
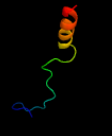

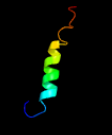

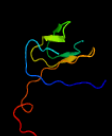

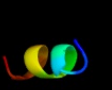

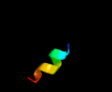





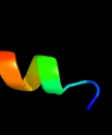

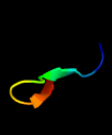



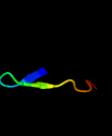

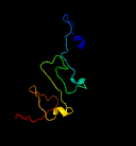

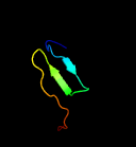
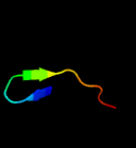
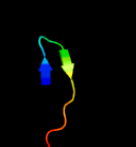
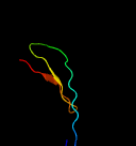

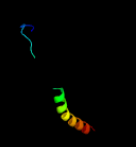


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2926c_(-)_3240558_3241181
Date	Thu Aug 8 16:20:08 BST 2019
Unique Job ID	440f368f52ab6c53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5iy9Q_</a>	 Alignment		28.3	15	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> Q; <b>PDB Molecule:</b> general transcription factor iie subunit 1; <b>PDBTitle:</b> human holo-pic in the initial transcribing state (no iis)
2	<a href="#">c2c55A_</a>	 Alignment		23.3	31	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein p6; <b>PDBTitle:</b> solution structure of the human immunodeficiency virus type2 1 p6 protein
3	<a href="#">c5ezdB_</a>	 Alignment		19.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> kunitz-type protease inhibitor 1; <b>PDBTitle:</b> crystal structure of a hepatocyte growth factor activator inhibitor-12 (hai-1) fragment covering the pkd-like 'internal' domain and kunitz3 domain 1
4	<a href="#">cli7xD_</a>	 Alignment		19.0	45	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> epithelial-cadherin; <b>PDBTitle:</b> beta-catenin/e-cadherin complex
5	<a href="#">d2dofa1</a>	 Alignment		18.0	30	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> FF domain <b>Family:</b> FF domain
6	<a href="#">d1pfva3</a>	 Alignment		18.0	32	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Methionyl-tRNA synthetase (MetRS), Zn-domain <b>Family:</b> Methionyl-tRNA synthetase (MetRS), Zn-domain
7	<a href="#">c2i9vA_</a>	 Alignment		16.4	40	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> pre-mrna-processing factor 40 homolog a; <b>PDBTitle:</b> nmr structure of the ff domain l24a mutant's folding transition state
8	<a href="#">cli7wB_</a>	 Alignment		15.8	40	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> epithelial-cadherin; <b>PDBTitle:</b> beta-catenin/phosphorylated e-cadherin complex
9	<a href="#">d1yuja_</a>	 Alignment		14.3	31	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
10	<a href="#">c2a93B_</a>	 Alignment		13.9	44	<b>PDB header:</b> leucine zippers <b>Chain:</b> B; <b>PDB Molecule:</b> c-myc-max heterodimeric leucine zipper; <b>PDBTitle:</b> nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures
11	<a href="#">d3d3ra1</a>	 Alignment		12.4	54	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like

