







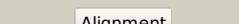


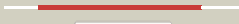



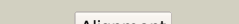













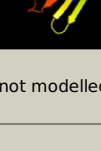


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3472_(-)_3889541_3890047
Date	Fri Aug 9 18:20:14 BST 2019
Unique Job ID	fb45404e140a6944

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2chca1	 Alignment		100.0	99	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
2	d2rgqa1	 Alignment		99.9	24	Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like
3	d3ejva1	 Alignment		99.9	27	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
4	d3ef8a1	 Alignment		99.9	20	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
5	c4lehA_	 Alignment		99.9	20	PDB header: lyase Chain: A: PDB Molecule: bile acid 7-alpha dehydratase, baie; PDBTitle: crystal structure of a bile-acid 7-alpha dehydratase (closj_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
6	d3b8la1	 Alignment		99.9	24	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
7	d2rfra1	 Alignment		99.9	22	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
8	c3a76B_	 Alignment		99.9	18	PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina
9	c4gb5A_	 Alignment		99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from kribbella flavida
10	d3e99a1	 Alignment		99.9	19	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
11	c3gzxB_	 Alignment		99.9	17	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

12	d3ebya1	Alignment		99.9	22	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
13	d3stda_	Alignment		99.9	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
14	d2b1xb1	Alignment		99.9	21	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
15	d1ulib_	Alignment		99.9	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
16	d1idpa_	Alignment		99.9	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase
17	d1wqlb1	Alignment		99.9	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
18	c2qbxF_	Alignment		99.8	15	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
19	c3robC_	Alignment		99.7	15	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	d1o7nb_	Alignment		99.7	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
21	d2bmob1	Alignment	not modelled	99.7	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
22	c3hx8A_	Alignment	not modelled	99.6	19	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
23	c4i4kB_	Alignment	not modelled	99.6	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6
24	d3d9ra1	Alignment	not modelled	99.5	22	Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like
25	c3h51A_	Alignment	not modelled	99.5	19	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
26	d3blza1	Alignment	not modelled	99.5	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like
27	c3gzaA_	Alignment	not modelled	99.5	20	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
						Fold: Cystatin-like

28	d3cxa1	Alignment	not modelled	99.4	14	Superfamily: NTF2-like Family: SAV4671-like
29	c4ovmE	Alignment	not modelled	99.3	15	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
30	d1hkxa	Alignment	not modelled	99.3	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
31	d3cu3a1	Alignment	not modelled	99.3	19	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
32	c3f7sA	Alignment	not modelled	99.3	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
33	d3b7ca1	Alignment	not modelled	99.2	11	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
34	c5ig4A	Alignment	not modelled	99.2	15	PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
35	d2ux0a1	Alignment	not modelled	99.2	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
36	d2r4ia1	Alignment	not modelled	99.2	10	Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like
37	c6of9G	Alignment	not modelled	99.2	16	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
38	c5ig5E	Alignment	not modelled	99.2	11	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
39	c3soyA	Alignment	not modelled	99.2	17	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
40	d2f86b1	Alignment	not modelled	99.1	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
41	c6bjuD	Alignment	not modelled	99.1	12	PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway
42	d2rcda1	Alignment	not modelled	99.1	18	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
43	c5ig0A	Alignment	not modelled	99.1	11	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
44	c3ke7A	Alignment	not modelled	99.0	11	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distansoni atcc 8503 at 1.45 a resolution
45	c3gwrA	Alignment	not modelled	99.0	11	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
46	c3bb9D	Alignment	not modelled	99.0	17	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
47	c3kspA	Alignment	not modelled	99.0	11	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
48	d2gxfa1	Alignment	not modelled	98.9	15	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
49	d3bb9a1	Alignment	not modelled	98.9	17	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
50	d2owpa1	Alignment	not modelled	98.9	16	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
51	c3fsdA	Alignment	not modelled	98.9	16	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: unknown function Chain: D: PDB Molecule: ntf2-like protein of unknown function;

52	c3dukD	Alignment	not modelled	98.9	19	PDBTitle: crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
53	d3en8a1	Alignment	not modelled	98.5	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
54	c5cxoA	Alignment	not modelled	98.5	18	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
55	d1oh0a	Alignment	not modelled	98.3	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
56	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
57	c3wmdA	Alignment	not modelled	98.3	13	PDB header: isomerase Chain: A: PDB Molecule: probable monensin biosynthesis isomerase; PDBTitle: crystal structure of epoxide hydrolase monbi
58	d1ohpa1	Alignment	not modelled	98.3	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
59	c4u13B	Alignment	not modelled	98.3	19	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
60	d1nwwa	Alignment	not modelled	98.3	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
61	c3rgaA	Alignment	not modelled	98.2	23	PDB header: isomerase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis
62	d2a15a1	Alignment	not modelled	98.2	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
63	c3fkaD	Alignment	not modelled	98.2	22	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	d3dmca1	Alignment	not modelled	98.2	11	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
65	d1z1sa1	Alignment	not modelled	98.2	20	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
66	c1z1sa	Alignment	not modelled	98.2	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa3332; PDBTitle: crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
67	c3f8xD	Alignment	not modelled	98.1	14	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 pectobacterium atrosepticum scri1043 at 1.55 a3 resolution
68	c6fejA	Alignment	not modelled	98.1	15	PDB header: photosynthesis Chain: A: PDB Molecule: all4940 protein; PDBTitle: anabaena apo-c-terminal domain homolog protein
69	c3f8hA	Alignment	not modelled	98.1	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
70	c5evhA	Alignment	not modelled	98.0	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of known function protein from kribbella flavida dsm2 17836
71	c3msoA	Alignment	not modelled	98.0	18	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
72	d3ebta1	Alignment	not modelled	98.0	13	Fold: Cystatin-like Superfamily: NTF2-like Family: SnoaL-like polyketide cyclase
73	c3b4oB	Alignment	not modelled	98.0	15	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
74	c5aigA	Alignment	not modelled	98.0	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
75	c5aiiP	Alignment	not modelled	98.0	16	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
76	d2k54a1	Alignment	not modelled	98.0	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0742-like
						PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein;

77	c4h3uB_	Alignment	not modelled	97.9	12	PDBTitle: crystal structure of hypothetical protein with ketosteroid isomerase-2 like protein fold from catenulispora acidiphila dsm 44928
78	c3f14A_	Alignment	not modelled	97.9	13	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 cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
79	d1m98a2	Alignment	not modelled	97.9	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Orange carotenoid protein, C-terminal domain
80	d3dxoa1	Alignment	not modelled	97.9	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0744-like
81	c1tuhA_	Alignment	not modelled	97.9	14	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein egc068; PDBTitle: structure of bal32a from a soil-derived mobile gene cassette
82	d1tuha_	Alignment	not modelled	97.9	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette
83	d1s5aa_	Alignment	not modelled	97.9	17	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
84	d2bnga1	Alignment	not modelled	97.8	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
85	d3ec9a1	Alignment	not modelled	97.8	12	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
86	c3i0yC_	Alignment	not modelled	97.8	14	PDB header: isomerase Chain: C: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
87	c3f7xA_	Alignment	not modelled	97.8	14	PDB header: unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
88	c6d34B_	Alignment	not modelled	97.8	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: terc; PDBTitle: apo crystal structure of terc, a terfestatin biosynthesis enzyme
89	d3dm8a1	Alignment	not modelled	97.8	19	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
90	c3k0zB_	Alignment	not modelled	97.8	21	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
91	c3f40A_	Alignment	not modelled	97.7	11	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
92	c3h3hA_	Alignment	not modelled	97.7	11	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
93	d2geya1	Alignment	not modelled	97.7	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
94	c5x9jB_	Alignment	not modelled	97.7	18	PDB header: isomerase Chain: B: PDB Molecule: prhc; PDBTitle: strcuture of prhc from penicillium brasilianum nbrc 6234
95	c3hk4B_	Alignment	not modelled	97.6	18	PDB header: lyase Chain: B: PDB Molecule: mlr7391 protein; PDBTitle: crystal structure of a snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
96	c6a5hB_	Alignment	not modelled	97.6	15	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
97	c3ff0A_	Alignment	not modelled	97.6	19	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
98	c4lmiA_	Alignment	not modelled	97.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative ketosteroid isomerase from kribbella2 flavida dsm 17836
99	c3fh1A_	Alignment	not modelled	97.6	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
100	c3fgyB_	Alignment	not modelled	97.6	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein (bx_e_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
101	d2f99a1	Alignment	not modelled	97.6	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
						Fold: Cystatin-like

102	d1sjwa_	Alignment	not modelled	97.5	13	Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
103	d2gexa1	Alignment	not modelled	97.5	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
104	c3fijA_	Alignment	not modelled	97.5	14	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
105	c4lqqA_	Alignment	not modelled	97.4	13	PDB header: lyase Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (cv_0247) from2 chromobacterium violaceum atcc 12472 at 2.72 a resolution
106	c5x7lA_	Alignment	not modelled	97.4	19	PDB header: isomerase Chain: A: PDB Molecule: tsrd; PDBTitle: structure of tsrd from streptomyces laurentii
107	c3ff2A_	Alignment	not modelled	97.3	13	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 novosphingobium aromaticivorans dsm at 1.90 a3 resolution
108	c3g8zA_	Alignment	not modelled	97.3	15	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
109	c3f9sB_	Alignment	not modelled	97.1	8	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
110	c3ehcA_	Alignment	not modelled	97.0	8	PDB header: unknown function Chain: A: PDB Molecule: snoal-like polyketide cyclase; PDBTitle: crystal structure of ntf2-superfamily protein with unknown function2 (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
111	c3grdA_	Alignment	not modelled	97.0	10	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
112	d3er7a1	Alignment	not modelled	96.8	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Exig0174-like
113	c1m98A_	Alignment	not modelled	96.5	15	PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein
114	c3g0kA_	Alignment	not modelled	96.2	17	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
115	c5wqhE_	Alignment	not modelled	96.0	8	PDB header: isomerase Chain: E: PDB Molecule: isomerase trt14; PDBTitle: structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d
116	c4y4vB_	Alignment	not modelled	95.9	9	PDB header: hydrolase Chain: B: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd6 in the d-ala-bound state
117	c5x9kA_	Alignment	not modelled	95.8	6	PDB header: isomerase Chain: A: PDB Molecule: austinol synthesis protein h; PDBTitle: strucutre of aush from aspergillus nidulans
118	d1jkqb_	Alignment	not modelled	95.4	15	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
119	d1gy7a_	Alignment	not modelled	94.2	14	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
120	d1gy6a_	Alignment	not modelled	94.1	14	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like