
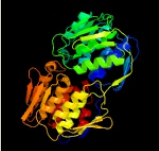
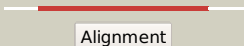
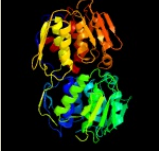


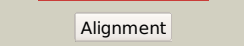
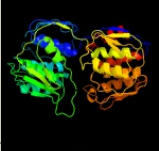



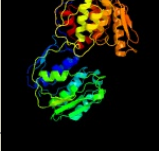
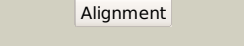

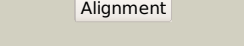

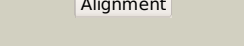

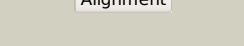
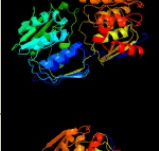
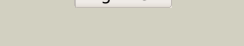
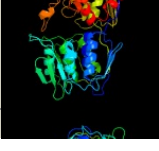
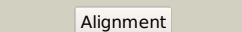



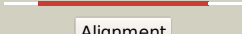

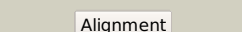











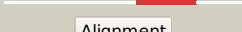


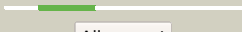
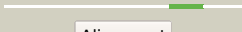
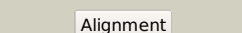




# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD3227_(aroA)_3603374_3604726 |
| Date          | Thu Aug 8 16:20:43 BST 2019     |
| Unique Job ID | 7ead958fbdf313c3                |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2o0zA_</a> |  Alignment   |    | 100.0      | 100    | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> mycobacterium tuberculosis epsp synthase in complex with product (eps)   |
| 2  | <a href="#">d1g6sa_</a> |  Alignment   |    | 100.0      | 32     | <b>Fold:</b> IF3-like<br><b>Superfamily:</b> EPT/RTPC-like<br><b>Family:</b> Enolpyruvate transferase, EPT   |
| 3  | <a href="#">c5xwbB_</a> |  Alignment   |    | 100.0      | 31     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> crystal structure of 5-enolpyruvylshikimate-3-phosphate synthase from2 a psychrophilic bacterium, colwellia psychrerythraea                      |
| 4  | <a href="#">c5bufA_</a> |  Alignment   |   | 100.0      | 26     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> 2.37 angstrom structure of epsp synthase from acinetobacter baumannii  |
| 5  | <a href="#">d1rf6a_</a> |  Alignment |  | 100.0      | 24     | <b>Fold:</b> IF3-like<br><b>Superfamily:</b> EPT/RTPC-like<br><b>Family:</b> Enolpyruvate transferase, EPT   |
| 6  | <a href="#">c3roiA_</a> |  Alignment |  | 100.0      | 29     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> 2.20 angstrom resolution structure of 3-phosphoshikimate 1-2 carboxyvinyltransferase (aroa) from coxiella burnetii                               |
| 7  | <a href="#">c3r38A_</a> |  Alignment |  | 100.0      | 19     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase 1;<br><b>PDBTitle:</b> 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e |
| 8  | <a href="#">c2pqdA_</a> |  Alignment |  | 100.0      | 28     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> a100g cp4 epsps liganded with (r)-difluoromethyl tetrahedral reaction2 intermediate analog   |
| 9  | <a href="#">c5ujsB_</a> |  Alignment |  | 100.0      | 19     | <b>PDB header:</b> hydrolase,oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> 2.45 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from campylobacter jejuni.    |
| 10 | <a href="#">c3rmtB_</a> |  Alignment |  | 100.0      | 27     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase 1;<br><b>PDBTitle:</b> crystal structure of putative 5-enolpyruvylshikimate-3-phosphate2 synthase from bacillus halodurans c-125                                      |
| 11 | <a href="#">d1ejda_</a> |  Alignment |  | 100.0      | 19     | <b>Fold:</b> IF3-like<br><b>Superfamily:</b> EPT/RTPC-like<br><b>Family:</b> Enolpyruvate transferase, EPT   |
|    |                         |   |   |            |        | <b>PDB header:</b> lipid-binding protein   |

|    |                         |   |   |       |    |  |
|----|-------------------------|---|---|-------|----|--|
| 12 | <a href="#">c5u4hB_</a> |  Alignment   |     | 100.0 | 18 | <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> 1.05 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from acinetobacter baumannii in covalently3 bound complex with (2r)-2-(phosphonoxy)propanoic acid.   |
| 13 | <a href="#">d1uaea_</a> |  Alignment   |    | 100.0 | 18 | <b>Fold:</b> IF3-like<br><b>Superfamily:</b> EPT/RTPC-like<br><b>Family:</b> Enolpyruvate transferase, EPT   |
| 14 | <a href="#">c5wi5C_</a> |  Alignment   |    | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase 1;<br><b>PDBTitle:</b> 2.0 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from streptococcus pneumoniae in complex3 with uridine-diphosphate-2(n-acetylglucosaminy) butyric acid, (2r)-4 2-(phosphonoxy)propanoic acid and magnesium. |
| 15 | <a href="#">c5bq2C_</a> |  Alignment   |    | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 (udp-n-acetylglucosamine enolpyruvyl transferase, ept) from3 pseudomonas aeruginosa   |
| 16 | <a href="#">c3zh3A_</a> |  Alignment   |    | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> crystal structure of s. pneumoniae d39 native mura1   |
| 17 | <a href="#">c4fqdA_</a> |  Alignment   |    | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> niko protein;<br><b>PDBTitle:</b> crystal structure of the enolpyruvyl transferase niko from2 streptomyces tendae  |
| 18 | <a href="#">c2yvva_</a> |  Alignment |  | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase;<br><b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 from aquifex aeolicus vf5   |
| 19 | <a href="#">d1p88a_</a> |  Alignment |  | 100.0 | 31 | <b>Fold:</b> IF3-like<br><b>Superfamily:</b> EPT/RTPC-like<br><b>Family:</b> Enolpyruvate transferase, EPT   |
| 20 | <a href="#">d1qmha2</a> |  Alignment |  | 96.1  | 19 | <b>Fold:</b> IF3-like<br><b>Superfamily:</b> EPT/RTPC-like<br><b>Family:</b> RNA 3'-terminal phosphate cyclase, RTPC   |
| 21 | <a href="#">c3pqvD_</a> |  Alignment | not modelled  | 95.3  | 16 | <b>PDB header:</b> unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> rc11 protein;<br><b>PDBTitle:</b> cyclase homolog   |
| 22 | <a href="#">c1qmiC_</a> |  Alignment | not modelled  | 94.5  | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> rna 3'-terminal phosphate cyclase;<br><b>PDBTitle:</b> crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology  |
| 23 | <a href="#">c4o8jB_</a> |  Alignment | not modelled  | 71.8  | 21 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> rna 3'-terminal phosphate cyclase;<br><b>PDBTitle:</b> crystal structure of rtca, the rna 3'-terminal phosphate cyclase from2 pyrococcus horikoshii, in complex with racaaa3'phosphate and adenine.   |
| 24 | <a href="#">c4muoB_</a> |  Alignment | not modelled  | 58.1  | 17 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ybib;<br><b>PDBTitle:</b> the trpd2 enzyme from e.coli: ybib   |
| 25 | <a href="#">d1x9za_</a> |  Alignment | not modelled  | 55.6  | 19 | <b>Fold:</b> DNA mismatch repair protein MutL<br><b>Superfamily:</b> DNA mismatch repair protein MutL<br><b>Family:</b> DNA mismatch repair protein MutL   |
| 26 | <a href="#">c1khdD_</a> |  Alignment | not modelled  | 42.7  | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase;<br><b>PDBTitle:</b> crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.9 resolution3 (current name, pectobacterium carotovorum)  |
| 27 | <a href="#">c1v8gB_</a> |  Alignment | not modelled  | 35.1  | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase;<br><b>PDBTitle:</b> crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8  |
| 28 | <a href="#">c2ox1C_</a> |  Alignment | not modelled  | 34.0  | 12 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase;<br><b>PDBTitle:</b> archaeal dehydroquinase  |
