




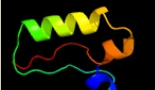



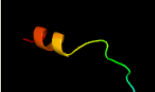
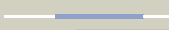
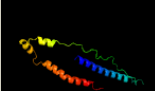

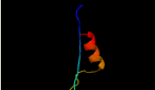



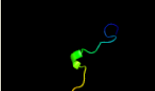



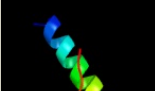


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1949c (-)_2199082_2200038
Date	Mon Aug 5 13:25:04 BST 2019
Unique Job ID	945d94d52e0f2574

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4evxA_	 Alignment		53.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative phage endolysin; PDBTitle: crystal structure of putative phage endolysin from s. enterica
2	c2lxeA_	 Alignment		42.6	50	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase suvr4; PDBTitle: s4wyild
3	d1yrra2	 Alignment		29.1	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
4	c3o6xC_	 Alignment		28.0	27	PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
5	c6iuhC_	 Alignment		27.5	35	PDB header: protein binding Chain: C: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of git1 pbd domain in complex with liprin-alpha2
6	c4wj2A_	 Alignment		25.0	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
7	c4r1dB_	 Alignment		24.6	18	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tle4-tli4 complex
8	c3gr1A_	 Alignment		21.7	30	PDB header: membrane protein Chain: A: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-392)
9	c6i9fA_	 Alignment		20.5	20	PDB header: lipid binding protein Chain: A: PDB Molecule: fatty acid-binding protein homolog; PDBTitle: solution structure of as-p18 reveals that nematode fatty acid binding2 proteins exhibit unusual structural features
10	c1wy1B_	 Alignment		19.4	22	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein ph0671; PDBTitle: crystal structure of the ph0671 protein from pyrococcus horikoshii ot3
11	d1u5wa1	 Alignment		17.7	31	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: yjx-like

12	c4evuB_	Alignment		15.9	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative periplasmic protein ydgh; PDBTitle: crystal structure of c-terminal domain of putative periplasmic protein2 ydgh from s. enterica
13	d1eeja2	Alignment		15.8	31	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
14	c6et6A_	Alignment		15.7	19	PDB header: antimicrobial protein Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of muramidase from acinetobacter baumannii ab 5075uw2 prophage
15	d1x6ma_	Alignment		15.5	43	Fold: Mss4-like Superfamily: Mss4-like Family: Glutathione-dependent formaldehyde-activating enzyme, Gfa
16	c1htmB_	Alignment		15.1	33	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin ha2 chain; PDBTitle: structure of influenza haemagglutinin at the ph of membrane2 fusion
17	d1v9pa3	Alignment		14.7	23	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
18	d1kbbh_	Alignment		13.7	31	Fold: Nuclear receptor coactivator interlocking domain Superfamily: Nuclear receptor coactivator interlocking domain Family: Nuclear receptor coactivator interlocking domain
19	d1t3ba2	Alignment		12.8	19	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
20	d1ivs1	Alignment		12.3	19	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
21	d1dgsa3	Alignment	not modelled	11.9	23	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
22	c4kwyB_	Alignment	not modelled	11.9	16	PDB header: transport protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative lipoprotein (cc_3750) from caulobacter2 crescentus cb15 at 2.40 a resolution
23	c2jq3A_	Alignment	not modelled	11.8	50	PDB header: lipid binding protein Chain: A: PDB Molecule: apolipoprotein c-iii; PDBTitle: structure and dynamics of human apolipoprotein c-iii
24	d1ta8a_	Alignment	not modelled	11.8	13	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
25	d1u14a_	Alignment	not modelled	11.3	31	Fold: Anticodon-binding domain-like Superfamily: TPase-like Family: YjyX-like
26	c2vo9C_	Alignment	not modelled	11.2	41	PDB header: hydrolase Chain: C: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: crystal structure of the enzymatically active domain of the listeria2 monocytogenes bacteriophage 500 endolysin ply500
27	c2lyjA_	Alignment	not modelled	10.5	31	PDB header: isomerase Chain: A: PDB Molecule: thiol disulfide interchange protein dsbc; PDBTitle: crystal structure of the n-terminal dimer domain of e.coli2 dsbc
28	d176la_	Alignment	not modelled	10.0	21	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
						Fold: Lysozyme-like

29	d1xjua_	Alignment	not modelled	10.0	18	Superfamily: Lysozyme-like Family: Phage lysozyme
30	c3m5gD_	Alignment	not modelled	9.6	33	PDB header: viral protein Chain: D: PDB Molecule: hemagglutinin; PDBTitle: crystal structure of a h7 influenza virus hemagglutinin
31	c6b29B_	Alignment	not modelled	9.5	36	PDB header: protein binding Chain: B: PDB Molecule: sh3 and cysteine-rich domain-containing protein 3; PDBTitle: crystal structure of the second sh3 domain of stac3 (309-364)
32	d1u7ka_	Alignment	not modelled	9.3	67	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
33	d2gcxa1	Alignment	not modelled	9.0	30	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
34	c5d6sB_	Alignment	not modelled	8.9	36	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
35	c5d0bB_	Alignment	not modelled	8.8	24	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
36	d1zway1	Alignment	not modelled	8.7	31	Fold: Anticodon-binding domain-like Superfamily: !TPase-like Family: YjyX-like
37	d1cexa_	Alignment	not modelled	8.6	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
38	c2mulA	Alignment	not modelled	8.6	38	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: solution structure of the ubm1 domain of human huwe1/arf-bp1
39	c1w8xM_	Alignment	not modelled	8.6	32	PDB header: virus Chain: M: PDB Molecule: protein p30; PDBTitle: structural analysis of prd1
40	c3gr0D_	Alignment	not modelled	8.4	36	PDB header: membrane protein Chain: D: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
41	c4fypA_	Alignment	not modelled	8.4	67	PDB header: plant protein Chain: A: PDB Molecule: vegetative storage protein 1; PDBTitle: crystal structure of plant vegetative storage protein
42	c4h32L_	Alignment	not modelled	8.3	42	PDB header: viral protein Chain: L: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of the hemagglutinin h17 derived the bat2 influenza a virus
43	c1ru7B_	Alignment	not modelled	8.3	50	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: 1934 human h1 hemagglutinin
44	d1un7a2	Alignment	not modelled	8.1	21	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
45	c1jsdB_	Alignment	not modelled	8.1	50	PDB header: viral protein Chain: B: PDB Molecule: haemagglutinin (ha2 chain); PDBTitle: crystal structure of swine h9 haemagglutinin
46	d2g84a1	Alignment	not modelled	8.0	36	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
47	c3dlmA_	Alignment	not modelled	7.9	32	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
48	d1cq3a_	Alignment	not modelled	7.9	26	Fold: Soluble secreted chemokine inhibitor, VCCI Superfamily: Soluble secreted chemokine inhibitor, VCCI Family: Soluble secreted chemokine inhibitor, VCCI
49	c1mqIB_	Alignment	not modelled	7.7	33	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin ha2 chain; PDBTitle: bha of ukr/63
50	c1hgeD_	Alignment	not modelled	7.7	33	PDB header: viral protein Chain: D: PDB Molecule: hemagglutinin, (g135r), ha1 chain; PDBTitle: binding of influenza virus hemagglutinin to analogs of its cell-2 surface receptor, sialic acid: analysis by proton nuclear magnetic3 resonance spectroscopy and x-ray crystallography
51	c3bt6B_	Alignment	not modelled	7.6	25	PDB header: viral protein Chain: B: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin
52	c5t0gV_	Alignment	not modelled	7.6	30	PDB header: hydrolase Chain: V: PDB Molecule: 26s proteasome non-atpase regulatory subunit 3; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
53	c1tfzA_	Alignment	not modelled	7.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: structural basis for herbicidal inhibitor selectivity revealed by2 comparison of crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
54	c6hwwA_	Alignment	not modelled	7.6	67	PDB header: viral protein Chain: A: PDB Molecule: putative gag polyprotein; PDBTitle: immature mlv capsid hexamer structure in intact virus particles
						PDB header: ligase

