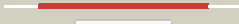



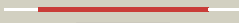























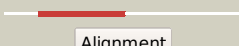



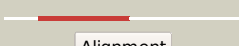










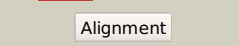
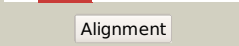




Phyre2

| | |
|---------------|--------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3704c_gshA_4147066_4148364 |
| Date | Fri Aug 9 18:20:40 BST 2019 |
| Unique Job ID | d62b28ae24183d16 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2gwcE_ |  Alignment |  | 100.0 | 24 | PDB header: ligase Chain: E: PDB Molecule: glutamate cysteine ligase; PDBTitle: crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue |
| 2 | d1tt4a_ |  Alignment |  | 100.0 | 20 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2) |
| 3 | c1tt4B_ |  Alignment |  | 100.0 | 20 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium |
| 4 | d1r8ga_ |  Alignment |  | 100.0 | 20 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2) |
| 5 | d2d32a1 |  Alignment |  | 99.7 | 17 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase |
| 6 | c3nztA_ |  Alignment |  | 99.5 | 15 | PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase; PDBTitle: 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ffrom francisella tularensis in complex with amp |
| 7 | c3lvwA_ |  Alignment |  | 99.5 | 22 | PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase; PDBTitle: glutathione-inhibited scgl |
| 8 | c3ln6A_ |  Alignment |  | 99.4 | 16 | PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae |
| 9 | c3ln7A_ |  Alignment |  | 99.3 | 13 | PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida |
| 10 | c4hppA_ |  Alignment |  | 98.4 | 19 | PDB header: ligase Chain: A: PDB Molecule: probable glutamine synthetase; PDBTitle: crystal structure of novel glutamine synthase homolog |
| 11 | c5zlpH_ |  Alignment |  | 98.4 | 19 | PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from helicobacter pylori |

| | | | | | | |
|----|-------------------------|---|---|------|----|---|
| 12 | c3qajL_ |  Alignment |  | 98.4 | 18 | PDB header: ligase Chain: L: PDB Molecule: glutamine synthetase; PDBTitle: x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp |
| 13 | d2bvca2 |  Alignment |  | 98.2 | 17 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain |
| 14 | d1f52a2 |  Alignment |  | 98.2 | 18 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain |
| 15 | c1htoB_ |  Alignment |  | 98.2 | 17 | PDB header: ligase Chain: B: PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from mycobacterium tuberculosis |
| 16 | c3ng0A_ |  Alignment |  | 98.2 | 16 | PDB header: ligase Chain: A: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803 |
| 17 | c2qc8J_ |  Alignment |  | 98.0 | 13 | PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate |
| 18 | c1fpyE_ |  Alignment |  | 98.0 | 18 | PDB header: ligase Chain: E: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin |
| 19 | c3o6xC_ |  Alignment |  | 97.9 | 16 | PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from bacteroides fragilis |
| 20 | c4s17E_ |  Alignment |  | 97.9 | 18 | PDB header: ligase Chain: E: PDB Molecule: glutamine synthetase; PDBTitle: the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703 |
| 21 | c2d3aj_ |  Alignment | not modelled | 97.7 | 17 | PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate |
| 22 | c2j9iL_ |  Alignment | not modelled | 97.1 | 19 | PDB header: ligase Chain: L: PDB Molecule: glutamate-ammonia ligase domain-containing protein 1; PDBTitle: lengsin is a survivor of an ancient family of class i glutamine2 synthetases in eukaryotes that has undergone evolutionary re-3 engineering for a tissue-specific role in the vertebrate eye lens. |
| 23 | c4baxH_ |  Alignment | not modelled | 96.9 | 18 | PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor |
| 24 | c4is4G_ |  Alignment | not modelled | 96.8 | 13 | PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer |
| 25 | c5dm3A_ |  Alignment | not modelled | 96.7 | 16 | PDB header: ligase Chain: A: PDB Molecule: l-glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from chromohalobacter2 salexigens dsm 3043(csa1_0679, target efi-550015) with bound adp |
| 26 | c3fkyD_ |  Alignment | not modelled | 96.0 | 18 | PDB header: ligase Chain: D: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae |
| 27 | c4b0tB_ |  Alignment | not modelled | 90.9 | 16 | PDB header: ligase Chain: B: PDB Molecule: pup--protein ligase; PDBTitle: structure of the pup ligase pafa of the prokaryotic2 ubiquitin-like modification pathway in complex with adp |

