



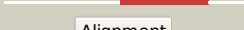

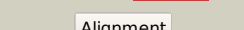

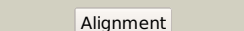

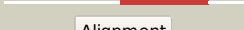





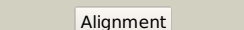



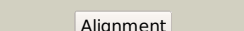



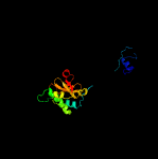

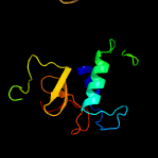






# Phyre2

|                  |                                 |
|------------------|---------------------------------|
| Email            | mdejesus@rockefeller.edu        |
| Description      | RVBD0024 (-<br>)_28362_29207    |
| Date             | Tue Jul 23 14:50:05 BST<br>2019 |
| Unique Job<br>ID | 346cc5e3475fa9aa                |

Detailed template  
information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">c2xivA_</a> | <br>Alignment   |    | 100.0      | 27     | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical invasion protein;<br><b>PDBTitle:</b> structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis   |
| 2  | <a href="#">c3pbiA_</a> | <br>Alignment   |    | 100.0      | 26     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> invasion protein;<br><b>PDBTitle:</b> structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution   |
| 3  | <a href="#">c6biqA_</a> | <br>Alignment   |    | 100.0      | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> clan ca, family c40, nlp/p60 superfamily cysteine<br><b>PDBTitle:</b> structure of nlp2 from trichomonas vaginalis  |
| 4  | <a href="#">c2fg0B_</a> | <br>Alignment   |    | 100.0      | 30     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cog0791: cell wall-associated hydrolases (invasion-<br><b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution |
| 5  | <a href="#">c4fdyA_</a> | <br>Alignment |  | 100.0      | 26     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> similar to lipoprotein, nlp/p60 family;<br><b>PDBTitle:</b> crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution                    |
| 6  | <a href="#">c3h41A_</a> | <br>Alignment |  | 100.0      | 29     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60 family protein;<br><b>PDBTitle:</b> crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution  |
| 7  | <a href="#">c3qt2A_</a> | <br>Alignment |  | 100.0      | 36     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c   |
| 8  | <a href="#">d2evra2</a> | <br>Alignment |  | 100.0      | 27     | <b>Fold:</b> Cysteine proteinases<br><b>Superfamily:</b> Cysteine proteinases<br><b>Family:</b> NlpC/P60  |
| 9  | <a href="#">c3nfpB_</a> | <br>Alignment |  | 100.0      | 34     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative dipeptidyl-peptidase vi;<br><b>PDBTitle:</b> crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution  |
| 10 | <a href="#">c3i86A_</a> | <br>Alignment |  | 99.9       | 34     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204  |
| 11 | <a href="#">c4hpeA_</a> | <br>Alignment |  | 99.9       | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cell wall hydrolase tn916-like,ctn1-orf17;<br><b>PDBTitle:</b> crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution                              |

