



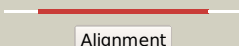

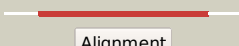

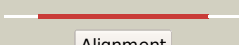

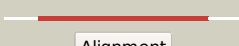







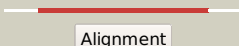


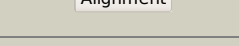

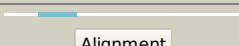

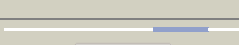


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3628_ppa_4067602_4068090
 Date Fri Aug 9 18:20:31 BST 2019
 Unique Job ID 97fe61144c4ac61b

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--------------------|----------|------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | c2uxsA_ | Alignment | | 100.0 | 100 | PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5 |
| 2 | d2prda_ | Alignment | | 100.0 | 52 | Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase |
| 3 | c4lugA_ | Alignment | | 100.0 | 39 | PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase ppa1 from arabidopsis2 thaliana |
| 4 | c3ld3A_ | Alignment | | 100.0 | 43 | PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution |
| 5 | d1i40a_ | Alignment | | 100.0 | 45 | Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase |
| 6 | c3fq3H_ | Alignment | | 100.0 | 45 | PDB header: hydrolase Chain: H: PDB Molecule: inorganic pyrophosphatase:bacterial/archaeal inorganic PDBTitle: crystal structure of inorganic phosphatase from brucella melitensis |
| 7 | c1ygzC_ | Alignment | | 100.0 | 43 | PDB header: hydrolase Chain: C: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from helicobacter2 pylori |
| 8 | c5teaF_ | Alignment | | 100.0 | 36 | PDB header: hydrolase Chain: F: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of an inorganic pyrophosphatase from neisseria2 gonorrhoeae |
| 9 | c6n1cB_ | Alignment | | 100.0 | 46 | PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from legionella2 pneumophila philadelphia 1 |
| 10 | d1udea_ | Alignment | | 100.0 | 48 | Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase |
| 11 | d1qeza_ | Alignment | | 100.0 | 46 | Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase |

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|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|-------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | c3tr4C_ |  Alignment |  | 100.0 | 47 | PDB header: hydrolase Chain: C: PDB Molecule: inorganic pyrophosphatase; PDBTitle: structure of an inorganic pyrophosphatase (ppa) from coxiella burnetii |
| 13 | c3d63B_ |  Alignment |  | 100.0 | 46 | PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from burkholderia2 pseudomallei |
| 14 | c3emjL_ |  Alignment |  | 100.0 | 44 | PDB header: hydrolase Chain: L: PDB Molecule: inorganic pyrophosphatase; PDBTitle: 2.2 a crystal structure of inorganic pyrophosphatase from2 rickettsia prowazekii (p21 form) |
| 15 | d1twla_ |  Alignment |  | 100.0 | 46 | Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase |
| 16 | d1e9ga_ |  Alignment |  | 100.0 | 28 | Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase |
| 17 | c6c45A_ |  Alignment |  | 100.0 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of human inorganic pyrophosphatase in the p2121212 space group |
| 18 | c4qlzA_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: sjchgc07024 protein; PDBTitle: the structure of inorganic pyrophosphatase from schistosoma japonicum |
| 19 | c5wrtB_ |  Alignment |  | 100.0 | 28 | PDB header: hydrolase Chain: B: PDB Molecule: soluble inorganic pyrophosphatase; PDBTitle: crystal structure of type i inorganic pyrophosphatase from toxoplasma2 gondii. |
| 20 | c5c5vB_ |  Alignment |  | 100.0 | 30 | PDB header: hydrolase Chain: B: PDB Molecule: acidocalcisomal pyrophosphatase; PDBTitle: recombinant inorganic pyrophosphatase from t brucei brucei |
| 21 | c5cuvB_ |  Alignment | not modelled | 100.0 | 31 | PDB header: metal binding protein Chain: B: PDB Molecule: acidocalcisomal pyrophosphatase; PDBTitle: crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form |
| 22 | c5wruA_ |  Alignment | not modelled | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: probable inorganic pyrophosphatase; PDBTitle: crystal structure of type i inorganic pyrophosphatase from p2 falciparum |
| 23 | c3lo0A_ |  Alignment | not modelled | 100.0 | 38 | PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis |
| 24 | c2dhxA_ |  Alignment | not modelled | 32.2 | 14 | PDB header: rna binding protein Chain: A: PDB Molecule: poly (adp-ribose) polymerase family, member 10 PDBTitle: solution structure of the rrm domain in the human poly (adp-2 ribose) polymerase family, member 10 variant |
| 25 | c3ideD_ |  Alignment | not modelled | 30.2 | 21 | PDB header: virus like particle Chain: D: PDB Molecule: capsid protein vp2; PDBTitle: structure of ipnv subviral particle |
| 26 | c1wwhB_ |  Alignment | not modelled | 30.0 | 15 | PDB header: protein transport Chain: B: PDB Molecule: nucleoporin 35; PDBTitle: crystal structure of the mppn domain of mouse nup35 |
| 27 | d1d02a_ |  Alignment | not modelled | 28.9 | 24 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease MunI |
| 28 | c2df7H_ |  Alignment | not modelled | 23.7 | 25 | PDB header: virus like particle Chain: H: PDB Molecule: structural polyprotein vp2; PDBTitle: crystal structure of infectious bursal disease virus vp2 subviral2 particle |

