

29	<a href="#">c2eheA</a>	Alignment	not modelled	25.6	29	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> four and a half lim domains 3; <b>PDBTitle:</b> solution structure of the first lim domain from human four2 and a half lim domains protein 3
30	<a href="#">c2p57A</a>	Alignment	not modelled	25.3	26	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase-activating protein znf289; <b>PDBTitle:</b> gap domain of znf289, an id1-regulated zinc finger protein
31	<a href="#">d1o26a</a>	Alignment	not modelled	25.3	37	<b>Fold:</b> Thymidylate synthase-complementing protein Thy1 <b>Superfamily:</b> Thymidylate synthase-complementing protein Thy1 <b>Family:</b> Thymidylate synthase-complementing protein Thy1
32	<a href="#">d1nuia2</a>	Alignment	not modelled	25.3	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> DNA primase zinc finger
33	<a href="#">d1mhxa</a>	Alignment	not modelled	25.1	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
34	<a href="#">d1wglA</a>	Alignment	not modelled	24.9	26	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
35	<a href="#">c2gviA</a>	Alignment	not modelled	24.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative formylmethanofuran dehydrogenase2 subunit e (ta1109) from thermoplasma acidophilum at 1.87 a resolution
36	<a href="#">d2a1ja1</a>	Alignment	not modelled	24.6	12	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
37	<a href="#">d1mi0a</a>	Alignment	not modelled	24.4	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
38	<a href="#">c2cuqA</a>	Alignment	not modelled	24.3	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> four and a half lim domains 3; <b>PDBTitle:</b> solution structure of second lim domain from human skeletal2 muscle lim-protein 2
39	<a href="#">c6j61B</a>	Alignment	not modelled	24.1	53	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin-dependent thymidylate synthase; <b>PDBTitle:</b> crystal structure of thymidylate synthase, thy1, from thermus2 thermophilus having an extra c terminal domain
40	<a href="#">d1fd6a</a>	Alignment	not modelled	24.0	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
41	<a href="#">c3dwdB</a>	Alignment	not modelled	24.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> adp-ribosylation factor gtpase-activating protein 1; <b>PDBTitle:</b> crystal structure of the arfgap domain of human arfgap1
42	<a href="#">c1x6aA</a>	Alignment	not modelled	24.0	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lim domain kinase 2; <b>PDBTitle:</b> solution structures of the second lim domain of human lim-2 kinase 2 (limk2)
43	<a href="#">c2dhyA</a>	Alignment	not modelled	23.9	24	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
44	<a href="#">d1gb4a</a>	Alignment	not modelled	23.7	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
45	<a href="#">c1x41A</a>	Alignment	not modelled	23.0	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> skeletal muscle lim-protein 3; <b>PDBTitle:</b> solution structure of lim domain in four and a half lim2 domains protein 2
46	<a href="#">c3jueA</a>	Alignment	not modelled	22.9	20	<b>PDB header:</b> protein transport/endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> arfgap with coiled-coil, ank repeat and ph domain- <b>PDBTitle:</b> crystal structure of arfgap and ank repeat domain of acap1
47	<a href="#">d1pgaa</a>	Alignment	not modelled	22.8	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
48	<a href="#">d1pgxa</a>	Alignment	not modelled	22.6	28	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
49	<a href="#">c2d91A</a>	Alignment	not modelled	22.6	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin-like protein rip; <b>PDBTitle:</b> solution structure of the arfgap domain of human rip
50	<a href="#">d1p7ea</a>	Alignment	not modelled	22.6	28	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
51	<a href="#">c2d8xA</a>	Alignment	not modelled	22.5	21	<b>PDB header:</b> structural protein, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein pinch; <b>PDBTitle:</b> solution structure of the second lim domain of particularly2 interesting new cys-his protein (pinch)
52	<a href="#">d1em7a</a>	Alignment	not modelled	22.4	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
53	<a href="#">c2kngA</a>	Alignment	not modelled	22.0	53	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> solution structure of c-domain of lsr2
54	<a href="#">d1qkza</a>	Alignment	not modelled	21.5	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
						<b>PDB header:</b> protein binding <b>Chain:</b> X: <b>PDB Molecule:</b> fusion protein of lmo4 protein and lim

55	<a href="#">c1rutX_</a>	Alignment	not modelled	21.1	19	domain-binding <b>PDBTitle:</b> complex of lmo4 lim domains 1 and 2 with the ldb1 lid domain
56	<a href="#">c2gajA_</a>	Alignment	not modelled	20.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase i; <b>PDBTitle:</b> structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
57	<a href="#">c3f6qB_</a>	Alignment	not modelled	20.4	21	<b>PDB header:</b> signaling protein/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> lim and senescent cell antigen-like-containing <b>PDBTitle:</b> crystal structure of integrin-linked kinase ankyrin repeat2 domain in complex with pinch1 lim1 domain
58	<a href="#">d1fcla_</a>	Alignment	not modelled	20.2	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
59	<a href="#">c1x3hA_</a>	Alignment	not modelled	19.9	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leupaxin; <b>PDBTitle:</b> solution structure of the lim domain of human leupaxin
60	<a href="#">c4qglA_</a>	Alignment	not modelled	19.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acireductone dioxygenase; <b>PDBTitle:</b> acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
61	<a href="#">c3t9kA_</a>	Alignment	not modelled	19.7	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> arf-gap with coiled-coil, ank repeat and ph domain- <b>PDBTitle:</b> crystal structure of acap1 c-portion mutant s554d fused with integrin2 beta1 peptide
62	<a href="#">c6gvwF_</a>	Alignment	not modelled	19.5	20	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> brca1-a complex subunit abraxas 1; <b>PDBTitle:</b> crystal structure of the brca1-a complex
63	<a href="#">c2l3kA_</a>	Alignment	not modelled	19.4	29	<b>PDB header:</b> oncoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> rhombotin-2, linker, lim domain-binding protein 1; <b>PDBTitle:</b> solution structure of lmo2(lim2)-ldb1(lid)
64	<a href="#">c3k7aM_</a>	Alignment	not modelled	19.1	17	<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
65	<a href="#">c2co8A_</a>	Alignment	not modelled	19.1	23	<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
66	<a href="#">c2crrA_</a>	Alignment	not modelled	18.9	28	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> stromal membrane-associated protein smap1b; <b>PDBTitle:</b> solution structure of arfgap domain from human smap1
67	<a href="#">c2xjyA_</a>	Alignment	not modelled	18.9	29	<b>PDB header:</b> oncoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> rhombotin-2; <b>PDBTitle:</b> crystal structure of the lmo2:ldb1-lid complex, p21 crystal2 form
68	<a href="#">c2jtnA_</a>	Alignment	not modelled	18.8	21	<b>PDB header:</b> protein binding/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lim domain-binding protein 1, lim/homeobox <b>PDBTitle:</b> nmr solution structure of a ldb1-lid:lhx3-lim complex
69	<a href="#">c1x63A_</a>	Alignment	not modelled	18.8	21	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> skeletal muscle lim-protein 1; <b>PDBTitle:</b> solution structure of the second lim domain of skeletal2 muscle lim protein 1
70	<a href="#">c2ypdB_</a>	Alignment	not modelled	18.7	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable jmjc domain-containing histone demethylation prot <b>PDBTitle:</b> crystal structure of the jumonji domain of human jumonji domain2 containing 1c protein
71	<a href="#">c2cwrA_</a>	Alignment	not modelled	18.4	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor gtpase-activating <b>PDBTitle:</b> solution structure of the arfgap domain of adp-ribosylation2 factor gtpaseactivating protein 3 (arfgap 3)
72	<a href="#">c1x61A_</a>	Alignment	not modelled	17.8	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> thyroid receptor interacting protein 6; <b>PDBTitle:</b> solution structure of the first lim domain of thyroid2 receptor interacting protein 6 (trip6)
73	<a href="#">c2naaA_</a>	Alignment	not modelled	17.7	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-36 and h4 <b>PDBTitle:</b> nsd1-phd_5-c5hch tandem domain structure
74	<a href="#">c2d8zA_</a>	Alignment	not modelled	17.5	33	<b>PDB header:</b> signaling protein, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> four and a half lim domains 2; <b>PDBTitle:</b> solution structure of the third lim domain of four and a2 half lim domains protein 2 (fhl-2)
75	<a href="#">c2k8dA_</a>	Alignment	not modelled	17.0	31	<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
