



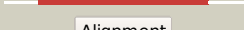

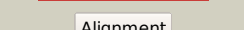

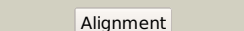





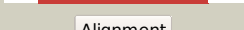

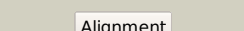

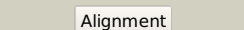





# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD1000c_(-)_1116535_1117152 |
| Date          | Wed Jul 31 22:05:07 BST 2019  |
| Unique Job ID | cbee898b6feb6c9c              |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c3btzA_</a> | <br>Alignment   |    | 100.0      | 27     | <b>PDB header:</b> oxidoreductase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent dioxygenase alkb homolog 2;<br><b>PDBTitle:</b> crystal structure of human abh2 cross-linked to dsdna   |
| 2  | <a href="#">c2iuwA_</a> | <br>Alignment   |    | 100.0      | 30     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alkylated repair protein alkb homolog 3;<br><b>PDBTitle:</b> crystal structure of human abh3 in complex with iron ion and 2-2 oxoglutarate  |
| 3  | <a href="#">d2iuwa1</a> | <br>Alignment   |    | 100.0      | 30     | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminic synthase-like<br><b>Family:</b> AlkB-like  |
| 4  | <a href="#">d2fdia1</a> | <br>Alignment   |   | 100.0      | 23     | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminic synthase-like<br><b>Family:</b> AlkB-like  |
| 5  | <a href="#">c4qkbA_</a> | <br>Alignment |  | 100.0      | 20     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent dioxygenase alkb homolog 7,<br><b>PDBTitle:</b> crystal structure of seleno-methionine labelled human alkbh7 in2 complex with alpha-ketoglutarate and mn(ii)  |
| 6  | <a href="#">c3thtB_</a> | <br>Alignment |  | 100.0      | 22     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alkylated dna repair protein alkb homolog 8;<br><b>PDBTitle:</b> crystal structure and rna binding properties of the rrm/alkb domains2 in human abh8, an enzyme catalyzing trna hypermodification, northeast3 structural genomics consortium target hr5601b |
| 7  | <a href="#">c5ylbA_</a> | <br>Alignment |  | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein p8a3.02c;<br><b>PDBTitle:</b> crystal structure of ofd2 from schizosaccharomyces pombe at 1.80 a  |
| 8  | <a href="#">c5xoiA_</a> | <br>Alignment |  | 100.0      | 18     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, 2og-fe oxygenase family protein, putative,<br><b>PDBTitle:</b> the structure of osalkbh1  |
| 9  | <a href="#">c4nj4A_</a> | <br>Alignment |  | 100.0      | 23     | <b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> rna demethylase alkbh5;<br><b>PDBTitle:</b> crystal structure of human alkbh5  |
| 10 | <a href="#">c3fma_</a>  | <br>Alignment |  | 99.1       | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein fto;<br><b>PDBTitle:</b> crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity  |
| 11 | <a href="#">c3dkqB_</a> | <br>Alignment |  | 97.8       | 16     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pkhd-type hydroxylase sba1_3634;<br><b>PDBTitle:</b> crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | <a href="#">c2g19A_</a> | Alignment |              | 97.7 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> egl nine homolog 1;<br><b>PDBTitle:</b> cellular oxygen sensing: crystal structure of hypoxia-inducible factor2 prolyl hydroxylase (phd2)  |
| 13 | <a href="#">c3ouia_</a> | Alignment |              | 97.5 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> egl nine homolog 1;<br><b>PDBTitle:</b> phd2-r717 with 40787422  |
| 14 | <a href="#">c4iw3J_</a> | Alignment |              | 97.0 | 12 | <b>PDB header:</b> metal binding protein/translation<br><b>Chain:</b> J: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a pseudomonas putida prolyl-4-hydroxylase (p4h)2 in complex with elongation factor tu (ef-tu)  |
| 15 | <a href="#">c6f0wA_</a> | Alignment |              | 96.9 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hif prolyl hydroxylase;<br><b>PDBTitle:</b> prolyl hydroxylase in complex with hypoxia inducible factor oxygen2 degradation domain peptide fragment from trichoplax adhaerens  |
| 16 | <a href="#">c6n1fD_</a> | Alignment |              | 96.2 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, 2og-fe(ii) oxygenase family;<br><b>PDBTitle:</b> crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei   |
| 17 | <a href="#">c4zonB_</a> | Alignment |              | 95.8 | 17 | <b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> verruculogen synthase;<br><b>PDBTitle:</b> structure of ftmxo1 with fumitremorgen b complex   |
| 18 | <a href="#">c3gjbA_</a> | Alignment |              | 95.6 | 18 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytc3;<br><b>PDBTitle:</b> cytc3 with fe(ii) and alpha-ketoglutarate   |
| 19 | <a href="#">c5c3qB_</a> | Alignment |              | 95.5 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thymine dioxygenase;<br><b>PDBTitle:</b> crystal structure of the full-length neurospora crassa t7h in complex2 with alpha-kg and thymine (t)  |
| 20 | <a href="#">c4diqA_</a> | Alignment |              | 95.5 | 20 | <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  |
| 21 | <a href="#">c5m0tA_</a> | Alignment | not modelled | 94.8 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash;<br><b>PDBTitle:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash   |
| 22 | <a href="#">c4nubA_</a> | Alignment | not modelled | 94.7 | 19 | <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   |
| 23 | <a href="#">c2jiiA_</a> | Alignment | not modelled | 94.7 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prolyl-4 hydroxylase;<br><b>PDBTitle:</b> crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i   |
| 24 | <a href="#">c4cswA_</a> | Alignment | not modelled | 94.6 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cupin 4 family protein;<br><b>PDBTitle:</b> rhodothermus marinus ycfd-like ribosomal protein l16 arginyl2 hydroxylase  |
| 25 | <a href="#">c5yboA_</a> | Alignment | not modelled | 94.5 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prha;<br><b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoid a1  |
| 26 | <a href="#">c2xdvA_</a> | Alignment | not modelled | 94.5 | 26 | <b>PDB header:</b> nuclear protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> myc-induced nuclear antigen;<br><b>PDBTitle:</b> crystal structure of the catalytic domain of flj14393  |
| 27 | <a href="#">c4nhyC_</a> | Alignment | not modelled | 94.5 | 17 | <b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor<br><b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate and iron-dependent oxygenase domain-<br><b>PDBTitle:</b> crystal structure of human ogfod1, 2-oxoglutarate and iron-dependent2 oxygenase domain containing 1, in complex with pyridine-2,4-3 dicarboxylic acid (2,4-pdca)<br><b>PDB header:</b> oxidoreductase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 28 | <a href="#">c3on7C_</a> | Alignment | not modelled | 94.5 | 22 | <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, iron/ascorbate family;<br><b>PDBTitle:</b> crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution  |
| 29 | <a href="#">c5daqA_</a> | Alignment | not modelled | 94.3 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phytanoyl-coa dioxygenase family protein (afu_orthologue<br><b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase asqj in complex with2 4-methoxycyclopeptin                         |
| 30 | <a href="#">c5epaE_</a> | Alignment | not modelled | 94.2 | 17 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> snok;<br><b>PDBTitle:</b> crystal structure of non-heme alpha ketoglutarate dependent2 carbocyclase snok from nogalamycin biosynthesis   |
| 31 | <a href="#">c4xaaA_</a> | Alignment | not modelled | 94.1 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative oxygenase;<br><b>PDBTitle:</b> crystal structure of avio1 from streptomyces viridochromogenes tue57  |
| 32 | <a href="#">c5zm4B_</a> | Alignment | not modelled | 94.1 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dioxygenase anda;<br><b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c  |
| 33 | <a href="#">c2opwA_</a> | Alignment | not modelled | 93.9 | 17 | <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)   |
| 34 | <a href="#">c3ooxA_</a> | Alignment | not modelled | 93.6 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative 2og-fe(ii) oxygenase family protein;<br><b>PDBTitle:</b> crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution |
| 35 | <a href="#">c6jyvA_</a> | Alignment | not modelled | 93.2 | 18 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable iron/ascorbate oxidoreductase;<br><b>PDBTitle:</b> structure of an isopenicillin n synthase from pseudomonas aeruginosa2 pao1   |
| 36 | <a href="#">d1w9ya1</a> | Alignment | not modelled | 93.1 | 22 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminat synthase-like<br><b>Family:</b> Penicillin synthase-like   |
| 37 | <a href="#">c3itqB_</a> | Alignment | not modelled | 93.0 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prolyl 4-hydroxylase, alpha subunit domain protein;<br><b>PDBTitle:</b> crystal structure of a prolyl 4-hydroxylase from bacillus anthracis   |
| 38 | <a href="#">c4naoA_</a> | Alignment | not modelled | 92.9 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative oxygenase;<br><b>PDBTitle:</b> crystal structure of eash   |
| 39 | <a href="#">c5gj9A_</a> | Alignment | not modelled | 92.4 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1-aminocyclopropane-1-carboxylate oxidase 2;<br><b>PDBTitle:</b> crystal structure of arabidopsis thaliana aco2 in complex with poa   |
| 40 | <a href="#">c5o7yA_</a> | Alignment | not modelled | 92.4 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thebaine 6-o-demethylase;<br><b>PDBTitle:</b> thebaine 6-o-demethylase (t6odm) from papaver somniferum in complex2 with succinate   |
| 41 | <a href="#">d1gp6a_</a> | Alignment | not modelled | 91.2 | 14 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminat synthase-like<br><b>Family:</b> Penicillin synthase-like   |
| 42 | <a href="#">c4xaeB_</a> | Alignment | not modelled | 89.4 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> feruloyl coa ortho-hydroxylase 1;<br><b>PDBTitle:</b> structure of feruloyl-coa 6-hydroxylase (f6h) from arabidopsis2 thaliana  |
| 43 | <a href="#">c4lt5A_</a> | Alignment | not modelled | 87.3 | 23 | <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  |
| 44 | <a href="#">c5c5tB_</a> | Alignment | not modelled | 86.7 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prolyl 4-hydroxylase;<br><b>PDBTitle:</b> the crystal structure of viral collagen prolyl hydroxylase vcph from2 paramecium bursaria chlorella virus-1 - 2og complex                               |
| 45 | <a href="#">c3kt4A_</a> | Alignment | not modelled | 86.5 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pkhd-type hydroxylase tpa1;<br><b>PDBTitle:</b> crystal structure of tpa1 from saccharomyces cerevisiae, a component2 of the messenger ribonucleoprotein complex                                  |
| 46 | <a href="#">c6ax6B_</a> | Alignment | not modelled | 85.5 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> procollagen lysyl hydroxylase and glycosyltransferase;<br><b>PDBTitle:</b> the crystal structure of a lysyl hydroxylase from acanthamoeba2 polyphaga mimivirus                                    |
| 47 | <a href="#">c4xabA_</a> | Alignment | not modelled | 84.6 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> evdo2;<br><b>PDBTitle:</b> crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca   |
| 48 | <a href="#">c6ec3C_</a> | Alignment | not modelled | 83.8 | 15 | <b>PDB header:</b> transferase, oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein;<br><b>PDBTitle:</b> crystal structure of evdmo1   |
| 49 | <a href="#">c4nm6A_</a> | Alignment | not modelled | 82.2 | 14 | <b>PDB header:</b> oxidoreductase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> methylcytosine dioxygenase tet2;<br><b>PDBTitle:</b> crystal structure of tet2-dna complex  |
| 50 | <a href="#">c2rdsA_</a> | Alignment | not modelled | 80.9 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha-<br><b>PDBTitle:</b> crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound                              |
| 51 | <a href="#">c4mhuB_</a> | Alignment | not modelled | 78.9 | 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   |
| 52 | <a href="#">c3bvcA_</a> | Alignment | not modelled | 78.8 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ism_01780;<br><b>PDBTitle:</b> crystal structure of uncharacterized protein ism_01780  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | from2 roseovarius nubinhibens ism  |
| 53 | <a href="#">d2a1xa1</a> | Alignment | not modelled | 78.0 | 11 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> PhyH-like   |
| 54 | <a href="#">d1vr3a1</a> | Alignment | not modelled | 77.4 | 22 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmIC-like cupins<br><b>Family:</b> Acireductone dioxygenase   |
| 55 | <a href="#">d2fcta1</a> | Alignment | not modelled | 77.0 | 14 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> PhyH-like   |
| 56 | <a href="#">d1vrba1</a> | Alignment | not modelled | 74.6 | 15 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> Asparaginyl hydroxylase-like  |
| 57 | <a href="#">c5lunC</a>  | Alignment | not modelled | 68.9 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate-dependent ethylene/succinate-forming enzyme;<br><b>PDBTitle:</b> ethylene forming enzyme from pseudomonas syringae pv. phaseolicola -2 p1 ultra-high resolution crystal form in complex with iron, n-3 oxalyglycine and arginine |
| 58 | <a href="#">c6iuqA</a>  | Alignment | not modelled | 67.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prolyl 4-hydroxylase;<br><b>PDBTitle:</b> crystal structure and expression patterns of prolyl 4-hydroxylases2 from phytophthora capsici   |
| 59 | <a href="#">c5ncjB</a>  | Alignment | not modelled | 64.4 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> leucine hydroxylase;<br><b>PDBTitle:</b> grie in complex with manganese, succinate and (2s,4r)-5-hydroxyleucine   |
| 60 | <a href="#">c5erID</a>  | Alignment | not modelled | 57.7 | 29 | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> snon,snon;<br><b>PDBTitle:</b> crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro   |
| 61 | <a href="#">c3al6C</a>  | Alignment | not modelled | 54.2 | 24 | <b>PDB header:</b> unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> jmjc domain-containing protein c2orf60;<br><b>PDBTitle:</b> crystal structure of human tyw5   |
| 62 | <a href="#">d1odma</a>  | Alignment | not modelled | 52.5 | 20 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> Penicillin synthase-like  |
| 63 | <a href="#">c4p7xA</a>  | Alignment | not modelled | 51.6 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-proline cis-4-hydroxylase;<br><b>PDBTitle:</b> l-pipecolic acid-bound l-proline cis-4-hydroxylase   |
| 64 | <a href="#">c3mguA</a>  | Alignment | not modelled | 50.4 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pkhd-type hydroxylase tpa1;<br><b>PDBTitle:</b> structure of s. cerevisiae tpa1 protein, a proline hydroxylase2 modifying ribosomal protein rps23   |
| 65 | <a href="#">c4b6wA</a>  | Alignment | not modelled | 45.7 | 7  | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> tubulin-specific chaperone;<br><b>PDBTitle:</b> architecture of trypanosoma brucei tubulin-binding cofactor b  |
| 66 | <a href="#">c3al6A</a>  | Alignment | not modelled | 42.3 | 26 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> jmjc domain-containing protein c2orf60;<br><b>PDBTitle:</b> crystal structure of human tyw5   |
| 67 | <a href="#">c2kjrA</a>  | Alignment | not modelled | 42.1 | 12 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> cg11242;<br><b>PDBTitle:</b> solution nmr structure of the n-terminal ubiquitin-like2 domain from tubulin-binding cofactor b, cg11242, from3 drosophila melanogaster. northeast structural genomics4 consortium target fr629a (residues 8-92)        |
| 68 | <a href="#">d1dcsa</a>  | Alignment | not modelled | 42.1 | 19 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Clavaminatase synthase-like<br><b>Family:</b> Penicillin synthase-like  |
| 69 | <a href="#">c3uyjA</a>  | Alignment | not modelled | 32.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase 8;<br><b>PDBTitle:</b> crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg  |
| 70 | <a href="#">d2bpa1</a>  | Alignment | not modelled | 29.1 | 40 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Microviridae-like VP  |
| 71 | <a href="#">d1kvpa</a>  | Alignment | not modelled | 28.0 | 40 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Microviridae-like VP  |
| 72 | <a href="#">c2l05A</a>  | Alignment | not modelled | 25.5 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase b-raf;<br><b>PDBTitle:</b> 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                 |
| 73 | <a href="#">c4xc9B</a>  | Alignment | not modelled | 24.6 | 18 | <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  |
| 74 | <a href="#">c3emrA</a>  | Alignment | not modelled | 22.8 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ectcd;<br><b>PDBTitle:</b> crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens   |
| 75 | <a href="#">c2kj6A</a>  | Alignment | not modelled | 22.4 | 17 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> tubulin folding cofactor b;<br><b>PDBTitle:</b> nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a   |
| 76 | <a href="#">c4qszB</a>  | Alignment | not modelled | 20.6 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein, jmjc domain-containing<br><b>PDBTitle:</b> crystal structure of mouse jmjd7 fused with maltose-binding protein  |
| 77 | <a href="#">d1zvfa1</a> | Alignment | not modelled | 20.1 | 7  | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmIC-like cupins  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
|    |                         |           |              |      |    | <b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like   |
| 78 | <a href="#">c4xbzB_</a> | Alignment | not modelled | 19.1 | 18 | <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  |
