

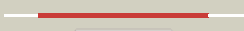



















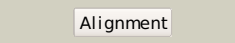

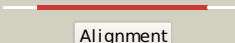


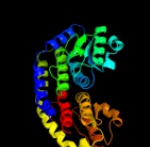
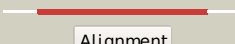



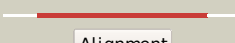














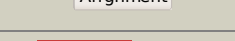


| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2a3nA_</a> |  Alignment   |    | 100.0      | 24     | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative glucosamine-fructose-6-phosphate aminotransferase;<br><b>PDBTitle:</b> crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution |
| 2  | <a href="#">c1jxaA_</a> |  Alignment   |    | 100.0      | 19     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate synthase;<br><b>PDBTitle:</b> glucosamine 6-phosphate synthase with glucose 6-phosphate  |
| 3  | <a href="#">c3fkjA_</a> |  Alignment   |    | 100.0      | 26     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerases;<br><b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution  |
| 4  | <a href="#">c3euaD_</a> |  Alignment   |    | 100.0      | 28     | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative fructose-aminoacid-6-phosphate deglycase;<br><b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution  |
| 5  | <a href="#">c2amlB_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sis domain protein;<br><b>PDBTitle:</b> crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution   |
| 6  | <a href="#">c3g68A_</a> |  Alignment |  | 100.0      | 15     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase;<br><b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution  |
| 7  | <a href="#">c2zj3A_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate<br><b>PDBTitle:</b> isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase   |
| 8  | <a href="#">c3odpA_</a> |  Alignment |  | 100.0      | 15     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase;<br><b>PDBTitle:</b> crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution                           |
| 9  | <a href="#">d1moqa_</a> |  Alignment |  | 100.0      | 19     | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> double-SIS domain  |
| 10 | <a href="#">c3fj1A_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase;<br><b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution   |
| 11 | <a href="#">c3i0zB_</a> |  Alignment |  | 100.0      | 14     | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase;<br><b>PDBTitle:</b> crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution          |

