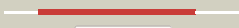






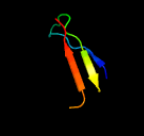

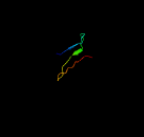

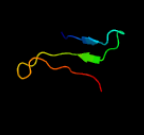

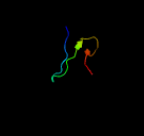



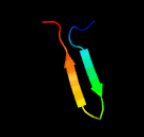



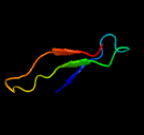


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0493c_(-)_583704_584693
Date	Fri Jul 26 01:50:03 BST 2019
Unique Job ID	a9d7ecbc83406aad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2icha1</a>	 Alignment		99.4	11	<b>Fold:</b> Atth-like <b>Superfamily:</b> Atth-like <b>Family:</b> Atth-like
2	<a href="#">d1l1da_</a>	 Alignment		83.5	13	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> SelR domain
3	<a href="#">c3cezA_</a>	 Alignment		67.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase; <b>PDBTitle:</b> crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
4	<a href="#">c2k8dA_</a>	 Alignment		64.6	16	<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
5	<a href="#">c3e0mB_</a>	 Alignment		56.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra/msrb <b>PDBTitle:</b> crystal structure of fusion protein of msra and msrb
6	<a href="#">c5fa9B_</a>	 Alignment		54.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra; <b>PDBTitle:</b> bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
7	<a href="#">d1xm0a1</a>	 Alignment		53.7	13	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> SelR domain
8	<a href="#">c2l1uA_</a>	 Alignment		50.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase b2, mitochondrial; <b>PDBTitle:</b> structure-functional analysis of mammalian msrb2 protein
9	<a href="#">c4g6tB_</a>	 Alignment		48.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> type iii effector hopa1; <b>PDBTitle:</b> structure of the hopa1-scha chaperone-effector complex
10	<a href="#">c3hcjB_</a>	 Alignment		43.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase; <b>PDBTitle:</b> structure of msrb from xanthomonas campestris (oxidized2 form)
11	<a href="#">c2kaoA_</a>	 Alignment		34.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase b1; <b>PDBTitle:</b> structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)

12	<a href="#">c3ttoD_</a>	Alignment		30.6	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dextranucrase; <b>PDBTitle:</b> crystal structure of leuconostoc mesenteroides nrml b-1299 n-2 terminally truncated dextranucrase dsr-e in triclinic form
13	<a href="#">c5xf9F_</a>	Alignment		23.2	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-reducing hydrogenase; <b>PDBTitle:</b> crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
14	<a href="#">c4pw1B_</a>	Alignment		22.1	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein with unknown function (clolep_02462)2 from clostridium leptum dsm 753 at 2.10 a resolution
15	<a href="#">c3hiaB_</a>	Alignment		18.7	19	<b>PDB header:</b> choline-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> choline binding protein; <b>PDBTitle:</b> crystal structure of the choline binding domain of spr1274 in2 streptococcus pneumoniae
16	<a href="#">c4nc2A_</a>	Alignment		18.2	19	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> toxin b; <b>PDBTitle:</b> crystal structure of tcdb-b1 bound to b39 vhh
17	<a href="#">c1nvpC_</a>	Alignment		17.8	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor iia beta chain; <b>PDBTitle:</b> human tfiia/tbp/dna complex
18	<a href="#">d1nvpC_</a>	Alignment		17.8	10	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
19	<a href="#">d1nh2c_</a>	Alignment		16.5	5	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
20	<a href="#">c1nh2C_</a>	Alignment		16.5	5	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor iia large chain; <b>PDBTitle:</b> crystal structure of a yeast tfiia/tbp/dna complex
21	<a href="#">c2ibjA_</a>	Alignment	not modelled	13.4	5	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b5; <b>PDBTitle:</b> structure of house fly cytochrome b5
22	<a href="#">d2dcya1</a>	Alignment	not modelled	13.2	17	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
23	<a href="#">d1yfc_</a>	Alignment	not modelled	13.1	5	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
24	<a href="#">c4b8nC_</a>	Alignment	not modelled	12.6	0	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome b5-host origin; <b>PDBTitle:</b> cytochrome b5 of ostreococcus tauri virus 2
25	<a href="#">d1hixa_</a>	Alignment	not modelled	12.4	22	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
26	<a href="#">d1hkoa_</a>	Alignment	not modelled	12.2	6	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
27	<a href="#">d1euea_</a>	Alignment	not modelled	12.1	0	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
28	<a href="#">c1rm1C_</a>	Alignment	not modelled	11.5	5	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor iia large chain; <b>PDBTitle:</b> structure of a yeast tfiia/tbp/tata-box dna complex
29	<a href="#">c3lh9C_</a>	Alignment	not modelled	11.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> endo-1,4-beta-xylanase;