| 79 | <a href="#">d1miau1</a> | Alignment | not modelled | 18.2 | 29 | <b>Fold:</b> BRCA2 helical domain<br><b>Superfamily:</b> BRCA2 helical domain<br><b>Family:</b> BRCA2 helical domain  |
| 80 | <a href="#">d1m06f_</a> | Alignment | not modelled | 18.0 | 47 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Microviridae-like VP   |
| 81 | <a href="#">c4ar0A_</a> | Alignment | not modelled | 14.7 | 23 | <b>PDB header:</b> transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> type iv pilus biogenesis and competence protein pilq;<br><b>PDBTitle:</b> n0 domain of neisseria meningitidis pilus assembly protein pilq   |
| 82 | <a href="#">d1v6ea_</a> | Alignment | not modelled | 14.1 | 10 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> Ubiquitin-like<br><b>Family:</b> Ubiquitin-related  |
| 83 | <a href="#">c3rcqA_</a> | Alignment | not modelled | 13.8 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl/asparaginyl beta-hydroxylase;<br><b>PDBTitle:</b> crystal structure of human aspartate beta-hydroxylase isoform a   |
| 84 | <a href="#">d1gff1_</a> | Alignment | not modelled | 13.7 | 47 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> ssDNA viruses<br><b>Family:</b> Microviridae-like VP   |
| 85 | <a href="#">c3k2oB_</a> | Alignment | not modelled | 10.8 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional arginine demethylase and lysyl-hydroxylase<br><b>PDBTitle:</b> structure of an oxygenase  |
| 86 | <a href="#">d1t0ya_</a> | Alignment | not modelled | 10.6 | 7  | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> Ubiquitin-like<br><b>Family:</b> Ubiquitin-related  |
| 87 | <a href="#">c1t0yA_</a> | Alignment | not modelled | 10.6 | 7  | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> tubulin folding cofactor b;<br><b>PDBTitle:</b> solution structure of a ubiquitin-like domain from tubulin-2 binding cofactor b   |
| 88 | <a href="#">d1ra0a1</a> | Alignment | not modelled | 10.2 | 23 | <b>Fold:</b> Composite domain of metallo-dependent hydrolases<br><b>Superfamily:</b> Composite domain of metallo-dependent hydrolases<br><b>Family:</b> Cytosine deaminase  |
| 89 | <a href="#">c5jqvA_</a> | Alignment | not modelled | 9.4  | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl/asparaginyl beta-hydroxylase;<br><b>PDBTitle:</b> aspartyl/asparaginyl beta-hydroxylase (asph)oxxygenase and tpr domains2 in complex with manganese, n-oxalyglycine and factor x substrate3 peptide fragment(39mer-4ser)                            |
| 90 | <a href="#">d1yfua1</a> | Alignment | not modelled | 7.3  | 15 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmLC-like cupins<br><b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like  |
| 91 | <a href="#">d2ijra1</a> | Alignment | not modelled | 7.3  | 25 | <b>Fold:</b> Api92-like<br><b>Superfamily:</b> Api92-like<br><b>Family:</b> Api92-like  |
| 92 | <a href="#">c3dg8B_</a> | Alignment | not modelled | 7.0  | 24 | <b>PDB header:</b> oxidoreductase, transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional dihydrofolate reductase-thymidylate synthase;<br><b>PDBTitle:</b> quadruple mutant (n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase (pdfhfr-ts) complexed3 with rjf670, nadph, and dump |
| 93 | <a href="#">c3pl0B_</a> | Alignment | not modelled | 6.7  | 27 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution   |
| 94 | <a href="#">d1kxpd3</a> | Alignment | not modelled | 6.6  | 5  | <b>Fold:</b> Serum albumin-like<br><b>Superfamily:</b> Serum albumin-like<br><b>Family:</b> Serum albumin-like  |
| 95 | <a href="#">d1j3ka_</a> | Alignment | not modelled | 6.4  | 24 | <b>Fold:</b> Dihydrofolate reductase-like<br><b>Superfamily:</b> Dihydrofolate reductase-like<br><b>Family:</b> Dihydrofolate reductases  |
| 96 | <a href="#">d1iyb1</a>  | Alignment | not modelled | 6.3  | 24 | <b>Fold:</b> BRCA2 helical domain<br><b>Superfamily:</b> BRCA2 helical domain<br><b>Family:</b> BRCA2 helical domain  |
| 97 | <a href="#">c4kheE_</a> | Alignment | not modelled | 5.9  | 40 | <b>PDB header:</b> transcription/replication<br><b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein spt16d;<br><b>PDBTitle:</b> structure of the spt16d pob3n heterodimer   |
| 98 | <a href="#">c5c33B_</a> | Alignment | not modelled | 5.8  | 18 | <b>PDB header:</b> contractile protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ryanodine receptor 2;<br><b>PDBTitle:</b> crystal structure of mouse ryanodine receptor 2 spry1 domain  |
| 99 | <a href="#">c4idxA_</a> | Alignment | not modelled | 5.8  | 24 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nucleocapsid protein;<br><b>PDBTitle:</b> hexameric crystal structure of schmallenberg virus nucleoprotein  |