|    |                         |  |   |       |    |   |
|----|-------------------------|--|---|-------|----|---|
| 12 | <a href="#">d1j5xa_</a> |  <div>Alignment</div>   |     | 100.0 | 18 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> double-SIS domain   |
| 13 | <a href="#">c3tbfA_</a> |  <div>Alignment</div>   |    | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate aminotransferase<br><b>PDBTitle:</b> c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.   |
| 14 | <a href="#">c3knzA_</a> |  <div>Alignment</div>   |    | 100.0 | 17 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar binding protein;<br><b>PDBTitle:</b> crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution   |
| 15 | <a href="#">c2decA_</a> |  <div>Alignment</div>   |    | 100.0 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> 325aa long hypothetical protein;<br><b>PDBTitle:</b> crystal structure of the ph0510 protein from pyrococcus horikoshii ot3   |
| 16 | <a href="#">c3c3jA_</a> |  <div>Alignment</div>   |    | 100.0 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase;<br><b>PDBTitle:</b> crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli   |
| 17 | <a href="#">c3hbaA_</a> |  <div>Alignment</div>   |   | 100.0 | 19 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase;<br><b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution   |
| 18 | <a href="#">c2puwA_</a> |  <div>Alignment</div> |  | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isomerase domain of glutamine-fructose-6-phosphate<br><b>PDBTitle:</b> the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans   |
| 19 | <a href="#">d1x9ia_</a> |  <div>Alignment</div> |  | 100.0 | 14 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> double-SIS domain   |
| 20 | <a href="#">c3shoA_</a> |  <div>Alignment</div> |  | 99.9  | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rpri family;<br><b>PDBTitle:</b> crystal structure of rpri transcription factor from spheraobacter2 thermophilus (sugar isomerase domain)  |
| 21 | <a href="#">c2xhzC_</a> |  <div>Alignment</div> | not modelled  | 99.9  | 12 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase;<br><b>PDBTitle:</b> probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography  |
| 22 | <a href="#">c3etnD_</a> |  <div>Alignment</div> | not modelled  | 99.9  | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative phosphosugar isomerase involved in capsule<br><b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution |
| 23 | <a href="#">c3fxaA_</a> |  <div>Alignment</div> | not modelled  | 99.9  | 14 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sis domain protein;<br><b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution                                      |
| 24 | <a href="#">c1nriA_</a> |  <div>Alignment</div> | not modelled  | 99.8  | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hi0754;<br><b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae   |
| 25 | <a href="#">d1nria_</a> |  <div>Alignment</div> | not modelled  | 99.8  | 16 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> mono-SIS domain   |
| 26 | <a href="#">d1vima_</a> |  <div>Alignment</div> | not modelled  | 99.8  | 16 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> mono-SIS domain   |
| 27 | <a href="#">d1m3sa_</a> |  <div>Alignment</div> | not modelled  | 99.8  | 14 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> mono-SIS domain   |
|    |                         |  <div></div>          |   |       |    | <b>Fold:</b> SIS domain   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 28 | <a href="#">d1tk9a_</a> | Alignment | not modelled | 99.8 | 17 | <b>Superfamily:</b> SIS domain<br><b>Family:</b> mono-SIS domain   |
| 29 | <a href="#">d1x94a_</a> | Alignment | not modelled | 99.8 | 14 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> mono-SIS domain  |
| 30 | <a href="#">d1x92a_</a> | Alignment | not modelled | 99.8 | 16 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> mono-SIS domain  |
| 31 | <a href="#">c2x3yA_</a> | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase;<br><b>PDBTitle:</b> crystal structure of gmha from burkholderia pseudomallei   |
| 32 | <a href="#">c3trjC_</a> | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase;<br><b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis  |
| 33 | <a href="#">c3cvjB_</a> | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase;<br><b>PDBTitle:</b> crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution  |
| 34 | <a href="#">c2yvaB_</a> | Alignment | not modelled | 99.7 | 13 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> dnaa initiator-associating protein diaa;<br><b>PDBTitle:</b> crystal structure of escherichia coli diaa  |
| 35 | <a href="#">d1jeoa_</a> | Alignment | not modelled | 99.7 | 12 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> mono-SIS domain  |
| 36 | <a href="#">c3ff1B_</a> | Alignment | not modelled | 99.3 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> structure of glucose 6-phosphate isomerase from staphylococcus aureus   |
| 37 | <a href="#">c1zzgB_</a> | Alignment | not modelled | 99.3 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8   |
| 38 | <a href="#">d1wiwa_</a> | Alignment | not modelled | 99.3 | 15 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> double-SIS domain  |
| 39 | <a href="#">d1c7qa_</a> | Alignment | not modelled | 99.3 | 13 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> Phosphoglucose isomerase, PGI  |
| 40 | <a href="#">c2q8nB_</a> | Alignment | not modelled | 99.2 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution    |
| 41 | <a href="#">c3ljkA_</a> | Alignment | not modelled | 99.2 | 12 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> glucose-6-phosphate isomerase from francisella tularensis.  |
| 42 | <a href="#">d1gzda_</a> | Alignment | not modelled | 99.1 | 15 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> Phosphoglucose isomerase, PGI  |
| 43 | <a href="#">d1q50a_</a> | Alignment | not modelled | 99.1 | 14 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> Phosphoglucose isomerase, PGI  |
| 44 | <a href="#">c1t10A_</a> | Alignment | not modelled | 99.0 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate                         |
| 45 | <a href="#">c3pr3B_</a> | Alignment | not modelled | 99.0 | 8  | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate  |
| 46 | <a href="#">c2o2cB_</a> | Alignment | not modelled | 99.0 | 10 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase, glycosomal;<br><b>PDBTitle:</b> crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site |
| 47 | <a href="#">c3hjbA_</a> | Alignment | not modelled | 99.0 | 14 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.                                      |
| 48 | <a href="#">d1iata_</a> | Alignment | not modelled | 99.0 | 11 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> Phosphoglucose isomerase, PGI  |
| 49 | <a href="#">c3nbuC_</a> | Alignment | not modelled | 98.9 | 10 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of pgi glucosephosphate isomerase   |
| 50 | <a href="#">d1u0fa_</a> | Alignment | not modelled | 98.9 | 12 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> Phosphoglucose isomerase, PGI  |
| 51 | <a href="#">d1hm5a_</a> | Alignment | not modelled | 98.9 | 10 | <b>Fold:</b> SIS domain<br><b>Superfamily:</b> SIS domain<br><b>Family:</b> Phosphoglucose isomerase, PGI  |
| 52 | <a href="#">c2wu8A_</a> | Alignment | not modelled | 98.8 | 9  | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv                                       |
| 53 | <a href="#">c3ujhB_</a> | Alignment | not modelled | 98.8 | 15 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii                                  |
| 54 | <a href="#">d2iv2x2</a> | Alignment | not modelled | 98.0 | 11 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-   |

