


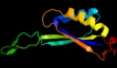

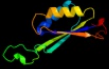
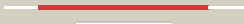
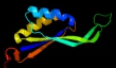

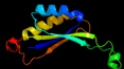





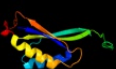





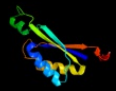

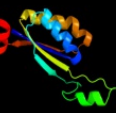








| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">d2piia_</a> | <br>Alignment   |    | 100.0      | 100    | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> Prokaryotic signal transducing protein  |
| 2  | <a href="#">d2ns1b1</a> | <br>Alignment   |    | 100.0      | 67     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> Prokaryotic signal transducing protein  |
| 3  | <a href="#">c3mhyC_</a> | <br>Alignment   |    | 100.0      | 64     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> pii-like protein pz;<br><b>PDBTitle:</b> a new pii protein structure  |
| 4  | <a href="#">d1qy7a_</a> | <br>Alignment   |    | 100.0      | 66     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> Prokaryotic signal transducing protein  |
| 5  | <a href="#">d1vfja_</a> | <br>Alignment |  | 100.0      | 45     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> Prokaryotic signal transducing protein  |
| 6  | <a href="#">c2rd5D_</a> | <br>Alignment |  | 100.0      | 49     | <b>PDB header:</b> protein binding<br><b>Chain:</b> D: <b>PDB Molecule:</b> pii protein;<br><b>PDBTitle:</b> structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana  |
| 7  | <a href="#">c3ncpD_</a> | <br>Alignment |  | 100.0      | 56     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii (glnb-2);<br><b>PDBTitle:</b> glnk2 from archaeoglobus fulgidus  |
| 8  | <a href="#">d1hwua_</a> | <br>Alignment |  | 100.0      | 71     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> Prokaryotic signal transducing protein  |
| 9  | <a href="#">d1ul3a_</a> | <br>Alignment |  | 100.0      | 63     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> Prokaryotic signal transducing protein  |
| 10 | <a href="#">c3bzqA_</a> | <br>Alignment |  | 100.0      | 58     | <b>PDB header:</b> signaling protein/transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii;<br><b>PDBTitle:</b> high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis |
| 11 | <a href="#">c2j9dG_</a> | <br>Alignment |  | 100.0      | 57     | <b>PDB header:</b> membrane transport<br><b>Chain:</b> G: <b>PDB Molecule:</b> hypothetical nitrogen regulatory pii-like<br><b>PDBTitle:</b> structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake                     |



|    |                         |           |   |       |    |  |
|----|-------------------------|-----------|---|-------|----|--|
| 12 | <a href="#">c3o8wA</a>  | Alignment |    | 100.0 | 56 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii (glnb-1);<br><b>PDBTitle:</b> archaeoglobus fulgidus glnk1  |
| 13 | <a href="#">c3l7pA</a>  | Alignment |    | 99.9  | 55 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative nitrogen regulatory protein pii;<br><b>PDBTitle:</b> crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans                                |
| 14 | <a href="#">d2cz4a1</a> | Alignment |    | 99.8  | 17 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> Prokaryotic signal transducing protein   |
| 15 | <a href="#">c3ce8A</a>  | Alignment |    | 98.6  | 17 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative pii-like nitrogen regulatory protein;<br><b>PDBTitle:</b> crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution              |
| 16 | <a href="#">c3m05A</a>  | Alignment |    | 98.2  | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pepe_1480;<br><b>PDBTitle:</b> the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745        |
| 17 | <a href="#">d1o51a</a>  | Alignment |   | 96.7  | 27 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> DUF190/COG1993   |
| 18 | <a href="#">c2dclB</a>  | Alignment |  | 95.3  | 30 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical upf0166 protein ph1503;<br><b>PDBTitle:</b> structure of ph1503 protein from pyrococcus horikoshii ot3  |
| 19 | <a href="#">c2gx8B</a>  | Alignment |  | 90.8  | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> nif3-related protein;<br><b>PDBTitle:</b> the crystal stucture of bacillus cereus protein related to nif3  |
| 20 | <a href="#">d2gx8a1</a> | Alignment |  | 88.5  | 20 | <b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like<br><b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like<br><b>Family:</b> NIF3 (NGG1p interacting factor 3)-like   |
| 21 | <a href="#">c3dfeA</a>  | Alignment | not modelled  | 86.6  | 26 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative pii-like signaling protein;<br><b>PDBTitle:</b> crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution |
| 22 | <a href="#">c3hluA</a>  | Alignment | not modelled  | 84.7  | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf2179;<br><b>PDBTitle:</b> crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum             |
| 23 | <a href="#">d1nh8a2</a> | Alignment | not modelled  | 84.3  | 16 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain   |
| 24 | <a href="#">c2nydB</a>  | Alignment | not modelled  | 81.3  | 20 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> upf0135 protein sa1388;<br><b>PDBTitle:</b> crystal structure of staphylococcus aureus hypothetical protein sa1388  |
| 25 | <a href="#">c2vd3B</a>  | Alignment | not modelled  | 74.5  | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase;<br><b>PDBTitle:</b> the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum  |
| 26 | <a href="#">c1nh7A</a>  | Alignment | not modelled  | 71.1  | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase;<br><b>PDBTitle:</b> atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis   |
| 27 | <a href="#">d1h3da2</a> | Alignment | not modelled  | 57.0  | 14 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain   |
| 28 | <a href="#">c2cz9A</a>  | Alignment | not modelled  | 56.9  | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable galactokinase;<br><b>PDBTitle:</b> crystal structure of galactokinase from pyrococcus   |