12	<a href="#">c3fqmA</a>	Alignment		11.9	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 5a; <b>PDBTitle:</b> crystal structure of a novel dimeric form of hcv ns5a domain i protein
13	<a href="#">d1j58a</a>	Alignment		11.8	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
14	<a href="#">d2fyia1</a>	Alignment		11.5	30	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
15	<a href="#">d2a90a2</a>	Alignment		10.4	23	<b>Fold:</b> WWE domain <b>Superfamily:</b> WWE domain <b>Family:</b> WWE domain
16	<a href="#">c3d3rA</a>	Alignment		10.4	54	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase assembly chaperone hupc/hupf; <b>PDBTitle:</b> crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
17	<a href="#">d2z1ca1</a>	Alignment		10.3	54	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
18	<a href="#">c5buxB</a>	Alignment		9.5	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-acp dehydratase (fabz) from yersinia pestis with glycerol bound
19	<a href="#">c2n8dA</a>	Alignment		9.4	25	<b>PDB header:</b> de novo protein, antimicrobial peptide <b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide lavracin; <b>PDBTitle:</b> in silico designed antimicrobial peptide lavracin
20	<a href="#">c5fywW</a>	Alignment		9.1	23	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha; <b>PDBTitle:</b> transcription initiation complex structures elucidate dna opening (oc)
21	<a href="#">d2ot2a1</a>	Alignment	not modelled	8.8	38	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
22	<a href="#">c2nx6A</a>	Alignment	not modelled	8.5	44	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematocyst outer wall antigen; <b>PDBTitle:</b> structure of nowa cysteine rich domain 6
23	<a href="#">d1lv3a</a>	Alignment	not modelled	8.1	45	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Hypothetical zinc finger protein YacG
24	<a href="#">d2grea1</a>	Alignment	not modelled	8.0	13	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminopeptidase/glucanase lid domain <b>Family:</b> Aminopeptidase/glucanase lid domain
25	<a href="#">d1kf6b2</a>	Alignment	not modelled	7.6	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
26	<a href="#">c3lpeF</a>	Alignment	not modelled	7.5	23	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> dna-directed rna polymerase subunit e"; <b>PDBTitle:</b> crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
27	<a href="#">c6fw2A</a>	Alignment	not modelled	6.9	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial amidoxime-reducing component 1, endolysin, <b>PDBTitle:</b> crystal structure of human marc1
28	<a href="#">c5zb8B</a>	Alignment	not modelled	6.6	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pfluendoq; <b>PDBTitle:</b> crystal structure of the novel lesion-specific endonuclease pfluendoq2 from pyrococcus furiosus
						<b>Fold:</b> Rubredoxin-like

29	<a href="#">d2akla2</a>	Alignment	not modelled	6.5	26	<b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> PhnA zinc-binding domain
30	<a href="#">c1bi6H_</a>	Alignment	not modelled	6.5	67	<b>PDB header:</b> cysteine protease inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> bromelain inhibitor vi; <b>PDBTitle:</b> nmr structure of bromelain inhibitor vi from pineapple stem
31	<a href="#">c5ijlA_</a>	Alignment	not modelled	6.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase ii large subunit; <b>PDBTitle:</b> d-family dna polymerase - dp2 subunit (catalytic subunit)
32	<a href="#">d1ex0a2</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
33	<a href="#">d1pvma3</a>	Alignment	not modelled	6.2	46	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Hypothetical protein Ta0289 C-terminal domain <b>Family:</b> Hypothetical protein Ta0289 C-terminal domain
34	<a href="#">c2bi6H_</a>	Alignment	not modelled	6.1	46	<b>PDB header:</b> cysteine protease inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> bromelain inhibitor vi; <b>PDBTitle:</b> nmr study of bromelain inhibitor vi from pineapple stem
35	<a href="#">c2hm3A_</a>	Alignment	not modelled	6.1	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematocyst outer wall antigen; <b>PDBTitle:</b> nematocyst outer wall antigen, cysteine rich domain nw1
36	<a href="#">d1vja2</a>	Alignment	not modelled	5.8	29	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
37	<a href="#">c5mfR_</a>	Alignment	not modelled	5.8	38	<b>PDB header:</b> transcription <b>Chain:</b> R: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha, tfa1; <b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex
38	<a href="#">c3wwnB_</a>	Alignment	not modelled	5.7	44	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orff; <b>PDBTitle:</b> crystal structure of lysz from thermus thermophilus complex with lysw
39	<a href="#">d1zfoa_</a>	Alignment	not modelled	5.5	56	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LASP-1
40	<a href="#">d2cupa2</a>	Alignment	not modelled	5.5	63	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
41	<a href="#">c3mjhD_</a>	Alignment	not modelled	5.4	55	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> early endosome antigen 1; <b>PDBTitle:</b> crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
42	<a href="#">c2hm4A_</a>	Alignment	not modelled	5.3	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematocyst outer wall antigen; <b>PDBTitle:</b> nematocyst outer wall antigen, nw1 k21p
43	<a href="#">c2oa2A_</a>	Alignment	not modelled	5.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2720 protein; <b>PDBTitle:</b> crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution