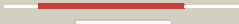



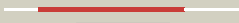
























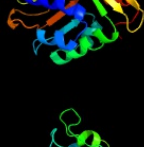
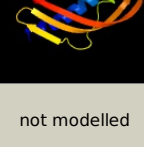


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0762c_(-)_855928_856473
Date	Fri Jul 26 01:50:34 BST 2019
Unique Job ID	3db945a9dd753f3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hx8A_	 Alignment		99.5	18	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
2	c3robC_	 Alignment		99.5	23	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
3	d2gxfa1	 Alignment		99.5	17	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
4	d3d9ra1	 Alignment		99.4	21	Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like
5	c3wmdA_	 Alignment		99.4	15	PDB header: isomerase Chain: A: PDB Molecule: probable monensin biosynthesis isomerase; PDBTitle: crystal structure of epoxide hydrolase monbi
6	c5cxoA_	 Alignment		99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: intriguing role of epoxide hydrolase/cyclase-like enzyme salbiii in2 pyran ring formation in polyether salinomycin
7	c5aigA_	 Alignment		99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: limonene-1,2-epoxide hydrolase; PDBTitle: discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries. tomsk-sample-3 valpromide complex
8	d1s5aa_	 Alignment		99.3	14	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
9	d2a15a1	 Alignment		99.3	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
10	d1oh0a_	 Alignment		99.3	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
11	d3bb9a1	 Alignment		99.2	7	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like

12	d2gexa1	Alignment		99.2	13	Fold: Cystatin-like Superfamily: NTF2-like Family: SnoaL-like polyketide cyclase
13	c3bb9D_	Alignment		99.2	8	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
14	c3b4oB_	Alignment		99.2	9	PDB header: biosynthetic protein Chain: B: PDB Molecule: phenazine biosynthesis protein a/b; PDBTitle: crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
15	c3ff0A_	Alignment		99.2	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: phenazine biosynthesis protein phzb 2; PDBTitle: crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
16	d1ohpa1	Alignment		99.1	21	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
17	c3ke7A_	Alignment		99.1	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
18	c4h3uB_	Alignment		99.1	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein with ketosteroid isomerase-2 like protein fold from catenulispora acidiphila dsm 44928
19	d1nwwa_	Alignment		99.1	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
20	c3soyA_	Alignment		99.1	12	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
21	d3cu3a1	Alignment	not modelled	99.1	12	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
22	c5x9jB_	Alignment	not modelled	99.1	15	PDB header: isomerase Chain: B: PDB Molecule: prhc; PDBTitle: strucutre of prhc from penicillium brasilianum nbrc 6234
23	c5aiiP_	Alignment	not modelled	99.1	21	PDB header: hydrolase Chain: P: PDB Molecule: limonene-1,2-epoxide hydrolase; PDBTitle: discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries.3 ch55-sample-peg complex
24	c3hk4B_	Alignment	not modelled	99.1	11	PDB header: lyase Chain: B: PDB Molecule: mlr7391 protein; PDBTitle: crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
25	c3k0zB_	Alignment	not modelled	99.1	9	PDB header: lyase Chain: B: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
26	c3h3hA_	Alignment	not modelled	99.1	7	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
27	c3msoA_	Alignment	not modelled	99.1	16	PDB header: isomerase Chain: A: PDB Molecule: steroid delta-isomerase; PDBTitle: crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
						Fold: Cystatin-like

28	d3ec9a1	Alignment	not modelled	99.1	15	Superfamily: NTF2-like Family: PhzA/PhzB-like
29	c3i0yC	Alignment	not modelled	99.0	23	PDB header: isomerase Chain: C: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (xcc0381) from <i>Xanthomonas campestris</i> pv. <i>campestris</i> at 1.50 a resolution
30	d3dmca1	Alignment	not modelled	99.0	16	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
31	c3fh1A	Alignment	not modelled	99.0	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (ml8193)2 from <i>Mesorhizobium loti</i> at 1.60 a resolution
32	c3fygB	Alignment	not modelled	99.0	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein (bx_e_b1094) from <i>Burkholderia xenovorans</i> lb400 at 1.59 a resolution
33	c3gzaA	Alignment	not modelled	99.0	17	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 <i>Caulobacter vibrioides</i> at 1.40 a resolution
34	c3f7xA	Alignment	not modelled	99.0	13	PDB header: unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (pp0894) from <i>Pseudomonas putida</i> kt2440 at 1.24 a resolution
35	c4ovmE	Alignment	not modelled	99.0	13	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from <i>Streptomyces carzinostaticus</i>
36	d3dm8a1	Alignment	not modelled	99.0	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
37	d2bnga1	Alignment	not modelled	99.0	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
38	d1z1sa1	Alignment	not modelled	99.0	15	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
39	d2rfra1	Alignment	not modelled	99.0	12	Fold: Cystatin-like Superfamily: NTF2-like Family: BalE/LinA-like
40	c3f8xD	Alignment	not modelled	98.9	18	PDB header: isomerase Chain: D: PDB Molecule: putative delta-5-3-ketosteroid isomerase; PDBTitle: crystal structure of a putative delta-5-3-ketosteroid isomerase2 (eca2236) from <i>Pectobacterium atrosepticum</i> scri1043 at 1.55 a3 resolution
41	d2geya1	Alignment	not modelled	98.9	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
42	c3f7sA	Alignment	not modelled	98.9	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 <i>Pseudomonas putida</i> kt2440 at 2.11 a resolution
43	c6d34B	Alignment	not modelled	98.9	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: terc; PDBTitle: apo crystal structure of terc, a terfestatin biosynthesis enzyme
44	c4lgqa	Alignment	not modelled	98.9	16	PDB header: lyase Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (cv_0247) from <i>Chromobacterium violaceum</i> atcc 12472 at 2.72 a resolution
45	c3h51A	Alignment	not modelled	98.9	18	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 <i>Xanthomonas campestris</i> at 1.70 a resolution
46	c3rgaA	Alignment	not modelled	98.9	13	PDB header: isomerase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis
47	c3f14A	Alignment	not modelled	98.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from <i>Cytophaga hutchinsonii</i> atcc 33406 at 1.45 a3 resolution
48	c3gwrA	Alignment	not modelled	98.9	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 <i>Thiobacillus denitrificans</i> atcc 25259 at 2.00 a resolution
49	c3ff2A	Alignment	not modelled	98.9	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized cystatin fold protein (yp_497570.1) from PDBTitle: crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from <i>Novosphingobium aromaticivorans</i> dsm at 1.90 a3 resolution
50	d2k54a1	Alignment	not modelled	98.9	19	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0742-like
						PDB header: unknown function

51	c1tuhA_	Alignment	not modelled	98.9	16	Chain: A: PDB Molecule: hypothetical protein egc068; PDBTitle: structure of bal32a from a soil-derived mobile gene cassette
52	d1tuha_	Alignment	not modelled	98.9	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette
53	c3f8hA_	Alignment	not modelled	98.9	15	PDB header: unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
54	c1z1sA_	Alignment	not modelled	98.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa3332; PDBTitle: crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
55	d3dxa01	Alignment	not modelled	98.9	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0744-like
56	c5x7IA_	Alignment	not modelled	98.9	16	PDB header: isomerase Chain: A: PDB Molecule: tsrd; PDBTitle: structure of tsrd from streptomyces laurentii
57	d3ebta1	Alignment	not modelled	98.8	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
58	c3f9sB_	Alignment	not modelled	98.8	10	PDB header: lyase Chain: B: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
59	c3g8zA_	Alignment	not modelled	98.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function with cystatin-like fold; PDBTitle: crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
60	c3grdA_	Alignment	not modelled	98.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-superfamily protein; PDBTitle: crystal structure of ntf2-superfamily protein with unknown function2 (np_977240.1) from bacillus cereus atcc 10987 at 1.25 a resolution
61	c3kkGA_	Alignment	not modelled	98.8	14	PDB header: lyase Chain: A: PDB Molecule: putative snoal-like polyketide cyclase; PDBTitle: crystal structure of putative snoal-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
62	d3en8a1	Alignment	not modelled	98.8	18	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
63	c4i4kB_	Alignment	not modelled	98.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6
64	d3b8la1	Alignment	not modelled	98.7	15	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
65	d1m98a2	Alignment	not modelled	98.7	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Orange carotenoid protein, C-terminal domain
66	c5wqhE_	Alignment	not modelled	98.7	13	PDB header: isomerase Chain: E: PDB Molecule: isomerase trt14; PDBTitle: structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d
67	c3a76B_	Alignment	not modelled	98.7	10	PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina
68	d1sjwa_	Alignment	not modelled	98.7	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
69	c6of9G_	Alignment	not modelled	98.7	16	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
70	d1hkxa_	Alignment	not modelled	98.6	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
71	d3b7ca1	Alignment	not modelled	98.6	17	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
72	c3ehcA_	Alignment	not modelled	98.6	14	PDB header: unknown function Chain: A: PDB Molecule: snoal-like polyketide cyclase; PDBTitle: crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
73	c4lmiA_	Alignment	not modelled	98.6	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative ketosteroid isomerase from kribbella2 flavidia dsm 17836
74	d2ux0a1	Alignment	not modelled	98.6	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
75	d3cnxa1	Alignment	not modelled	98.6	18	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like
76	c5x9kA_	Alignment	not modelled	98.6	16	PDB header: isomerase Chain: A: PDB Molecule: austinol synthesis protein h;

						PDBTitle: structre of aush from aspergillus nidulans
77	c5evhA	Alignment	not modelled	98.6	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of known function protein from kribbella flavida dsm2 17836
78	c6fejA	Alignment	not modelled	98.6	17	PDB header: photosynthesis Chain: A: PDB Molecule: all4940 protein; PDBTitle: anabaena apo-c-terminal domain homolog protein
79	d2rgqa1	Alignment	not modelled	98.6	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
80	c3fjJA	Alignment	not modelled	98.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein conserved in bacteria with a PDBTitle: crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
81	d2f86b1	Alignment	not modelled	98.5	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
82	d2f99a1	Alignment	not modelled	98.5	14	Fold: Cystatin-like Superfamily: NTF2-like Family: SnoaL-like polyketide cyclase
83	c5ig4A	Alignment	not modelled	98.5	13	PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
84	c5ig0A	Alignment	not modelled	98.5	10	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
85	d2rcda1	Alignment	not modelled	98.5	16	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
86	c5ig5E	Alignment	not modelled	98.4	11	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
87	c6a5hB	Alignment	not modelled	98.4	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: 101015d; PDBTitle: the structure of [4+2] and [6+4] cyclase in the biosynthetic pathway2 of unidentified natural product
88	d2owpa1	Alignment	not modelled	98.4	8	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
89	c6bjuD	Alignment	not modelled	98.4	9	PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway
90	d3ef8a1	Alignment	not modelled	98.4	13	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
91	c4u13B	Alignment	not modelled	98.3	16	PDB header: transferase Chain: B: PDB Molecule: putative polyketide cyclase sma1630; PDBTitle: crystal structure of putative polyketide cyclase (protein sma1630)2 from sinorhizobium meliloti at 2.3 a resolution
92	d2chca1	Alignment	not modelled	98.3	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
93	c4kvhA	Alignment	not modelled	98.3	15	PDB header: unknown function Chain: A: PDB Molecule: ketosteroid isomerase fold protein hmuk_0747; PDBTitle: crystal structure of ketosteroid isomerase fold protein hmuk_0747
94	d2r4ia1	Alignment	not modelled	98.3	15	Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like
95	c3f40A	Alignment	not modelled	98.3	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution
96	d1ulib	Alignment	not modelled	98.3	7	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
97	c3g0kA	Alignment	not modelled	98.2	13	PDB header: ca-binding protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
98	d1wqlb1	Alignment	not modelled	98.2	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
99	c4lehA	Alignment	not modelled	98.2	8	PDB header: lyase Chain: A: PDB Molecule: bile acid 7-alpha dehydratase, baie; PDBTitle: crystal structure of a bile-acid 7-alpha dehydratase (closi_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
100	c3fsdA	Alignment	not modelled	98.2	17	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
						PDB header: oxidoreductase

101	c3gzxB_	Alignment	not modelled	98.0	12	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
102	d2b1xb1	Alignment	not modelled	98.0	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
103	d3er7a1	Alignment	not modelled	97.9	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Exig0174-like
104	d3ebye1	Alignment	not modelled	97.9	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
105	c3kspA_	Alignment	not modelled	97.9	9	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
106	c4gb5A_	Alignment	not modelled	97.8	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from kribbella flavida
107	c2gbxF_	Alignment	not modelled	97.7	9	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
108	d3e99a1	Alignment	not modelled	97.6	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
109	d3stda_	Alignment	not modelled	97.5	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
110	d3ejva1	Alignment	not modelled	97.5	17	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
111	d1idpa_	Alignment	not modelled	97.3	9	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
112	d3blza1	Alignment	not modelled	97.0	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like
113	d1o7nb_	Alignment	not modelled	97.0	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
114	d2bmob1	Alignment	not modelled	96.9	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
115	c1m98A_	Alignment	not modelled	96.6	18	PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein
116	d1jkqb_	Alignment	not modelled	94.4	15	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
117	d1zo2a1	Alignment	not modelled	92.5	14	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
118	c5xe7A_	Alignment	not modelled	92.1	16	PDB header: dna binding protein Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
119	c3ujmB_	Alignment	not modelled	92.1	15	PDB header: signaling protein Chain: B: PDB Molecule: rasputin; PDBTitle: crystal structure of the ntf2-like domain of the drosophila2 melanogaster rasputin protein
120	d2qiya1	Alignment	not modelled	88.4	15	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like