|    |                         |           |              |      |  |
|----|-------------------------|-----------|--------------|------|--|
|    |                         |           |              |      | horikoshi  |
| 29 | <a href="#">c3rrkA_</a> | Alignment | not modelled | 53.8 | 16<br><b>PDB header:</b> proton transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> v-type atpase 116 kda subunit;<br><b>PDBTitle:</b> crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase                                |
| 30 | <a href="#">c2dtjA_</a> | Alignment | not modelled | 53.7 | 13<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartokinase;<br><b>PDBTitle:</b> crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum  |
| 31 | <a href="#">c1q1kA_</a> | Alignment | not modelled | 40.6 | 13<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase;<br><b>PDBTitle:</b> structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp  |
| 32 | <a href="#">c2hk3A_</a> | Alignment | not modelled | 29.5 | 16<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> diphosphomevalonate decarboxylase;<br><b>PDBTitle:</b> crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)                                     |
| 33 | <a href="#">c2f06B_</a> | Alignment | not modelled | 24.7 | 16<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein;<br><b>PDBTitle:</b> crystal structure of protein bt0572 from bacteroides thetaiotaomicron  |
| 34 | <a href="#">d1zhva2</a> | Alignment | not modelled | 23.2 | 19<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Atu0741-like  |
| 35 | <a href="#">c2zvxB_</a> | Alignment | not modelled | 22.6 | 11<br><b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> chemotaxis protein motb;<br><b>PDBTitle:</b> structure of the periplasmic domain of motb from salmonella2 (crystal form ii)   |
| 36 | <a href="#">c2re1A_</a> | Alignment | not modelled | 21.0 | 10<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartokinase, alpha and beta subunits;<br><b>PDBTitle:</b> crystal structure of aspartokinase alpha and beta subunits   |
| 37 | <a href="#">c2zhoB_</a> | Alignment | not modelled | 20.6 | 15<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase;<br><b>PDBTitle:</b> crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)   |
| 38 | <a href="#">d2hmfa2</a> | Alignment | not modelled | 19.7 | 18<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Aspartokinase allosteric domain-like  |
| 39 | <a href="#">d1v6za2</a> | Alignment | not modelled | 17.3 | 30<br><b>Fold:</b> alpha/beta knot<br><b>Superfamily:</b> alpha/beta knot<br><b>Family:</b> YggJ C-terminal domain-like  |
| 40 | <a href="#">c2nuxB_</a> | Alignment | not modelled | 17.0 | 20<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate<br><b>PDBTitle:</b> 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution       |
| 41 | <a href="#">c3hulA_</a> | Alignment | not modelled | 16.9 | 21<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> homoserine kinase;<br><b>PDBTitle:</b> structure of putative homoserine kinase thrb from listeria2 monocytogenes   |
| 42 | <a href="#">d1w1oa1</a> | Alignment | not modelled | 16.9 | 13<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> FAD-linked oxidases, C-terminal domain<br><b>Family:</b> Cytokinin dehydrogenase 1   |
| 43 | <a href="#">d2f06a2</a> | Alignment | not modelled | 15.2 | 28<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> BT0572-like   |
| 44 | <a href="#">c3dz1A_</a> | Alignment | not modelled | 14.7 | 17<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution   |
| 45 | <a href="#">c3fluD_</a> | Alignment | not modelled | 14.7 | 16<br><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 from the pathogen2 neisseria meningitidis  |
| 46 | <a href="#">d2a5la1</a> | Alignment | not modelled | 13.0 | 17<br><b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> Flavoproteins<br><b>Family:</b> WrbA-like  |
| 47 | <a href="#">c3lerA_</a> | Alignment | not modelled | 12.2 | 19<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168  |
| 48 | <a href="#">c3n2xB_</a> | Alignment | not modelled | 12.1 | 17<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yage;<br><b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate |
| 49 | <a href="#">d2j0wa3</a> | Alignment | not modelled | 11.9 | 9<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Aspartokinase allosteric domain-like   |
| 50 | <a href="#">c2a2cA_</a> | Alignment | not modelled | 11.7 | 18<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylgalactosamine kinase;<br><b>PDBTitle:</b> x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg-adt and n-acetyl galactosamine 1-3 phosphate                       |
| 51 | <a href="#">d1vi2a2</a> | Alignment | not modelled | 11.3 | 17<br><b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Family:</b> Shikimate dehydrogenase-like   |
| 52 | <a href="#">d1nxza2</a> | Alignment | not modelled | 10.7 | 13<br><b>Fold:</b> alpha/beta knot<br><b>Superfamily:</b> alpha/beta knot<br><b>Family:</b> YggJ C-terminal domain-like  |
| 53 | <a href="#">c3pueA_</a> | Alignment | not modelled | 10.6 | 12<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of the complex of dihydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution                      |
|    |                         |           |              |      | <b>PDB header:</b> lyase   |