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|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | d2df7a1 | Alignment | not modelled | 22.5 | 25 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Birnaviridae-like VP |
| 30 | c2yueA | Alignment | not modelled | 22.4 | 15 | PDB header: rna binding protein Chain: A: PDB Molecule: protein neuralized; PDBTitle: solution structure of the neuZ (nhr) domain in neuralized2 from drosophila melanogaster |
| 31 | d1wwha1 | Alignment | not modelled | 17.5 | 15 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 32 | c5cioA | Alignment | not modelled | 17.5 | 15 | PDB header: metal binding protein Chain: A: PDB Molecule: pyrroloquinoline quinone biosynthesis protein pqqf; PDBTitle: crystal structure of pqqf |
| 33 | c5hnmC | Alignment | not modelled | 16.9 | 10 | PDB header: hydrolase Chain: C: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-pentapeptidase vanY2 e175a mutant from vanB-type resistance cassette in complex with3 zn(ii) |
| 34 | c2vtvA | Alignment | not modelled | 16.2 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei |
| 35 | d2fgea4 | Alignment | not modelled | 15.3 | 17 | Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like |
| 36 | d1hr6a1 | Alignment | not modelled | 15.3 | 9 | Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like |
| 37 | c2opdA | Alignment | not modelled | 15.1 | 19 | PDB header: cell adhesion Chain: A: PDB Molecule: pilx; PDBTitle: structure of the neisseria meningitidis minor type iv pilin, pilx |
| 38 | c2l76A | Alignment | not modelled | 14.8 | 33 | PDB header: transcription Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto |
| 39 | c4joiA | Alignment | not modelled | 14.5 | 18 | PDB header: dna binding protein Chain: A: PDB Molecule: cst complex subunit stn1; PDBTitle: crystal structure of the human telomeric stn1-ten1 complex |
| 40 | c2e63A | Alignment | not modelled | 13.3 | 29 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa1787 protein; PDBTitle: solution structure of the neuZ domain in kiaa1787 protein |
| 41 | c3kztB | Alignment | not modelled | 12.9 | 22 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution |
| 42 | d1ppja1 | Alignment | not modelled | 11.5 | 9 | Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like |
| 43 | c1p0yA | Alignment | not modelled | 11.5 | 50 | PDB header: transferase Chain: A: PDB Molecule: ribulose-1,5 bisphosphate carboxylase/oxygenase PDBTitle: crystal structure of the set domain of lsmt bound to2 melsyne and adohcy |
| 44 | c4q7jD | Alignment | not modelled | 10.6 | 16 | PDB header: translation/transferase Chain: D: PDB Molecule: 30s ribosomal protein s1; PDBTitle: complex structure of viral rna polymerase |
| 45 | d1p9qc3 | Alignment | not modelled | 10.1 | 30 | Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain |
| 46 | d1t95a3 | Alignment | not modelled | 9.5 | 30 | Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain |
| 47 | c6jo52 | Alignment | not modelled | 9.3 | 43 | PDB header: photosynthesis Chain: 2: PDB Molecule: chlorophyll a-b binding protein, chloroplastic; PDBTitle: structure of the green algal photosystem i supercomplex with light-2 harvesting complex i |
| 48 | d1x9na2 | Alignment | not modelled | 9.2 | 17 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain |
| 49 | c3mjdA | Alignment | not modelled | 9.2 | 20 | PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis. |
| 50 | c4qmfB | Alignment | not modelled | 8.7 | 12 | PDB header: rna binding protein Chain: B: PDB Molecule: krr1 small subunit processome component; PDBTitle: structure of the krr1 and faf1 complex from saccharomyces cerevisiae |
| 51 | c4eskA | Alignment | not modelled | 8.4 | 19 | PDB header: immune system Chain: A: PDB Molecule: leukocyte-associated immunoglobulin-like receptor 1; PDBTitle: crystal structure of a strand-swapped dimer of mouse leukocyte-2 associated immunoglobulin-like receptor 1 (nysgrc-006047)jig-like3 domain |
| 52 | c4jw1A | Alignment | not modelled | 8.3 | 24 | PDB header: hydrolase activator Chain: A: PDB Molecule: effector protein b; PDBTitle: crystal structure of n-terminal 618-residue fragment of lepB from2 legionella pneumophila |
| 53 | c2jnsA | Alignment | not modelled | 7.9 | 7 | PDB header: unknown function Chain: A: PDB Molecule: bromodomain-containing protein 4; PDBTitle: solution structure of the bromodomain-containing protein |

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|----|-------------------------|-----------|--------------|-----|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | | | | 42 et domain |
| 54 | c5xswA_ | Alignment | not modelled | 7.8 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of an archaeal chitinase in the substrate-complex2 form (p63) |
| 55 | c2rukA_ | Alignment | not modelled | 7.7 | 33 | PDB header: transcription Chain: A: PDB Molecule: cellular tumor antigen p53; PDBTitle: solution structure of the complex between p53 transactivation domain 22 and tfiih p62 ph domain |
| 56 | d1tlea2 | Alignment | not modelled | 7.6 | 15 | Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors |
| 57 | c2mmpA_ | Alignment | not modelled | 7.4 | 24 | PDB header: ribosomal protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a ribosomal protein |
| 58 | c4zgnA_ | Alignment | not modelled | 6.9 | 9 | PDB header: cell cycle Chain: A: PDB Molecule: cell division cycle protein 123; PDBTitle: structure cdc123 complexed with the c-terminal domain of eif2gamma |
| 59 | c3k7bA_ | Alignment | not modelled | 6.4 | 50 | PDB header: viral protein Chain: A: PDB Molecule: protein a33; PDBTitle: the structure of the poxvirus a33 protein reveals a dimer of unique c-2 type lectin-like domains. |
| 60 | d1pzna1 | Alignment | not modelled | 6.2 | 9 | Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 61 | c5hytC_ | Alignment | not modelled | 6.2 | 5 | PDB header: immune system Chain: C: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein |
| 62 | c5hytE_ | Alignment | not modelled | 6.2 | 5 | PDB header: immune system Chain: E: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein |
| 63 | c2e4mC_ | Alignment | not modelled | 6.1 | 27 | PDB header: toxin Chain: C: PDB Molecule: ha-17; PDBTitle: crystal structure of hemagglutinin subcomponent complex (ha-2 33/ha-17) from clostridium botulinum serotype d strain 4947 |
| 64 | c5hytA_ | Alignment | not modelled | 6.0 | 5 | PDB header: immune system Chain: A: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein |
| 65 | c5hytG_ | Alignment | not modelled | 6.0 | 5 | PDB header: immune system Chain: G: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein |
| 66 | c2przB_ | Alignment | not modelled | 5.9 | 22 | PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp |
| 67 | c4x8yA_ | Alignment | not modelled | 5.9 | 16 | PDB header: membrane protein Chain: A: PDB Molecule: membrane-associated progesterone receptor component 1; PDBTitle: crystal structure of human pgrmc1 cytochrome b5-like domain |
| 68 | d1hmca_ | Alignment | not modelled | 5.7 | 22 | Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines |
| 69 | c5yl1A_ | Alignment | not modelled | 5.7 | 43 | PDB header: viral protein Chain: A: PDB Molecule: capsid protein; PDBTitle: t=1 subviral particle of penaeus vannamei nodavirus capsid protein2 deletion mutant (delta 1-37 & 251-368) |
| 70 | c4yn7A_ | Alignment | not modelled | 5.7 | 16 | PDB header: transcription Chain: A: PDB Molecule: yfir; PDBTitle: non-oxidized yfir |
| 71 | c3cx5L_ | Alignment | not modelled | 5.7 | 8 | PDB header: oxidoreductase Chain: L: PDB Molecule: cytochrome b-c1 complex subunit 1, mitochondrial; PDBTitle: structure of complex iii with bound cytochrome c in reduced state and2 definition of a minimal core interface for electron transfer. |
| 72 | d2ghpa1 | Alignment | not modelled | 5.6 | 11 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 73 | c1ayrA_ | Alignment | not modelled | 5.6 | 18 | PDB header: sensory transduction Chain: A: PDB Molecule: arrestin; PDBTitle: arrestin from bovine rod outer segments |
| 74 | c6izlB_ | Alignment | not modelled | 5.6 | 43 | PDB header: virus Chain: B: PDB Molecule: mud crab tombus-like virus; PDBTitle: cryo-em structure of mud crab tombus-like virus at 3.3 angstroms2 resolution |
| 75 | d1w7ca3 | Alignment | not modelled | 5.4 | 24 | Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region |
| 76 | c6ab6A_ | Alignment | not modelled | 5.3 | 43 | PDB header: virus like particle Chain: A: PDB Molecule: capsid protein; PDBTitle: cryo-em structure of t=3 penaeus vannamei nodavirus |
| 77 | d1q2la1 | Alignment | not modelled | 5.3 | 11 | Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like |
| | | | | | | Fold: TraM-like |

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|----|-------------------------|-----------|--------------|-----|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 78 | d2g7oa1 | Alignment | not modelled | 5.3 | 15 | Superfamily: TraM-like Family: TraM-like |
| 79 | c4cw5B_ | Alignment | not modelled | 5.2 | 8 | PDB header: oxidoreductase Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens |
| 80 | c6i9bA_ | Alignment | not modelled | 5.2 | 14 | PDB header: rna binding protein Chain: A: PDB Molecule: la-related protein 4; PDBTitle: nmr structure of the la module from human larp4a |