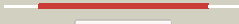



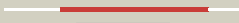




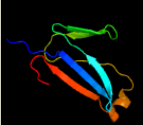





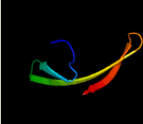





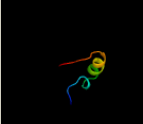











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0813c_(-)_907341_908021
Date	Fri Jul 26 01:50:40 BST 2019
Unique Job ID	76108984b43f692a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fwvA_	 Alignment		100.0	99	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein mtubf_01000852; PDBTitle: crystal structure of rv0813
2	c3ia8A_	 Alignment		100.0	22	PDB header: metal binding protein Chain: A: PDB Molecule: thap domain-containing protein 4; PDBTitle: the structure of the c-terminal heme nitrobindin domain of thap2 domain-containing protein 4 from homo sapiens
3	d2a13a1	 Alignment		100.0	32	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
4	d2fr2a1	 Alignment		100.0	32	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
5	d1v8ha1	 Alignment		45.3	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: SoxZ-like
6	c3zueB_	 Alignment		40.7	16	PDB header: virus Chain: B: PDB Molecule: capsid structural protein vp60; PDBTitle: rabbit hemorrhagic disease virus (rhdv) capsid protein
7	d1jvaa2	 Alignment		36.9	26	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
8	d2h9fa2	 Alignment		34.9	12	Fold: Diaminopimelate epimerase-like Superfamily: Diaminopimelate epimerase-like Family: PA0793-like
9	c2kq8A_	 Alignment		32.8	29	PDB header: hydrolase Chain: A: PDB Molecule: cell wall hydrolase; PDBTitle: solution nmr structure of a domain from bt9727_4915 from 2 bacillus thuringiensis, northeast structural genomics3 consortium target bur95a
10	c6otfA_	 Alignment		31.4	33	PDB header: virus like particle Chain: A: PDB Molecule: viral protein 1; PDBTitle: symmetric reconstruction of human norovirus gii.2 snow mountain virus2 strain vlp in t=3 symmetry
11	c1ihmC_	 Alignment		27.4	38	PDB header: virus Chain: C: PDB Molecule: capsid protein; PDBTitle: crystal structure analysis of norwalk virus capsid

12	d1ihma_	Alignment		27.4	38	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Caliciviridae-like VP
13	c6ouuB_	Alignment		26.5	29	PDB header: virus like particle Chain: B: PDB Molecule: major capsid protein; PDBTitle: symmetric reconstruction of human norovirus gii.4 minerva strain vlp2 in t=4 symmetry
14	c5z4gA_	Alignment		25.7	33	PDB header: unknown function Chain: A: PDB Molecule: sahs4; PDBTitle: crystal structure of secretory abundant heat soluble protein 4 from2 ramazzottius varieornatus
15	c6crjC_	Alignment		23.1	38	PDB header: virus Chain: C: PDB Molecule: norwalk virus, mnv-1 capsid protein chimera; PDBTitle: mouse norovirus model using the crystal structure of mnv p domain and2 the norwalkvirus shell domain
16	c6ou9A_	Alignment		22.7	33	PDB header: virus like particle Chain: A: PDB Molecule: major capsid protein; PDBTitle: asymmetric focused reconstruction of human norovirus gi.7 houston2 strain vlp asymmetric unit in t=3 symmetry
17	c2pw0A_	Alignment		21.7	14	PDB header: unknown function Chain: A: PDB Molecule: prpf methylaconitate isomerase; PDBTitle: crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis
18	d2o62a1	Alignment		20.8	27	Fold: Lipocalins Superfamily: Lipocalins Family: All1756-like
19	c4mveB_	Alignment		16.2	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata
20	c5yznA_	Alignment		15.9	17	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
21	d1qcsa2	Alignment	not modelled	15.2	13	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
22	c3qefB_	Alignment	not modelled	15.0	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-xylosidase/alpha-l-arabinofuranosidase, gly43n; PDBTitle: the structure and function of an arabinan-specific alpha-1,2-2 arabinofuranosidase identified from screening the activities of3 bacterial gh43 glycoside hydrolases
23	c3i6pF_	Alignment	not modelled	14.4	21	PDB header: structural protein Chain: F: PDB Molecule: ethanolamine utilization protein eutm; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutm
24	c3ngkA_	Alignment	not modelled	14.3	21	PDB header: unknown function Chain: A: PDB Molecule: propanediol utilization protein pdua; PDBTitle: pdua from salmonella enterica typhimurium
25	c3fqmA_	Alignment	not modelled	14.2	60	PDB header: metal binding protein Chain: A: PDB Molecule: non-structural protein 5a; PDBTitle: crystal structure of a novel dimeric form of hcv ns5a domain i protein
26	c5i38A_	Alignment	not modelled	14.1	23	PDB header: structural protein Chain: A: PDB Molecule: msm0272 - rmm microcompartment shell protein; PDBTitle: the structure of the hexagonal shell protein msm0272 from the rmm2 microcompartment
27	c3m8IA_	Alignment	not modelled	13.9	33	PDB header: virus Chain: A: PDB Molecule: capsid protein; PDBTitle: crystal structure analysis of the feline calicivirus capsid protein
						Fold: Four-helical up-and-down bundle Superfamily: Mannose-6-phosphate receptor binding protein 1

28	d1szia_	Alignment	not modelled	13.5	43	Tip47 , C-terminal domain Family: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
29	c5y9vA_	Alignment	not modelled	12.6	27	PDB header: transport protein Chain: A: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of diamondback moth ryanodine receptor n-terminal2 domain
30	c4jqpA_	Alignment	not modelled	12.6	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase; PDBTitle: x-ray crystal structure of a 4-hydroxythreonine-4-phosphate2 dehydrogenase from burkholderia phymatum
31	d1oqla_	Alignment	not modelled	12.6	30	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Hypothetical protein YesU
32	c4hboD_	Alignment	not modelled	12.0	50	PDB header: viral protein Chain: D: PDB Molecule: capsid protein; PDBTitle: crystal structure of rubella virus capsid protein (residues 127-277)
33	c4dguB_	Alignment	not modelled	11.8	31	PDB header: cell adhesion Chain: B: PDB Molecule: putative cell adhesion protein; PDBTitle: crystal structure of a putative cell adhesion protein (bt0320) from2 bacteroides thetaiotaomicron vpi-5482 at 2.37 a resolution
34	c5vztB_	Alignment	not modelled	11.2	21	PDB header: cell cycle Chain: B: PDB Molecule: fbx-only protein 31; PDBTitle: crystal structure of the skp1-fbxo31 complex
35	d1xqoa_	Alignment	not modelled	11.2	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: AgoG-like
36	c3cegA_	Alignment	not modelled	10.6	28	PDB header: ligase Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 6; PDBTitle: crystal structure of the ubc domain of baculoviral iap repeat-2 containing protein 6
37	d1meoa_	Alignment	not modelled	10.1	19	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
38	d1x3ha2	Alignment	not modelled	10.1	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
39	c3akgA_	Alignment	not modelled	9.5	24	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted alpha l-arabinofuranosidase ii; PDBTitle: crystal structure of exo-1,5-alpha-l-arabinofuranosidase complexed2 with alpha-1,5-l-arabinofuranobiose
40	c1qdnA_	Alignment	not modelled	9.4	29	PDB header: fusion protein Chain: A: PDB Molecule: protein (n-ethylmaleimide sensitive fusion PDBTitle: amino terminal domain of the n-ethylmaleimide sensitive2 fusion protein (nsf)
41	d1mv8a3	Alignment	not modelled	9.4	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain Family: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
42	c4zltA_	Alignment	not modelled	9.0	29	PDB header: chemokine binding protein/chemokine Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of viral chemokine binding protein r17 in complex2 with ccl3
43	c2ivzD_	Alignment	not modelled	8.9	15	PDB header: protein transport/hydrolase Chain: D: PDB Molecule: protein tolB; PDBTitle: structure of tolB in complex with a peptide of the colicin2 e9 t-domain
44	c2hi1A_	Alignment	not modelled	8.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 2; PDBTitle: the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
45	c6iczX_	Alignment	not modelled	8.5	71	PDB header: splicing Chain: X: PDB Molecule: prkr-interacting protein 1; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
46	d1ej7l1	Alignment	not modelled	8.3	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
47	d1mkfa_	Alignment	not modelled	7.9	16	Fold: Viral chemokine binding protein m3 Superfamily: Viral chemokine binding protein m3 Family: Viral chemokine binding protein m3
48	d1cr5a2	Alignment	not modelled	7.6	9	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
49	c5djbD_	Alignment	not modelled	7.6	28	PDB header: structural protein Chain: D: PDB Molecule: microcompartments protein; PDBTitle: structure of the hallangium ochraceum bmc-h shell protein
50	c4qivA_	Alignment	not modelled	7.5	28	PDB header: structural protein Chain: A: PDB Molecule: bacterial microcompartments family protein; PDBTitle: crystal structure of hexameric microcompart ment shell protein from2 aeromonas hydrophila
51	d2cu8a2	Alignment	not modelled	7.5	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
52	c4i0xA_	Alignment	not modelled	7.4	71	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex

53	c3qr5B_	Alignment	not modelled	7.4	29	PDB header: signaling protein Chain: B: PDB Molecule: cardiac ca2+ release channel; PDBTitle: structure of the first domain of a cardiac ryanodine receptor mutant2 with exon 3 deleted
54	c2kybA_	Alignment	not modelled	7.3	21	PDB header: toxin Chain: A: PDB Molecule: mannosyl-glycoprotein endo-beta-n-acetylglucosamidase PDBTitle: solution structure of cpr82g from clostridium perfringens. north east2 structural genomics consortium target cpr82g
55	c3r2cJ_	Alignment	not modelled	7.0	28	PDB header: transcription/rna Chain: J: PDB Molecule: 30s ribosomal protein s10; PDBTitle: crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna
56	c4m8rA_	Alignment	not modelled	7.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf4784 family protein (baccac_01631) from2 bacteroides caccae atcc 43185 at 2.50 a resolution
57	c3akjB_	Alignment	not modelled	6.9	24	PDB header: transferase Chain: B: PDB Molecule: ctka; PDBTitle: crystal structure of a helicobacter pylori proinflammatory kinase ctka
58	c3w6sA_	Alignment	not modelled	6.8	44	PDB header: transferase Chain: A: PDB Molecule: mpr1 protein; PDBTitle: yeast n-acetyltransferase mpr1 involved in oxidative stress tolerance2 via proline metabolism
59	d1svda1	Alignment	not modelled	6.8	22	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
60	c5t86A_	Alignment	not modelled	6.4	17	PDB header: toxin Chain: A: PDB Molecule: cdia toxin; PDBTitle: crystal structure of cdi complex from e. coli a0 34/86
61	c3e7dC_	Alignment	not modelled	6.4	12	PDB header: isomerase Chain: C: PDB Molecule: cobh, precorrin-8x methylmutase; PDBTitle: crystal structure of precorrin-8x methyl mutase cbic/cobh from2 brucella melitensis
62	d1lr0a_	Alignment	not modelled	6.3	33	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: ToIA
63	c4atyA_	Alignment	not modelled	6.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: terephthalate 1,2-cis-dihydrodiol dehydrogenase; PDBTitle: crystal structure of a terephthalate 1,2-cis-2 dihydrodioldehydrogenase from burkholderia xenovorans3 lb400
64	c3a1zC_	Alignment	not modelled	6.3	21	PDB header: transport protein Chain: C: PDB Molecule: hemolymph juvenile hormone binding protein; PDBTitle: crystal structure of juvenile hormone binding protein from silkworm
65	c2gh8B_	Alignment	not modelled	6.3	20	PDB header: virus Chain: B: PDB Molecule: capsid protein; PDBTitle: x-ray structure of a native calicivirus
66	c3tijA_	Alignment	not modelled	5.9	40	PDB header: membrane protein Chain: A: PDB Molecule: nupc family protein; PDBTitle: crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
67	c3tcqA_	Alignment	not modelled	5.8	35	PDB header: viral protein Chain: A: PDB Molecule: matrix protein vp40; PDBTitle: crystal structure of matrix protein vp40 from ebola virus sudan
68	c2mewA_	Alignment	not modelled	5.8	36	PDB header: structural protein Chain: A: PDB Molecule: 30s ribosomal protein s10; PDBTitle: solution structure of nuse (s10) from thermotoga maritima
69	d1u35c1	Alignment	not modelled	5.8	33	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
70	d1f2va_	Alignment	not modelled	5.8	29	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH
71	c1bctA_	Alignment	not modelled	5.8	22	PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution
72	c5l2bC_	Alignment	not modelled	5.7	30	PDB header: transport protein Chain: C: PDB Molecule: nucleoside permease; PDBTitle: structure of cntnw n149s, e332a in an outward-facing state
73	c4wbxC_	Alignment	not modelled	5.6	36	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit alpha; PDBTitle: conserved hypothetical protein pf1771 from pyrococcus furiosus solved2 by sulfur sad using swiss light source data
74	d1ou0a_	Alignment	not modelled	5.4	24	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH
75	d1imla2	Alignment	not modelled	5.4	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
76	c2c55A_	Alignment	not modelled	5.3	33	PDB header: viral protein Chain: A: PDB Molecule: protein p6; PDBTitle: solution structure of the human immunodeficiency virus type2 1 p6 protein
77	d1v9ca_	Alignment	not modelled	5.2	12	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH

78	d1ewka_	Alignment	not modelled	5.2	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
79	c2jraB_	Alignment	not modelled	5.2	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
80	d1jfma_	Alignment	not modelled	5.2	10	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
81	d2q07a3	Alignment	not modelled	5.2	33	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: AF0587 pre C-terminal domain-like
82	c1toIA_	Alignment	not modelled	5.1	31	PDB header: viral protein Chain: A: PDB Molecule: protein (fusion protein consisting of minor coat protein, PDBTitle: fusion of n-terminal domain of the minor coat protein from gene iii in2 phage m13, and c-terminal domain of e. coli protein-tola
83	c1b24A_	Alignment	not modelled	5.1	20	PDB header: intron-encoded Chain: A: PDB Molecule: protein (i-dmoi); PDBTitle: i-dmoi, intron-encoded endonuclease
84	c2kksA_	Alignment	not modelled	5.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of protein dsy2949 from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr27
85	c6qhgB_	Alignment	not modelled	5.1	83	PDB header: viral protein Chain: B: PDB Molecule: polymerase; PDBTitle: structure of the cap-binding domain of rift valley fever virus I2 protein