


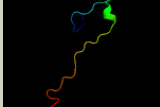

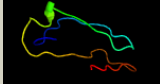

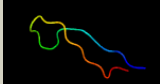









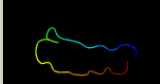




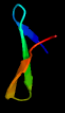
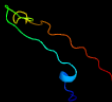
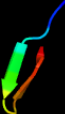

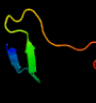

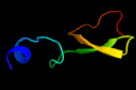




# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0344c\_(lpq)\_414381\_414941  
 Date Tue Jul 23 14:50:41 BST 2019  
 Unique Job ID c7cb479cdd590d99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1upsB_</a>	 Alignment		86.5	18	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glcnac-alpha-1,4-gal-releasing endo-beta-galactosidase; <b>PDBTitle:</b> glcnac[alpha]1-4gal releasing endo-[beta]-galactosidase from2 clostridium perfringens
2	<a href="#">c3iynQ_</a>	 Alignment		24.4	26	<b>PDB header:</b> virus <b>Chain:</b> Q: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
3	<a href="#">c2xfeA_</a>	 Alignment		18.1	27	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding module; <b>PDBTitle:</b> vcbm60 in complex with galactobiose
4	<a href="#">d1ylxa1</a>	 Alignment		17.8	31	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GK1464-like <b>Family:</b> GK1464-like
5	<a href="#">d2okfa1</a>	 Alignment		16.4	23	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> XisH-like
6	<a href="#">d2inba1</a>	 Alignment		16.2	23	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> XisH-like
7	<a href="#">d2hqha1</a>	 Alignment		12.3	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
8	<a href="#">d1zvca1</a>	 Alignment		12.2	17	<b>Fold:</b> AOC barrel-like <b>Superfamily:</b> Allene oxide cyclase-like <b>Family:</b> Allene oxide cyclase-like
9	<a href="#">d2d81a1</a>	 Alignment		12.1	33	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PHB depolymerase-like
10	<a href="#">d1xoda1</a>	 Alignment		11.9	14	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
11	<a href="#">c4k08A_</a>	 Alignment		11.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis sensory transducer; <b>PDBTitle:</b> periplasmic sensor domain of chemotaxis protein, adeh_3718

12	<a href="#">c2mx4A_</a>	Alignment		10.8	36	<b>PDB header:</b> translation,protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 4e-binding protein <b>PDBTitle:</b> nmr structure of phosphorylated 4e-bp2
13	<a href="#">dlut1a_</a>	Alignment		10.1	26	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Dr-family adhesin
14	<a href="#">d2brja1</a>	Alignment		9.9	17	<b>Fold:</b> AOC barrel-like <b>Superfamily:</b> Allene oxide cyclase-like <b>Family:</b> Allene oxide cyclase-like
15	<a href="#">d2coya1</a>	Alignment		9.4	29	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
16	<a href="#">c2lieA_</a>	Alignment		9.4	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc12 lectin; <b>PDBTitle:</b> nmr structure of the lectin ccl2
17	<a href="#">d1ixda_</a>	Alignment		9.1	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
18	<a href="#">d1tdha3</a>	Alignment		9.0	19	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
19	<a href="#">c5xtaC_</a>	Alignment		9.0	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> virk protein; <b>PDBTitle:</b> crystal structure of lpg1832, a virk family protein from legionella2 pneumophila
20	<a href="#">c1ym0B_</a>	Alignment		8.5	47	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fibrinotic enzyme component b; <b>PDBTitle:</b> crystal structure of earthworm fibrinolytic enzyme component b: a2 novel, glycosylated two-chained trypsin
21	<a href="#">d1iwma_</a>	Alignment	not modelled	8.4	26	<b>Fold:</b> LoLA-like prokaryotic lipoproteins and lipoprotein localization factors <b>Superfamily:</b> Prokaryotic lipoproteins and lipoprotein localization factors <b>Family:</b> Outer membrane lipoprotein receptor LolB
22	<a href="#">c3ixxE_</a>	Alignment	not modelled	7.6	30	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> peptide pr; <b>PDBTitle:</b> the pseudo-atomic structure of west nile immature virus in complex2 with fab fragments of the anti-fusion loop antibody e53
23	<a href="#">c2bcmB_</a>	Alignment	not modelled	7.3	29	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> f1845 fimbrial protein; <b>PDBTitle:</b> daae adhesin
24	<a href="#">d1whla_</a>	Alignment	not modelled	7.2	21	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
25	<a href="#">c4akaA_</a>	Alignment	not modelled	7.1	45	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> il-4-inducing protein; <b>PDBTitle:</b> ipse alpha-1, an ige-binding crystallin
26	<a href="#">c2k14A_</a>	Alignment	not modelled	6.5	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yuaf protein; <b>PDBTitle:</b> solution structure of the soluble domain of the nfd2 protein yuaf from bacillus subtilis
27	<a href="#">c1fwxB_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrous oxide reductase; <b>PDBTitle:</b> crystal structure of nitrous oxide reductase from p. denitrificans
28	<a href="#">c2k5rA_</a>	Alignment	not modelled	6.2	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein xf2673; <b>PDBTitle:</b> solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39

29	<a href="#">c5g4yA_</a>	Alignment	not modelled	6.2	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein; <b>PDBTitle:</b> structural basis for carboxylic acid recognition by a cache2 chemosensory domain.
30	<a href="#">c2krxA_</a>	Alignment	not modelled	6.2	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> asl3597 protein; <b>PDBTitle:</b> solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
31	<a href="#">c4b2gB_</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> gh3-1 auxin conjugating enzyme; <b>PDBTitle:</b> crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
32	<a href="#">c2g8gA_</a>	Alignment	not modelled	5.8	16	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> capsid; <b>PDBTitle:</b> structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4
33	<a href="#">c3iynR_</a>	Alignment	not modelled	5.8	41	<b>PDB header:</b> virus <b>Chain:</b> R: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
34	<a href="#">d1qnia2</a>	Alignment	not modelled	5.7	18	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> Nitrous oxide reductase, N-terminal domain <b>Family:</b> Nitrous oxide reductase, N-terminal domain
35	<a href="#">d1vdra_</a>	Alignment	not modelled	5.7	23	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
36	<a href="#">d1x9la_</a>	Alignment	not modelled	5.4	20	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> DR1885-like metal-binding protein <b>Family:</b> DR1885-like metal-binding protein
37	<a href="#">c2kkyA_</a>	Alignment	not modelled	5.3	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ecs2156; <b>PDBTitle:</b> solution structure of c-terminal domain of oxidized nleg2-3 (residue2 90-191) from pathogenic e. coli o157:h7. northeast structural3 genomics consortium and midwest center for structural genomics target4 et109a
38	<a href="#">c2waqG_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> dna-directed rna polymerase rpo8 subunit; <b>PDBTitle:</b> the complete structure of the archaeal 13-subunit dna-directed rna2 polymerase
39	<a href="#">d2cowa1</a>	Alignment	not modelled	5.2	19	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
40	<a href="#">c5kodA_</a>	Alignment	not modelled	5.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-acetic acid-amido synthetase gh3.5; <b>PDBTitle:</b> crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana