


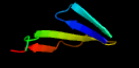

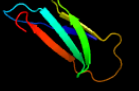



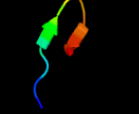

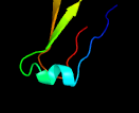

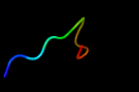







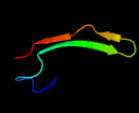


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3483c (- )_3902329_3902991
Date	Fri Aug 9 18:20:16 BST 2019
Unique Job ID	e12136cfc814537b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1zpsa1</a>	 Alignment		49.2	15	<b>Fold:</b> His1-like <b>Superfamily:</b> His1-like <b>Family:</b> His1-like
2	<a href="#">d1sy6a1</a>	 Alignment		46.2	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
3	<a href="#">c3pdgA_</a>	 Alignment		30.3	5	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> fibronectin(iii)-like module; <b>PDBTitle:</b> structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
4	<a href="#">d1pj5a1</a>	 Alignment		28.5	24	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
5	<a href="#">d2p3pa1</a>	 Alignment		24.7	9	<b>Fold:</b> PG1388-like <b>Superfamily:</b> PG1388-like <b>Family:</b> PG1388-like
6	<a href="#">c3pe9D_</a>	 Alignment		23.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> fibronectin(iii)-like module; <b>PDBTitle:</b> structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
7	<a href="#">c5e24D_</a>	 Alignment		21.6	27	<b>PDB header:</b> transport/dna binding/dna <b>Chain:</b> D: <b>PDB Molecule:</b> protein hairless; <b>PDBTitle:</b> structure of the su(h)-hairless-dna repressor complex
8	<a href="#">c1jbaA_</a>	 Alignment		21.4	16	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cd3 epsilon and gamma ectodomain fragment <b>PDBTitle:</b> cd3 epsilon and gamma ectodomain fragment complex in single-2 chain construct
9	<a href="#">c2ifmA_</a>	 Alignment		20.2	19	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> pf1 filamentous bacteriophage; <b>PDBTitle:</b> pf1 filamentous bacteriophage: refinement of a molecular2 model by simulated annealing using 3.3 angstroms3 resolution x-ray fibre diffraction data
10	<a href="#">c1ql1A_</a>	 Alignment		20.2	19	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> pf1 bacteriophage coat protein b; <b>PDBTitle:</b> inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
11	<a href="#">d1jba1</a>	 Alignment		19.8	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains

12	<a href="#">c3pe9B_</a>	Alignment		14.8	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> fibronectin(iii)-like module; <b>PDBTitle:</b> structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
13	<a href="#">c5y31B_</a>	Alignment		14.7	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-rich glioma-inactivated protein 1; <b>PDBTitle:</b> crystal structure of human Igi1-adam22 complex
14	<a href="#">d2hfa1</a>	Alignment		11.7	33	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> HyaE-like
15	<a href="#">c4c87A_</a>	Alignment		10.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> esterase Ipest1 from lactobacillus plantarum wcfs1
16	<a href="#">d1inva_</a>	Alignment		10.5	19	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
17	<a href="#">d1gpla1</a>	Alignment		9.9	38	<b>Fold:</b> Lipase/lipoxygenase domain (PLAT/LH2 domain) <b>Superfamily:</b> Lipase/lipoxygenase domain (PLAT/LH2 domain) <b>Family:</b> Colipase-binding domain
18	<a href="#">c5naoA_</a>	Alignment		9.7	35	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> toll-like receptor 4; <b>PDBTitle:</b> nmr structure of tir4 transmembrane domain (624-657) in dpc micelles
19	<a href="#">c2qsiB_</a>	Alignment		9.5	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrogenase expression/formation protein hupg; <b>PDBTitle:</b> crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
20	<a href="#">c4qn3B_</a>	Alignment		9.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> neuraminidase; <b>PDBTitle:</b> crystal structure of neuraminidase n7
21	<a href="#">c2yyoA_</a>	Alignment	not modelled	8.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> spry domain-containing protein 3; <b>PDBTitle:</b> crystal structure of human spry domain
22	<a href="#">c2zsha_</a>	Alignment	not modelled	8.8	27	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> probable gibberellin receptor gid111; <b>PDBTitle:</b> structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
23	<a href="#">c2fynO_</a>	Alignment	not modelled	8.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
24	<a href="#">c3cb0B_</a>	Alignment	not modelled	8.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxyphenylacetate 3-monoxygenase; <b>PDBTitle:</b> cobr
25	<a href="#">c4m6tA_</a>	Alignment	not modelled	8.4	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase ii-associated factor 1 homolog, linker, rna <b>PDBTitle:</b> structure of human paf1 and leo1 complex
26	<a href="#">d1o5ha_</a>	Alignment	not modelled	8.3	22	<b>Fold:</b> Methenyltetrahydrofolate cyclohydrolase-like <b>Superfamily:</b> Methenyltetrahydrofolate cyclohydrolase-like <b>Family:</b> Methenyltetrahydrofolate cyclohydrolase-like
27	<a href="#">c2lnhC_</a>	Alignment	not modelled	8.3	83	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> secreted effector protein espf(u); <b>PDBTitle:</b> enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
28	<a href="#">c2ecrA_</a>	Alignment	not modelled	7.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase component (hpac) of 4-hydroxyphenylacetate <b>PDBTitle:</b> crystal structure of the ligand-free form of the flavin

						reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monooxygenase
29	<a href="#">c2r0xA</a>	Alignment	not modelled	7.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible flavin reductase; <b>PDBTitle:</b> crystal structure of a putative flavin reductase (ycdh, hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
30	<a href="#">c4hx6D</a>	Alignment	not modelled	7.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> streptomyces globisporus c-1027 nadh:fad oxidoreductase sgce6
31	<a href="#">c6chgB</a>	Alignment	not modelled	7.3	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> klla0c10945p; <b>PDBTitle:</b> crystal structure of the yeast compass catalytic module
32	<a href="#">c5namA</a>	Alignment	not modelled	7.1	35	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> toll-like receptor 4; <b>PDBTitle:</b> nmr structure of tir4 transmembrane domain (624-670) in dmpg/dhpc2 bicelles
33	<a href="#">c2we7A</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xanthine dehydrogenase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
34	<a href="#">c2pm8A</a>	Alignment	not modelled	6.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> crystal structure of recombinant full length human2 butyrylcholinesterase
35	<a href="#">d1dx4a</a>	Alignment	not modelled	6.3	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
36	<a href="#">c5xebC</a>	Alignment	not modelled	6.2	22	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> structure of the envelope glycoprotein of dhori virus
37	<a href="#">d1ivga</a>	Alignment	not modelled	6.1	22	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
38	<a href="#">c3tiaC</a>	Alignment	not modelled	6.0	22	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> neuraminidase; <b>PDBTitle:</b> crystal structure of 1957 pandemic h2n2 neuraminidase complexed with2 laninamivir
39	<a href="#">c3u6gB</a>	Alignment	not modelled	6.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf4425; <b>PDBTitle:</b> crystal structure of a domain of unknown function, duf4425 (bvu_3708)2 from bacteroides vulgatus atcc 8482 at 1.35 a resolution
40	<a href="#">c4fvkA</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neuraminidase; <b>PDBTitle:</b> structural and functional characterization of neuraminidase-like2 molecule n10 derived from bat influenza a virus
41	<a href="#">c3d7rB</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a putative esterase from staphylococcus aureus
42	<a href="#">c1vlyA</a>	Alignment	not modelled	5.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> unknown protein from 2d-page; <b>PDBTitle:</b> crystal structure of a putative aminomethyltransferase (ygfz) from2 escherichia coli at 1.30 a resolution
43	<a href="#">c2wirB</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha/beta hydrolase fold-3 domain protein; <b>PDBTitle:</b> hyperthermophilic esterase from the archeon pyrobaculum2 caldifontis
44	<a href="#">c1nmbN</a>	Alignment	not modelled	5.6	22	<b>PDB header:</b> complex (hydrolase/immunoglobulin) <b>Chain:</b> N: <b>PDB Molecule:</b> n9 neuraminidase; <b>PDBTitle:</b> the structure of a complex between the nc10 antibody and influenza2 virus neuraminidase and comparison with the overlapping binding site3 of the nc41 antibody
45	<a href="#">d1fo5a</a>	Alignment	not modelled	5.6	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
46	<a href="#">d1qvpa</a>	Alignment	not modelled	5.5	26	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
47	<a href="#">c3ga7A</a>	Alignment	not modelled	5.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl esterase; <b>PDBTitle:</b> 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
48	<a href="#">d1f8ea</a>	Alignment	not modelled	5.4	22	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
49	<a href="#">c6i2tC</a>	Alignment	not modelled	5.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
50	<a href="#">c2hu4D</a>	Alignment	not modelled	5.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> neuraminidase; <b>PDBTitle:</b> n1 neuraminidase in complex with oseltamivir 2
51	<a href="#">c6ijo2</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> lhca2; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
52	<a href="#">d1qe3a</a>	Alignment	not modelled	5.2	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
53	<a href="#">d2aepa1</a>	Alignment	not modelled	5.2	22	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
						<b>PDB header:</b> dna binding protein