76	<a href="#">c1wyhA_</a>	Alignment	not modelled	16.8	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> skeletal muscle lim-protein 2; <b>PDBTitle:</b> solution structure of the lim domain from human skeletal2 muscle lim-protein 2
77	<a href="#">d1mvka_</a>	Alignment	not modelled	16.8	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
78	<a href="#">c2jwuA_</a>	Alignment	not modelled	16.6	11	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gb88; <b>PDBTitle:</b> solution nmr structures of two designed proteins with 88%2 sequence identity but different fold and function
79	<a href="#">c5ldeB_</a>	Alignment	not modelled	16.6	19	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> immunoglobulin g-binding protein g,viral flice protein; <b>PDBTitle:</b> crystal structure of a vflip-ikkgamma stapled peptide

						dimer
80	<a href="#">c1ibiA_</a>	Alignment	not modelled	16.4	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine-rich protein 2; <b>PDBTitle:</b> quail cysteine and glycine-rich protein, nmr, 15 minimized2 model structures
81	<a href="#">d1x3ha2</a>	Alignment	not modelled	16.3	35	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
82	<a href="#">c1zxhA_</a>	Alignment	not modelled	16.1	22	<b>PDB header:</b> immune system/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin g binding protein g; <b>PDBTitle:</b> g311 mutant protein
83	<a href="#">c2wryA_</a>	Alignment	not modelled	16.1	14	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> interleukin-1beta; <b>PDBTitle:</b> crystal structure of chicken cytokine interleukin 1 beta
84	<a href="#">c2l6yB_</a>	Alignment	not modelled	15.6	29	<b>PDB header:</b> transcription regulation/oncoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> lim domain only 2, linker, lim domain-binding protein 1; <b>PDBTitle:</b> haddock model of gata1nf:lmo2lim2-ldb1lid
85	<a href="#">c1nltA_</a>	Alignment	not modelled	15.1	32	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial protein import protein mas5; <b>PDBTitle:</b> the crystal structure of hsp40 ydj1
86	<a href="#">c4p5aB_</a>	Alignment	not modelled	14.9	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate synthase thyx; <b>PDBTitle:</b> crystal structure of a ump/dump methylase polb from streptomyces2 cacaai bound with 5-br ump
87	<a href="#">d1yrnb_</a>	Alignment	not modelled	14.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
88	<a href="#">d1du6a_</a>	Alignment	not modelled	14.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
89	<a href="#">c2egqA_</a>	Alignment	not modelled	14.6	24	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fhl1 protein; <b>PDBTitle:</b> solution structure of the fourth lim domain from human four2 and a half lim domains 1
90	<a href="#">c6f42V_</a>	Alignment	not modelled	14.4	26	<b>PDB header:</b> transcription <b>Chain:</b> V: <b>PDB Molecule:</b> transcription factor iiib 70 kda subunit; <b>PDBTitle:</b> rna polymerase iii closed complex cc1.
91	<a href="#">c2yrgA_</a>	Alignment	not modelled	14.3	23	<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
92	<a href="#">c1bg1A_</a>	Alignment	not modelled	14.1	18	<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
93	<a href="#">d1zrra1</a>	Alignment	not modelled	14.1	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Acireductone dioxygenase
94	<a href="#">c3wofB_</a>	Alignment	not modelled	14.1	47	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of p23-45 gp39 (6-132) bound to thermus thermophilus2 rna polymerase beta-flap domain
95	<a href="#">c6h9dB_</a>	Alignment	not modelled	13.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lysozyme; <b>PDBTitle:</b> muramidase domain of spmx from asticcacaulis excentricus
96	<a href="#">c1x4kA_</a>	Alignment	not modelled	13.8	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> skeletal muscle lim-protein 3; <b>PDBTitle:</b> solution structure of lim domain in lim-protein 3
97	<a href="#">c5vgiG_</a>	Alignment	not modelled	13.6	18	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> G: <b>PDB Molecule:</b> 1fd6-v1v2-wito; <b>PDBTitle:</b> crystal structure of the human fab vrc38.01, an hiv-1 v1v2-directed2 neutralizing antibody isolated from donor n90, bound to a scaffolded3 wito v1v2 domain
98	<a href="#">c5fz5M_</a>	Alignment	not modelled	13.4	17	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> transcription initiation complex structures elucidate dna opening (cc)
99	<a href="#">c4v1oM_</a>	Alignment	not modelled	13.4	17	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> architecture of the rna polymerase ii-mediator core transcription2 initiation complex