|    |                          |           |              |      |    |   |
|----|--------------------------|-----------|--------------|------|----|---|
| 54 | <a href="#">c2iv2A2</a>  | Alignment | not modelled | 90.0 | 11 | 3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit;<br><b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum  |
| 55 | <a href="#">c2ivfA</a>   | Alignment | not modelled | 95.9 | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahy;<br><b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus   |
| 56 | <a href="#">c2e7zA</a>   | Alignment | not modelled | 95.6 | 6  | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3   |
| 57 | <a href="#">d2jioa2</a>  | Alignment | not modelled | 95.3 | 9  | <b>Fold:</b> MurCD N-terminal domain<br><b>Superfamily:</b> MurCD N-terminal domain<br><b>Family:</b> MurCD N-terminal domain   |
| 58 | <a href="#">d1p3da1</a>  | Alignment | not modelled | 94.4 | 11 | <b>PDB header:</b> dehydrogenase<br><b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase (large subunit);<br><b>PDBTitle:</b> tungsten containing formate dehydrogenase from2 desulfovibrio gigas  |
| 59 | <a href="#">c1h0hA</a>   | Alignment | not modelled | 94.4 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trimethylamine n-oxide reductase;<br><b>PDBTitle:</b> trimethylamine n-oxide reductase from shewanella massilia  |
| 60 | <a href="#">c1tmoA</a>   | Alignment | not modelled | 94.0 | 4  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> thiosulfate reductase;<br><b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)  |
| 61 | <a href="#">c2vpyE</a>   | Alignment | not modelled | 93.6 | 10 | <b>Fold:</b> MurCD N-terminal domain<br><b>Superfamily:</b> MurCD N-terminal domain<br><b>Family:</b> MurCD N-terminal domain   |
| 62 | <a href="#">d1j6ua1</a>  | Alignment | not modelled | 92.9 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dmsd reductase;<br><b>PDBTitle:</b> dmsd reductase modified by the presence of dms and air   |
| 63 | <a href="#">c1h5nC</a>   | Alignment | not modelled | 92.5 | 12 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3   |
| 64 | <a href="#">d1tmoa2</a>  | Alignment | not modelled | 92.2 | 5  | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3   |
| 65 | <a href="#">d1vlfm2</a>  | Alignment | not modelled | 92.1 | 7  | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3   |
| 66 | <a href="#">d1logya2</a> | Alignment | not modelled | 91.6 | 12 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3   |
| 67 | <a href="#">d1vi6a</a>   | Alignment | not modelled | 91.6 | 10 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Ribosomal protein S2<br><b>Family:</b> Ribosomal protein S2   |
| 68 | <a href="#">c2v45A</a>   | Alignment | not modelled | 91.5 | 8  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase;<br><b>PDBTitle:</b> a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand |
| 69 | <a href="#">c3iz6A</a>   | Alignment | not modelled | 91.3 | 10 | <b>PDB header:</b> ribosome<br><b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa (s2p);<br><b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome   |
| 70 | <a href="#">d1dmra2</a>  | Alignment | not modelled | 90.7 | 12 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3   |
| 71 | <a href="#">c2zkb</a>    | Alignment | not modelled | 90.4 | 7  | <b>PDB header:</b> ribosomal protein/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> rna expansion segment es3;<br><b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map                                 |
| 72 | <a href="#">c2f00A</a>   | Alignment | not modelled | 89.9 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase;<br><b>PDBTitle:</b> escherichia coli murc  |
| 73 | <a href="#">c1vlfQ</a>   | Alignment | not modelled | 89.7 | 7  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> Q: <b>PDB Molecule:</b> pyrogallol hydroxytransferase large subunit;<br><b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene                              |
| 74 | <a href="#">c2nyaF</a>   | Alignment | not modelled | 89.3 | 8  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> periplasmic nitrate reductase;<br><b>PDBTitle:</b> crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli   |
| 75 | <a href="#">c1y5iA</a>   | Alignment | not modelled | 88.5 | 9  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> respiratory nitrate reductase 1 alpha chain;<br><b>PDBTitle:</b> the crystal structure of the narghi mutant nari-k86a  |
| 76 | <a href="#">d1h0ha2</a>  | Alignment | not modelled | 88.4 | 12 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3   |
| 77 | <a href="#">c3izbA</a>   | Alignment | not modelled | 88.0 | 9  | <b>PDB header:</b> ribosome<br><b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein rps0 (s2p);<br><b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome  |
| 78 | <a href="#">c2iv2X</a>   | Alignment | not modelled | 88.0 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> X: <b>PDB Molecule:</b> formate dehydrogenase h;<br><b>PDBTitle:</b> reinterpretation of reduced form of formate dehydrogenase h2 from e. coli   |