|    |                         |           |   |      |    |  |
|----|-------------------------|-----------|---|------|----|--|
| 12 | <a href="#">c2k1gA</a>  | Alignment |     | 99.9 | 33 | <b>PDB header:</b> lipoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein spr;<br><b>PDBTitle:</b> solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162   |
| 13 | <a href="#">c6b8cA</a>  | Alignment |    | 99.9 | 37 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60;<br><b>PDBTitle:</b> crystal structure of nlpC/p60 domain of peptidoglycan hydrolase saga  |
| 14 | <a href="#">c4xcmB</a>  | Alignment |    | 99.9 | 32 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cell wall-binding endopeptidase-related protein;<br><b>PDBTitle:</b> crystal structure of the putative nlpC/p60 d,l endopeptidase from t.2 thermophilus  |
| 15 | <a href="#">c3m1uB</a>  | Alignment |    | 99.8 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative gamma-d-glutamyl-l-diamino acid2 endopeptidase;<br><b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dVu_0896) from desulfovibrio vulgaris hildenborough at 3.175 Å resolution   |
| 16 | <a href="#">c2p1gA</a>  | Alignment |    | 99.0 | 28 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative xylanase;<br><b>PDBTitle:</b> crystal structure of a putative xylanase from bacteroides fragilis  |
| 17 | <a href="#">c2kytA</a>  | Alignment |   | 97.7 | 29 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> group xvi phospholipase a2;<br><b>PDBTitle:</b> solution structure of the h-rev107 n-terminal domain   |
| 18 | <a href="#">c2lktA</a>  | Alignment |  | 97.4 | 37 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> retinoic acid receptor responder protein 3;<br><b>PDBTitle:</b> solution structure of n-terminal domain of human tig3 in 2 m urea  |
| 19 | <a href="#">c3kw0D</a>  | Alignment |  | 97.1 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> cysteine peptidase;<br><b>PDBTitle:</b> crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 Å resolution  |
| 20 | <a href="#">c4cgkA</a>  | Alignment |  | 97.0 | 12 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> secreted 45 kda protein;<br><b>PDBTitle:</b> crystal structure of the essential protein pcsb from streptococcus2 pneumoniae   |
| 21 | <a href="#">d2if6a1</a> | Alignment | not modelled  | 95.9 | 24 | <b>Fold:</b> Cysteine proteinases<br><b>Superfamily:</b> Cysteine proteinases<br><b>Family:</b> YiiX-like  |
| 22 | <a href="#">c4hzbA</a>  | Alignment | not modelled  | 95.7 | 29 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein;<br><b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii  |
| 23 | <a href="#">c2lrjA</a>  | Alignment | not modelled  | 95.5 | 27 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> staphyloxanthin biosynthesis protein, putative;<br><b>PDBTitle:</b> nmr solution structure of staphyloxanthin biosynthesis protein  |
| 24 | <a href="#">c5udmA</a>  | Alignment | not modelled  | 95.4 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phage-associated cell wall hydrolase;<br><b>PDBTitle:</b> phage-associated cell wall hydrolase plypy from streptococcus2 pyogenes, space group p6522   |
| 25 | <a href="#">c5t1qB</a>  | Alignment | not modelled  | 95.1 | 26 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase domain-containing<br><b>PDBTitle:</b> 2.15 angstrom crystal structure of n-acetylmuramoyl-l-alanine amidase2 from staphylococcus aureus.  |
| 26 | <a href="#">c2k3aA</a>  | Alignment | not modelled  | 93.6 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> chap domain protein;<br><b>PDBTitle:</b> nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11 |
| 27 | <a href="#">d2im9a1</a> | Alignment | not modelled  | 92.8 | 30 | <b>Fold:</b> Cysteine proteinases<br><b>Superfamily:</b> Cysteine proteinases<br><b>Family:</b> Lpg0564-like   |
|    |                         |           |   |      |    | <b>PDB header:</b> structural genomics, unknown function   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 28 | <a href="#">c2im9A</a>  | Alignment | not modelled | 92.8 | 30 | <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460  |
| 29 | <a href="#">c4olkB</a>  | Alignment | not modelled | 92.6 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> endolysin;<br><b>PDBTitle:</b> the chap domain of lysgh15  |
| 30 | <a href="#">c4f4mA</a>  | Alignment | not modelled | 92.2 | 33 | <b>PDB header:</b> hydrolase regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> papain peptidoglycan amidase effector tse1;<br><b>PDBTitle:</b> structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa   |