29	<a href="#">c3b2c_</a>	Alignment	not modelled	11.4	17	<b>PDBTitle:</b> crystal structure of the b. circulans cpa123 circular permutant
30	<a href="#">d1mj4a_</a>	Alignment	not modelled	11.1	11	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
31	<a href="#">d1fu9a_</a>	Alignment	not modelled	11.0	20	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> C2HC finger
32	<a href="#">d1cyoa_</a>	Alignment	not modelled	10.8	6	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
33	<a href="#">d1xyna_</a>	Alignment	not modelled	10.5	9	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
34	<a href="#">d1do9a_</a>	Alignment	not modelled	10.5	6	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
35	<a href="#">d1m4wa_</a>	Alignment	not modelled	10.3	17	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
36	<a href="#">c2r2cA_</a>	Alignment	not modelled	9.7	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 28 kda outer membrane protein omp28; <b>PDBTitle:</b> crystal structure of a domain of the outer membrane lipoprotein omp282 from porphyromonas gingivalis
37	<a href="#">d1kbia2</a>	Alignment	not modelled	9.6	0	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
38	<a href="#">d1soxa2</a>	Alignment	not modelled	9.2	11	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
39	<a href="#">d1m2ia_</a>	Alignment	not modelled	9.1	6	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
40	<a href="#">d1iccc_</a>	Alignment	not modelled	8.8	0	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
41	<a href="#">c5hdwA_</a>	Alignment	not modelled	8.8	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fb-box only protein 3; <b>PDBTitle:</b> apag domain of fbxo3
42	<a href="#">c1x3xA_</a>	Alignment	not modelled	8.5	10	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b5; <b>PDBTitle:</b> crystal structure of cytochrome b5 from ascaris suum
43	<a href="#">c3lf5B_</a>	Alignment	not modelled	8.5	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome b5 reductase 4; <b>PDBTitle:</b> structure of human nadh cytochrome b5 oxidoreductase (ncb5or) b52 domain to 1.25a resolution
44	<a href="#">c5lnkc_</a>	Alignment	not modelled	8.5	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
45	<a href="#">d1yu8x1</a>	Alignment	not modelled	8.3	36	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
46	<a href="#">c3ixzB_</a>	Alignment	not modelled	8.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
47	<a href="#">c4ox3A_</a>	Alignment	not modelled	8.1	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxypeptidase yodj; <b>PDBTitle:</b> structure of the ldcb ld-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition
48	<a href="#">d1axxa_</a>	Alignment	not modelled	7.8	0	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
49	<a href="#">c2wwcA_</a>	Alignment	not modelled	7.8	0	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-beta-n-acetylmuramidase; <b>PDBTitle:</b> 3d-structure of the modular autolysin lytc from2 streptococcus pneumoniae in complex with synthetic3 peptidoglycan ligand
50	<a href="#">d1lj0a_</a>	Alignment	not modelled	7.8	0	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
51	<a href="#">c2j8fA_</a>	Alignment	not modelled	7.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme; <b>PDBTitle:</b> crystal structure of the modular cpl-1 endolysin complexed with a2 peptidoglycan analogue (e94q mutant in complex with a disaccharide-3 pentapeptide)
52	<a href="#">d1ywka1</a>	Alignment	not modelled	7.7	7	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Kdul-like
53	<a href="#">d1lunca_</a>	Alignment	not modelled	7.5	45	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
54	<a href="#">c1ywkE_</a>	Alignment	not modelled	7.5	7	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-deoxy-1-threo-5-hexosulose-uronate ketol- <b>PDBTitle:</b> crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
55	<a href="#">d1ligoa_</a>	Alignment	not modelled	7.5	22	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases

						<b>Family:</b> Xylanase/endoglucanase 11/12
56	<a href="#">c6bl5A_</a>	Alignment	not modelled	7.4	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> head decoration protein; <b>PDBTitle:</b> head decoration protein from the hyperthermophilic phage p74-26
57	<a href="#">d1aqa_</a>	Alignment	not modelled	7.4	0	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
58	<a href="#">c2dylA_</a>	Alignment	not modelled	7.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity mitogen-activated protein kinase2 kinase 7 activated mutant (s287d, t291d)
59	<a href="#">c2vijC_</a>	Alignment	not modelled	7.3	23	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> exoenzyme s synthesis protein b; <b>PDBTitle:</b> structural characterization of a secretin pilot protein2 from the type iii secretion system (t3s) of pseudomonas3 aeruginosa
60	<a href="#">c3jtzA_</a>	Alignment	not modelled	7.0	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> structure of the arm-type binding domain of hpi integrase
61	<a href="#">c3imoC_</a>	Alignment	not modelled	6.9	0	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> integron cassette protein; <b>PDBTitle:</b> structure from the mobile metagenome of vibrio cholerae. integron2 cassette protein vch_cass14
62	<a href="#">c2vyuA_</a>	Alignment	not modelled	6.9	7	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline binding protein f; <b>PDBTitle:</b> crystal structure of choline binding protein f from2 streptococcus pneumoniae in the presence of a3 peptidoglycan analogue (tetrasaccharide-pentapeptide)
63	<a href="#">c5iydN_</a>	Alignment	not modelled	6.7	10	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> N: <b>PDB Molecule:</b> transcription initiation factor iia subunit 1; <b>PDBTitle:</b> human core-pic in the initial transcribing state (no iis)
64	<a href="#">c3ecjC_</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> protein (homoprotocatechuate 2,3-dioxygenase); <b>PDBTitle:</b> structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
65	<a href="#">d1ihna_</a>	Alignment	not modelled	6.4	27	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
66	<a href="#">c2keoA_</a>	Alignment	not modelled	6.1	0	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> probable e3 ubiquitin-protein ligase herc2; <b>PDBTitle:</b> solution nmr structure of human protein hs00059, cytochrome-b5-like2 domain of the herc2 e3 ligase. northeast structural genomics3 consortium (nsg) target ht98a
67	<a href="#">c4ox5A_</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ldcb ld-carboxypeptidase; <b>PDBTitle:</b> structure of the ldcb ld-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition
68	<a href="#">d2biba1</a>	Alignment	not modelled	6.0	7	<b>Fold:</b> beta-hairpin stack <b>Superfamily:</b> Cell wall binding repeat <b>Family:</b> Cell wall binding repeat
69	<a href="#">d1unda_</a>	Alignment	not modelled	5.8	45	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
70	<a href="#">c6gcsY_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Y: <b>PDB Molecule:</b> nuym subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
71	<a href="#">d1cxya_</a>	Alignment	not modelled	5.7	5	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
72	<a href="#">c4f78A_</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d,d-dipeptidase/d,d-carboxypeptidase; <b>PDBTitle:</b> crystal structure of vancomycin resistance d,d-dipeptidase vanxyg
73	<a href="#">c2a45J_</a>	Alignment	not modelled	5.5	6	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> J: <b>PDB Molecule:</b> fibrinogen alpha chain; <b>PDBTitle:</b> crystal structure of the complex between thrombin and the central "e"2 region of fibrin
74	<a href="#">d2q0zx2</a>	Alignment	not modelled	5.4	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Sec63 C-terminal domain-like
75	<a href="#">d1dgja2</a>	Alignment	not modelled	5.4	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
76	<a href="#">c2n67B_</a>	Alignment	not modelled	5.3	10	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> hemolysin ii; <b>PDBTitle:</b> c-terminal domain of hemolysin ii-p87m-bmrb
77	<a href="#">c2k6nA_</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> supervillin; <b>PDBTitle:</b> solution structure of human supervillin headpiece, minimized2 average
78	<a href="#">d1legza_</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
79	<a href="#">c2v04A_</a>	Alignment	not modelled	5.2	7	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline binding protein f; <b>PDBTitle:</b> crystal structure of choline binding protein f from streptococcus2 pneumoniae