55	c1dgsB	Alignment	not modelled	7.5	23	Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
56	c2qnlA	Alignment	not modelled	7.4	25	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
57	c2bfuL	Alignment	not modelled	7.4	33	PDB header: virus Chain: L: PDB Molecule: cowpea mosaic virus, large (l) subunit; PDBTitle: x-ray structure of cpmv top component
58	c3nh8A	Alignment	not modelled	7.3	20	PDB header: hydrolase Chain: A: PDB Molecule: aspartoacylase-2; PDBTitle: crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
59	c6hwyB	Alignment	not modelled	7.2	67	PDB header: viral protein Chain: B: PDB Molecule: putative gag polyprotein; PDBTitle: mature mlv capsid pentamer structure in intact virus particles
60	c3gbsA	Alignment	not modelled	7.2	21	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
61	c1zauA	Alignment	not modelled	7.2	17	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: adenylation domain of nad+ dependent dna ligase from m.tuberculosis
62	c1v9pB	Alignment	not modelled	7.1	23	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
63	d1dl6a	Alignment	not modelled	7.0	55	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
64	c3hdfA	Alignment	not modelled	7.0	13	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of truncated endolysin r21 from phage 21
65	c6e1rA	Alignment	not modelled	7.0	43	PDB header: hydrolase Chain: A: PDB Molecule: tailspike protein; PDBTitle: crystal structure of the acinetobacter phage vb_apip_p1 tailspike2 protein
66	d2gycf2	Alignment	not modelled	6.9	26	Fold: Mbth/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
67	c6gvwD	Alignment	not modelled	6.9	31	PDB header: signaling protein Chain: D: PDB Molecule: brisc and brca1-a complex member 1; PDBTitle: crystal structure of the brca1-a complex
68	d1q08a	Alignment	not modelled	6.7	11	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
69	d1rutx4	Alignment	not modelled	6.7	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
70	c2wrhl	Alignment	not modelled	6.7	42	PDB header: viral protein Chain: I: PDB Molecule: hemagglutinin ha2 chain; PDBTitle: structure of h1 duck albert hemagglutinin with human2 receptor
71	c2anxB	Alignment	not modelled	6.6	23	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme; PDBTitle: crystal structure of bacteriophage p22 lysozyme mutant i87m
72	c2mxzA	Alignment	not modelled	6.6	17	PDB header: hydrolase Chain: A: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: bacteriophage t5 l-alanyl-d-glutamate peptidase complex with zn2+2 (endo t5-zn2+)
73	c5nv4A	Alignment	not modelled	6.5	32	PDB header: transferase Chain: A: PDB Molecule: udp-glucose-glycoprotein glucosyltransferase-like protein; PDBTitle: udp-glucose glycoprotein glucosyltransferase from chaetomium2 thermophilum double mutant d611c:g1050c
74	d1xjta	Alignment	not modelled	6.4	21	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
75	d1pfta	Alignment	not modelled	6.4	63	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
76	c2qv6D	Alignment	not modelled	6.3	21	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
77	d2vo9a1	Alignment	not modelled	6.0	41	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like
78	d1ny722	Alignment	not modelled	6.0	71	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
79	c4idmA	Alignment	not modelled	5.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase; PDBTitle: crystal structure of the delta-pyrroline-5-carboxylate dehydrogenase2 from mycobacterium tuberculosis
80	d1pgl22	Alignment	not modelled	5.9	86	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP

81	d1p5ca_	Alignment	not modelled	5.9	15	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
82	c2fkkA_	Alignment	not modelled	5.8	22	PDB header: viral protein Chain: A: PDB Molecule: baseplate structural protein gp10; PDBTitle: crystal structure of the c-terminal domain of the bacteriophage t42 gene product 10
83	c3qd7X_	Alignment	not modelled	5.8	6	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized protein ydal; PDBTitle: crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
84	d1ni3a2	Alignment	not modelled	5.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
85	d1ywsa1	Alignment	not modelled	5.7	24	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
86	d1wgea1	Alignment	not modelled	5.7	24	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
87	d1sp9a_	Alignment	not modelled	5.6	16	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
88	c5x88A_	Alignment	not modelled	5.6	25	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
89	c2jr7A_	Alignment	not modelled	5.6	24	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
90	c5opzB_	Alignment	not modelled	5.6	39	PDB header: hydrolase Chain: B: PDB Molecule: chix; PDBTitle: crystal structure of serratia marcescens l-ala d-glu endopeptidase2 chix
91	d1nt2b_	Alignment	not modelled	5.6	15	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
92	c4fiuC_	Alignment	not modelled	5.5	50	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
93	c4v1ao_	Alignment	not modelled	5.5	24	PDB header: ribosome Chain: O: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
94	c1tr8A_	Alignment	not modelled	5.5	20	PDB header: chaperone Chain: A: PDB Molecule: conserved protein (mth177); PDBTitle: crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
95	d2pxrc1	Alignment	not modelled	5.4	29	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
96	d1jbsa_	Alignment	not modelled	5.4	25	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Ribotoxin
97	c6c8rA_	Alignment	not modelled	5.3	20	PDB header: transferase Chain: A: PDB Molecule: loganic acid o-methyltransferase; PDBTitle: loganic acid o-methyltransferase complexed with sah and loganic acid
98	c2lvuA_	Alignment	not modelled	5.2	71	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 10
99	c3dd5F_	Alignment	not modelled	5.1	21	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex