
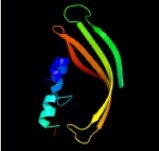


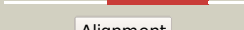











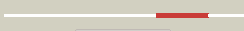











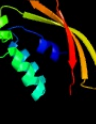

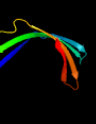


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0178 (-) _208936_209670
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	5c0410d6e32c5284

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5u9oD_	 Alignment		97.2	13	PDB header: cell cycle Chain: D: PDB Molecule: plastid division protein cdp1, chloroplastic,plastid PDBTitle: cocrystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1
2	c5d9rA_	 Alignment		97.1	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: protein accumulation and replication of chloroplasts 6, PDBTitle: crystal structure of a conserved domain in the intermembrane space2 region of the plastid division protein arc6
3	c3wz4F_	 Alignment		96.9	15	PDB header: unknown function Chain: F: PDB Molecule: doti; PDBTitle: structure of the periplasmic domain of doti (crystal form i)
4	c5cn1A_	 Alignment		96.7	14	PDB header: protein transport Chain: A: PDB Molecule: icml-like; PDBTitle: crystal structure of an icml-like type iv secretion system protein2 (lpg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution
5	d2rfr1	 Alignment		96.7	19	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
6	c3a76B_	 Alignment		96.2	12	PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina
7	d3b81a1	 Alignment		96.2	15	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
8	d2ux0a1	 Alignment		96.1	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
9	d3stda_	 Alignment		96.1	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
10	d3cu3a1	 Alignment		96.0	10	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
11	c4i4kB_	 Alignment		95.9	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6

12	c3gzaA	Alignment		95.9	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein with a ntf2-like fold; PDBTitle: crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
13	d1idpa	Alignment		95.6	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
14	c3h51A	Alignment		95.4	16	PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin dependent protein kinase ii PDBTitle: crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
15	c3wz3A	Alignment		95.2	9	PDB header: unknown function Chain: A: PDB Molecule: tram protein; PDBTitle: structure of a periplasmic fragment of tram
16	c4ovmE	Alignment		94.7	11	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
17	d1hkxa	Alignment		94.5	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
18	c4nhfF	Alignment		94.3	11	PDB header: protein transport Chain: F: PDB Molecule: trwg protein; PDBTitle: crystal structure of the soluble domain of trwg type iv secretion2 machinery from bartonella grahamii
19	c5i97C	Alignment		94.2	10	PDB header: protein transport Chain: C: PDB Molecule: conjugal transfer protein; PDBTitle: structural analysis and inhibition of traE from the pkm101 type iv2 secretion system
20	d3ef8a1	Alignment		94.1	11	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
21	d2rgqa1	Alignment	not modelled	94.1	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
22	c3robC	Alignment	not modelled	93.9	10	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
23	c5ig5E	Alignment	not modelled	93.7	12	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
24	c3k7cC	Alignment	not modelled	93.4	15	PDB header: protein binding Chain: C: PDB Molecule: putative ntf2-like transpeptidase; PDBTitle: crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
25	d2chca1	Alignment	not modelled	93.2	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
26	d2cc3a1	Alignment	not modelled	93.1	11	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
27	d3ebya1	Alignment	not modelled	92.9	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
28	d3ejva1	Alignment	not modelled	92.7	17	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
						PDB header: lyase Chain: A: PDB Molecule: bile acid 7-alpha dehydratase, baie;

