

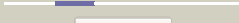
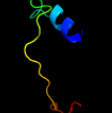

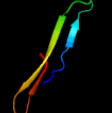

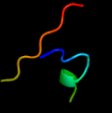





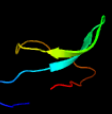

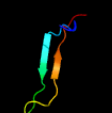



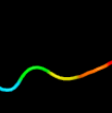


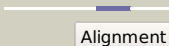
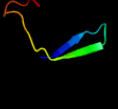
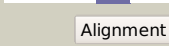
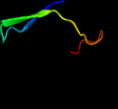

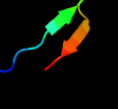

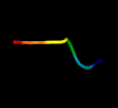
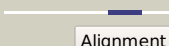

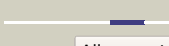
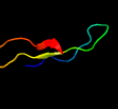


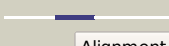
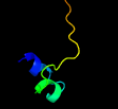

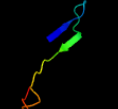
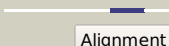
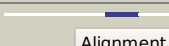
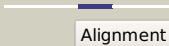


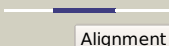
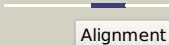



Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0448c (-) _536507_537172 |
| Date | Tue Jul 23 14:50:52 BST 2019 |
| Unique Job ID | 3651a83fc730acd9 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | d1wspa1 |  Alignment |  | 32.4 | 17 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: DIX domain |
| 2 | c2vycA_ |  Alignment |  | 18.7 | 11 | PDB header: lyase Chain: A: PDB Molecule: biodegradative arginine decarboxylase; PDBTitle: crystal structure of acid induced arginine decarboxylase2 from e. coli |
| 3 | c4xhfD_ |  Alignment |  | 17.9 | 21 | PDB header: oxidoreductase Chain: D: PDB Molecule: na-translocating nadh-quinone reductase subunit c nqrc; PDBTitle: crystal structure of shewanella oneidensis nqrc |
| 4 | c6cn0B_ |  Alignment |  | 17.1 | 35 | PDB header: transferase Chain: B: PDB Molecule: 16s rrna (guanine(1405)-n(7))-methyltransferase; PDBTitle: 2.95 angstrom crystal structure of 16s rrna methylase from proteus2 mirabilis |
| 5 | c3l20A_ |  Alignment |  | 13.9 | 8 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from staphylococcus aureus |
| 6 | d1wxma1 |  Alignment |  | 13.0 | 28 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD |
| 7 | c3pz7A_ |  Alignment |  | 12.7 | 10 | PDB header: signaling protein Chain: A: PDB Molecule: dixin; PDBTitle: crystal structure of ccd1-dix domain |
| 8 | c4e8uA_ |  Alignment |  | 12.0 | 20 | PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein t8p19.180; PDBTitle: crystal structure of arabidopsis idn2 xs domain along with a small2 segment of adjacent coiled-coil region |
| 9 | d1jg1a_ |  Alignment |  | 11.8 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 10 | c2mxqA_ |  Alignment |  | 11.6 | 50 | PDB header: antimicrobial protein Chain: A: PDB Molecule: paneth cell-specific alpha-defensin 1; PDBTitle: the solution structure of defa1, a highly potent antimicrobial peptide2 from the horse |
| 11 | d2cs7a1 |  Alignment |  | 10.8 | 67 | Fold: !L8-like Superfamily: PhtA domain-like Family: PhtA domain-like |