|    |                         |   |   |       |    | <b>Fold:</b> Common fold of diphtheria toxin/transcription   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">d1a66a_</a> | Alignment | not modelled | 31.1 | 33 | factors/cytochrome f<br><b>Superfamily:</b> p53-like transcription factors<br><b>Family:</b> Rel/Dorsal transcription factors, DNA-binding domain  |
| 30 | <a href="#">d2fvta1</a> | Alignment | not modelled | 29.9 | 12 | <b>Fold:</b> MTH938-like<br><b>Superfamily:</b> MTH938-like<br><b>Family:</b> MTH938-like  |
| 31 | <a href="#">d1ml4a2</a> | Alignment | not modelled | 29.8 | 13 | <b>Fold:</b> ATC-like<br><b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase<br><b>Family:</b> Aspartate/ornithine carbamoyltransferase   |
| 32 | <a href="#">c4gtnA_</a> | Alignment | not modelled | 29.6 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase;<br><b>PDBTitle:</b> structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi  |
| 33 | <a href="#">d1a9xa1</a> | Alignment | not modelled | 27.1 | 25 | <b>Fold:</b> Carbamoyl phosphate synthetase, large subunit connection domain<br><b>Superfamily:</b> Carbamoyl phosphate synthetase, large subunit connection domain<br><b>Family:</b> Carbamoyl phosphate synthetase, large subunit connection domain  |
| 34 | <a href="#">d1ekxa2</a> | Alignment | not modelled | 26.0 | 13 | <b>Fold:</b> ATC-like<br><b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase<br><b>Family:</b> Aspartate/ornithine carbamoyltransferase   |
| 35 | <a href="#">c3ncvB_</a> | Alignment | not modelled | 25.5 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein mutl;<br><b>PDBTitle:</b> ngol   |
| 36 | <a href="#">c2zxrA_</a> | Alignment | not modelled | 24.6 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna specific exonuclease recj;<br><b>PDBTitle:</b> crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8   |
| 37 | <a href="#">d2atca2</a> | Alignment | not modelled | 24.4 | 13 | <b>Fold:</b> ATC-like<br><b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase<br><b>Family:</b> Aspartate/ornithine carbamoyltransferase   |
| 38 | <a href="#">c2gm2A_</a> | Alignment | not modelled | 24.1 | 11 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein;<br><b>PDBTitle:</b> nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35                                |
| 39 | <a href="#">c3gabC_</a> | Alignment | not modelled | 23.9 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dna mismatch repair protein mutl;<br><b>PDBTitle:</b> c-terminal domain of bacillus subtilis mutl crystal form i   |
| 40 | <a href="#">c5f56A_</a> | Alignment | not modelled | 22.3 | 31 | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded-dna-specific exonuclease;<br><b>PDBTitle:</b> structure of recj complexed with dna and ssb-ct  |
| 41 | <a href="#">c2yswB_</a> | Alignment | not modelled | 17.8 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase;<br><b>PDBTitle:</b> crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5   |
| 42 | <a href="#">c4kjeA_</a> | Alignment | not modelled | 16.4 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> atomic resolution structure of pfgxr1   |
| 43 | <a href="#">c2ltkA_</a> | Alignment | not modelled | 16.2 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mono-cysteine glutaredoxin;<br><b>PDBTitle:</b> solution structure of a monomeric truncated mutant of trypanosoma2 brucei 1-c-grx1  |
| 44 | <a href="#">c1o17A_</a> | Alignment | not modelled | 16.0 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase;<br><b>PDBTitle:</b> anthranilate phosphoribosyl-transferase (trpd)   |
| 45 | <a href="#">d2fi9a1</a> | Alignment | not modelled | 15.3 | 10 | <b>Fold:</b> MTH938-like<br><b>Superfamily:</b> MTH938-like<br><b>Family:</b> MTH938-like  |
| 46 | <a href="#">c5yq7L_</a> | Alignment | not modelled | 14.8 | 15 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> L: <b>PDB Molecule:</b> precursor for l subunits of photosynthetic reaction center;<br><b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii  |
| 47 | <a href="#">d1jcb2</a>  | Alignment | not modelled | 14.6 | 28 | <b>Fold:</b> Putative DNA-binding domain<br><b>Superfamily:</b> Putative DNA-binding domain<br><b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT  |
| 48 | <a href="#">d1ni9a_</a> | Alignment | not modelled | 14.5 | 30 | <b>Fold:</b> Carbohydrate phosphatase<br><b>Superfamily:</b> Carbohydrate phosphatase<br><b>Family:</b> GlpX-like bacterial fructose-1,6-bisphosphatase  |
| 49 | <a href="#">d1u0bb1</a> | Alignment | not modelled | 14.1 | 18 | <b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br><b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br><b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases |
| 50 | <a href="#">c1vqzA_</a> | Alignment | not modelled | 14.0 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lipoate-protein ligase, putative;<br><b>PDBTitle:</b> crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution  |
| 51 | <a href="#">c1ml4A_</a> | Alignment | not modelled | 13.2 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate transcarbamoylase;<br><b>PDBTitle:</b> the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi   |
| 52 | <a href="#">d1vpka1</a> | Alignment | not modelled | 12.5 | 20 | <b>Fold:</b> DNA clamp<br><b>Superfamily:</b> DNA clamp<br><b>Family:</b> DNA polymerase III, beta subunit   |
| 53 | <a href="#">c3js3C_</a> | Alignment | not modelled | 12.4 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase;<br><b>PDBTitle:</b> crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate<br><b>PDB header:</b> transferase        |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 54 | <a href="#">c2bpqB_</a> | Alignment | not modelled | 11.7 | 19 | <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)   |
| 55 | <a href="#">c5nofB_</a> | Alignment | not modelled | 11.3 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase from thermococcus kodakaraensis   |
| 56 | <a href="#">d2dy1a4</a> | Alignment | not modelled | 11.2 | 12 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> EF-G C-terminal domain-like<br><b>Family:</b> EF-G/eEF-2 domains III and V  |
| 57 | <a href="#">c2yr1B_</a> | Alignment | not modelled | 10.9 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426  |
| 58 | <a href="#">c4yegA_</a> | Alignment | not modelled | 10.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyphosphate kinase 2; <b>PDBTitle:</b> characterisation of polyphosphate kinase 2 from the intracellular2 pathogen francisella tularensis   |
| 59 | <a href="#">c3czqA_</a> | Alignment | not modelled | 10.6 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative polyphosphate kinase 2; <b>PDBTitle:</b> crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti   |
| 60 | <a href="#">c2gjhA_</a> | Alignment | not modelled | 10.5 | 29 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)  |
| 61 | <a href="#">c3nr6A_</a> | Alignment | not modelled | 10.3 | 32 | <b>PDB header:</b> hydrolase/inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> protease p14; <b>PDBTitle:</b> crystal structure of xenotropic murine leukemia virus-related virus2 (xmrv) protease   |
| 62 | <a href="#">d1sr9a3</a> | Alignment | not modelled | 10.1 | 21 | <b>Fold:</b> 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain<br><b>Superfamily:</b> 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain<br><b>Family:</b> 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain |
| 63 | <a href="#">c5m64M_</a> | Alignment | not modelled | 10.0 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> M: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa49; <b>PDBTitle:</b> rna polymerase i elongation complex with a49 tandem winged helix2 domain  |
| 64 | <a href="#">c6ayyB_</a> | Alignment | not modelled | 9.9  | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fructose-1,6-bisphosphatase class 2; <b>PDBTitle:</b> crystal structure of apo fructose-1,6-bisphosphatase from2 mycobacterium tuberculosis   |
| 65 | <a href="#">c5ld1D_</a> | Alignment | not modelled | 9.7  | 7  | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> polyphosphate:amp phosphotransferase; <b>PDBTitle:</b> crystal structure of polyphosphate kinase from meiothermus ruber bound2 to atp   |
| 66 | <a href="#">d1nh2a1</a> | Alignment | not modelled | 9.4  | 14 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> TATA-box binding protein-like<br><b>Family:</b> TATA-box binding protein (TBP), C-terminal domain  |
| 67 | <a href="#">c2zc3F_</a> | Alignment | not modelled | 9.3  | 11 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> penicillin-binding protein 2x; <b>PDBTitle:</b> penicillin-binding protein 2x (pbp 2x) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae                       |
| 68 | <a href="#">c6aqeB_</a> | Alignment | not modelled | 9.3  | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> molecule a; <b>PDBTitle:</b> crystal structure of ppk2 in complex with mg atp   |
| 69 | <a href="#">c3rojD_</a> | Alignment | not modelled | 9.1  | 35 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-<br><b>PDBTitle:</b> d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase2 of synechocystis sp. pcc 6803    |
| 70 | <a href="#">c3rhfB_</a> | Alignment | not modelled | 8.9  | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative polyphosphate kinase 2 family protein; <b>PDBTitle:</b> crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1                                       |
| 71 | <a href="#">d1k8ba_</a> | Alignment | not modelled | 8.7  | 15 | <b>Fold:</b> Ribosome binding domain-like<br><b>Superfamily:</b> Translation initiation factor 2 beta, aIF2beta, N-terminal domain<br><b>Family:</b> Translation initiation factor 2 beta, aIF2beta, N-terminal domain                                      |
| 72 | <a href="#">c2cxiA_</a> | Alignment | not modelled | 8.7  | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of an n-terminal fragment of the phenylalanyl-trna2 synthetase beta subunit from pyrococcus horikoshii       |
| 73 | <a href="#">d1r7ma2</a> | Alignment | not modelled | 8.6  | 15 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease  |
| 74 | <a href="#">c3nfiB_</a> | Alignment | not modelled | 8.3  | 19 | <b>PDB header:</b> dna binding protein, transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa49; <b>PDBTitle:</b> crystal structure of tandem winged helix domain of rna polymerase i2 subunit a49               |
| 75 | <a href="#">c3oqqA_</a> | Alignment | not modelled | 8.1  | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (bacova_00967) from2 bacteroides ovatus at 2.08 a resolution           |
| 76 | <a href="#">c3c6aA_</a> | Alignment | not modelled | 7.6  | 22 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> terminase large subunit; <b>PDBTitle:</b> crystal structure of the rb49 gp17 nuclease domain  |
| 77 | <a href="#">c4tr1A_</a> | Alignment | not modelled | 7.5  | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 3; <b>PDBTitle:</b> crystal structure of gsh-bound cgrx2/c15s   |
|    |                         |           |              |      |    | <b>Fold:</b> TBP-like   |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 78 | <a href="#">d1cdwa1</a> | Alignment | not modelled | 7.5 | 18 | <b>Superfamily:</b> TATA-box binding protein-like<br><b>Family:</b> TATA-box binding protein (TBP), C-terminal domain  |
| 79 | <a href="#">c2rgwD</a>  | Alignment | not modelled | 7.0 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> aspartate carbamoyltransferase;<br><b>PDBTitle:</b> catalytic subunit of m. jannaschii aspartate2 transcarbamoylase  |
| 80 | <a href="#">c5w66M</a>  | Alignment | not modelled | 7.0 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> M: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa49;<br><b>PDBTitle:</b> rna polymerase i initial transcribing complex state 3   |
| 81 | <a href="#">c5mwwA</a>  | Alignment | not modelled | 7.0 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor siga;<br><b>PDBTitle:</b> sigma1.1 domain of sigmaa from bacillus subtilis   |
| 82 | <a href="#">c2hp0A</a>  | Alignment | not modelled | 6.9 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ids-epimerase;<br><b>PDBTitle:</b> crystal structure of iminodisuccinate epimerase   |
| 83 | <a href="#">c2jugB</a>  | Alignment | not modelled | 6.9 | 21 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> tubc protein;<br><b>PDBTitle:</b> multienzyme docking in hybrid megasynthetases   |
| 84 | <a href="#">c3l9cA</a>  | Alignment | not modelled | 6.9 | 12 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase;<br><b>PDBTitle:</b> the crystal structure of smu.777 from streptococcus mutans ua159   |
| 85 | <a href="#">c3fs2A</a>  | Alignment | not modelled | 6.8 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase;<br><b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 brucella melitensis at 1.85a resolution  |
| 86 | <a href="#">c5lj6A</a>  | Alignment | not modelled | 6.8 | 10 | <b>PDB header:</b> ligase,transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lipoate--protein ligase;<br><b>PDBTitle:</b> crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-1) in complex with lipoic acid  |
| 87 | <a href="#">d1omha</a>  | Alignment | not modelled | 6.8 | 30 | <b>Fold:</b> Origin of replication-binding domain, RBD-like<br><b>Superfamily:</b> Origin of replication-binding domain, RBD-like<br><b>Family:</b> Relaxase domain  |
| 88 | <a href="#">c2k2eA</a>  | Alignment | not modelled | 6.7 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bp2786;<br><b>PDBTitle:</b> solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31 |
| 89 | <a href="#">d1sqia1</a> | Alignment | not modelled | 6.6 | 12 | <b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br><b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br><b>Family:</b> Extradiol dioxygenases   |
| 90 | <a href="#">c2k6xA</a>  | Alignment | not modelled | 6.5 | 27 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpod;<br><b>PDBTitle:</b> autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure  |
| 91 | <a href="#">d1tuga1</a> | Alignment | not modelled | 6.4 | 15 | <b>Fold:</b> ATC-like<br><b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase<br><b>Family:</b> Aspartate/ornithine carbamoyltransferase   |
| 92 | <a href="#">d1qnaa1</a> | Alignment | not modelled | 6.3 | 22 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> TATA-box binding protein-like<br><b>Family:</b> TATA-box binding protein (TBP), C-terminal domain   |
| 93 | <a href="#">c5zjgD</a>  | Alignment | not modelled | 6.2 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> gamma-glutamyltransferase 1 threonine peptidase. merops<br><b>PDBTitle:</b> gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly  |
| 94 | <a href="#">c5jxpA</a>  | Alignment | not modelled | 6.2 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase;<br><b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation  |
| 95 | <a href="#">d1gqna</a>  | Alignment | not modelled | 6.2 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 96 | <a href="#">c4p71B</a>  | Alignment | not modelled | 6.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanine--trna ligase beta subunit;<br><b>PDBTitle:</b> apo phers from p. aeruginosa   |
| 97 | <a href="#">c3b8iF</a>  | Alignment | not modelled | 5.9 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase;<br><b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.   |
| 98 | <a href="#">d1eysl</a>  | Alignment | not modelled | 5.8 | 23 | <b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits   |
| 99 | <a href="#">c5tgtA</a>  | Alignment | not modelled | 5.6 | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase;<br><b>PDBTitle:</b> crystal structure of glytamyl-trna synthetase glurs from pseudomonas2 aeruginosa  |