29	c4lehA	Alignment	not modelled	92.2	9	PDBTitle: crystal structure of a bile-acid 7-alpha dehydratase (closci_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
30	d3d9ra1	Alignment	not modelled	91.7	14	Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like
31	c3f7sA	Alignment	not modelled	89.1	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
32	c3hx8A	Alignment	not modelled	89.0	14	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
33	c6of9G	Alignment	not modelled	88.9	15	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
34	c5ig4A	Alignment	not modelled	88.5	10	PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
35	d2f86b1	Alignment	not modelled	88.2	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
36	c4gb5A	Alignment	not modelled	87.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from kribbella flavida
37	c4hzbE	Alignment	not modelled	85.9	21	PDB header: hydrolase Chain: E: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
38	c2bhmE	Alignment	not modelled	85.4	14	PDB header: bacterial protein Chain: E: PDB Molecule: type iv secretion system protein virb8; PDBTitle: crystal structure of virb8 from brucella suis
39	c3bb9D	Alignment	not modelled	85.2	11	PDB header: unknown function Chain: D: PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
40	d3b7ca1	Alignment	not modelled	85.0	14	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
41	d2b1xb1	Alignment	not modelled	84.8	8	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
42	c2gbxF	Alignment	not modelled	84.6	12	PDB header: oxidoreductase Chain: F: PDB Molecule: biphenyl 2,3-dioxygenase beta subunit; PDBTitle: crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
43	d2bhma1	Alignment	not modelled	83.4	13	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
44	c3soyA	Alignment	not modelled	82.7	13	PDB header: membrane protein Chain: A: PDB Molecule: ntf2-like superfamily protein; PDBTitle: nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
45	d3blza1	Alignment	not modelled	82.3	18	Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like
46	c4meiA	Alignment	not modelled	81.2	6	PDB header: protein transport Chain: A: PDB Molecule: virb8 protein; PDBTitle: crystal structure of a virb8 type iv secretion system machinery2 soluble domain from bartonella tribocorum
47	c3gwrA	Alignment	not modelled	79.7	9	PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
48	d2r4ia1	Alignment	not modelled	75.9	17	Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like
49	c3ub1C	Alignment	not modelled	75.4	20	PDB header: transport protein Chain: C: PDB Molecule: orf13-like protein; PDBTitle: ntf2 like protein involved in plasmid conjugation
50	d3bb9a1	Alignment	not modelled	72.4	16	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
51	c3dukD	Alignment	not modelled	68.8	17	PDB header: unknown function Chain: D: PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
52	c5ig0A	Alignment	not modelled	68.5	10	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
53	d3cnxa1	Alignment	not modelled	67.8	12	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like
54	c2rsvA	Alignment	not modelled	67.2	14	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein yoeb;

54	c419aA	Alignment	not modelled	67.2	14	PDBTitle: solution structure of iesa, an inhibitor protein of di-endopeptidases2 from bacillus subtilis PDB header: unknown function
55	c3fkaD	Alignment	not modelled	67.0	17	Chain: D: PDB Molecule: uncharacterized ntf-2 like protein; PDBTitle: crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
56	d3e99a1	Alignment	not modelled	66.2	6	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
57	d2owpa1	Alignment	not modelled	58.5	11	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
58	c2qguA	Alignment	not modelled	58.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable signal peptide protein; PDBTitle: three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
59	c4o3vA	Alignment	not modelled	54.3	8	PDB header: protein transport Chain: A: PDB Molecule: virb8-like protein of type iv secretion system; PDBTitle: crystal structure of a virb8-like protein of type iv secretion system2 from rickettsia typhi
60	c5uwaB	Alignment	not modelled	49.4	11	PDB header: transport protein Chain: B: PDB Molecule: probable phospholipid-binding protein mlac; PDBTitle: structure of e. coli phospholipid binding protein mlac
61	c3ke7A	Alignment	not modelled	43.9	14	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution
62	c3kspA	Alignment	not modelled	36.5	7	PDB header: unknown function Chain: A: PDB Molecule: calcium/calmodulin-dependent kinase ii association domain; PDBTitle: crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
63	c4r4gA	Alignment	not modelled	31.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative lipoprotein ycda; PDBTitle: crystal structure of a putative lipoprotein (ycda) from bacillus2 subtilis subsp. subtilis str. 168 at 2.62 a resolution
64	c2ml6A	Alignment	not modelled	31.3	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein zp_02069618.1 from bacteroides uniformis atcc2 8492
65	d1o7nb	Alignment	not modelled	29.8	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
66	c4fczB	Alignment	not modelled	29.7	8	PDB header: transport protein Chain: B: PDB Molecule: toluene-tolerance protein; PDBTitle: crystal structure of toluene-tolerance protein from pseudomonas putida2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
67	c3gzxB	Alignment	not modelled	29.5	5	PDB header: oxidoreductase Chain: B: PDB Molecule: biphenyl dioxygenase subunit beta; PDBTitle: crystal structure of the biphenyl dioxygenase in complex with biphenyl2 from comamonas testosteroni sp. strain b-356
68	c5up5A	Alignment	not modelled	29.1	36	PDB header: de novo protein Chain: A: PDB Molecule: ehee_rd1_0284; PDBTitle: solution structure of the de novo mini protein ehee_rd1_0284
69	c3fsdA	Alignment	not modelled	27.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntf2-like protein of unknown function in nutrient uptake; PDBTitle: crystal structure of ntf2-like protein of unknown function in nutrient2 uptake (yp_427473.1) from rhodospirillum rubrum atcc 11170 at 1.70 a3 resolution
70	c1zeqX	Alignment	not modelled	21.5	5	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
71	c6bjuD	Alignment	not modelled	21.0	14	PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway
72	c1mwuA	Alignment	not modelled	20.9	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: penicillin-binding protein 2a; PDBTitle: structure of methicillin acyl-penicillin binding protein 2a from2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution.
73	c4or1A	Alignment	not modelled	20.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4783 family protein (bacova_04304) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
74	c3j6vl	Alignment	not modelled	20.1	26	PDB header: ribosome Chain: I: PDB Molecule: 28s ribosomal protein s9, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
75	c5ve9C	Alignment	not modelled	19.7	38	PDB header: protein binding Chain: C: PDB Molecule: microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; PDBTitle: structure of hacf7 ef1-ef2-gar domains
76	c4ouqA	Alignment	not modelled	19.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4783 family protein (bf1468) from2 bacteroides fragilis ych46 at 1.55 a resolution
						Fold: Cystatin-like