|     |                          |           |              |      |    |  |
|-----|--------------------------|-----------|--------------|------|----|--|
| 79  | <a href="#">d1m2ka_</a>  | Alignment | not modelled | 86.5 | 11 | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Sir2 family of transcriptional regulators  |
| 80  | <a href="#">c1kqgA_</a>  | Alignment | not modelled | 86.5 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, major subunit;<br><b>PDBTitle:</b> formate dehydrogenase n from e. coli   |
| 81  | <a href="#">d1y5ia2</a>  | Alignment | not modelled | 86.4 | 10 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3  |
| 82  | <a href="#">d2b4ya1</a>  | Alignment | not modelled | 86.3 | 13 | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Sir2 family of transcriptional regulators  |
| 83  | <a href="#">d2jfga1</a>  | Alignment | not modelled | 85.8 | 8  | <b>Fold:</b> MurCD N-terminal domain<br><b>Superfamily:</b> MurCD N-terminal domain<br><b>Family:</b> MurCD N-terminal domain  |
| 84  | <a href="#">d1yc5a1</a>  | Alignment | not modelled | 85.5 | 6  | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Sir2 family of transcriptional regulators  |
| 85  | <a href="#">c1j6uA_</a>  | Alignment | not modelled | 85.4 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc;<br><b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution  |
| 86  | <a href="#">d1eu1a2</a>  | Alignment | not modelled | 85.2 | 6  | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3  |
| 87  | <a href="#">c3jwpA_</a>  | Alignment | not modelled | 85.0 | 0  | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein sir2 homologue;<br><b>PDBTitle:</b> crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp   |
| 88  | <a href="#">d1ma3a_</a>  | Alignment | not modelled | 84.5 | 9  | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Sir2 family of transcriptional regulators  |
| 89  | <a href="#">c3k35D_</a>  | Alignment | not modelled | 83.7 | 7  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6;<br><b>PDBTitle:</b> crystal structure of human sirt6  |
| 90  | <a href="#">c3pkiF_</a>  | Alignment | not modelled | 82.4 | 7  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> F: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6;<br><b>PDBTitle:</b> human sirt6 crystal structure in complex with adp ribose  |
| 91  | <a href="#">c2h0rD_</a>  | Alignment | not modelled | 81.9 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamidase;<br><b>PDBTitle:</b> structure of the yeast nicotinamidase pnc1p  |
| 92  | <a href="#">c2xznB_</a>  | Alignment | not modelled | 81.7 | 6  | <b>PDB header:</b> ribosome<br><b>Chain:</b> B: <b>PDB Molecule:</b> rps0e;<br><b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2  |
| 93  | <a href="#">c1s1hB_</a>  | Alignment | not modelled | 81.2 | 10 | <b>PDB header:</b> ribosome<br><b>Chain:</b> B: <b>PDB Molecule:</b> 40s ribosomal protein s0-a;<br><b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i. |
| 94  | <a href="#">d1dkua1</a>  | Alignment | not modelled | 80.6 | 16 | <b>Fold:</b> PRTase-like<br><b>Superfamily:</b> PRTase-like<br><b>Family:</b> Phosphoribosylpyrophosphate synthetase-like  |
| 95  | <a href="#">d1u9ya1</a>  | Alignment | not modelled | 78.4 | 16 | <b>Fold:</b> PRTase-like<br><b>Superfamily:</b> PRTase-like<br><b>Family:</b> Phosphoribosylpyrophosphate synthetase-like  |
| 96  | <a href="#">d1g8ka2</a>  | Alignment | not modelled | 77.6 | 12 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3  |
| 97  | <a href="#">d2gy9b1</a>  | Alignment | not modelled | 77.6 | 18 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Ribosomal protein S2<br><b>Family:</b> Ribosomal protein S2  |
| 98  | <a href="#">c3bchA_</a>  | Alignment | not modelled | 75.8 | 9  | <b>PDB header:</b> cell adhesion, ribosomal protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa;<br><b>PDBTitle:</b> crystal structure of the human laminin receptor precursor   |
| 99  | <a href="#">c3jx9B_</a>  | Alignment | not modelled | 75.5 | 11 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase;<br><b>PDBTitle:</b> crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution   |
| 100 | <a href="#">c1ogyA_</a>  | Alignment | not modelled | 75.4 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase;<br><b>PDBTitle:</b> crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides   |
| 101 | <a href="#">c2z04A_</a>  | Alignment | not modelled | 75.3 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase<br><b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus  |
| 102 | <a href="#">d1kqfa2</a>  | Alignment | not modelled | 73.2 | 11 | <b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3  |
| 103 | <a href="#">d1kjqaa2</a> | Alignment | not modelled | 72.7 | 18 | <b>Fold:</b> PreATP-grasp domain<br><b>Superfamily:</b> PreATP-grasp domain<br><b>Family:</b> BC N-terminal domain-like  |



