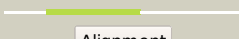

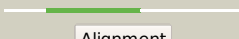

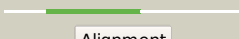
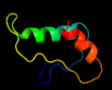







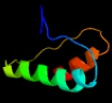
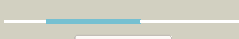

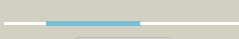
















Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0395 (-) _474943_475347 |
| Date | Tue Jul 23 14:50:46 BST 2019 |
| Unique Job ID | dff7f8b4043cba10 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2f7IA_ |  Alignment |  | 66.0 | 9 | PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase |
| 2 | c3pdkB_ |  Alignment |  | 54.7 | 15 | PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis |
| 3 | c1c4gB_ |  Alignment |  | 54.4 | 11 | PDB header: transferase Chain: B: PDB Molecule: protein (alpha-d-glucose 1-phosphate phosphoglucomutase); PDBTitle: phosphoglucomutase vanadate based transition state analog complex |
| 4 | c1kfiA_ |  Alignment |  | 52.9 | 14 | PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase 1; PDBTitle: crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium |
| 5 | d1kfiA1 |  Alignment |  | 42.5 | 11 | Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains |
| 6 | c6gyzB_ |  Alignment |  | 42.0 | 17 | PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus |
| 7 | c4hjhA_ |  Alignment |  | 36.8 | 15 | PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: iodide sad phased crystal structure of a phosphoglucomutase from2 brucella melitensis complexed with glucose-6-phosphate |
| 8 | c5bmpA_ |  Alignment |  | 35.6 | 22 | PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate |
| 9 | c2z0fA_ |  Alignment |  | 34.5 | 19 | PDB header: isomerase Chain: A: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8 |
| 10 | c1wqaB_ |  Alignment |  | 32.7 | 20 | PDB header: isomerase Chain: B: PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+ |
| 11 | d1p5dx1 |  Alignment |  | 30.5 | 15 | Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|--|
| 12 | c5n4cG_ | Alignment |  | 28.0 | 39 | PDB header: hydrolase Chain: G: PDB Molecule: alpha-amanitin proprotein; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 35mer2 hydrolysis and macrocyclization substrate - s577a mutant |
| 13 | c2fuvB_ | Alignment |  | 26.1 | 20 | PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium. |
| 14 | d3pma1 | Alignment |  | 22.3 | 11 | Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains |
| 15 | c2gamA_ | Alignment |  | 21.4 | 23 | PDB header: transferase Chain: A: PDB Molecule: beta-1,6-n-acetylglucosaminyltransferase; PDBTitle: x-ray crystal structure of murine leukocyte-type core 2 b1,6-n-2 acetylglucosaminyltransferase (c2gnt-l) in complex with galb1,3galnac |
| 16 | c3uw2A_ | Alignment |  | 20.5 | 13 | PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase/phosphomannomutase family protein; PDBTitle: x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_i1489)from burkholderia thailandensis |
| 17 | c1tuoA_ | Alignment |  | 20.2 | 17 | PDB header: biosynthetic protein Chain: A: PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8 |
| 18 | c3c04A_ | Alignment |  | 16.7 | 15 | PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa |
| 19 | c3nybA_ | Alignment |  | 14.4 | 38 | PDB header: transferase/rna binding protein Chain: A: PDB Molecule: poly(a) rna polymerase protein 2; PDBTitle: structure and function of the polymerase core of tramp, a rna2 surveillance complex |
| 20 | c3djca_ | Alignment |  | 14.3 | 26 | PDB header: transferase Chain: A: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of pantothenate kinase from legionella pneumophila |
| 21 | d2phpa1 | Alignment | not modelled | 13.0 | 20 | Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: Phosphomethylpyrimidine kinase C-terminal domain-like |
| 22 | c3bf1C_ | Alignment | not modelled | 12.2 | 23 | PDB header: transferase Chain: C: PDB Molecule: type iii pantothenate kinase; PDBTitle: type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp |
| 23 | c3i3wB_ | Alignment | not modelled | 12.2 | 11 | PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis |
| 24 | c4ev1A_ | Alignment | not modelled | 10.5 | 26 | PDB header: chaperone Chain: A: PDB Molecule: anabena tic22; PDBTitle: anabaena tic22 (protein transport) |
| 25 | d2otaa1 | Alignment | not modelled | 9.7 | 29 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |
| 26 | c2f9tB_ | Alignment | not modelled | 9.5 | 32 | PDB header: transferase Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the type iii coaa from pseudomonas aeruginosa |
| 27 | c5uazB_ | Alignment | not modelled | 9.0 | 44 | PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin |
| 28 | c2l61A_ | Alignment | not modelled | 8.8 | 58 | PDB header: metal binding protein Chain: A: PDB Molecule: ec protein i/ii; PDBTitle: protein and metal cluster structure of the wheat metallothionein2 domain g-ec-1. the second part of the puzzle. |
| | | | | | | Fold: Ribonuclease H-like motif |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|---|
| 29 | d2e1za1 | Alignment | not modelled | 8.5 | 23 | Superfamily: Actin-like ATPase domain Family: Acetokinase-like |
| 30 | c5fk0F_ | Alignment | not modelled | 8.2 | 47 | PDB header: structural protein Chain: F: PDB Molecule: coatomer subunit delta; PDBTitle: yeast delta-cop-i mu-homology domain |
| 31 | c4o8qA_ | Alignment | not modelled | 8.1 | 50 | PDB header: protein transport Chain: A: PDB Molecule: coatomer subunit delta; PDBTitle: crystal structure of bovine mhd domain of the cop1 delta subunit at 2.15 a resolution |
| 32 | c2l62A_ | Alignment | not modelled | 8.1 | 58 | PDB header: metal binding protein Chain: A: PDB Molecule: ec protein i/ii; PDBTitle: protein and metal cluster structure of the wheat metallothionein2 domain g-ec-1. the second part of the puzzle. |
| 33 | c2q2eA_ | Alignment | not modelled | 8.0 | 27 | PDB header: isomerase Chain: A: PDB Molecule: type ii dna topoisomerase vi subunit a; PDBTitle: crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei |
| 34 | c2qn5B_ | Alignment | not modelled | 7.6 | 67 | PDB header: hydrolase inhibitor/hydrolase Chain: B: PDB Molecule: bowman-birk type bran trypsin inhibitor; PDBTitle: crystal structure and functional study of the bowman-birk2 inhibitor from rice bran in complex with bovine trypsin |
| 35 | c5wmmB_ | Alignment | not modelled | 7.6 | 27 | PDB header: biosynthetic protein Chain: B: PDB Molecule: mbth homologue; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios |
| 36 | c5h1nB_ | Alignment | not modelled | 7.2 | 33 | PDB header: unknown function Chain: B: PDB Molecule: upf0253 protein yaep; PDBTitle: crystal structure of sf173 from shigella flexneri |
| 37 | d2j7ja2 | Alignment | not modelled | 7.2 | 53 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 38 | c6cegA_ | Alignment | not modelled | 7.1 | 75 | PDB header: toxin Chain: A: PDB Molecule: conotoxin movib; PDBTitle: solution nmr structure of the omega conotoxin movib from conus moncuri |
| 39 | c2mfpA_ | Alignment | not modelled | 6.8 | 58 | PDB header: metal binding protein Chain: A: PDB Molecule: ec protein i/ii; PDBTitle: solution structure of the circular g-domain analog from the wheat2 metallothionein ec-1 |
| 40 | c4o8kB_ | Alignment | not modelled | 6.6 | 19 | PDB header: transferase Chain: B: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of type iii pantothenate kinase from burkholderia2 thailandensis, apo structure |
| 41 | c4ebaH_ | Alignment | not modelled | 6.6 | 50 | PDB header: structural protein/rna binding protein Chain: H: PDB Molecule: rna15; PDBTitle: crystal structure of the rna14-rna15 complex |
| 42 | d2juza1 | Alignment | not modelled | 6.6 | 38 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |
| 43 | c5ja1B_ | Alignment | not modelled | 6.3 | 18 | PDB header: ligase Chain: B: PDB Molecule: enterobactin biosynthesis protein ybdz; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 mbth-like protein ybdz |
| 44 | c6ce1A_ | Alignment | not modelled | 6.1 | 42 | PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-3; PDBTitle: crystal structure of peptidyl arginine deiminase type iii (padi3) |
| 45 | d1d3ya_ | Alignment | not modelled | 6.0 | 30 | Fold: DNA topoisomerase IV, alpha subunit Superfamily: DNA topoisomerase IV, alpha subunit Family: DNA topoisomerase IV, alpha subunit |
| 46 | d2gpfa1 | Alignment | not modelled | 5.8 | 23 | Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like |
| 47 | c4uoiB_ | Alignment | not modelled | 5.7 | 80 | PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: unexpected structure for the n-terminal domain of hepatitis c virus2 envelope glycoprotein e1 |
| 48 | c3fm3B_ | Alignment | not modelled | 5.6 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase 2; PDBTitle: crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2 |
| 49 | d2pstx1 | Alignment | not modelled | 5.5 | 23 | Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like |
| 50 | d1g0da4 | Alignment | not modelled | 5.5 | 25 | Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core |
| 51 | d2p06a1 | Alignment | not modelled | 5.1 | 43 | Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: AF0060-like |
| 52 | c2p06A_ | Alignment | not modelled | 5.1 | 43 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af_0060; PDBTitle: crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304 |
| 53 | c5u89B_ | Alignment | not modelled | 5.1 | 18 | PDB header: hydrolase/inhibitor Chain: B: PDB Molecule: mbth domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dhbf |