| 31 | <a href="#">c4f0wA</a>  | Alignment | not modelled | 91.6 | 33 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of type effector tse1 c30a mutant from pseudomonas2 aeruginosa   |
| 32 | <a href="#">c4h4jA</a>  | Alignment | not modelled | 91.0 | 26 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of a n-acetylmuramoyl-l-alanine amidase2 (bacuni_02947) from bacteroides uniformis atcc 8492 at 1.15 a3 resolution                   |
| 33 | <a href="#">d2ba0a2</a> | Alignment | not modelled | 90.8 | 33 | <b>Fold:</b> Barrel-sandwich hybrid<br><b>Superfamily:</b> Ribosomal L27 protein-like<br><b>Family:</b> ECR1 N-terminal domain-like  |
| 34 | <a href="#">c4eyzB</a>  | Alignment | not modelled | 88.0 | 43 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cellulosome-related protein module from ruminococcus<br><b>PDBTitle:</b> crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases |
| 35 | <a href="#">c4pa5A</a>  | Alignment | not modelled | 87.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase;<br><b>PDBTitle:</b> tgl - a bacterial spore coat transglutaminase - cystamine complex   |
| 36 | <a href="#">d2io8a2</a> | Alignment | not modelled | 85.9 | 30 | <b>Fold:</b> Cysteine proteinases<br><b>Superfamily:</b> Cysteine proteinases<br><b>Family:</b> CHAP domain  |
| 37 | <a href="#">d2gbsa1</a> | Alignment | not modelled | 82.2 | 32 | <b>Fold:</b> PUA domain-like<br><b>Superfamily:</b> PUA domain-like<br><b>Family:</b> Atu2648/PH1033-like  |
| 38 | <a href="#">d1zcea1</a> | Alignment | not modelled | 80.9 | 26 | <b>Fold:</b> PUA domain-like<br><b>Superfamily:</b> PUA domain-like<br><b>Family:</b> Atu2648/PH1033-like  |
| 39 | <a href="#">d2ar1a1</a> | Alignment | not modelled | 80.6 | 37 | <b>Fold:</b> PUA domain-like<br><b>Superfamily:</b> PUA domain-like<br><b>Family:</b> Atu2648/PH1033-like  |
| 40 | <a href="#">d2g2xa1</a> | Alignment | not modelled | 78.1 | 35 | <b>Fold:</b> PUA domain-like<br><b>Superfamily:</b> PUA domain-like<br><b>Family:</b> Atu2648/PH1033-like  |
| 41 | <a href="#">d2eyqa1</a> | Alignment | not modelled | 77.6 | 17 | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> CarD-like<br><b>Family:</b> CarD-like  |
| 42 | <a href="#">d2evea1</a> | Alignment | not modelled | 77.6 | 32 | <b>Fold:</b> PUA domain-like<br><b>Superfamily:</b> PUA domain-like<br><b>Family:</b> Atu2648/PH1033-like  |
| 43 | <a href="#">c3eopB</a>  | Alignment | not modelled | 76.3 | 35 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> thymocyte nuclear protein 1;<br><b>PDBTitle:</b> crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1  |
| 44 | <a href="#">c2ioaA</a>  | Alignment | not modelled | 71.7 | 26 | <b>PDB header:</b> ligase, hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional glutathionylspermidine<br><b>PDBTitle:</b> e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor                                       |
| 45 | <a href="#">d1zx8a1</a> | Alignment | not modelled | 71.4 | 32 | <b>Fold:</b> Cyclophilin-like<br><b>Superfamily:</b> Cyclophilin-like<br><b>Family:</b> TM1367-like  |
| 46 | <a href="#">c2wbqA</a>  | Alignment | not modelled | 70.6 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-arginine beta-hydroxylase;<br><b>PDBTitle:</b> crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine  |
| 47 | <a href="#">c2vpmB</a>  | Alignment | not modelled | 70.3 | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trypanothione synthetase;<br><b>PDBTitle:</b> trypanothione synthetase  |
| 48 | <a href="#">c6d6rH</a>  | Alignment | not modelled | 70.3 | 28 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> H: <b>PDB Molecule:</b> exosome complex component rrp4;<br><b>PDBTitle:</b> human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction   |
| 49 | <a href="#">c4kbmB</a>  | Alignment | not modelled | 70.2 | 21 | <b>PDB header:</b> transferase/transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase-binding transcription factor card;<br><b>PDBTitle:</b> structure of the mtb card/rnap beta subunit b1-b2 domains complex  |
| 50 | <a href="#">c4ifdH</a>  | Alignment | not modelled | 69.8 | 37 | <b>PDB header:</b> hydrolase/rna<br><b>Chain:</b> H: <b>PDB Molecule:</b> exosome complex component rrp4;<br><b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna  |
| 51 | <a href="#">c4xbzB</a>  | Alignment | not modelled | 68.6 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> evdo1;<br><b>PDBTitle:</b> crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca   |
| 52 | <a href="#">c6dawA</a>  | Alignment | not modelled | 68.1 | 40 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> non-heme iron hydroxylase;<br><b>PDBTitle:</b> x-ray crystal structure of napi l-arginine desaturase bound to fe(ii),2 l-arginine, and acetate  |

|    |                          |           |              |      |    |  |
|----|--------------------------|-----------|--------------|------|----|--|
| 53 | <a href="#">c5z9tB_</a>  | Alignment | not modelled | 67.6 | 28 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alginate lyase alyf-ou02;<br><b>PDBTitle:</b> a new pl6 alginate lyase complex with trisaccharide  |
| 54 | <a href="#">c6f6jC_</a>  | Alignment | not modelled | 66.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> l-lysine 3-hydroxylase;<br><b>PDBTitle:</b> crystal structure of the fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo1 with fe(ii)/succinate/(3s)-3-hydroxy-l-lysine                       |
| 55 | <a href="#">c4dbhA_</a>  | Alignment | not modelled | 65.7 | 22 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase;<br><b>PDBTitle:</b> crystal structure of cg1458 with inhibitor  |
| 56 | <a href="#">c2og5A_</a>  | Alignment | not modelled | 65.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative oxygenase;<br><b>PDBTitle:</b> crystal structure of asparagine oxygenase (asno)  |
| 57 | <a href="#">d1jr7a_</a>  | Alignment | not modelled | 64.4 | 14 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> Gab protein (hypothetical protein YgaT)   |
| 58 | <a href="#">c5hsxB_</a>  | Alignment | not modelled | 64.4 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-ketoglutarate-dependent taurine dioxygenase;<br><b>PDBTitle:</b> crystal structure of a putative alpha-ketoglutarate-dependent taurine2 dioxygenase from burkholderia xenovorans |
| 59 | <a href="#">c4ne0A_</a>  | Alignment | not modelled | 64.1 | 25 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-arginine beta-hydroxylase;<br><b>PDBTitle:</b> crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg  |
| 60 | <a href="#">c4nubA_</a>  | Alignment | not modelled | 64.0 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l16 arginine hydroxylase;<br><b>PDBTitle:</b> crystal structure of escherichia coli ribosomal oxygenase ycfD  |
| 61 | <a href="#">c5eqnA_</a>  | Alignment | not modelled | 63.2 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> frbj;<br><b>PDBTitle:</b> structure of phosphonate hydroxylase   |
| 62 | <a href="#">d1ds1a_</a>  | Alignment | not modelled | 63.0 | 30 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> Clavaminatase synthase  |
| 63 | <a href="#">d1otja_</a>  | Alignment | not modelled | 62.9 | 19 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> TauD/TfdA-like  |
| 64 | <a href="#">d2fcta1</a>  | Alignment | not modelled | 62.9 | 15 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> PhyH-like   |
| 65 | <a href="#">c6exhA_</a>  | Alignment | not modelled | 62.3 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine 4-hydroxylase;<br><b>PDBTitle:</b> crystal structure of the complex fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo5 with fe(ii)/succinate/(4r)-4-hydroxy-l-lysine               |
| 66 | <a href="#">c2lwjA_</a>  | Alignment | not modelled | 62.0 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, card family;<br><b>PDBTitle:</b> nmr solution structure myxococcus xanthus cdnl   |
| 67 | <a href="#">c4xc9B_</a>  | Alignment | not modelled | 61.8 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oxidase/hydroxylase;<br><b>PDBTitle:</b> crystal structure of apo hygx from streptomyces hygroscopicus  |
| 68 | <a href="#">c4yxB_A_</a> | Alignment | not modelled | 61.5 | 17 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> flagellar motor switch protein flim,flagellar motor switch<br><b>PDBTitle:</b> flim(spoa)::flin fusion protein   |
| 69 | <a href="#">c3nnlB_</a>  | Alignment | not modelled | 61.4 | 29 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> cura;<br><b>PDBTitle:</b> halogenase domain from cura module (crystal form iii)   |
| 70 | <a href="#">c2nnzA_</a>  | Alignment | not modelled | 61.4 | 25 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus   |
| 71 | <a href="#">c3kopB_</a>  | Alignment | not modelled | 61.3 | 23 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution    |
| 72 | <a href="#">c4ne0B_</a>  | Alignment | not modelled | 61.0 | 25 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-arginine beta-hydroxylase;<br><b>PDBTitle:</b> crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg  |
| 73 | <a href="#">c2eygA_</a>  | Alignment | not modelled | 60.4 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription-repair coupling factor;<br><b>PDBTitle:</b> crystal structure of escherichia coli transcription-repair2 coupling factor  |
| 74 | <a href="#">d1nkqa_</a>  | Alignment | not modelled | 60.4 | 18 | <b>Fold:</b> FAH<br><b>Superfamily:</b> FAH<br><b>Family:</b> FAH  |
| 75 | <a href="#">d1wpga1</a>  | Alignment | not modelled | 59.7 | 26 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Calcium ATPase, transduction domain A<br><b>Family:</b> Calcium ATPase, transduction domain A   |
| 76 | <a href="#">c3eatX_</a>  | Alignment | not modelled | 59.3 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> X: <b>PDB Molecule:</b> pyoverdine biosynthesis protein pvcB;<br><b>PDBTitle:</b> crystal structure of the pvcB (pa2255) protein from2 pseudomonas aeruginosa   |
| 77 | <a href="#">c4afpA_</a>  | Alignment | not modelled | 59.2 | 29 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> metacaspase mca2;<br><b>PDBTitle:</b> the structure of metacaspase 2 from t. brucei determined in the2 presence of samarium  |
| 78 | <a href="#">c6d1oD_</a>  | Alignment | not modelled | 59.1 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> (r)-phenoxypropionate/alpha-ketoglutarate-dioxygenase;  |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
|     |                         |           |              |      |    | <b>PDBTitle:</b> ft_5 dioxygenase apoenzyme   |
| 79  | <a href="#">c2opwA_</a> | Alignment | not modelled | 59.0 | 42 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phyhd1 protein;<br><b>PDBTitle:</b> crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)  |
| 80  | <a href="#">c5xrwD_</a> | Alignment | not modelled | 58.9 | 7  | <b>PDB header:</b> motor protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> flyi;<br><b>PDBTitle:</b> crystal structure of flagellar motor switch complex from h. pylori  |
| 81  | <a href="#">c3uepB_</a> | Alignment | not modelled | 58.7 | 26 | <b>PDB header:</b> protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> ysqc-c, type iii secretion protein;<br><b>PDBTitle:</b> crystal structure of ysqc-c from yersinia pseudotuberculosis  |
| 82  | <a href="#">d1e8ca2</a> | Alignment | not modelled | 58.6 | 25 | <b>Fold:</b> MurD-like peptide ligases, peptide-binding domain<br><b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain<br><b>Family:</b> MurCDEF C-terminal domain   |
| 83  | <a href="#">c2lqkA_</a> | Alignment | not modelled | 58.5 | 24 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> nmr solution structure of the n-terminal domain of the cdnl protein2 from thermus thermophilus                                   |
| 84  | <a href="#">d2nn6h2</a> | Alignment | not modelled | 58.0 | 33 | <b>Fold:</b> Barrel-sandwich hybrid<br><b>Superfamily:</b> Ribosomal L27 protein-like<br><b>Family:</b> ECR1 N-terminal domain-like   |
| 85  | <a href="#">c6dchA_</a> | Alignment | not modelled | 57.7 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> scoe protein;<br><b>PDBTitle:</b> structure of isonitrile biosynthesis enzyme scoe   |
| 86  | <a href="#">c2lt4A_</a> | Alignment | not modelled | 57.5 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, card family;<br><b>PDBTitle:</b> cdnlnt from myxococcus xanthus  |