|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | <a href="#">c2yxgD_</a> | Alignment | not modelled | 10.6 | 16 | <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase (dapa)   |
| 55 | <a href="#">c3b4uB_</a> | Alignment | not modelled | 10.3 | 13 | <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 agrobacterium2 tumefaciens str. c58   |
| 56 | <a href="#">c1zr6A_</a> | Alignment | not modelled | 10.2 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucooligosaccharide oxidase;<br><b>PDBTitle:</b> the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation   |
| 57 | <a href="#">c1z85B_</a> | Alignment | not modelled | 10.0 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein tm1380;<br><b>PDBTitle:</b> crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution   |
| 58 | <a href="#">c2gs8A_</a> | Alignment | not modelled | 9.9  | 10 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate pyrophosphate decarboxylase;<br><b>PDBTitle:</b> structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes   |
| 59 | <a href="#">d1mwza_</a> | Alignment | not modelled | 9.8  | 19 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> HMA, heavy metal-associated domain<br><b>Family:</b> HMA, heavy metal-associated domain  |
| 60 | <a href="#">c3mahA_</a> | Alignment | not modelled | 9.7  | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartokinase;<br><b>PDBTitle:</b> a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.   |
| 61 | <a href="#">c3lciA_</a> | Alignment | not modelled | 9.7  | 16 | <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   |
| 62 | <a href="#">d1nvta2</a> | Alignment | not modelled | 9.7  | 33 | <b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Family:</b> Shikimate dehydrogenase-like   |
| 63 | <a href="#">c3cprB_</a> | Alignment | not modelled | 9.5  | 17 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthetase;<br><b>PDBTitle:</b> the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution  |
| 64 | <a href="#">d1x8da1</a> | Alignment | not modelled | 9.4  | 11 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Dimeric alpha+beta barrel<br><b>Family:</b> YiiL-like  |
| 65 | <a href="#">c2zodB_</a> | Alignment | not modelled | 9.4  | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase;<br><b>PDBTitle:</b> crystal structure of selenophosphate synthetase from2 aquifex aeolicus   |
| 66 | <a href="#">d1vhka2</a> | Alignment | not modelled | 9.3  | 17 | <b>Fold:</b> alpha/beta knot<br><b>Superfamily:</b> alpha/beta knot<br><b>Family:</b> YggJ C-terminal domain-like  |
| 67 | <a href="#">d1p77a2</a> | Alignment | not modelled | 9.1  | 21 | <b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Family:</b> Shikimate dehydrogenase-like   |
| 68 | <a href="#">c3nngA_</a> | Alignment | not modelled | 9.1  | 16 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-terminal domain of moloney murine leukemia virus<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3           |
| 69 | <a href="#">c2qlxA_</a> | Alignment | not modelled | 9.0  | 11 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase;<br><b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose  |
| 70 | <a href="#">c2qlwA_</a> | Alignment | not modelled | 9.0  | 11 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rhau;<br><b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum  |
| 71 | <a href="#">d1xxxa1</a> | Alignment | not modelled | 9.0  | 12 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 72 | <a href="#">c2cx8B_</a> | Alignment | not modelled | 8.8  | 30 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase;<br><b>PDBTitle:</b> crystal structure of methyltransferase with ligand(sah)  |
| 73 | <a href="#">d1fx0a2</a> | Alignment | not modelled | 8.8  | 21 | <b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like<br><b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase<br><b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase  |
| 74 | <a href="#">c3mdoB_</a> | Alignment | not modelled | 8.8  | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoribosylformylglycinamide cyclo-ligase;<br><b>PDBTitle:</b> crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution |
| 75 | <a href="#">d2cdqa3</a> | Alignment | not modelled | 8.8  | 22 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Aspartokinase allosteric domain-like  |
| 76 | <a href="#">c3daqB_</a> | Alignment | not modelled | 8.7  | 12 | <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   |
| 77 | <a href="#">c2zkru_</a> | Alignment | not modelled | 8.6  | 25 | <b>PDB header:</b> ribosomal protein/rna<br><b>Chain:</b> U: <b>PDB Molecule:</b> rna expansion segment es41;<br><b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map         |
| 78 | <a href="#">d1vqou1</a> | Alignment | not modelled | 8.2  | 50 | <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain)<br><b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain)<br><b>Family:</b> Ribosomal protein L24e   |
|    |                         |           |              |      |    | <b>PDB header:</b> ribosome  |



