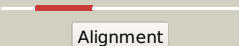

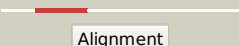

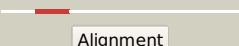

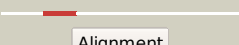

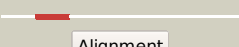

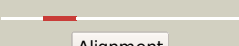


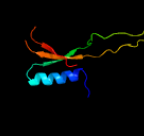



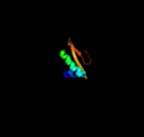




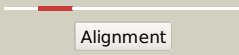

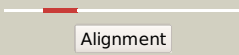

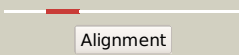

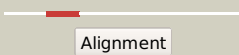
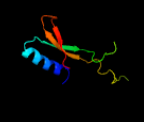
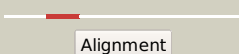
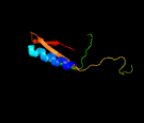
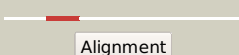


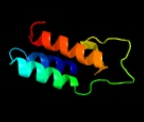
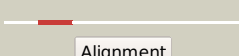

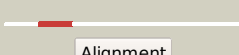

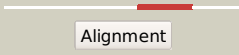
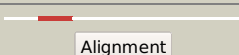
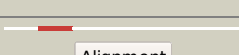

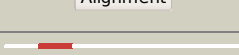
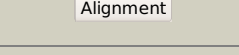
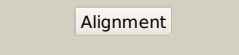
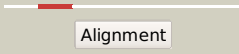


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2566 (-)_2886383_2889805
Date	Wed Aug 7 12:50:20 BST 2019
Unique Job ID	f9117bae346dcb80

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lsrB_	 Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: transglutaminase-like enzymes, putative cysteine protease; PDBTitle: the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
2	c6g49A_	 Alignment		99.9	23	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of the periplasmic domain of tgpa from pseudomonas2 aeruginosa
3	c4xz7A_	 Alignment		99.3	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a tgase
4	d1g0da4	 Alignment		99.3	28	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
5	d2f4ma1	 Alignment		99.3	21	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
6	d2q3za4	 Alignment		99.2	32	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
7	d1vjia4	 Alignment		99.2	29	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
8	d1ex0a4	 Alignment		99.1	31	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
9	d1x3za1	 Alignment		98.6	35	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
10	c4u65F_	 Alignment		98.4	27	PDB header: transferase/hydrolase Chain: F: PDB Molecule: putative cystine protease; PDBTitle: structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lapg
11	c3kd4A_	 Alignment		98.2	14	PDB header: hydrolase Chain: A: PDB Molecule: putative protease; PDBTitle: crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution

12	c2qshA_	 Alignment		98.0	16	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna repair protein rad4; PDBTitle: crystal structure of rad4-rad23 bound to a mismatch dna
13	c3eswA_	 Alignment		97.9	34	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
14	c1g0dA_	 Alignment		97.5	27	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of red sea bream transglutaminase
15	c19mB_	 Alignment		97.3	24	PDB header: transferase Chain: B: PDB Molecule: protein-glutamine glutamyltransferase e3; PDBTitle: three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
16	c1f13A_	 Alignment		97.2	34	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
17	c1kv3F_	 Alignment		97.2	29	PDB header: transferase Chain: F: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: human tissue transglutaminase in gdp bound form
18	c4fgpB_	 Alignment		97.0	19	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic protein; PDBTitle: legionella pneumophila lapp (egta-treated)
19	c2pfrB_	 Alignment		95.0	16	PDB header: transferase Chain: B: PDB Molecule: arylamine n-acetyltransferase 2; PDBTitle: human n-acetyltransferase 2
20	d1e2ta_	 Alignment		94.8	17	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
21	d1r8ga_	 Alignment	not modelled	94.7	15	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
22	c3lnbA_	 Alignment	not modelled	93.5	15	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase family protein; PDBTitle: crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
23	d1w5ra1	 Alignment	not modelled	93.4	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
24	d1w4ta1	 Alignment	not modelled	93.3	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
25	c2vfbA_	 Alignment	not modelled	93.1	19	PDB header: transferase Chain: A: PDB Molecule: arylamine n-acetyltransferase; PDBTitle: the structure of mycobacterium marinum arylamine n-2 acetyltransferase
26	c3d9wA_	 Alignment	not modelled	92.9	16	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure analysis of nocardia farcinica arylamine n-2 acetyltransferase
27	c4guzA_	 Alignment	not modelled	92.7	15	PDB header: transferase Chain: A: PDB Molecule: probable arylamine n-acetyl transferase; PDBTitle: structure of the arylamine n-acetyltransferase from mycobacterium2 abscessus
28	c4dmoB_	 Alignment	not modelled	91.8	16	PDB header: transferase Chain: B: PDB Molecule: n-hydroxyarylamine o-acetyltransferase; PDBTitle: crystal structure of the (baccr)nat3 arylamine n-acetyltransferase2 from bacillus cereus reveals a unique cys-his-glu catalytic triad