| 87  | <a href="#">c4j5iH_</a> | Alignment | not modelled | 56.9 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent taurine dioxygenase;<br><b>PDBTitle:</b> crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis           |
| 88  | <a href="#">c4lt5A_</a> | Alignment | not modelled | 56.7 | 46 | <b>PDB header:</b> oxidoreductase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> naegleria tet-like dioxygenase;<br><b>PDBTitle:</b> structure of a naegleria tet-like dioxygenase in complex with 5-2 methylcytosine dna   |
| 89  | <a href="#">c2xxzA_</a> | Alignment | not modelled | 55.6 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase 6b;<br><b>PDBTitle:</b> crystal structure of the human jmjd3 jumonji domain  |
| 90  | <a href="#">d1nx4a_</a> | Alignment | not modelled | 55.3 | 25 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> gamma-Butyrobetaine hydroxylase  |
| 91  | <a href="#">c3r1jB_</a> | Alignment | not modelled | 55.2 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent taurine dioxygenase;<br><b>PDBTitle:</b> crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form     |
| 92  | <a href="#">d1gtta1</a> | Alignment | not modelled | 55.2 | 23 | <b>Fold:</b> FAH<br><b>Superfamily:</b> FAH<br><b>Family:</b> FAH   |
| 93  | <a href="#">c3pvjB_</a> | Alignment | not modelled | 55.1 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent taurine dioxygenase;<br><b>PDBTitle:</b> crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440 |
| 94  | <a href="#">c2nbgA_</a> | Alignment | not modelled | 55.1 | 13 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2;<br><b>PDBTitle:</b> structure of the geobacillus stearothermophilus if2 g3-subdomain  |
| 95  | <a href="#">c4mhuB_</a> | Alignment | not modelled | 55.0 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ectoine hydroxylase;<br><b>PDBTitle:</b> crystal structure of ectd from s. alaskensis with bound fe  |
| 96  | <a href="#">d1y0za_</a> | Alignment | not modelled | 55.0 | 19 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> gamma-Butyrobetaine hydroxylase  |
| 97  | <a href="#">c5vn6B_</a> | Alignment | not modelled | 54.9 | 5  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> taurine dioxygenase;<br><b>PDBTitle:</b> crystal structure of taurine dioxygenase from burkholderia ambifaria  |
| 98  | <a href="#">c5j92B_</a> | Alignment | not modelled | 54.8 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha kg dependent 2,4-d dioxygenase;<br><b>PDBTitle:</b> crystal structure of a putative alpha-ketoglutarate dependent 2,4-d2 dioxygenase from burkholderia xenovorans         |
| 99  | <a href="#">c2kijA_</a> | Alignment | not modelled | 54.4 | 28 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1;<br><b>PDBTitle:</b> solution structure of the actuator domain of the copper-2 transporting atpase atp7a   |
| 100 | <a href="#">c4y0eB_</a> | Alignment | not modelled | 54.2 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative dioxygenase;<br><b>PDBTitle:</b> x-ray crystal structure of a putative dioxygenase from mycobacterium2 abscessus  |
| 101 | <a href="#">c2hc8A_</a> | Alignment | not modelled | 53.9 | 35 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cation-transporting atpase, p-type;<br><b>PDBTitle:</b> structure of the a. fulgidus copa a-domain  |
| 102 | <a href="#">c5d74B_</a> | Alignment | not modelled | 53.8 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative phage lysin;<br><b>PDBTitle:</b> the crystal structure of ly7917   |
| 103 | <a href="#">c2q1dX_</a> | Alignment | not modelled | 53.7 | 8  | <b>PDB header:</b> lyase<br><b>Chain:</b> X: <b>PDB Molecule:</b> 2-keto-3-deoxy-d-arabinonate dehydratase;<br><b>PDBTitle:</b> 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and 2,5-dioxopentanoate   |