| | | | | | | |
|----|-------------------------|---|---|------|----|---|
| 12 | c2jn4A_ |  |  | 10.7 | 25 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein fixu, nift; PDBTitle: solution nmr structure of protein rp4601 from rhodospseudomonas2 palustris. northeast structural genomics consortium target rpt2;3 ontario center for structural proteomics target rp4601. |
| 13 | d2jn4a1 |  |  | 10.7 | 25 | Fold: NifT/FixU barrel-like Superfamily: NifT/FixU-like Family: NifT/FixU |
| 14 | c2wshC_ |  |  | 10.6 | 7 | PDB header: hydrolase Chain: C: PDB Molecule: endonuclease ii; PDBTitle: structure of bacteriophage t4 endoii e118a mutant |
| 15 | c6cslA_ |  |  | 10.0 | 50 | PDB header: metal binding protein Chain: A: PDB Molecule: histidine triad protein d; PDBTitle: pneumococcal phtd protein 269-339 fragment with bound zn(ii) |
| 16 | d1u7ia_ |  |  | 9.9 | 12 | Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase |
| 17 | c3bt3B_ |  |  | 9.4 | 12 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: glyoxalase-related enzyme, arac type; PDBTitle: crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans |
| 18 | c5kkmA_ |  |  | 9.4 | 57 | PDB header: unknown function Chain: A: PDB Molecule: o2_contryphan_vc1 prepropeptide; PDBTitle: con-vc11-22 |
| 19 | c1c4kA_ |  |  | 9.2 | 14 | PDB header: lyase Chain: A: PDB Molecule: protein (ornithine decarboxylase); PDBTitle: ornithine decarboxylase mutant (gly121tyr) |
| 20 | c3vg8F_ |  |  | 9.0 | 32 | PDB header: unknown function Chain: F: PDB Molecule: hypothetical protein tthb210; PDBTitle: crystal structure of hypothetical protein tthb210 from thermus2 thermophilus hb8 |
| 21 | d1u6ia_ |  | not modelled | 8.9 | 8 | Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase |
| 22 | c6eiwD_ |  | not modelled | 8.8 | 29 | PDB header: virus Chain: D: PDB Molecule: minor capsid protein micp; PDBTitle: sacbrood virus of honeybee empty particle |
| 23 | d2foka1 |  | not modelled | 8.5 | 42 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain |
| 24 | d1e32a3 |  | not modelled | 8.5 | 27 | Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like |
| 25 | d1m1ha2 |  | not modelled | 8.2 | 15 | Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain Family: N-utilization substance G protein NusG, N-terminal domain |
| 26 | c4pv3D_ |  | not modelled | 8.1 | 19 | PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with na+ cations |
| 27 | c1kriA_ |  | not modelled | 8.1 | 18 | PDB header: viral protein Chain: A: PDB Molecule: vp4; PDBTitle: nmr solution structures of the rhesus rotavirus vp4 sialic acid2 binding domain without ligand |
| 28 | d1kqra_ |  | not modelled | 8.1 | 18 | Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: vp4 sialic acid binding domain |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 29 | c6eh1D | Alignment | not modelled | 8.1 | 29 | PDB header: virus Chain: D: PDB Molecule: minor capsid protein micp; PDBTitle: sacbrood virus of honeybee - expansion state ii |
| 30 | c6egvD | Alignment | not modelled | 8.1 | 29 | PDB header: virus Chain: D: PDB Molecule: minor capsid protein micp; PDBTitle: sacbrood virus of honeybee |
| 31 | c5oypD | Alignment | not modelled | 8.1 | 29 | PDB header: virus Chain: D: PDB Molecule: minor capsid protein micp; PDBTitle: sacbrood virus of honeybee |
| 32 | c5lsfD | Alignment | not modelled | 8.1 | 29 | PDB header: virus Chain: D: PDB Molecule: vp4; PDBTitle: sacbrood honeybee virus |
| 33 | c6egxD | Alignment | not modelled | 8.1 | 29 | PDB header: virus Chain: D: PDB Molecule: minor capsid protein micp; PDBTitle: sacbrood virus of honeybee - expansion state i |
| 34 | c2aenH | Alignment | not modelled | 7.9 | 18 | PDB header: viral protein Chain: H: PDB Molecule: outer capsid protein vp4, vp8* core; PDBTitle: crystal structure of the rotavirus strain ds-1 vp8* core |
| 35 | c3wz3A | Alignment | not modelled | 7.8 | 19 | PDB header: unknown function Chain: A: PDB Molecule: tram protein; PDBTitle: structure of a periplasmic fragment of tram |
| 36 | d1mqea | Alignment | not modelled | 7.8 | 2 | Fold: Nudix Superfamily: Nudix Family: MutT-like |
| 37 | c3oqhB | Alignment | not modelled | 7.7 | 50 | PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein yvmc; PDBTitle: crystal structure of b. licheniformis cdps yvmc-blic |
| 38 | d1qhva | Alignment | not modelled | 7.6 | 26 | Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain |
| 39 | d1dt9a3 | Alignment | not modelled | 7.5 | 11 | Fold: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Superfamily: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Family: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 |
| 40 | c5icuA | Alignment | not modelled | 7.5 | 19 | PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b |
| 41 | c4drvA | Alignment | not modelled | 7.4 | 27 | PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein vp4; PDBTitle: cell attachment protein vp8* of a human rotavirus specifically2 interacts with a-type histo-blood group antigen |
| 42 | c2q48A | Alignment | not modelled | 7.4 | 8 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein at5g48480; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at5g48480 |
| 43 | d1xy7a | Alignment | not modelled | 7.4 | 8 | Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Hypothetical protein At5g48480 |
| 44 | d1kaca | Alignment | not modelled | 7.2 | 22 | Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain |
| 45 | c6q2zB | Alignment | not modelled | 7.2 | 21 | PDB header: unknown function Chain: B: PDB Molecule: upf0339 family protein; PDBTitle: nmr solution structure of the hvo_2922 protein from haloferax volcanii |
| 46 | d2o39a1 | Alignment | not modelled | 7.2 | 11 | Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain |
| 47 | c2xvsA | Alignment | not modelled | 7.1 | 15 | PDB header: antitumor protein Chain: A: PDB Molecule: tetratricopeptide repeat protein 5; PDBTitle: crystal structure of human ttc5 (strap) c-terminal ob2 domain |
| 48 | c2n24A | Alignment | not modelled | 7.1 | 57 | PDB header: toxin Chain: A: PDB Molecule: o2_contryphan_vc1; PDBTitle: solution nmr structure of contryphan-vc1 |
| 49 | d1xvsa | Alignment | not modelled | 7.1 | 16 | Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like |
| 50 | c3omsA | Alignment | not modelled | 6.8 | 4 | PDB header: transferase Chain: A: PDB Molecule: phnb protein; PDBTitle: putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus. |
| 51 | c5hdwA | Alignment | not modelled | 6.6 | 17 | PDB header: protein binding Chain: A: PDB Molecule: if-box only protein 3; PDBTitle: apag domain of fbx3 |
| 52 | c5lnk2 | Alignment | not modelled | 6.5 | 21 | PDB header: oxidoreductase Chain: 2: PDB Molecule: mitochondrial complex i, 24 kda subunit; PDBTitle: entire ovine respiratory complex i |
| 53 | d1xq4a | Alignment | not modelled | 6.5 | 18 | Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like |
| 54 | c3fg7A | Alignment | not modelled | 6.5 | 19 | PDB header: structural protein Chain: A: PDB Molecule: villin-1; PDBTitle: the crystal structure of villin domain 6 |
| | | | | | | Fold: Virus attachment protein globular domain |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 55 | d1knba_ | Alignment | not modelled | 6.4 | 15 | Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain |
| 56 | c6gcsH_ | Alignment | not modelled | 6.3 | 15 | PDB header: oxidoreductase Chain: H: PDB Molecule: 24-kda subunit (nuhm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 57 | c4yg3A_ | Alignment | not modelled | 6.2 | 14 | PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein vp4; PDBTitle: structural basis of glycan recognition in neonate-specific rotaviruses |
| 58 | c4nvsB_ | Alignment | not modelled | 6.2 | 8 | PDB header: unknown function Chain: B: PDB Molecule: putative enzyme, glyoxalase family; PDBTitle: crystal structure of the q18cp6_clod6 protein from glyoxalase family.2 northeast structural genomics consortium target cfr3 |
| 59 | d1a0ea_ | Alignment | not modelled | 6.2 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase |
| 60 | c2mmwA_ | Alignment | not modelled | 6.1 | 13 | PDB header: antibiotic Chain: A: PDB Molecule: microcin j25; PDBTitle: lasso peptide based integrin inhibitor: microcin j25 variant with rgd2 substitution of gly12-ile13-gly14 |
| 61 | c2i05A_ | Alignment | not modelled | 6.1 | 22 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase b-raf; PDBTitle: solution nmr structure of the ras-binding domain of serine/threonine-2 protein kinase b-raf from homo sapiens, northeast structural genomics3 consortium target hr4694f |
| 62 | c5vx8A_ | Alignment | not modelled | 6.1 | 23 | PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein vp4; PDBTitle: vp8* of p[6] human rotavirus rv3 |
| 63 | c2i99X_ | Alignment | not modelled | 6.0 | 13 | PDB header: de novo protein, antimicrobial protein Chain: X: PDB Molecule: lak160-p10; PDBTitle: solution structure of lak160-p10 |
| 64 | c4xkmB_ | Alignment | not modelled | 6.0 | 15 | PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of xylose isomerase from an human intestinal tract2 microbe bacteroides thetaiotaomicron |
| 65 | c2x9qA_ | Alignment | not modelled | 6.0 | 38 | PDB header: ligase Chain: A: PDB Molecule: cyclodipeptide synthetase; PDBTitle: structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases. |
| 66 | d3bida1 | Alignment | not modelled | 5.8 | 21 | Fold: YegP-like Superfamily: YegP-like Family: YegP-like |
| 67 | c2q2kA_ | Alignment | not modelled | 5.8 | 14 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein |
| 68 | c3cncD_ | Alignment | not modelled | 5.8 | 11 | PDB header: viral protein Chain: D: PDB Molecule: fiber protein; PDBTitle: crystal structure of ad16 fiber knob |
| 69 | d2k7ia1 | Alignment | not modelled | 5.7 | 26 | Fold: YegP-like Superfamily: YegP-like Family: YegP-like |
| 70 | c2k7iB_ | Alignment | not modelled | 5.7 | 26 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0339 protein atu0232; PDBTitle: solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223. |
| 71 | d2j12a1 | Alignment | not modelled | 5.7 | 13 | Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain |
| 72 | c4zdtB_ | Alignment | not modelled | 5.6 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: structure-specific endonuclease subunit slx4; PDBTitle: crystal structure of the ring finger domain of slx1 in complex with2 the c-terminal domain of slx4 |
| 73 | c3htrB_ | Alignment | not modelled | 5.6 | 18 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris |
| 74 | c6ez3C_ | Alignment | not modelled | 5.6 | 50 | PDB header: rna binding protein Chain: C: PDB Molecule: cyclo(l-leucyl-l-leucyl) synthase; PDBTitle: structure of cdps from staphylococcus haemolyticus |
| 75 | c1rrbA_ | Alignment | not modelled | 5.5 | 26 | PDB header: transferase Chain: A: PDB Molecule: raf proto-oncogene serine/threonine-protein PDBTitle: the ras-binding domain of raf-1 from rat, nmr, 1 structure |
| 76 | d2fug21 | Alignment | not modelled | 5.5 | 23 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like |
| 77 | d1c1yb_ | Alignment | not modelled | 5.5 | 26 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD |
| 78 | c4gdkA_ | Alignment | not modelled | 5.5 | 26 | PDB header: protein binding Chain: A: PDB Molecule: ubiquitin-like protein atg12; PDBTitle: crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1 |
| 79 | c4i0xl_ | Alignment | not modelled | 5.3 | 32 | PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex |
| | | | | | | Fold: TIM beta/alpha-barrel |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 80 | d1a0da_ | Alignment | not modelled | 5.3 | 7 | Superfamily: Xylose isomerase-like Family: Xylose isomerase |
| 81 | c4xl8B_ | Alignment | not modelled | 5.2 | 38 | PDB header: viral protein Chain: B: PDB Molecule: fiber-1; PDBTitle: crystal structure of human adenovirus 52 short fiber knob in complex2 with 2-o-methyl-5-n-acetylneuraminic acid |
| 82 | c5yxiA_ | Alignment | not modelled | 5.2 | 19 | PDB header: de novo protein Chain: A: PDB Molecule: drafx6; PDBTitle: designed protein drafx6 |
| 83 | d1srqa_ | Alignment | not modelled | 5.2 | 21 | Fold: Rap/Ran-GAP Superfamily: Rap/Ran-GAP Family: Rap/Ran-GAP |
| 84 | c5fkzE_ | Alignment | not modelled | 5.2 | 21 | PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, constitutive; PDBTitle: structure of e.coli constitutive lysine decarboxylase |
| 85 | c2i7xA_ | Alignment | not modelled | 5.1 | 17 | PDB header: rna binding protein, protein binding Chain: A: PDB Molecule: protein cft2; PDBTitle: structure of yeast cpsf-100 (ydh1p) |
| 86 | d2i7xa1 | Alignment | not modelled | 5.1 | 17 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases |
| 87 | d2rkya1 | Alignment | not modelled | 5.1 | 20 | Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module |
| 88 | c1qiuC_ | Alignment | not modelled | 5.1 | 26 | PDB header: fibre protein Chain: C: PDB Molecule: adenovirus fibre; PDBTitle: a triple beta-spiral in the adenovirus fibre shaft reveals a new2 structural motif for biological fibres |