




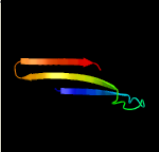

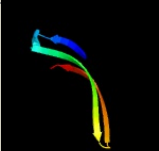





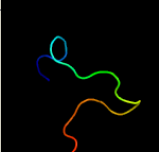



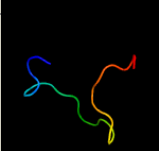



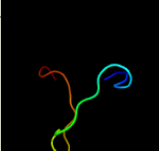
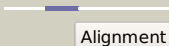
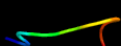
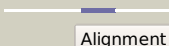




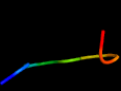
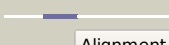
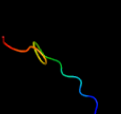
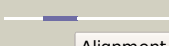






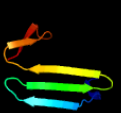
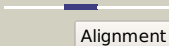
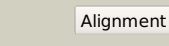
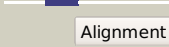
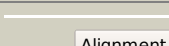
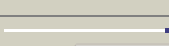
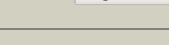
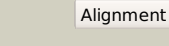
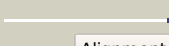


Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0999_(-)_1115771_1116529 |
| Date | Wed Jul 31 22:05:06 BST 2019 |
| Unique Job ID | aefa88ccd87a2986 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4tmdA |  Alignment |  | 100.0 | 58 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: x-ray structure of putative uncharacterized protein (rv0999 ortholog)2 from mycobacterium smegmatis |
| 2 | c4h69A |  Alignment |  | 49.6 | 33 | PDB header: isomerase Chain: A: PDB Molecule: allene oxide cyclase; PDBTitle: crystal structure of the allene oxide cyclase 2 from physcomitrella2 patens complexed with substrate analog |
| 3 | d1zvca1 |  Alignment |  | 48.2 | 29 | Fold: AOC barrel-like Superfamily: Allene oxide cyclase-like Family: Allene oxide cyclase-like |
| 4 | d2brja1 |  Alignment |  | 25.7 | 25 | Fold: AOC barrel-like Superfamily: Allene oxide cyclase-like Family: Allene oxide cyclase-like |
| 5 | c2dzqA |  Alignment |  | 17.0 | 30 | PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna |
| 6 | c2ed2A |  Alignment |  | 16.4 | 17 | PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna |
| 7 | c2dn4A |  Alignment |  | 16.2 | 17 | PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna |
| 8 | c2d99A |  Alignment |  | 16.2 | 30 | PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna |
| 9 | d1q60a |  Alignment |  | 16.2 | 26 | Fold: GTF2I-like repeat Superfamily: GTF2I-like repeat Family: GTF2I-like repeat |
| 10 | c2dn5A |  Alignment |  | 15.4 | 26 | PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna |
| 11 | c2ejeA |  Alignment |  | 14.8 | 30 | PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna |

| | | | | | | |
|----|--------------------------|---|---|------|----|--|
| 12 | c1af7A_ |  |  | 14.4 | 33 | PDB header: methyltransferase Chain: A: PDB Molecule: chemotaxis receptor methyltransferase cher; PDBTitle: cher from salmonella typhimurium |
| 13 | c2e3lA_ |  |  | 14.1 | 22 | PDB header: transcription Chain: A: PDB Molecule: transcription factor gtf2ird2 beta; PDBTitle: solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna |
| 14 | c2dztA_ |  |  | 14.1 | 26 | PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna |
| 15 | c5xlyA_ |  |  | 12.7 | 56 | PDB header: transferase Chain: A: PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of cher1 in complex with c-di-gmp-bound mapz |
| 16 | c5mz6l_ |  |  | 12.1 | 27 | PDB header: cell cycle Chain: 1: PDB Molecule: separase; PDBTitle: cryo-em structure of a separase-securin complex from caenorhabditis2 elegans at 3.8 a resolution |
| 17 | c5u1sA_ |  |  | 11.3 | 50 | PDB header: hydrolase Chain: A: PDB Molecule: separin; PDBTitle: crystal structure of the saccharomyces cerevisiae separase-securin2 complex at 3.0 angstrom resolution |
| 18 | c2m9lA_ |  |  | 10.6 | 67 | PDB header: toxin Chain: A: PDB Molecule: beta-theraphotoxin-tp1a; PDBTitle: solution structure of protoxin-1 |
| 19 | c2yuuvA_ |  |  | 10.5 | 11 | PDB header: cell adhesion Chain: A: PDB Molecule: myosin-binding protein c, slow-type; PDBTitle: solution structure of 2nd immunoglobulin domain of slow2 type myosin-binding protein c |
| 20 | c6nu9A_ |  |  | 9.7 | 22 | PDB header: viral protein Chain: A: PDB Molecule: zinc-binding non-structural protein; PDBTitle: crystal structure of a zinc-binding non-structural protein from the2 hepatitis e virus |
| 21 | d1wmhb_ |  | not modelled | 9.7 | 25 | Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain |
| 22 | c3ldlA_ |  | not modelled | 8.7 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: replicase polyprotein 1a; PDBTitle: crystal structure of ibv nsp2a |
| 23 | c5ftwA_ |  | not modelled | 8.4 | 50 | PDB header: transferase Chain: A: PDB Molecule: chemotaxis protein methyltransferase; PDBTitle: crystal structure of glutamate o-methyltransferase in2 complex with s- adenosyl-l-homocysteine (sah) from3 bacillus subtilis |
| 24 | c3nuhB_ |  | not modelled | 7.7 | 32 | PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function |
| 25 | c2fvnA_ |  | not modelled | 7.3 | 24 | PDB header: cell adhesion Chain: A: PDB Molecule: protein afad; PDBTitle: the fibrillar tip complex of the afa/dr adhesins from2 pathogen e. coli displays synergistic binding to 5 1 and v3 3 integrins |
| 26 | c3zrhA_ |  | not modelled | 7.3 | 32 | PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin thioesterase zranb1; PDBTitle: crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd) |
| 27 | c4phxE_ |  | not modelled | 7.1 | 22 | PDB header: cell adhesion Chain: E: PDB Molecule: protein aggb; PDBTitle: crystal structure of aggb, the minor subunit of aggregative adherence2 fimbriae type i from the escherichia coli o4h104 |
| 28 | c2ehdB_ |  | not modelled | 6.5 | 6 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family; |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| | | | | | | PDBTitle: crystal structure analysis of oxidoreductase |
| 29 | c5fc2A_ | Alignment | not modelled | 6.0 | 63 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: pamk, peptide containing a phospho-serine; PDBTitle: structure of a separase in complex with a pamk peptide containing a2 phospho-serine |
| 30 | c4bm5A_ | Alignment | not modelled | 5.9 | 28 | PDB header: protein transport Chain: A: PDB Molecule: similar to chloroplast inner membrane protein tic110; PDBTitle: chloroplast inner membrane protein tic110 |
| 31 | c2myxA_ | Alignment | not modelled | 5.9 | 12 | PDB header: ubiquitin-binding protein Chain: A: PDB Molecule: coupling of ubiquitin conjugation to er degradation protein PDBTitle: structure of the cue domain of yeast cue1 |
| 32 | c5sujB_ | Alignment | not modelled | 5.8 | 19 | PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg2148 from legionella2 pneumophila |
| 33 | c2jf1A_ | Alignment | not modelled | 5.7 | 25 | PDB header: cell adhesion Chain: A: PDB Molecule: filamin-a; PDBTitle: crystal structure of the filamin a repeat 21 complexed with2 the integrin beta2 cytoplasmic tail peptide |
| 34 | d1te1b_ | Alignment | not modelled | 5.3 | 27 | Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12 |
| 35 | c2vulA_ | Alignment | not modelled | 5.2 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: gh11 xylanase; PDBTitle: thermostable mutant of environmentally isolated gh112 xylanase |