
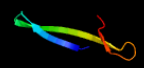
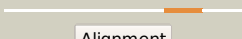

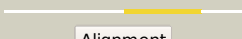








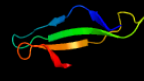


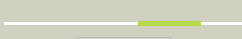








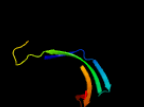

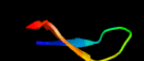





Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2116_(lppK)_2376579_2377148 |
| Date | Mon Aug 5 13:25:23 BST 2019 |
| Unique Job ID | ba247782895a4edb |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c2rsxA_ |  Alignment |  | 92.6 | 19 | PDB header: hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein yoeb; PDBTitle: solution structure of izea, an inhibitor protein of dl-endopeptidases2 from bacillus subtilis |
| 2 | c3k7cC_ |  Alignment |  | 86.8 | 9 | PDB header: protein binding Chain: C: PDB Molecule: putative ntf2-like transpeptidase; PDBTitle: crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution |
| 3 | c3dukD_ |  Alignment |  | 79.5 | 17 | PDB header: unknown function Chain: D: PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution |
| 4 | d3blza1 |  Alignment |  | 77.0 | 20 | Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like |
| 5 | c3robC_ |  Alignment |  | 75.3 | 10 | 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 |
| 6 | c3fkaD_ |  Alignment |  | 73.3 | 14 | 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 |
| 7 | c4hzbE_ |  Alignment |  | 72.8 | 14 | 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 |
| 8 | c4ovmE_ |  Alignment |  | 68.8 | 7 | PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus |
| 9 | c4i4kB_ |  Alignment |  | 68.7 | 10 | 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 | c4lehA_ |  Alignment |  | 65.5 | 4 | 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 |
| 11 | d3ebya1 |  Alignment |  | 65.3 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|--|
| 12 | d3cu3a1 | Alignment |  | 62.0 | 7 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 13 | d2owpa1 | Alignment |  | 61.3 | 8 | Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like |
| 14 | d3b8la1 | Alignment |  | 57.9 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 15 | d3ef8a1 | Alignment |  | 55.2 | 18 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 16 | c3bb9D_ | Alignment |  | 53.5 | 8 | PDB header: unknown function Chain: D: PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from <i>Shewanella frigidimarina</i> ncbi 400 at 1.80 Å resolution |
| 17 | c4gb5A_ | Alignment |  | 51.6 | 46 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from <i>Kribbella flavida</i> |
| 18 | c3a76B_ | Alignment |  | 51.0 | 16 | PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina |
| 19 | c4iffC_ | Alignment |  | 51.0 | 27 | PDB header: cell cycle Chain: C: PDB Molecule: fusion of phage phi29 gp7 protein and cell division protein PDBTitle: structural organization of ftsb, a transmembrane protein of the bacterial divisome |
| 20 | d3bb9a1 | Alignment |  | 50.4 | 9 | Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like |
| 21 | c1nohB_ | Alignment | not modelled | 49.8 | 27 | PDB header: viral protein Chain: B: PDB Molecule: head morphogenesis protein; PDBTitle: the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly |
| 22 | d2chca1 | Alignment | not modelled | 48.7 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like |
| 23 | d2rgga1 | Alignment | not modelled | 48.5 | 15 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like |
| 24 | c5ig4A_ | Alignment | not modelled | 45.5 | 12 | PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of <i>N. vectensis</i> camkii-a hub |
| 25 | d3eipa_ | Alignment | not modelled | 45.2 | 22 | Fold: FKBP-like Superfamily: Colicin E3 immunity protein Family: Colicin E3 immunity protein |
| 26 | c3ub1C_ | Alignment | not modelled | 42.5 | 10 | PDB header: transport protein Chain: C: PDB Molecule: orf13-like protein; PDBTitle: ntf2 like protein involved in plasmid conjugation |
| 27 | d2rcda1 | Alignment | not modelled | 39.8 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like |
| 28 | d2rfra1 | Alignment | not modelled | 39.8 | 29 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 29 | c6hiuD | Alignment | not modelled | 39.1 | 10 | PDB header: unknown function Chain: D: PDB Molecule: atzh; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c0jjuB | Alignment | not modelled | 39.1 | 10 | PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin-dependent protein kinase type |
| 30 | c3gwrA | Alignment | not modelled | 39.0 | 10 | PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thioobacillus3 denitrificans atcc 25259 at 2.00 a resolution |
| 31 | d3b7ca1 | Alignment | not modelled | 37.5 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like |
| 32 | d1hkxa | Alignment | not modelled | 35.4 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 33 | c3hx8A | Alignment | not modelled | 29.0 | 13 | 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 |
| 34 | d1ulib | Alignment | not modelled | 28.9 | 15 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 35 | c5lfiA | Alignment | not modelled | 28.9 | 12 | PDB header: immune system Chain: A: PDB Molecule: lactococcin-a immunity protein; PDBTitle: lactococcin a immunity protein |
| 36 | d1xdpa1 | Alignment | not modelled | 27.2 | 26 | Fold: Spectrin repeat-like Superfamily: PPK N-terminal domain-like Family: PPK N-terminal domain-like |
| 37 | d3e99a1 | Alignment | not modelled | 26.9 | 0 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 38 | d2o8ra1 | Alignment | not modelled | 26.0 | 26 | Fold: Spectrin repeat-like Superfamily: PPK N-terminal domain-like Family: PPK N-terminal domain-like |
| 39 | c3mtuE | Alignment | not modelled | 25.7 | 30 | PDB header: contractile protein Chain: E: PDB Molecule: capsid assembly scaffolding protein,tropomyosin alpha-1 PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle |
| 40 | d3d9ra1 | Alignment | not modelled | 25.5 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like |
| 41 | c3f7sA | Alignment | not modelled | 24.6 | 7 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution |
| 42 | d2ux0a1 | Alignment | not modelled | 23.7 | 11 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 43 | d1ldpa | Alignment | not modelled | 23.6 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase |
| 44 | c3fsdA | Alignment | not modelled | 22.5 | 14 | 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 |
| 45 | c3kspA | Alignment | not modelled | 21.6 | 20 | 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 |
| 46 | d3ejva1 | Alignment | not modelled | 20.5 | 11 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 47 | c3ke7A | Alignment | not modelled | 19.5 | 5 | PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distazonis atcc 8503 at 1.45 a resolution |
| 48 | c3gzrA | Alignment | not modelled | 19.5 | 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 |
| 49 | c2gbxF | Alignment | not modelled | 19.0 | 4 | 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 |
| 50 | c5d9rA | Alignment | not modelled | 18.9 | 33 | 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 |
| 51 | c3h51A | Alignment | not modelled | 18.2 | 9 | 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 |
| | | | | | | Fold: Cystatin-like |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 52 | d3stda_ | Alignment | not modelled | 17.4 | 6 | Superfamily: NTF2-like Family: Scytalone dehydratase |
| 53 | c5wlgA_ | Alignment | not modelled | 17.0 | 27 | PDB header: motor protein Chain: A: PDB Molecule: capsid assembly scaffolding protein,myosin-7,microtubule- PDBTitle: crystal structure of amino acids 1677-1755 of human beta cardiac2 myosin fused to gp7 and eb1 |
| 54 | c5uwaB_ | Alignment | not modelled | 15.8 | 20 | PDB header: transport protein Chain: B: PDB Molecule: probable phospholipid-binding protein mlac; PDBTitle: structure of e. coli phospholipid binding protein mlac |
| 55 | c1e0tD_ | Alignment | not modelled | 15.0 | 26 | PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase |
| 56 | c5hsbA_ | Alignment | not modelled | 14.3 | 13 | PDB header: transcription Chain: A: PDB Molecule: rna polymerase; PDBTitle: andes virus endonuclease |
| 57 | c4qpoB_ | Alignment | not modelled | 14.3 | 60 | PDB header: transcription Chain: B: PDB Molecule: relaxosome protein tram; PDBTitle: mechanistic basis of plasmid-specific dna binding of the f plasmid2 regulatory protein, tram |
| 58 | d3cnxa1 | Alignment | not modelled | 14.2 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like |
| 59 | d1e0ta2 | Alignment | not modelled | 14.0 | 26 | Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase |
| 60 | c4fczB_ | Alignment | not modelled | 13.2 | 18 | 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 |
| 61 | c4c1oA_ | Alignment | not modelled | 13.2 | 44 | PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase; PDBTitle: geobacillus thermoglucosidasius gh family 52 xylosidase |
| 62 | d1bh9a_ | Alignment | not modelled | 12.2 | 22 | Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs |
| 63 | c5u9oD_ | Alignment | not modelled | 11.9 | 8 | PDB header: cell cycle Chain: D: PDB Molecule: plastid division protein cdp1, chloroplastic,plastid PDBTitle: cocrystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1 |
| 64 | c2jq5A_ | Alignment | not modelled | 11.6 | 9 | PDB header: structural genomics Chain: A: PDB Molecule: sec-c motif; PDBTitle: solution structure of rpa3114, a sec-c motif containing protein from2 rhodopseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097 |
| 65 | d2r4ia1 | Alignment | not modelled | 11.5 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like |
| 66 | c5n02B_ | Alignment | not modelled | 11.0 | 33 | PDB header: lyase Chain: B: PDB Molecule: glutaconate coa-transferase family, subunit b; PDBTitle: crystal structure of the decarboxylase aiba/aibb c56s variant |
| 67 | d1dp3a_ | Alignment | not modelled | 10.4 | 50 | Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: DNA-binding domain (fragment?) of the TraM protein |
| 68 | d2f86b1 | Alignment | not modelled | 9.5 | 6 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 69 | c2n5dA_ | Alignment | not modelled | 9.0 | 27 | PDB header: protein binding Chain: A: PDB Molecule: fusion protein of two pks domains; PDBTitle: nmr structure of pks domains |
| 70 | c3omyB_ | Alignment | not modelled | 9.0 | 50 | PDB header: dna binding protein Chain: B: PDB Molecule: protein tram; PDBTitle: crystal structure of the ped208 tram n-terminal domain |
| 71 | d2gqba1 | Alignment | not modelled | 8.8 | 7 | Fold: RPA2825-like Superfamily: RPA2825-like Family: RPA2825-like |
| 72 | c5ig5E_ | Alignment | not modelled | 8.5 | 14 | PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2 |
| 73 | c2xgyA_ | Alignment | not modelled | 8.3 | 20 | PDB header: viral protein/isomerase Chain: A: PDB Molecule: relik capsid n-terminal domain; PDBTitle: complex of rabbit endogenous lentivirus (relik)capsid with2 cyclophilin a |
| 74 | c6mzIS_ | Alignment | not modelled | 7.6 | 23 | PDB header: transcription Chain: S: PDB Molecule: transcription initiation factor tfiid subunit 13; PDBTitle: human tfiid canonical state |
| 75 | d1jkea_ | Alignment | not modelled | 7.4 | 27 | Fold: DTD-like Superfamily: DTD-like Family: DTD-like |
| 76 | c2oI5B_ | Alignment | not modelled | 7.4 | 18 | PDB header: transcription regulator Chain: B: PDB Molecule: pai 2 protein; PDBTitle: crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearotherophilus |
| 77 | d1vqqa1 | Alianment | not modelled | 7.4 | 15 | Fold: Cystatin-like Superfamily: NTF2-like |

| | | | | Family: Penicillin binding protein 2a (PBP2A), N-terminal domain | |
|----|-------------------------|-----------|--------------|---|--|
| 78 | c5xmB_ | Alignment | not modelled | 7.3 | 14 PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pknI; PDBTitle: monomer form of m.tuberculosis pknI sensor domain |
| 79 | d1gp6a_ | Alignment | not modelled | 7.3 | 12 Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like |
| 80 | d1j7ga_ | Alignment | not modelled | 7.2 | 18 Fold: DTD-like Superfamily: DTD-like Family: DTD-like |
| 81 | c3l6tB_ | Alignment | not modelled | 7.0 | 19 PDB header: hydrolase Chain: B: PDB Molecule: mobilization protein trai; PDBTitle: crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain |
| 82 | d2fp7b1 | Alignment | not modelled | 6.6 | 30 Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases |
| 83 | c2mdaB_ | Alignment | not modelled | 6.0 | 15 PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase |
| 84 | c6rdvP_ | Alignment | not modelled | 5.9 | 19 PDB header: proton transport Chain: P: PDB Molecule: mitochondrial atp synthase subunit oscp; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 focussed refinement of f1 head and rotor |
| 85 | d1e8qa_ | Alignment | not modelled | 5.8 | 27 Fold: Cellulose docking domain, docking Superfamily: Cellulose docking domain, docking Family: Cellulose docking domain, docking |
| 86 | d2auna1 | Alignment | not modelled | 5.6 | 13 Fold: The "swivelling" beta/beta/alpha domain Superfamily: LD-carboxypeptidase A C-terminal domain-like Family: LD-carboxypeptidase A C-terminal domain-like |
| 87 | c4kdwA_ | Alignment | not modelled | 5.5 | 16 PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of a bacterial immunoglobulin-like domain from the2 m. primoryensis ice-binding adhesin |
| 88 | d1lfoa_ | Alignment | not modelled | 5.5 | 33 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like |
| 89 | c3d0fA_ | Alignment | not modelled | 5.4 | 40 PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718 |
| 90 | c6of9G_ | Alignment | not modelled | 5.4 | 14 PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain |
| 91 | c3zmnA_ | Alignment | not modelled | 5.4 | 17 PDB header: viral protein Chain: A: PDB Molecule: vp17; PDBTitle: vp17, a capsid protein of bacteriophage p23-77 |
| 92 | c3onjA_ | Alignment | not modelled | 5.3 | 19 PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain |
| 93 | d2ftba1 | Alignment | not modelled | 5.2 | 45 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like |