



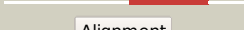






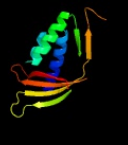
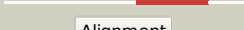






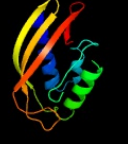













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0176 (-)_207450_208418
Date	Tue Jul 23 14:50:22 BST 2019
Unique Job ID	69af26e9597d060d

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5u9oD_	 Alignment		96.9	10	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	c4i4kB_	 Alignment		96.7	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6
3	d2ux0a1	 Alignment		96.7	8	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
4	c3wz4F_	 Alignment		96.6	6	PDB header: unknown function Chain: F: PDB Molecule: doti; PDBTitle: structure of the periplasmic domain of doti (crystal form i)
5	d1hkxa_	 Alignment		96.5	8	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
6	c5d9rA_	 Alignment		96.4	14	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
7	c5cn1A_	 Alignment		96.1	12	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
8	d2r4ia1	 Alignment		96.0	9	Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like
9	d3d9ra1	 Alignment		96.0	14	Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like
10	c3gzrA_	 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
11	c3a76B_	 Alignment		95.5	9	PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina

12	d3b8la1	Alignment		95.4	8	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
13	c4ovmE	Alignment		95.4	9	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
14	d3ebya1	Alignment		95.3	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
15	c3wz3A	Alignment		95.3	6	PDB header: unknown function Chain: A: PDB Molecule: stram protein; PDBTitle: structure of a periplasmic fragment of tram
16	c3hx8A	Alignment		94.6	11	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
17	d3cu3a1	Alignment		94.5	10	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
18	d2f86b1	Alignment		93.8	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
19	d2rfra1	Alignment		93.7	17	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
20	d1ldpa	Alignment		93.7	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
21	d2rgqa1	Alignment	not modelled	93.3	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
22	d3stda	Alignment	not modelled	93.3	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
23	c3kspA	Alignment	not modelled	93.3	10	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
24	c3h51A	Alignment	not modelled	93.2	13	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
25	d3b7ca1	Alignment	not modelled	93.1	7	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
26	c3robC	Alignment	not modelled	91.7	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
27	c5ig5E	Alignment	not modelled	91.3	11	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
						PDB header: transferase

28	c5ig4A_	Alignment	not modelled	91.2	12	Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
29	d3ejva1	Alignment	not modelled	90.6	9	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
30	c3soyA_	Alignment	not modelled	90.6	11	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
31	d2chca1	Alignment	not modelled	90.5	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
32	c3f7sA_	Alignment	not modelled	90.3	9	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
33	c3fsdA_	Alignment	not modelled	89.4	11	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
34	d3ef8a1	Alignment	not modelled	89.1	8	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
35	d3e99a1	Alignment	not modelled	88.6	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
36	c3bb9D_	Alignment	not modelled	88.1	5	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
37	d2cc3a1	Alignment	not modelled	88.0	13	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
38	c3gwrA_	Alignment	not modelled	87.9	12	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
39	c5ig0A_	Alignment	not modelled	86.6	9	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
40	c4lehA_	Alignment	not modelled	86.3	9	PDB header: lyase Chain: A: PDB Molecule: bile acid 7-alpha dehydratase, baie; PDBTitle: crystal structure of a bile-acid 7-alpha dehydratase (closci_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
41	d3blza1	Alignment	not modelled	85.2	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like
42	d3cnxa1	Alignment	not modelled	85.2	12	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like
43	c3k7cC_	Alignment	not modelled	78.2	8	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
44	c4hzbE_	Alignment	not modelled	78.1	7	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
45	c6of9G_	Alignment	not modelled	75.1	11	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
46	d2owpa1	Alignment	not modelled	72.5	11	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
47	c4gb5A_	Alignment	not modelled	72.3	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from kribbella flavida
48	c4o3vA_	Alignment	not modelled	71.5	12	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
49	c2gbxF_	Alignment	not modelled	70.3	11	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
50	d2bhma1	Alignment	not modelled	70.0	16	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
51	c5i97C_	Alignment	not modelled	68.0	14	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
52	c6bjuD_	Alignment	not modelled	67.0	10	PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the

						atrazine breakdown2 pathway
53	c4nhff_	Alignment	not modelled	65.9	13	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
54	c2bhmE_	Alignment	not modelled	65.5	16	PDB header: bacterial protein Chain: E: PDB Molecule: type iv secretion system protein virb8; PDBTitle: crystal structure of virb8 from brucella suis
55	c3hzpA_	Alignment	not modelled	65.4	21	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 natl2a at 1.40 a resolution
56	d2b1xb1	Alignment	not modelled	63.6	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
57	c2rsxA_	Alignment	not modelled	62.7	21	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein yoeb; PDBTitle: solution structure of isea, an inhibitor protein of dl-endopeptidases2 from bacillus subtilis
58	c4r4gA_	Alignment	not modelled	58.8	28	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
59	d2rcda1	Alignment	not modelled	58.7	8	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
60	c4meiA_	Alignment	not modelled	54.9	4	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
61	c4fczB_	Alignment	not modelled	53.5	13	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
62	c3dukD_	Alignment	not modelled	52.5	25	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
63	c3fkaD_	Alignment	not modelled	48.2	25	PDB header: unknown function 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
64	d1vqqa1	Alignment	not modelled	47.9	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Penicillin binding protein 2a (PBP2A), N-terminal domain
65	c3j6vl_	Alignment	not modelled	45.2	30	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
66	c4ce4i_	Alignment	not modelled	39.2	17	PDB header: ribosome Chain: I: PDB Molecule: mrpl9; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
67	c2qguA_	Alignment	not modelled	37.2	19	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
68	d3bb9a1	Alignment	not modelled	36.2	9	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
69	c2ml6A_	Alignment	not modelled	29.8	29	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
70	c1mwuA_	Alignment	not modelled	24.7	14	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.
71	c4js0B_	Alignment	not modelled	24.7	29	PDB header: signaling protein/signaling protein Chain: B: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: complex of cdc42 with the crib-pr domain of irsp53
72	c5uwaB_	Alignment	not modelled	21.7	9	PDB header: transport protein Chain: B: PDB Molecule: probable phospholipid-binding protein mlac; PDBTitle: structure of e. coli phospholipid binding protein mlac
73	c2voyB_	Alignment	not modelled	21.5	18	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
74	d1t33a1	Alignment	not modelled	19.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
75	c5up5A_	Alignment	not modelled	19.0	29	PDB header: de novo protein Chain: A: PDB Molecule: ehee_rd1_0284; PDBTitle: solution structure of the de novo mini protein ehee_rd1_0284
76	c1t33B_	Alignment	not modelled	16.3	11	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional repressor (tetr/acrr family); PDBTitle: structural genomics, the crystal structure of a putative2

						transcriptional repressor (tetr/carr family) from salmonella3 typhimurim lt2
77	c6gf8B_	Alignment	not modelled	15.9	14	PDB header: cell adhesion Chain: B: PDB Molecule: zona pellucida sperm-binding protein 1,zona pellucida PDBTitle: molecular basis of egg coat filament cross-linking: structure of the2 glycosylated zp1 zp-n1 domain homodimer
78	c3ke7A_	Alignment	not modelled	14.6	9	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
79	c4or1A_	Alignment	not modelled	13.8	15	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
80	d1hywa_	Alignment	not modelled	13.7	29	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
81	c4ouqA_	Alignment	not modelled	13.2	5	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
82	d1ulib_	Alignment	not modelled	12.0	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
83	c3qk9B_	Alignment	not modelled	11.8	16	PDB header: protein transport Chain: B: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: yeast tim44 c-terminal domain complexed with cymal-3
84	c4jgiB_	Alignment	not modelled	11.1	7	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
85	d2gxfa1	Alignment	not modelled	11.1	10	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
86	c2n6uA_	Alignment	not modelled	9.2	29	PDB header: unknown function Chain: A: PDB Molecule: astexin2-dc4; PDBTitle: solution study of astexin2-dc4
87	d2f1la1	Alignment	not modelled	8.9	27	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: RimM C-terminal domain-like
88	c3d00A_	Alignment	not modelled	8.3	12	PDB header: metal binding protein Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit e; PDBTitle: crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
89	c4jcbD_	Alignment	not modelled	8.2	50	PDB header: photosynthesis Chain: D: PDB Molecule: light-harvesting protein b-875 alpha chain; PDBTitle: rc-lh1-pufx dimer complex from rhodobacter sphaeroides
90	c4za6A_	Alignment	not modelled	8.1	10	PDB header: signaling protein Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: structure of the r. erythropolis transcriptional repressor qsdr from2 tetr family
91	d1xk7a1	Alignment	not modelled	7.9	18	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
92	c2pv7B_	Alignment	not modelled	7.8	11	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
93	c5yq72_	Alignment	not modelled	7.7	24	PDB header: photosynthesis Chain: 2: PDB Molecule: beta subunit of light-harvesting 1; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
94	c5yx6D_	Alignment	not modelled	7.3	17	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein rv3272; PDBTitle: crystal structure of rv3272 from m. tuberculosis orthorhombic form
95	c4aq5C_	Alignment	not modelled	7.2	3	PDB header: membrane protein Chain: C: PDB Molecule: acetylcholine receptor delta subunit; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
96	c2bg9C_	Alignment	not modelled	7.2	3	PDB header: ion channel/receptor Chain: C: PDB Molecule: acetylcholine receptor protein, delta chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
97	c1xa3B_	Alignment	not modelled	6.5	16	PDB header: transferase Chain: B: PDB Molecule: crotonobetainyl-coa:carnitine coa-transferase; PDBTitle: crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
98	c5ts4A_	Alignment	not modelled	6.5	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
99	d1xrda1	Alignment	not modelled	6.4	44	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits