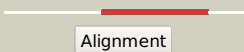

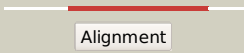



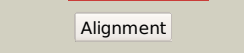



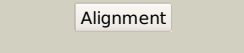

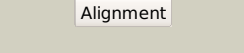



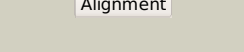

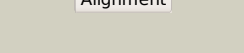

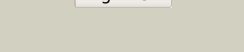



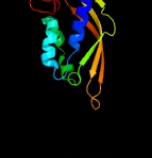


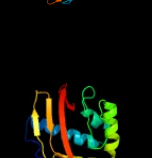


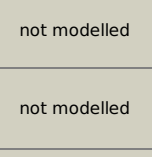


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0177 (-)_208415_208969
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	5f1080f62b59f8e4

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5d9rA_	 Alignment		96.7	15	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
2	d2ux0a1	 Alignment		96.4	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
3	c3a76B_	 Alignment		95.9	8	PDB header: lyase Chain: B; PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina
4	d1hkxa_	 Alignment		95.9	9	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
5	d3ef8a1	 Alignment		95.6	13	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
6	c3wz4F_	 Alignment		95.6	10	PDB header: unknown function Chain: F; PDB Molecule: doti; PDBTitle: structure of the periplasmic domain of doti (crystal form i)
7	d1idpa_	 Alignment		95.4	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
8	d3stda_	 Alignment		95.3	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
9	d2f86b1	 Alignment		95.0	5	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
10	c5ig5E_	 Alignment		94.8	10	PDB header: transferase Chain: E; PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
11	c5ig4A_	 Alignment		94.5	8	PDB header: transferase Chain: A; PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub

12	d3d9ra1	Alignment		94.3	18	Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like
13	c3f7sA	Alignment		94.3	7	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
14	c5cn1A	Alignment		94.0	4	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
15	c5u9oD	Alignment		93.9	8	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
16	d3cu3a1	Alignment		93.7	13	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
17	c4lehA	Alignment		93.6	13	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
18	c3h51A	Alignment		93.4	6	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
19	d3b81a1	Alignment		93.2	15	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
20	d2cc3a1	Alignment		93.2	14	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
21	c3wz3A	Alignment	not modelled	93.0	12	PDB header: unknown function Chain: A: PDB Molecule: tram protein; PDBTitle: structure of a periplasmic fragment of tram
22	c5i97C	Alignment	not modelled	92.8	8	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
23	d3ebya1	Alignment	not modelled	92.7	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
24	c3gzaA	Alignment	not modelled	92.6	13	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
25	d2b1xb1	Alignment	not modelled	92.4	8	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
26	d2rfa1	Alignment	not modelled	92.3	8	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
27	c3robC	Alignment	not modelled	91.6	17	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
28	d3b7ca1	Alignment	not modelled	91.5	9	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like

29	c4ovmE_	Alignment	not modelled	91.4	8	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
30	c4i4kB_	Alignment	not modelled	91.3	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6
31	c4nhfF_	Alignment	not modelled	90.6	9	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
32	d2rgga1	Alignment	not modelled	90.4	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
33	c4gb5A_	Alignment	not modelled	89.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from kribbella flavida
34	c3gwrA_	Alignment	not modelled	87.9	10	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
35	d2r4ia1	Alignment	not modelled	87.8	14	Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like
36	c6of9G_	Alignment	not modelled	87.3	15	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
37	c2rsxA_	Alignment	not modelled	86.9	35	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
38	d2chca1	Alignment	not modelled	86.7	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
39	c3soyA_	Alignment	not modelled	84.9	9	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
40	c2gbxF_	Alignment	not modelled	82.8	13	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
41	c4hzbE_	Alignment	not modelled	82.0	22	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
42	c5ig0A_	Alignment	not modelled	79.4	16	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
43	d3cnxa1	Alignment	not modelled	78.5	12	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like
44	d3ejva1	Alignment	not modelled	76.4	18	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
45	c6bjuD_	Alignment	not modelled	75.5	15	PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway
46	d2owpa1	Alignment	not modelled	70.9	10	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
47	d3bb9a1	Alignment	not modelled	66.2	11	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
48	c4meiA_	Alignment	not modelled	65.7	8	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
49	c4o3vA_	Alignment	not modelled	64.9	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
50	c3bb9D_	Alignment	not modelled	63.8	21	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
51	c2qguA_	Alignment	not modelled	61.6	20	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
52	c2bhmE_	Alignment	not modelled	60.7	11	PDB header: bacterial protein Chain: E: PDB Molecule: type iv secretion system protein virb8; PDBTitle: crystal structure of virb8 from brucella suis
53	c3kspA_	Alignment	not modelled	58.9	16	PDB header: unknown function Chain: A: PDB Molecule: calcium/calmodulin-dependent kinase ii association domain;

53	c3kspA	Alignment	not modelled	58.9	10	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
54	c3hx8A	Alignment	not modelled	56.9	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
55	c3dukD	Alignment	not modelled	56.6	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
56	d2bhma1	Alignment	not modelled	55.9	10	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
57	c5uwaB	Alignment	not modelled	54.4	13	PDB header: transport protein Chain: B: PDB Molecule: probable phospholipid-binding protein mlac; PDBTitle: structure of e. coli phospholipid binding protein mlac
58	c4fczB	Alignment	not modelled	52.7	16	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
59	c3fkaD	Alignment	not modelled	51.4	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
60	d1ulib	Alignment	not modelled	50.0	8	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
61	d3e99a1	Alignment	not modelled	49.6	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
62	c3k7cC	Alignment	not modelled	44.7	9	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
63	c3ke7A	Alignment	not modelled	41.7	20	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
64	c3gzxB	Alignment	not modelled	31.9	11	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
65	c3fsdA	Alignment	not modelled	31.8	9	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
66	c4r4gA	Alignment	not modelled	31.2	15	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
67	d1vqqa1	Alignment	not modelled	29.4	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Penicillin binding protein 2a (PBP2A), N-terminal domain
68	d2cw9a1	Alignment	not modelled	26.3	5	Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like
69	c3qk9B	Alignment	not modelled	24.7	6	PDB header: protein transport Chain: B: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: yeast tim44 c-terminal domain complexed with cymal-3
70	c6f0kA	Alignment	not modelled	23.0	13	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
71	c5ve9C	Alignment	not modelled	22.4	25	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
72	c5up5A	Alignment	not modelled	22.2	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
73	d3blza1	Alignment	not modelled	19.9	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like
74	d1v5ra1	Alignment	not modelled	19.8	25	Fold: N domain of copper amine oxidase-like Superfamily: GAS2 domain-like Family: GAS2 domain
75	c2n6uA	Alignment	not modelled	19.0	29	PDB header: unknown function Chain: A: PDB Molecule: astexin2-dc4; PDBTitle: solution study of astexin2-dc4
76	c4or1A	Alignment	not modelled	18.9	20	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
77	c4ouqA	Alignment	not modelled	18.3	15	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

78	d2rcda1	Alignment	not modelled	15.6	15	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
79	d1wqlb1	Alignment	not modelled	15.2	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
80	c5z1lL_	Alignment	not modelled	14.9	24	PDB header: protein fibril Chain: L: PDB Molecule: flagellin; PDBTitle: cryo-em structure of methanococcus maripaludis archaeum
81	c3r2cj_	Alignment	not modelled	14.7	6	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
82	d2gxfa1	Alignment	not modelled	13.3	11	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
83	c1mwuA_	Alignment	not modelled	12.3	9	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.
84	c5o4uK_	Alignment	not modelled	12.2	22	PDB header: cell adhesion Chain: K: PDB Molecule: flagellin; PDBTitle: the flagellin of pyrococcus furiosus
85	c5tfyl_	Alignment	not modelled	12.1	18	PDB header: cell adhesion Chain: J: PDB Molecule: flagellin; PDBTitle: the archaeal flagellum of methanospirillum hungatei strain jf1.
86	c6hwhX_	Alignment	not modelled	11.2	16	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
87	c3hzpA_	Alignment	not modelled	10.5	9	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
88	c1zeqX_	Alignment	not modelled	10.5	15	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
89	c5ts4A_	Alignment	not modelled	10.1	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
90	c5kzoA_	Alignment	not modelled	10.0	16	PDB header: transcription Chain: A: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated juxtamembrane segment
91	c4irnF_	Alignment	not modelled	9.8	16	PDB header: oxidoreductase Chain: F: PDB Molecule: prolyl-acc dehydrogenase; PDBTitle: crystal structure of the prolyl acyl carrier protein oxidase anab
92	c2mewA_	Alignment	not modelled	9.8	17	PDB header: structural protein Chain: A: PDB Molecule: 30s ribosomal protein s10; PDBTitle: solution structure of nuse (s10) from thermotoga maritima
93	c3gf6B_	Alignment	not modelled	9.0	23	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized bacterial lipoprotein; PDBTitle: crystal structure of a bacterial lipoprotein (bt_1233) from2 bacteroides thetaiotaomicron vpi-5482 at 1.69 a resolution
94	c5zwwA_	Alignment	not modelled	8.9	7	PDB header: gene regulation Chain: A: PDB Molecule: agenet domain-containing protein; PDBTitle: crystal structure of arabidopsis thaliana agdp1 agd34
95	c6hwhB_	Alignment	not modelled	8.7	14	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
96	c1wazA_	Alignment	not modelled	8.5	18	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
97	c2kncA_	Alignment	not modelled	8.3	12	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIiB-beta3 transmembrane-cytoplasmic2 heterocomplex
98	c3efyB_	Alignment	not modelled	7.8	18	PDB header: cell cycle Chain: B: PDB Molecule: cif (cell cycle inhibiting factor); PDBTitle: structure of the cyclomodulin cif from pathogenic2 escherichia coli
99	c1r2jA_	Alignment	not modelled	7.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: protein fkbi; PDBTitle: fkbi for biosynthesis of methoxymalonyl extender unit of fk5202 polyketide immunosuppressant