|     |                         |   |              |      |    |   |
|-----|-------------------------|---|--------------|------|----|---|
| 104 | <a href="#">c5bkeF_</a> |  Alignment    | not modelled | 53.7 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate<br><b>PDBTitle:</b> crystal structure of aad-2 in complex with mn(ii) and n-oxalylglycine   |
| 105 | <a href="#">d1oiha_</a> |  Alignment   | not modelled | 53.5 | 15 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavamate synthase-like<br><b>Family:</b> TauD/TfdA-like   |
| 106 | <a href="#">c2zauB_</a> |  Alignment   | not modelled | 53.4 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase;<br><b>PDBTitle:</b> crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus  |
| 107 | <a href="#">c6npcB_</a> |  Alignment   | not modelled | 53.3 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tmpa, 2-trimethylaminoethylphosphonate hydroxylase;<br><b>PDBTitle:</b> x-ray crystal structure of tmpa, 2-trimethylaminoethylphosphonate2 hydroxylase, with fe, 2og, and 2-trimethylaminoethylphosphonate |
| 108 | <a href="#">c3ibmB_</a> |  Alignment   | not modelled | 53.0 | 36 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein;<br><b>PDBTitle:</b> crystal structure of cupin 2 domain-containing protein hha_0468 from2 halorhodospira halophila                        |
| 109 | <a href="#">d2nn6i2</a> |  Alignment   | not modelled | 53.0 | 21 | <b>Fold:</b> Barrel-sandwich hybrid<br><b>Superfamily:</b> Ribosomal L27 protein-like<br><b>Family:</b> ECR1 N-terminal domain-like   |
| 110 | <a href="#">c6gmaA_</a> |  Alignment   | not modelled | 52.6 | 17 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> rb1-inducible coiled-coil protein 1;<br><b>PDBTitle:</b> crystal structure of the fip200 c-terminal region  |
| 111 | <a href="#">d1o6aa_</a> |  Alignment   | not modelled | 52.5 | 12 | <b>Fold:</b> Surface presentation of antigens (SPOA)<br><b>Superfamily:</b> Surface presentation of antigens (SPOA)<br><b>Family:</b> Surface presentation of antigens (SPOA)   |
| 112 | <a href="#">c5y9vA_</a> |  Alignment   | not modelled | 52.4 | 11 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ryanodine receptor 1;<br><b>PDBTitle:</b> crystal structure of diamondback moth ryanodine receptor n-terminal2 domain   |
| 113 | <a href="#">d2hd9a1</a> |  Alignment   | not modelled | 52.3 | 21 | <b>Fold:</b> PUA domain-like<br><b>Superfamily:</b> PUA domain-like<br><b>Family:</b> Atu2648/PH1033-like   |
| 114 | <a href="#">cli7oC_</a> |  Alignment  | not modelled | 52.0 | 19 | <b>PDB header:</b> isomerase, lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxyphenylacetate degradation bifunctional<br><b>PDBTitle:</b> crystal structure of hpce  |
| 115 | <a href="#">c4cswA_</a> |  Alignment | not modelled | 51.5 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cupin 4 family protein;<br><b>PDBTitle:</b> rhodothermus marinus ycf-d-like ribosomal protein l16 arginyl2 hydroxylase   |
| 116 | <a href="#">c6b8wB_</a> |  Alignment | not modelled | 51.2 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> xre family transcriptional regulator;<br><b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of cupin_2 domain (pfam2 07883) of xre family transcriptional regulator from enterobacter3 cloacae.     |
| 117 | <a href="#">c4rgkA_</a> |  Alignment | not modelled | 51.1 | 37 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of putative phytanoyl-coa dioxygenase family protein2 ybiu from yersinia pestis                                      |
| 118 | <a href="#">d1we3o_</a> |  Alignment | not modelled | 51.1 | 24 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> GroES   |
| 119 | <a href="#">c4diqA_</a> |  Alignment | not modelled | 51.1 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase no66;<br><b>PDBTitle:</b> crystal structure of human no66  |
| 120 | <a href="#">c3ms5A_</a> |  Alignment | not modelled | 51.1 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gamma-butyrobetaine dioxygenase;<br><b>PDBTitle:</b> crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)  |