|     |                         |   |              |      |    |  |
|-----|-------------------------|---|--------------|------|----|--|
| 104 | <a href="#">c2dwcB_</a> |  Alignment   | not modelled | 72.7 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 433aa long hypothetical phosphoribosylglycinamide formyl<br><b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp |
| 105 | <a href="#">c1kjjA_</a> |  Alignment   | not modelled | 72.5 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase 2;<br><b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s  |
| 106 | <a href="#">c3e96B_</a> |  Alignment   | not modelled | 72.1 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 bacillus clausii   |
| 107 | <a href="#">c2z2uA_</a> |  Alignment   | not modelled | 70.9 | 16 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0026 protein mj0257;<br><b>PDBTitle:</b> crystal structure of archaeal tyw1   |
| 108 | <a href="#">c2ehhE_</a> |  Alignment   | not modelled | 70.4 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus   |
| 109 | <a href="#">d1xjca_</a> |  Alignment   | not modelled | 70.2 | 23 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 110 | <a href="#">c3bbnB_</a> |  Alignment   | not modelled | 70.1 | 32 | <b>PDB header:</b> ribosome<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal protein s2;<br><b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.   |
| 111 | <a href="#">d2ji7a1</a> |  Alignment   | not modelled | 68.8 | 4  | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain  |
| 112 | <a href="#">c3q2oB_</a> |  Alignment  | not modelled | 68.4 | 19 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit;<br><b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase   |
| 113 | <a href="#">c3uvzB_</a> |  Alignment | not modelled | 68.3 | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit;<br><b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria                         |
| 114 | <a href="#">c1eu1A_</a> |  Alignment | not modelled | 67.2 | 6  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase;<br><b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.              |
| 115 | <a href="#">c3lciA_</a> |  Alignment | not modelled | 67.0 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase;<br><b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w   |
| 116 | <a href="#">c2rfgB_</a> |  Alignment | not modelled | 66.3 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution  |
| 117 | <a href="#">c2yxgD_</a> |  Alignment | not modelled | 65.9 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase (dapa)   |
| 118 | <a href="#">c3dahB_</a> |  Alignment | not modelled | 65.3 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase;<br><b>PDBTitle:</b> 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei  |
| 119 | <a href="#">c3daqB_</a> |  Alignment | not modelled | 65.0 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus   |
| 120 | <a href="#">d1o5ka_</a> |  Alignment | not modelled | 64.6 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |