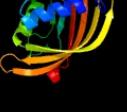
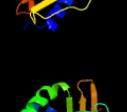
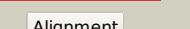
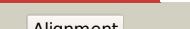
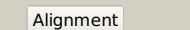
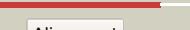
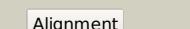
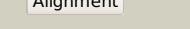
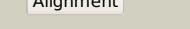
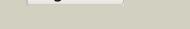
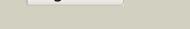
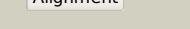
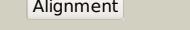
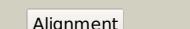
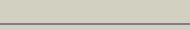
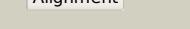


Phyre²

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0760c_(-)_854270_854689 |
| Date | Fri Jul 26 01:50:34 BST 2019 |
| Unique Job ID | e5a184fab950b78a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|----------|--------------------|---|------------|--------|--|
| 1 | d2a15a1 | Alignment |  | 100.0 | 100 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like |
| 2 | c3wmdA_ | Alignment |  | 99.9 | 21 | PDB header: isomerase Chain: A: PDB Molecule: probable monensin biosynthesis isomerase; PDBTitle: crystal structure of epoxide hydrolase monbi |
| 3 | d3dm8a1 | Alignment |  | 99.8 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like |
| 4 | d1oh0a_ | Alignment |  | 99.8 | 20 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like |
| 5 | c5cxoA_ | Alignment |  | 99.8 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: intriguing role of epoxide hydrolase/cyclase-like enzyme salbiiii in2 pyran ring formation in polyether salinomycin |
| 6 | c6d34B_ | Alignment |  | 99.8 | 19 | PDB header: biosynthetic protein Chain: B: PDB Molecule: terc; PDBTitle: apo crystal structure of terc, a terfestatin biosynthesis enzyme |
| 7 | d3ebeta1 | Alignment |  | 99.8 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: SnoAL-like polyketide cyclase |
| 8 | c1tuha_ | Alignment |  | 99.8 | 14 | PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein egc068; PDBTitle: structure of bal32a from a soil-derived mobile gene cassette |
| 9 | d1tuha_ | Alignment |  | 99.8 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette |
| 10 | d1ohpa1 | Alignment |  | 99.8 | 23 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like |
| 11 | d1z1sa1 | Alignment |  | 99.8 | 19 | Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like |

| | | | | | | |
|----|--------------------------|---|---|------|----|--|
| 12 | d3dmca1 |  |  | 99.8 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like |
| 13 | c5aigA |  |  | 99.8 | 17 | 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 |
| 14 | d1s5aa |  |  | 99.8 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like |
| 15 | c1z1sA |  |  | 99.8 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa3332; PDBTitle: crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa |
| 16 | d2bnrga1 |  |  | 99.8 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like |
| 17 | c3rgaA |  |  | 99.8 | 20 | PDB header: isomerase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis |
| 18 | d1nwra |  |  | 99.8 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like |
| 19 | c3fgyB |  |  | 99.8 | 16 | PDB header: unknown function Chain: B: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein (bxe_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution |
| 20 | c3g8za |  |  | 99.8 | 17 | 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 |
| 21 | c3msoA |  | not modelled | 99.8 | 14 | 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 |
| 22 | d3ec9a1 |  | not modelled | 99.8 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like |
| 23 | c4h3ub |  | not modelled | 99.8 | 15 | 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 |
| 24 | c3i0yC |  | not modelled | 99.8 | 20 | 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 |
| 25 | c3b4oB |  | not modelled | 99.7 | 14 | 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 |
| 26 | c3f8hb |  | not modelled | 99.7 | 22 | 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 |
| 27 | c3hk4B |  | not modelled | 99.7 | 19 | 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 PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c3h3hA | Alignment | not modelled | 99.7 | 18 | PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_i0226) from burkholderia thailandensis e264 at 1.60 a3 resolution 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 |
| 29 | c5aiiP | Alignment | not modelled | 99.7 | 25 | 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 |
| 30 | c3f14A | Alignment | not modelled | 99.7 | 15 | Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase |
| 31 | d2f99a1 | Alignment | not modelled | 99.7 | 12 | 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 |
| 32 | c3f7xA | Alignment | not modelled | 99.7 | 19 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (ml18193)2 from mesorhizobium loti at 1.60 a resolution |
| 33 | c3fh1A | Alignment | not modelled | 99.7 | 26 | 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 |
| 34 | c3f8xD | Alignment | not modelled | 99.7 | 18 | 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 |
| 35 | c6a5hB | Alignment | not modelled | 99.7 | 11 | 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 |
| 36 | c3k0zB | Alignment | not modelled | 99.7 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase |
| 37 | d2gexa1 | Alignment | not modelled | 99.7 | 17 | 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 |
| 38 | c3grdA | Alignment | not modelled | 99.7 | 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 |
| 39 | c3ff0A | Alignment | not modelled | 99.7 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like |
| 40 | d3en8a1 | Alignment | not modelled | 99.7 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative ketosteroid isomerase from kribbella2 flava dsm 17836 |
| 41 | c4lmiA | Alignment | not modelled | 99.7 | 19 | Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0742-like |
| 42 | d2k54a1 | Alignment | not modelled | 99.7 | 15 | PDB header: isomerase Chain: B: PDB Molecule: prhc; PDBTitle: strucuture of prhc from penicillium brasiliannum nbrc 6234 |
| 43 | c5x9jB | Alignment | not modelled | 99.7 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0744-like |
| 44 | d3dxoa1 | Alignment | not modelled | 99.7 | 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_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution |
| 45 | c3f40A | Alignment | not modelled | 99.7 | 12 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of known function protein from kribbella flava dsm2 17836 |
| 46 | c5evhA | Alignment | not modelled | 99.7 | 18 | Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase |
| 47 | d1sjwa | Alignment | not modelled | 99.7 | 13 | PDB header: lyase Chain: B: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc 1.76 a resolution |
| 48 | c3f9sB | Alignment | not modelled | 99.7 | 11 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized cystatin fold protein (yp_497570.1) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution |
| 49 | c3ff2A | Alignment | not modelled | 99.7 | 13 | PDB header: lyase Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution |
| 50 | c4lgqA | Alignment | not modelled | 99.7 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: putative polyketide cyclase |
| 51 | d2geya1 | Alignment | not modelled | 99.6 | 10 | PDB header: unknown function |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 52 | c4kvhA | Alignment | not modelled | 99.6 | 16 | Chain: A: PDB Molecule: ketosteroid isomerase fold protein hmuk_0747; PDBTitle: crystal structure of ketosteroid isomerase fold protein hmuk_0747 |
| 53 | c3fljA | Alignment | not modelled | 99.6 | 17 | 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 |
| 54 | c5wqhE | Alignment | not modelled | 99.6 | 10 | PDB header: isomerase Chain: E: PDB Molecule: isomerase trt14; PDBTitle: structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d |
| 55 | c3kkgA | Alignment | not modelled | 99.6 | 15 | 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 |
| 56 | c4u13B | Alignment | not modelled | 99.6 | 17 | 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 |
| 57 | c5x7IA | Alignment | not modelled | 99.6 | 9 | PDB header: isomerase Chain: A: PDB Molecule: tsrd; PDBTitle: structure of tsrd from streptomyces laurentii |
| 58 | c5x9kA | Alignment | not modelled | 99.6 | 11 | PDB header: isomerase Chain: A: PDB Molecule: austinol synthesis protein h; PDBTitle: strucutre of aush from aspergillus nidulans |
| 59 | d1m98a2 | Alignment | not modelled | 99.5 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: Orange carotenoid protein, C-terminal domain |
| 60 | c3ehcA | Alignment | not modelled | 99.5 | 11 | 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 |
| 61 | c3ke7A | Alignment | not modelled | 99.5 | 13 | 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 |
| 62 | c6fejA | Alignment | not modelled | 99.4 | 16 | PDB header: photosynthesis Chain: A: PDB Molecule: all4940 protein; PDBTitle: anabaena apo-c-terminal domain homolog protein |
| 63 | c3g0kA | Alignment | not modelled | 99.4 | 15 | 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 |
| 64 | d3er7a1 | Alignment | not modelled | 99.1 | 15 | Fold: Cystatin-like Superfamily: NTF2-like Family: Exig0174-like |
| 65 | c3hx8A | Alignment | not modelled | 99.0 | 15 | 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 |
| 66 | c3g16A | Alignment | not modelled | 99.0 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein with cystatin-like fold; PDBTitle: crystal structure of protein of unknown function with cystatin-like2 fold (yp_001022489.1) from methylobium petroleophilum pm1 at 1.45 a3 resolution |
| 67 | c3h51A | Alignment | not modelled | 98.9 | 15 | 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 |
| 68 | d3cnxa1 | Alignment | not modelled | 98.9 | 15 | Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like |
| 69 | c3robC | Alignment | not modelled | 98.9 | 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 |
| 70 | c3gwrA | Alignment | not modelled | 98.8 | 18 | 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 |
| 71 | c1m98A | Alignment | not modelled | 98.8 | 17 | PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein |
| 72 | c3f7sA | Alignment | not modelled | 98.7 | 18 | 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 |
| 73 | d3d9ra1 | Alignment | not modelled | 98.7 | 15 | Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like |
| 74 | d2gxfa1 | Alignment | not modelled | 98.7 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like |
| | | | | | | Fold: Cystatin-like |

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|-----|---------|-----------|--------------|------|----|--|
| 75 | d3cu3a1 | Alignment | not modelled | 98.6 | 13 | Superfamily: NTF2-like Family: BaiE/LinA-like |
| 76 | d3bb9a1 | Alignment | not modelled | 98.6 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like |
| 77 | c3bb9D_ | Alignment | not modelled | 98.5 | 15 | 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 |
| 78 | d2owpa1 | Alignment | not modelled | 98.5 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like |
| 79 | d2ux0a1 | Alignment | not modelled | 98.5 | 11 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 80 | d2rcda1 | Alignment | not modelled | 98.5 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like |
| 81 | d1hkxa_ | Alignment | not modelled | 98.4 | 11 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 82 | c4ovmE_ | Alignment | not modelled | 98.4 | 17 | PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus |
| 83 | d3b7ca1 | Alignment | not modelled | 98.4 | 7 | Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like |
| 84 | c5ig0A_ | Alignment | not modelled | 98.4 | 14 | PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub |
| 85 | d2rgqa1 | Alignment | not modelled | 98.4 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like |
| 86 | c5ig4A_ | Alignment | not modelled | 98.3 | 13 | PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub |
| 87 | c6of9G_ | Alignment | not modelled | 98.3 | 12 | PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydamonas reinhardtii camkii hub homology domain |
| 88 | d2chca1 | Alignment | not modelled | 98.3 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like |
| 89 | d3b8la1 | Alignment | not modelled | 98.3 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 90 | c5xe7A_ | Alignment | not modelled | 98.3 | 12 | 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 |
| 91 | c3soyA_ | Alignment | not modelled | 98.3 | 13 | 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 |
| 92 | c3gzrA_ | Alignment | not modelled | 98.2 | 9 | 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 |
| 93 | 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 |
| 94 | c4i4kB_ | Alignment | not modelled | 98.2 | 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 |
| 95 | d2rfra1 | Alignment | not modelled | 98.2 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 96 | d3ejva1 | Alignment | not modelled | 98.2 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 97 | d2r4ia1 | Alignment | not modelled | 98.2 | 18 | Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like |
| 98 | c3gzxB_ | Alignment | not modelled | 98.1 | 15 | 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 |
| 99 | d2f86b1 | Alignment | not modelled | 98.1 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 100 | d2imja1 | Alignment | not modelled | 98.1 | 16 | Fold: Cystatin-like Superfamily: NTF2-like |

| | | | | | Family: PFL3262-like |
|-----|-------------------------|-----------|--------------|------|---|
| 101 | d3ebya1 | Alignment | not modelled | 97.9 | 14 Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 102 | c5ig5E | Alignment | not modelled | 97.9 | 13 PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2 |
| 103 | c6bjuD | Alignment | not modelled | 97.9 | 11 PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway |
| 104 | c4lehA | Alignment | not modelled | 97.9 | 11 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 |
| 105 | d1wqlb1 | Alignment | not modelled | 97.9 | 15 Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 106 | c3kspA | Alignment | not modelled | 97.7 | 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 |
| 107 | c3lygA | Alignment | not modelled | 97.6 | 15 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 function2 (yp_270605.1) from colwellia psychrerythraea 34h at 1.61 a resolution |
| 108 | c3a76B | Alignment | not modelled | 97.6 | 9 PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina |
| 109 | d3blza1 | Alignment | not modelled | 97.6 | 4 Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like |
| 110 | d3ef8a1 | Alignment | not modelled | 97.6 | 14 Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 111 | d1ulib | Alignment | not modelled | 97.6 | 7 Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 112 | c4gb5A | Alignment | not modelled | 97.4 | 13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from kribbella flava |
| 113 | c2gbxF | Alignment | not modelled | 97.4 | 11 PDB header: oxidoreductase Chain: F: PDB Molecule: biphenyl 2,3-dioxygenase beta subunit; PDBTitle: crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyaе b1 bound to biphenyl |
| 114 | d3e99a1 | Alignment | not modelled | 97.4 | 10 Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 115 | d3stda | Alignment | not modelled | 97.4 | 9 Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase |
| 116 | d1idpa | Alignment | not modelled | 97.3 | 9 Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase |
| 117 | d2b1xb1 | Alignment | not modelled | 97.0 | 16 Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 118 | c5tgnA | Alignment | not modelled | 96.9 | 25 PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein sthe_2403 from sphaerobacter thermophilus |
| 119 | c3dukD | Alignment | not modelled | 96.7 | 7 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 |
| 120 | c5tpjA | Alignment | not modelled | 96.5 | 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 |