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|----|-------------------------|-----------|--------------|------|----|--|
| 28 | c4b0sA | Alignment | not modelled | 88.3 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: deamidase-depupylase dop; PDBTitle: structure of the deamidase-depupylase dop of the prokaryotic2 ubiquitin-like modification pathway in complex with atp |
| 29 | c4bjrA | Alignment | not modelled | 82.3 | 15 | PDB header: ligase Chain: A: PDB Molecule: pup--protein ligase, prokaryotic ubiquitin-like protein PDBTitle: crystal structure of the complex between prokaryotic2 ubiquitin-like protein pup and its ligase pafa |
| 30 | c4eacC | Alignment | not modelled | 52.1 | 10 | PDB header: lyase Chain: C: PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12 |
| 31 | c3oqvA | Alignment | not modelled | 27.7 | 12 | PDB header: protein binding Chain: A: PDB Molecule: albc; PDBTitle: albc, a cyclodipeptide synthase from streptomyces noursei |
| 32 | d2eg6a1 | Alignment | not modelled | 26.8 | 33 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase |
| 33 | d3ci0k1 | Alignment | not modelled | 23.4 | 21 | Fold: SAM domain-like Superfamily: GspK insert domain-like Family: GspK insert domain-like |
| 34 | d1iv8a2 | Alignment | not modelled | 18.8 | 11 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain |
| 35 | c5z73A | Alignment | not modelled | 16.9 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: alr0819 protein; PDBTitle: crystal structure of alkaline/neutral invertase invb from anabaena sp.2 pcc 7120 |
| 36 | c5gorE | Alignment | not modelled | 16.7 | 20 | PDB header: hydrolase Chain: E: PDB Molecule: alkaline invertase; PDBTitle: crystal structure of alkaline invertase inva from anabaena sp. pcc2 7120 |
| 37 | c3jezC | Alignment | not modelled | 16.6 | 33 | PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2 |
| 38 | c3gtzA | Alignment | not modelled | 16.5 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative translation initiation inhibitor; PDBTitle: crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium |
| 39 | c3bdkB | Alignment | not modelled | 15.7 | 16 | PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue |
| 40 | c4lfbB | Alignment | not modelled | 12.2 | 42 | PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315 |
| 41 | c1iv8A | Alignment | not modelled | 11.8 | 11 | PDB header: isomerase Chain: A: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: crystal structure of maltooligosyl trehalose synthase |
| 42 | c5vgmA | Alignment | not modelled | 11.5 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase pyrc from vibrio cholerae in2 complex with zinc at 1.95 a resolution. |
| 43 | c5v0gE | Alignment | not modelled | 11.2 | 33 | PDB header: hydrolase Chain: E: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase pyrc from yersinia pestis in2 complex with zinc and unknown ligand at 2.4 a resolution. |
| 44 | d1tz9a | Alignment | not modelled | 10.2 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like |
| 45 | c5zet2 | Alignment | not modelled | 9.8 | 22 | PDB header: ribosome Chain: 2: PDB Molecule: 50s ribosomal protein l31; PDBTitle: m. smegmatis p/p state 50s ribosomal subunit |
| 46 | c3oqhB | Alignment | not modelled | 9.6 | 15 | PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein yvmc; PDBTitle: crystal structure of b. licheniformis cdps yvmc-blic |
| 47 | c3rj1G | Alignment | not modelled | 9.0 | 38 | PDB header: transcription Chain: G: PDB Molecule: mediator of rna polymerase ii transcription subunit 6; PDBTitle: architecture of the mediator head module |
| 48 | c3pnuA | Alignment | not modelled | 8.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni. |
| 49 | c3iwcD | Alignment | not modelled | 8.7 | 9 | PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with s-adenosylmethionine methyl ester |
| 50 | c2qsgX | Alignment | not modelled | 8.6 | 19 | PDB header: dna binding protein/dna Chain: X: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of rad4-rad23 bound to a uv-damaged dna |
| 51 | d1ik7a | Alignment | not modelled | 8.1 | 23 | Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD |
| 52 | c5v3nB | Alignment | not modelled | 7.2 | 33 | PDB header: hydrolase Chain: B: PDB Molecule: ulp2p,topoisomerase 1-associated factor 2 chimera; PDBTitle: structure of s. cerevisiae ulp2-tof2-csm1 complex |
| 53 | c5o60g | Alignment | not modelled | 7.0 | 20 | PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from |

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|----|-------------------------|-----------|--------------|-----|----|--|
| | | | | | | mycobacterium2 smegmatis |
| 54 | d1x3zb1 | Alignment | not modelled | 6.8 | 18 | Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain |
| 55 | d1ylea1 | Alignment | not modelled | 6.5 | 33 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like |
| 56 | c4gwpG_ | Alignment | not modelled | 6.2 | 25 | PDB header: transcription Chain: G: PDB Molecule: mediator of rna polymerase ii transcription subunit 6; PDBTitle: structure of the mediator head module from s. cerevisiae |
| 57 | c6ez3C_ | Alignment | not modelled | 6.0 | 6 | PDB header: rna binding protein Chain: C: PDB Molecule: cyclo(l-leucyl-l-leucyl) synthase; PDBTitle: structure of cdps from staphylococcus haemolyticus |
| 58 | c5ja1B_ | Alignment | not modelled | 5.7 | 11 | 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 |
| 59 | c2j034_ | Alignment | not modelled | 5.6 | 18 | PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii. |
| 60 | d2j0141 | Alignment | not modelled | 5.6 | 18 | Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p |
| 61 | d2ewca1 | Alignment | not modelled | 5.4 | 21 | Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP |
| 62 | c3ey7B_ | Alignment | not modelled | 5.4 | 4 | PDB header: oxidoreductase Chain: B: PDB Molecule: biphenyl-2,3-diol 1,2-dioxygenase iii-related PDBTitle: structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1 |
| 63 | d2idga1 | Alignment | not modelled | 5.3 | 7 | Fold: TorD-like Superfamily: TorD-like Family: TorD-like |
| 64 | c6avjB_ | Alignment | not modelled | 5.2 | 22 | PDB header: metal binding protein Chain: B: PDB Molecule: cdgsh iron-sulfur domain-containing protein 3, PDBTitle: crystal structure of human mitochondrial inner neet protein (mint)2 /cisd3 |