77	d2bmob1	Alignment	not modelled	19.2	15	Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
78	d1vqqa1	Alignment	not modelled	19.0	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Penicillin binding protein 2a (PBP2A), N-terminal domain
79	d1ulib_	Alignment	not modelled	17.2	4	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
80	c3hzaA_	Alignment	not modelled	17.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 nat12a at 1.40 a resolution
81	c5ts4A_	Alignment	not modelled	16.9	14	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
82	c3efyB_	Alignment	not modelled	16.2	24	PDB header: cell cycle Chain: B: PDB Molecule: cif (cell cycle inhibiting factor); PDBTitle: structure of the cyclomodulin cif from pathogenic2 escherichia coli
83	d1v5ra1	Alignment	not modelled	15.5	33	Fold: N domain of copper amine oxidase-like Superfamily: GAS2 domain-like Family: GAS2 domain
84	c3rgaA_	Alignment	not modelled	15.2	15	PDB header: isomerase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis
85	c6f0kA_	Alignment	not modelled	15.2	21	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
86	d2qxfa1	Alignment	not modelled	15.1	15	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
87	c1xofB_	Alignment	not modelled	13.7	20	PDB header: de novo protein Chain: B: PDB Molecule: bbahett1; PDBTitle: heterooligomeric beta beta alpha miniprotein
88	c2jnzA_	Alignment	not modelled	13.5	17	PDB header: allergen Chain: A: PDB Molecule: phl p 3 allergen; PDBTitle: solution structure of phl p 3, a major allergen from2 timothy grass pollen
89	c2n6uA_	Alignment	not modelled	11.2	36	PDB header: unknown function Chain: A: PDB Molecule: astexin2-dc4; PDBTitle: solution study of astexin2-dc4
90	d2h1ta1	Alignment	not modelled	11.1	13	Fold: Spiral beta-roll Superfamily: PA1994-like Family: PA1994-like
91	c2l55A_	Alignment	not modelled	10.8	0	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
92	c2lyyB_	Alignment	not modelled	9.5	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
93	d1wqlb1	Alignment	not modelled	9.2	5	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
94	c6hwhX_	Alignment	not modelled	8.8	14	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
95	c3r2cJ_	Alignment	not modelled	8.7	15	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
96	c6k4vA_	Alignment	not modelled	8.7	50	PDB header: antibiotic Chain: A: PDB Molecule: smart chimeric peptide g6; PDBTitle: the solution structure of the smart chimeric peptide g6
97	c2ls01_	Alignment	not modelled	8.5	15	PDB header: hydrolase Chain: 1: PDB Molecule: zoocin a endopeptidase; PDB Fragment: unp residues 170-285; PDBTitle: solution structure of the target recognition domain of zoocin a
98	d2nt0a1	Alignment	not modelled	8.0	20	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
99	c4d0uD_	Alignment	not modelled	7.9	50	PDB header: viral protein Chain: D: PDB Molecule: fiber protein; PDBTitle: crystal structure of the fiber head domain of the atadenovirus snake2 adenovirus 1, selenomethionine-derivative