|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 79 | <a href="#">c3ccjU_</a> | Alignment | not modelled | 8.2 | 50 | <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l24e;<br><b>PDBTitle:</b> structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u   |
| 80 | <a href="#">d2i0ka2</a> | Alignment | not modelled | 8.2 | 12 | <b>Fold:</b> FAD-binding/transporter-associated domain-like<br><b>Superfamily:</b> FAD-binding/transporter-associated domain-like<br><b>Family:</b> FAD-linked oxidases, N-terminal domain   |
| 81 | <a href="#">c3l76B_</a> | Alignment | not modelled | 8.2 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase;<br><b>PDBTitle:</b> crystal structure of aspartate kinase from synechocystis  |
| 82 | <a href="#">d1nyta2</a> | Alignment | not modelled | 8.1 | 21 | <b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain<br><b>Family:</b> Shikimate dehydrogenase-like   |
| 83 | <a href="#">d1oyia_</a> | Alignment | not modelled | 7.9 | 35 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Z-DNA binding domain  |
| 84 | <a href="#">cloyiA_</a> | Alignment | not modelled | 7.9 | 35 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> double-stranded rna-binding protein;<br><b>PDBTitle:</b> solution structure of the z-dna binding domain of the2 vaccinia virus gene e3l  |
| 85 | <a href="#">c2l26A_</a> | Alignment | not modelled | 7.7 | 20 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv0899/mt0922;<br><b>PDBTitle:</b> rv0899 from mycobacterium tuberculosis contains two separated domains  |
| 86 | <a href="#">c2y3rC_</a> | Alignment | not modelled | 7.7 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> taml;<br><b>PDBTitle:</b> structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group   |
| 87 | <a href="#">c3n3fB_</a> | Alignment | not modelled | 7.4 | 29 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(xv) chain;<br><b>PDBTitle:</b> crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens          |
| 88 | <a href="#">c3izcZ_</a> | Alignment | not modelled | 7.3 | 50 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein rpl24 (l24e);<br><b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 89 | <a href="#">c4a1eT_</a> | Alignment | not modelled | 7.2 | 38 | <b>PDB header:</b> ribosome<br><b>Chain:</b> T: <b>PDB Molecule:</b> rpl24;<br><b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1                      |
| 90 | <a href="#">c3oonA_</a> | Alignment | not modelled | 7.2 | 20 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein (tpn50);<br><b>PDBTitle:</b> the structure of an outer membrane protein from borrelia burgdorferi2 b31   |
| 91 | <a href="#">d1v7ra_</a> | Alignment | not modelled | 7.1 | 32 | <b>Fold:</b> Anticodon-binding domain-like<br><b>Superfamily:</b> ITPase-like<br><b>Family:</b> ITPase (Ham1)  |
| 92 | <a href="#">d1hl2a_</a> | Alignment | not modelled | 7.1 | 16 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 93 | <a href="#">c2qieA_</a> | Alignment | not modelled | 7.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2;<br><b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex2 with precursor z   |
| 94 | <a href="#">c2ipiD_</a> | Alignment | not modelled | 6.9 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> aclacinomycin oxidoreductase (aknox);<br><b>PDBTitle:</b> crystal structure of aclacinomycin oxidoreductase   |
| 95 | <a href="#">d1o5ka_</a> | Alignment | not modelled | 6.9 | 10 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 96 | <a href="#">c1vhkA_</a> | Alignment | not modelled | 6.9 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yqeu;<br><b>PDBTitle:</b> crystal structure of an hypothetical protein  |
| 97 | <a href="#">d1j3ma_</a> | Alignment | not modelled | 6.9 | 20 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> TT1751-like<br><b>Family:</b> TT1751-like   |
| 98 | <a href="#">d1ny5a2</a> | Alignment | not modelled | 6.8 | 28 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Extended AAA-ATPase domain   |
| 99 | <a href="#">d1t3ta6</a> | Alignment | not modelled | 6.8 | 7  | <b>Fold:</b> PurM C-terminal domain-like<br><b>Superfamily:</b> PurM C-terminal domain-like<br><b>Family:</b> PurM C-terminal domain-like  |