29	d2bsza1	Alignment	not modelled	91.5	17	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
30	c1tt4B_	Alignment	not modelled	89.8	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from <i>Salmonella typhimurium</i>
31	d1tt4a_	Alignment	not modelled	89.8	18	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
32	c4aghA	Alignment	not modelled	74.6	11	PDB header: transcription Chain: A: PDB Molecule: mosub1, transcription cofactor; PDBTitle: structural features of ssdna binding protein mosub1 from <i>Magnaporthe oryzae</i>
33	c2gwcE_	Alignment	not modelled	57.4	15	PDB header: ligase Chain: E: PDB Molecule: glutamate cysteine ligase; PDBTitle: crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
34	c2lzoA_	Alignment	not modelled	47.0	25	PDB header: toxin Chain: A: PDB Molecule: ugtX; PDBTitle: spatial structure of pi-anmtX ugr 9a-1
35	c3canA_	Alignment	not modelled	45.7	45	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from <i>Bacteroides vulgatus</i> atcc 8482
36	d2f2ha3	Alignment	not modelled	44.6	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Putative glucosidase YicI, domain 3
37	c3hn5B_	Alignment	not modelled	43.2	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative exported protein bf0290; PDBTitle: crystal structure of bf0290 (yp_210027.1) from <i>Bacteroides fragilis</i> nctc 9343 at 1.70 a resolution
38	c5td6A_	Alignment	not modelled	41.5	17	PDB header: rna binding protein Chain: A: PDB Molecule: fog-3 protein; PDBTitle: c. elegans fog-3 btg/tob domain - h47n, c117a
39	d2z15a1	Alignment	not modelled	38.2	33	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
40	c3evaA_	Alignment	not modelled	35.5	21	PDB header: transferase Chain: A: PDB Molecule: rna-directed rna polymerase ns5; PDBTitle: crystal structure of yellow fever virus methyltransferase complexed2 with s-adenosyl-l-homocysteine
41	d3e9va1	Alignment	not modelled	34.7	21	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
42	c4nkpD_	Alignment	not modelled	33.8	13	PDB header: chaperone Chain: D: PDB Molecule: putative extracellular heme-binding protein; PDBTitle: crystal structure of a putative extracellular heme-binding protein2 (despg_02683) from <i>Desulfovibrio piger</i> atcc 29098 at 1.24 a3 resolution
43	c4u4hA_	Alignment	not modelled	33.4	37	PDB header: viral protein Chain: A: PDB Molecule: tegument protein ul21; PDBTitle: crystal structure of hsv-1 ul21 n-terminal domain
44	c2gpzC_	Alignment	not modelled	32.8	24	PDB header: hydrolase Chain: C: PDB Molecule: transthyretin-like protein; PDBTitle: transthyretin-like protein from <i>Salmonella dublin</i>
45	c5anrC_	Alignment	not modelled	32.1	50	PDB header: rna binding protein Chain: C: PDB Molecule: eukaryotic translation initiation factor 4e transporter; PDBTitle: structure of a human 4e-t - ddx6 - cnot1 complex
46	d1pcfa_	Alignment	not modelled	32.0	20	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Transcriptional coactivator PC4 C-terminal domain
47	d1h8ba_	Alignment	not modelled	30.3	22	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
48	d1w1oa1	Alignment	not modelled	28.0	16	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
49	c2qzbB_	Alignment	not modelled	27.4	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yfey; PDBTitle: crystal structure of the uncharacterized protein yfey from <i>Escherichia coli</i>
50	d1h59b_	Alignment	not modelled	27.1	24	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain
51	c5o46A_	Alignment	not modelled	25.0	31	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: iristatin; PDBTitle: crystal structure of iristatin, a secreted salivary cystatin from the2 hard tick ixodes ricinus
52	c2ml7A_	Alignment	not modelled	24.9	56	PDB header: unknown function Chain: A: PDB Molecule: specific abundant protein 3; PDBTitle: ginsentides: characterization, structure and application of a new2 class of highly stable cystine knot peptides in ginseng
53	c3mxuA_	Alignment	not modelled	24.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from <i>Bartonella henselae</i>
54	c3fymA_	Alignment	not modelled	24.8	16	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of yfmf, a putative dna-binding membrane2 protein from <i>Staphylococcus aureus</i>

55	d1uc2a_	Alignment	not modelled	24.5	57	Fold: Hypothetical protein PH1602 Superfamily: Hypothetical protein PH1602 Family: Hypothetical protein PH1602
56	c5vglA_	Alignment	not modelled	24.4	18	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
57	c2epgB_	Alignment	not modelled	24.3	57	PDB header: ligase Chain: B: PDB Molecule: hypothetical protein ttha1785; PDBTitle: crystal structure of ttha1785
58	d1b63a1	Alignment	not modelled	24.3	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
59	c2lkyA_	Alignment	not modelled	24.2	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysm.17112.b
60	c2z2uA_	Alignment	not modelled	23.9	32	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
61	c1rpcA_	Alignment	not modelled	23.8	60	PDB header: replication inhibitor Chain: A: PDB Molecule: tricyclic peptide rp 71955; PDBTitle: solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
62	c3lssA_	Alignment	not modelled	23.8	31	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
63	c1rpbA_	Alignment	not modelled	22.7	60	PDB header: replication inhibitor Chain: A: PDB Molecule: tricyclic peptide rp 71955; PDBTitle: solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
64	d2fd6u3	Alignment	not modelled	22.2	19	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Extracellular domain of cell surface receptors
65	c2kvcA_	Alignment	not modelled	21.9	33	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
66	c3mwzA_	Alignment	not modelled	21.9	19	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: sialostatin I2; PDBTitle: crystal structure of the selenomethionine derivative of the I 22,47,2 100 m mutant of sialostatin I2
67	c4njkA_	Alignment	not modelled	21.8	23	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
68	c3elyA_	Alignment	not modelled	21.5	33	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: wesselsbron virus methyltransferase in complex with adohcy
69	d1iu4a_	Alignment	not modelled	21.4	40	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Microbial transglutaminase
70	c3gczA_	Alignment	not modelled	21.2	22	PDB header: transferase Chain: A: PDB Molecule: polyprotein; PDBTitle: yokose virus methyltransferase in complex with adomet
71	c3nrdB_	Alignment	not modelled	20.9	22	PDB header: nucleotide binding protein Chain: B: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
72	c6a42A_	Alignment	not modelled	20.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: rna-directed dna polymerase homolog (r1),polyubiquitin-c; PDBTitle: r1en(5-223)-ubiquitin fusion
73	c4uqtB_	Alignment	not modelled	20.0	36	PDB header: translation Chain: B: PDB Molecule: pre-mrna-splicing factor cwc26; PDBTitle: rrm-peptide structure in res complex
74	c5zn6D_	Alignment	not modelled	19.4	22	PDB header: hydrolase Chain: D: PDB Molecule: alpha-xylosidase mexyl31; PDBTitle: crystal structure of gh31 alpha-xylosidase from a soil metagenome
75	c3iu0A_	Alignment	not modelled	19.3	40	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: structural basis for zymogen activation and substrate binding of2 transglutaminase from streptomyces mobaraense
76	c3qzrC_	Alignment	not modelled	19.0	47	PDB header: hormone receptor Chain: C: PDB Molecule: abscisic acid receptor pyl5; PDBTitle: crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
77	d2pbza2	Alignment	not modelled	19.0	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
78	c2pbzC_	Alignment	not modelled	18.5	15	PDB header: ligase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
79	c5mlkB_	Alignment	not modelled	18.4	19	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
						PDB header: structural genomics, unknown function

80	c4kmgA	Alignment	not modelled	18.1	25	Chain: A: PDB Molecule: lmo2446 protein; PDBTitle: 1.9 angstrom resolution crystal structure of uncharacterized protein2 lmo2446 from listeria monocytogenes egd-e
81	c5f7sA	Alignment	not modelled	18.0	16	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 31; PDBTitle: cycloalternan-degrading enzyme from trueperella pyogenes
82	d1ddla	Alignment	not modelled	18.0	29	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
83	d1hyha2	Alignment	not modelled	17.8	23	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
84	c3lkzB	Alignment	not modelled	17.6	37	PDB header: viral protein Chain: B: PDB Molecule: non-structural protein 5; PDBTitle: structural and functional analyses of a conserved hydrophobic pocket2 of flavivirus methyltransferase
85	c6ak0A	Alignment	not modelled	17.6	70	PDB header: unknown function Chain: A: PDB Molecule: cys-leu-gly-val-gly-ser-cys-val-asp-phe-alg-gly-cys-gly- PDBTitle: solution nmr structure of a new lasso peptide specialicin
86	d2nrha1	Alignment	not modelled	17.6	67	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
87	d1w7ja1	Alignment	not modelled	17.5	25	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
88	c4q6uA	Alignment	not modelled	17.5	28	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
89	c5x7rB	Alignment	not modelled	17.4	18	PDB header: hydrolase, transferase Chain: B: PDB Molecule: glycoside hydrolase family 31 alpha-glucosidase; PDBTitle: crystal structure of paenibacillus sp. 598k alpha-1,6-2 glucosyltransferase complexed with isomaltohexaose
90	c4xpsA	Alignment	not modelled	17.1	9	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of the mutant d365a of pedobacter saltans gh312 alpha-galactosidase complexed with p-nitrophenyl-alpha-3 galactopyranoside
91	d1af7a2	Alignment	not modelled	17.0	29	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain
92	d1ju8a	Alignment	not modelled	17.0	80	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
93	d1lrza	Alignment	not modelled	16.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: GARP response regulators
94	c1xsiF	Alignment	not modelled	16.7	19	PDB header: hydrolase Chain: F: PDB Molecule: putative family 31 glucosidase yici; PDBTitle: structure of a family 31 alpha glycosidase
95	d1zo0a1	Alignment	not modelled	16.4	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Ornithine decarboxylase antizyme-like
96	d1k8rb	Alignment	not modelled	16.3	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
97	d1cgt4	Alignment	not modelled	16.3	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	d1p8ba	Alignment	not modelled	16.2	100	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
99	d1nyed	Alignment	not modelled	15.9	14	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins