

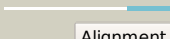

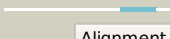



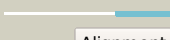




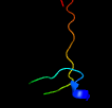



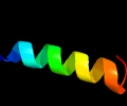



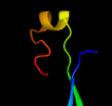

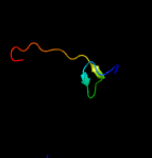
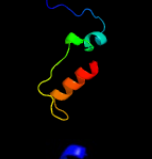

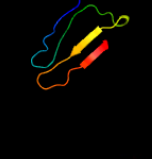


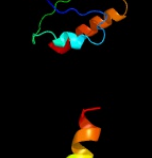
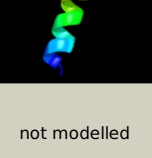


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0789c_(-)_883454_884053 |
| Date | Fri Jul 26 01:50:37 BST 2019 |
| Unique Job ID | 581211a59fdd0fc5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3f5dA_ |  Alignment |  | 39.9 | 16 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis |
| 2 | c3c4rC_ |  Alignment |  | 37.8 | 28 | PDB header: structural genomics, unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein encoded by2 cryptic prophage |
| 3 | d2bosa_ |  Alignment |  | 35.7 | 52 | Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits |
| 4 | d2fb5a1 |  Alignment |  | 34.8 | 27 | Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like |
| 5 | d2auna2 |  Alignment |  | 31.3 | 20 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like |
| 6 | c3n7tA_ |  Alignment |  | 28.2 | 10 | PDB header: protein binding Chain: A; PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis |
| 7 | c4rv7C_ |  Alignment |  | 26.2 | 27 | PDB header: transferase Chain: C; PDB Molecule: diadenylate cyclase; PDBTitle: characterization of an essential diadenylate cyclase |
| 8 | c4lruA_ |  Alignment |  | 23.1 | 12 | PDB header: lyase Chain: A; PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans |
| 9 | c1tr1B_ |  Alignment |  | 22.8 | 35 | PDB header: hydrolase (metalloprotease) Chain: B; PDB Molecule: thermolysin fragment 255 - 316; PDBTitle: nmr solution structure of the c-terminal fragment 255-3162 of thermolysin: a dimer formed by subunits having the3 native structure |
| 10 | c3kk1A_ |  Alignment |  | 22.2 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae |
| 11 | d1r4pb_ |  Alignment |  | 21.4 | 48 | Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|---|
| 12 | d1gq2a2 | Alignment |  | 20.5 | 19 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain |
| 13 | c6gyyB_ | Alignment |  | 18.9 | 19 | PDB header: transferase Chain: B: PDB Molecule: diadenylate cyclase; PDBTitle: crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant |
| 14 | c3gdfA_ | Alignment |  | 18.1 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable nadp-dependent mannitol dehydrogenase; PDBTitle: crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum. |
| 15 | d1d1da1 | Alignment |  | 13.2 | 43 | Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain |
| 16 | c3hj8A_ | Alignment |  | 11.8 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: catechol 1,2-dioxygenase; PDBTitle: crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol |
| 17 | d2j0wa1 | Alignment |  | 10.8 | 47 | Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like |
| 18 | d1zl0a2 | Alignment |  | 9.1 | 20 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like |
| 19 | d1pj3a2 | Alignment |  | 9.1 | 22 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain |
| 20 | d2cdqa1 | Alignment |  | 9.0 | 47 | Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like |
| 21 | c4o0lA_ | Alignment | not modelled | 8.7 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-dependent 3-quinuclidinone reductase; PDBTitle: crystal structure of nadph-dependent 3-quinuclidinone reductase from2 rhodotorula rubra |
| 22 | c3lyhB_ | Alignment | not modelled | 8.7 | 20 | PDB header: lyase Chain: B: PDB Molecule: cobalamin (vitamin b12) biosynthesis cbix protein; PDBTitle: crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution |
| 23 | c3up8B_ | Alignment | not modelled | 8.1 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase b; PDBTitle: crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b |
| 24 | d1xqla_ | Alignment | not modelled | 8.1 | 25 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 25 | d1c4qa_ | Alignment | not modelled | 8.1 | 48 | Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits |
| 26 | d1jba2 | Alignment | not modelled | 7.9 | 40 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains |
| 27 | d2bura1 | Alignment | not modelled | 7.8 | 25 | Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase |
| | | | | | | Fold: Aminoacid dehydrogenase-like, N-terminal domain |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|-----|--|
| 28 | d1o0sa2 | Alignment | not modelled | 7.7 | 23 | Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain |
| 29 | d2hmfal | Alignment | not modelled | 7.2 | 37 | Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like |
| 30 | c5xftA | Alignment | not modelled | 7.1 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: dehydroascorbate reductase; PDBTitle: crystal structure of chlamydomonas reinhardtii dehydroascorbate2 reductase |
| 31 | c6hauA | Alignment | not modelled | 6.4 | 15 | PDB header: rna binding protein Chain: A: PDB Molecule: mrna export factor icp27 homolog; PDBTitle: kshv pan rna mta-response element fragment complexed with the globular2 domain of herpesvirus saimiri orf57 |
| 32 | c3c1nA | Alignment | not modelled | 6.3 | 37 | PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine |
| 33 | c2azqA | Alignment | not modelled | 6.3 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: catechol 1,2-dioxygenase; PDBTitle: crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1 |
| 34 | c2hsiB | Alignment | not modelled | 6.3 | 48 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium |
| 35 | c1vw46 | Alignment | not modelled | 6.2 | 14 | PDB header: ribosome Chain: 6: PDB Molecule: 54s ribosomal protein l17, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit |
| 36 | d1g0wa1 | Alignment | not modelled | 6.2 | 28 | Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain |
| 37 | c5ou5C | Alignment | not modelled | 6.2 | 18 | PDB header: photosynthesis Chain: C: PDB Molecule: malic enzyme; PDBTitle: crystal structure of maize chloroplastic photosynthetic nadp(+)-2 dependent malic enzyme |
| 38 | c2j0wA | Alignment | not modelled | 5.9 | 47 | PDB header: transferase Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state) |
| 39 | d1zq1c1 | Alignment | not modelled | 5.9 | 35 | Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like |
| 40 | c5zb3B | Alignment | not modelled | 5.9 | 15 | PDB header: transcription Chain: B: PDB Molecule: orf57; PDBTitle: dimeric crystal structure of orf57 from kshv |
| 41 | c4z1mj | Alignment | not modelled | 5.8 | 86 | PDB header: hydrolase Chain: J: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: bovine f1-atpase inhibited by three copies of the inhibitor protein2 if1 crystallised in the presence of thiophosphate. |
| 42 | d1s68a | Alignment | not modelled | 5.6 | 14 | Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: RNA ligase |
| 43 | d2jb0b1 | Alignment | not modelled | 5.6 | 36 | Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif |
| 44 | c2aw5A | Alignment | not modelled | 5.5 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependant malic enzyme; PDBTitle: crystal structure of a human malic enzyme |
| 45 | c5vg2B | Alignment | not modelled | 5.4 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: intradial ring-cleavage dioxygenase; PDBTitle: intradiol ring-cleavage dioxygenase from tetranychus urticae |
| 46 | c4uhpA | Alignment | not modelled | 5.4 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex |
| 47 | c3pl0B | Alignment | not modelled | 5.4 | 26 | PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution |
| 48 | c3ty8A | Alignment | not modelled | 5.3 | 22 | PDB header: transferase Chain: A: PDB Molecule: polynucleotide 2',3'-cyclic phosphate phosphodiesterase / PDBTitle: crystal structure of c. thermocellum pnkp ligase domain apo form |
| 49 | c4tt3j | Alignment | not modelled | 5.2 | 86 | PDB header: hydrolase Chain: J: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: the pathway of binding of the intrinsically disordered mitochondrial2 inhibitor protein to f1-atpase |
| 50 | c1xofA | Alignment | not modelled | 5.1 | 100 | PDB header: de novo protein Chain: A: PDB Molecule: bbahett1; PDBTitle: heterooligomeric beta beta alpha miniprotein |
| 51 | c2jesG | Alignment | not modelled | 5.1 | 29 | PDB header: viral protein Chain: G: PDB Molecule: portal protein; PDBTitle: portal protein (gp6) from bacteriophage spp1 |
| 52 | c1fwxB | Alignment | not modelled | 5.1 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans |
| 53 | c2boyC | Alignment | not modelled | 5.1 | 19 | PDB header: oxidoreductase Chain: C: PDB Molecule: 3-chlorocatechol 1,2-dioxygenase; PDBTitle: crystal structure of 3-chlorocatechol 1,2-dioxygenase from rhodococcus2 opacus 1cp |