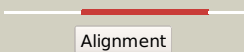

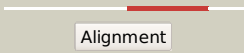



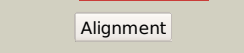



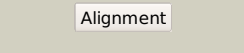

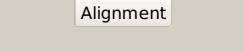



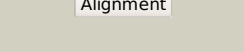

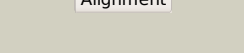

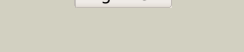



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1972_(-)_2216600_2217175
Date	Mon Aug 5 13:25:07 BST 2019
Unique Job ID	58369188165855c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5cnlA_	 Alignment		97.3	10	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
2	c3a76B_	 Alignment		97.2	15	PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina
3	c5d9rA_	 Alignment		97.2	9	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
4	c3wz4F_	 Alignment		97.1	15	PDB header: unknown function Chain: F: PDB Molecule: doti; PDBTitle: structure of the periplasmic domain of doti (crystal form i)
5	d3b8la1	 Alignment		97.0	15	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
6	d2ux0a1	 Alignment		97.0	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
7	c3wz3A_	 Alignment		96.7	16	PDB header: unknown function Chain: A: PDB Molecule: tram protein; PDBTitle: structure of a periplasmic fragment of tram
8	d3d9ra1	 Alignment		96.6	13	Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like
9	c4i4kB_	 Alignment		96.6	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6
10	d2rfra1	 Alignment		96.6	17	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
11	d1hkxa_	 Alignment		96.5	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A

12	c5u9oD_	Alignment		96.3	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
13	d3stda_	Alignment		96.1	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
14	d3cu3a1	Alignment		96.1	8	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
15	d3ef8a1	Alignment		96.0	13	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
16	c3gza_	Alignment		96.0	8	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
17	c3h51A_	Alignment		95.8	10	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
18	d2f86b1	Alignment		95.7	8	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
19	c3robC_	Alignment		95.7	7	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
20	d1idpa_	Alignment		95.6	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
21	c4ovmE_	Alignment	not modelled	95.5	10	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
22	d3ebya1	Alignment	not modelled	95.4	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
23	d2rgqa1	Alignment	not modelled	95.4	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
24	c5ig4A_	Alignment	not modelled	95.1	11	PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
25	d2chca1	Alignment	not modelled	95.0	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
26	c5ig5E_	Alignment	not modelled	94.9	10	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
27	c4lehA_	Alignment	not modelled	94.8	5	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
28	c4nhff_	Alignment	not modelled	94.7	10	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
29	c4gb5A_	Alignment	not modelled	94.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;

						PDBTitle: crystal structure of kfla4162 protein from krillbella flavida
30	d3b7ca1	Alignment	not modelled	93.8	9	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
31	d2b1xb1	Alignment	not modelled	93.4	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
32	d2cc3a1	Alignment	not modelled	93.2	8	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
33	c5i97C	Alignment	not modelled	93.0	9	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
34	c6of9G	Alignment	not modelled	92.9	9	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
35	c3f7sa	Alignment	not modelled	92.6	11	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
36	d3ejva1	Alignment	not modelled	92.4	19	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
37	c3soyaA	Alignment	not modelled	91.8	7	PDB header: membrane protein Chain: A: PDB Molecule: ntf2-like superfamily protein; PDBTitle: nuclear transport factor 2 (ntf2-like) superfamily protein from 2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
38	c3hx8A	Alignment	not modelled	91.1	11	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (np_103587.1) from 2 mesorhizobium loti at 1.45 a resolution
39	d2bhma1	Alignment	not modelled	90.7	15	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
40	c2bhmE	Alignment	not modelled	89.3	15	PDB header: bacterial protein Chain: E: PDB Molecule: type iv secretion system protein virb8; PDBTitle: crystal structure of virb8 from brucella suis
41	d3blza1	Alignment	not modelled	88.3	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like
42	c2gbxF	Alignment	not modelled	86.7	10	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	d2r4ia1	Alignment	not modelled	86.3	12	Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like
44	c5ig0A	Alignment	not modelled	85.1	14	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
45	c4hzbE	Alignment	not modelled	84.8	12	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
46	c3k7cC	Alignment	not modelled	84.7	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
47	d3cnxa1	Alignment	not modelled	84.6	14	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like
48	c3bb9D	Alignment	not modelled	83.9	15	PDB header: unknown function Chain: D: PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from 2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
49	c4o3vA	Alignment	not modelled	82.0	10	PDB header: protein transport Chain: A: PDB Molecule: virb8-like protein of type iv secretion system2 from rickettsia typhi
50	c4meiA	Alignment	not modelled	80.7	15	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
51	c6bjuD	Alignment	not modelled	79.6	15	PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway
52	c3gwrA	Alignment	not modelled	78.6	13	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
53	d3bb9a1	Alignment	not modelled	78.5	21	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
54	c2gcuA	Alignment	not modelled	76.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable signal peptide protein; PDBTitle: three-dimensional structure of the phospholipid-binding

54	c2qguA	Alignment	not modelled	70.3	23	protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
55	c5uwaB	Alignment	not modelled	75.4	12	PDB header: transport protein Chain: B: PDB Molecule: probable phospholipid-binding protein mlaC; PDBTitle: structure of e. coli phospholipid binding protein mlaC
56	d2owpa1	Alignment	not modelled	73.4	14	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
57	d3e99a1	Alignment	not modelled	72.3	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
58	c2rsxA	Alignment	not modelled	68.2	19	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein yoeb; PDBTitle: solution structure of iese, an inhibitor protein of dl-endopeptidases2 from bacillus subtilis
59	c3ub1C	Alignment	not modelled	67.8	19	PDB header: transport protein Chain: C: PDB Molecule: orf13-like protein; PDBTitle: ntf2 like protein involved in plasmid conjugation
60	c3fsdA	Alignment	not modelled	62.3	13	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
61	c3fkaD	Alignment	not modelled	62.0	17	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
62	c3kspA	Alignment	not modelled	57.1	12	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	c4fczB	Alignment	not modelled	54.2	15	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
64	d1vqa1	Alignment	not modelled	50.7	5	Fold: Cystatin-like Superfamily: NTF2-like Family: Penicillin binding protein 2a (PBP2A), N-terminal domain
65	c3dukD	Alignment	not modelled	47.1	11	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
66	c4ce4i	Alignment	not modelled	45.1	7	PDB header: ribosome Chain: I: PDB Molecule: mrp19; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
67	d2rcda1	Alignment	not modelled	40.7	13	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
68	c4ouqA	Alignment	not modelled	38.4	13	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
69	c4or1A	Alignment	not modelled	36.4	9	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
70	c1mwuA	Alignment	not modelled	33.9	7	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	c3ke7A	Alignment	not modelled	33.5	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
72	c5ve9C	Alignment	not modelled	29.5	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
73	d1v5ra1	Alignment	not modelled	27.7	33	Fold: N domain of copper amine oxidase-like Superfamily: GAS2 domain-like Family: GAS2 domain
74	c4r4gA	Alignment	not modelled	26.8	9	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
75	c6hwhB	Alignment	not modelled	20.7	16	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
76	c2z8nB	Alignment	not modelled	19.6	42	PDB header: lyase Chain: B: PDB Molecule: 27.5 kda virulence protein; PDBTitle: structural basis for the catalytic mechanism of phosphothreonine lyase
77	d1ulib	Alignment	not modelled	19.0	8	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit

78	c5ts4A_	Alignment	not modelled	17.6	19	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
79	c3gzxB_	Alignment	not modelled	17.0	9	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
80	c2n6uA_	Alignment	not modelled	16.9	29	PDB header: unknown function Chain: A: PDB Molecule: astexin2-dc4; PDBTitle: solution study of astexin2-dc4
81	c5up5A_	Alignment	not modelled	16.8	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
82	c3hzpA_	Alignment	not modelled	15.8	10	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
83	d1ciya1	Alignment	not modelled	15.3	21	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
84	c3qk9B_	Alignment	not modelled	13.2	14	PDB header: protein transport Chain: B: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: yeast tim44 c-terminal domain complexed with cymal-3
85	c3i0uA_	Alignment	not modelled	12.0	36	PDB header: lyase Chain: A: PDB Molecule: phosphothreonine lyase ospf; PDBTitle: structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
86	d1wqlb1	Alignment	not modelled	10.8	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
87	c6f0kA_	Alignment	not modelled	10.7	10	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
88	c2pg1J_	Alignment	not modelled	10.5	44	PDB header: structural protein Chain: J: PDB Molecule: cytoplasmic dynein 1 intermediate chain 2; PDBTitle: structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
89	c2pg1L_	Alignment	not modelled	10.5	44	PDB header: structural protein Chain: L: PDB Molecule: cytoplasmic dynein 1 intermediate chain 2; PDBTitle: structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
90	c1zeqX_	Alignment	not modelled	10.5	10	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
91	d1dlca1	Alignment	not modelled	9.9	38	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
92	c1ciyA_	Alignment	not modelled	9.8	21	PDB header: toxin Chain: A: PDB Molecule: cryia(a); PDBTitle: insecticidal toxin: structure and channel formation
93	d1ji6a1	Alignment	not modelled	9.7	15	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
94	c5kpeA_	Alignment	not modelled	9.6	16	PDB header: de novo protein Chain: A: PDB Molecule: de novo beta sheet design protein or664; PDBTitle: solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesh) target or664
95	d2cw9a1	Alignment	not modelled	9.4	10	Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like
96	c1i5pA_	Alignment	not modelled	9.2	18	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry2aa; PDBTitle: insecticidal crystal protein cry2aa
97	d2qxfa1	Alignment	not modelled	8.4	13	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
98	c3efyB_	Alignment	not modelled	8.3	24	PDB header: cell cycle Chain: B: PDB Molecule: cif (cell cycle inhibiting factor); PDBTitle: structure of the cyclomodulin cif from pathogenic2 escherichia coli
99	c6owkA_	Alignment	not modelled	8.0	14	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry1be, cry1k-like protein PDBTitle: crystal structure of a bacillus thuringiensis cry1b.867 tryptic core2 variant