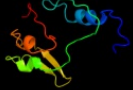
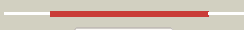
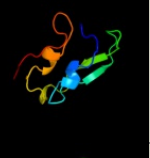
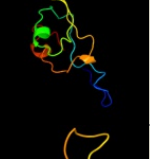
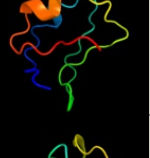
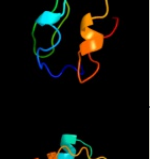
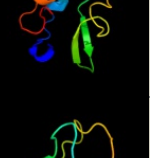
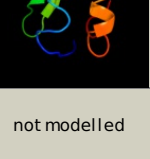


| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                       |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c2ivfB_</a> | <br>Alignment   |    | 99.8       | 36     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ethylbenzene dehydrogenase beta-subunit;<br><b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum                                             |
| 2  | <a href="#">c1kqfB_</a> | <br>Alignment   |    | 99.7       | 25     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, iron-sulfur<br><b>PDBTitle:</b> formate dehydrogenase n from e. coli                                                  |
| 3  | <a href="#">d1y5ib1</a> | <br>Alignment   |    | 99.7       | 39     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                      |
| 4  | <a href="#">d1kqfb1</a> | <br>Alignment   |    | 99.7       | 26     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                      |
| 5  | <a href="#">c2vpyB_</a> | <br>Alignment |  | 99.6       | 20     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nrfc protein;<br><b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor, 2-pentachlorophenol (pcp)                                                 |
| 6  | <a href="#">d1h0hb_</a> | <br>Alignment |  | 99.6       | 21     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                      |
| 7  | <a href="#">d1vlfm2</a> | <br>Alignment |  | 99.6       | 12     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                      |
| 8  | <a href="#">c1ti2F_</a> | <br>Alignment |  | 99.6       | 13     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> pyrogallol hydroxytransferase small subunit;<br><b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol 2 transhydroxylase from pelobacter acidigallici |
| 9  | <a href="#">c2fugG_</a> | <br>Alignment |  | 99.5       | 22     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 9;<br><b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus        |
| 10 | <a href="#">d2fug91</a> | <br>Alignment |  | 99.5       | 22     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                      |
| 11 | <a href="#">c1gthD_</a> | <br>Alignment |  | 99.4       | 31     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase;<br><b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil               |

|    |                          |           |                                                                                     |      |    |                                                                                                                                                                                                                                                       |
|----|--------------------------|-----------|-------------------------------------------------------------------------------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">dlxera_</a>  | Alignment |     | 99.4 | 34 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Archaeal ferredoxins                                                                                                                                         |
| 13 | <a href="#">c2gmhA_</a>  | Alignment |    | 99.3 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein-ubiquinone<br><b>PDBTitle:</b> structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone |
| 14 | <a href="#">dljb0c_</a>  | Alignment |    | 99.3 | 22 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> 7-Fe ferredoxin                                                                                                                                              |
| 15 | <a href="#">dlgtea5</a>  | Alignment |    | 99.3 | 25 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                 |
| 16 | <a href="#">dlhfel2</a>  | Alignment |    | 99.2 | 27 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                 |
| 17 | <a href="#">dlrgva_</a>  | Alignment |   | 99.2 | 34 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Short-chain ferredoxins                                                                                                                                      |
| 18 | <a href="#">dladura_</a> | Alignment |  | 99.2 | 45 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Short-chain ferredoxins                                                                                                                                      |
| 19 | <a href="#">d3c8ya3</a>  | Alignment |  | 99.2 | 29 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                 |
| 20 | <a href="#">dlbc6a_</a>  | Alignment |  | 99.2 | 43 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> 7-Fe ferredoxin                                                                                                                                              |
| 21 | <a href="#">d2c42a5</a>  | Alignment | not modelled                                                                        | 99.2 | 21 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                 |
| 22 | <a href="#">dlh98a_</a>  | Alignment | not modelled                                                                        | 99.1 | 37 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> 7-Fe ferredoxin                                                                                                                                              |
| 23 | <a href="#">c2zvsB_</a>  | Alignment | not modelled                                                                        | 99.1 | 37 | <b>PDB header:</b> electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized ferredoxin-like protein yfhI;<br><b>PDBTitle:</b> crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli                                  |
| 24 | <a href="#">c2c3yA_</a>  | Alignment | not modelled                                                                        | 99.1 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase;<br><b>PDBTitle:</b> crystal structure of the radical form of 2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus        |
| 25 | <a href="#">d2gmha3</a>  | Alignment |  | 99.1 | 19 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> ETF-QO domain-like                                                                                                                                           |
| 26 | <a href="#">d2fdna_</a>  | Alignment | not modelled                                                                        | 99.1 | 49 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Short-chain ferredoxins                                                                                                                                      |
| 27 | <a href="#">dlfcaa_</a>  | Alignment | not modelled                                                                        | 99.1 | 42 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Short-chain ferredoxins                                                                                                                                      |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                |
|----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 28 | <a href="#">d1blua_</a> | Alignment | not modelled | 99.0 | 38 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Short-chain ferredoxins                                                                                                                                                                                               |
| 29 | <a href="#">c3gyxl_</a> | Alignment | not modelled | 98.9 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> J: <b>PDB Molecule:</b> adenylylsulfate reductase;<br><b>PDBTitle:</b> crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas                                                                                                             |
| 30 | <a href="#">d3c7bb1</a> | Alignment | not modelled | 98.9 | 22 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                                                                          |
| 31 | <a href="#">d7fd1a_</a> | Alignment | not modelled | 98.9 | 23 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> 7-Fe ferredoxin                                                                                                                                                                                                       |
| 32 | <a href="#">d1jnrb_</a> | Alignment | not modelled | 98.8 | 24 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                                                                          |
| 33 | <a href="#">c1hfeL_</a> | Alignment | not modelled | 98.7 | 23 | <b>PDB header:</b> hydrogenase<br><b>Chain:</b> L: <b>PDB Molecule:</b> protein (fe-only hydrogenase (e.c.1.18.99.1)<br><b>PDBTitle:</b> 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans                                                                               |
| 34 | <a href="#">d1clfa_</a> | Alignment | not modelled | 98.7 | 26 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Short-chain ferredoxins                                                                                                                                                                                               |
| 35 | <a href="#">c1gx7A_</a> | Alignment | not modelled | 98.6 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic [fe] hydrogenase large subunit;<br><b>PDBTitle:</b> best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase                                                                             |
| 36 | <a href="#">c2fgoA_</a> | Alignment | not modelled | 98.6 | 26 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin;<br><b>PDBTitle:</b> structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa                                                                                                                              |
| 37 | <a href="#">d1sj1a_</a> | Alignment | not modelled | 98.5 | 36 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Single 4Fe-4S cluster ferredoxin                                                                                                                                                                                      |
| 38 | <a href="#">c2v2kB_</a> | Alignment | not modelled | 98.5 | 22 | <b>PDB header:</b> electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin;<br><b>PDBTitle:</b> the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis                                                                                                                   |
| 39 | <a href="#">d1vjwa_</a> | Alignment | not modelled | 98.5 | 24 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Single 4Fe-4S cluster ferredoxin                                                                                                                                                                                      |
| 40 | <a href="#">d2fug34</a> | Alignment | not modelled | 98.4 | 17 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                                                                          |
| 41 | <a href="#">d1iqza_</a> | Alignment | not modelled | 98.4 | 19 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Single 4Fe-4S cluster ferredoxin                                                                                                                                                                                      |
| 42 | <a href="#">c1dw1A_</a> | Alignment | not modelled | 98.3 | 16 | <b>PDB header:</b> electron transfer<br><b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin i;<br><b>PDBTitle:</b> the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation                                                                                                              |
| 43 | <a href="#">c2v4jE_</a> | Alignment | not modelled | 98.3 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit<br><b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration |
| 44 | <a href="#">c3c7bE_</a> | Alignment | not modelled | 98.3 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta;<br><b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus                                                                               |
| 45 | <a href="#">c3bk7A_</a> | Alignment | not modelled | 98.2 | 33 | <b>PDB header:</b> hydrolase/translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein;<br><b>PDBTitle:</b> structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi                                                                                  |
| 46 | <a href="#">c1c4cA_</a> | Alignment | not modelled | 98.2 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (fe-only hydrogenase);<br><b>PDBTitle:</b> binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum                                                 |
| 47 | <a href="#">c2fugC_</a> | Alignment | not modelled | 98.0 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 3;<br><b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus                                                                            |
| 48 | <a href="#">d2bs2b1</a> | Alignment | not modelled | 97.7 | 28 | <b>Fold:</b> Globin-like<br><b>Superfamily:</b> alpha-helical ferredoxin<br><b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain                                                                                                                                   |
| 49 | <a href="#">c3c7bA_</a> | Alignment | not modelled | 97.7 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha;<br><b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus                                                                              |
| 50 | <a href="#">d1fxra_</a> | Alignment | not modelled | 97.7 | 9  | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Single 4Fe-4S cluster ferredoxin                                                                                                                                                                                      |
| 51 | <a href="#">c2v4jA_</a> | Alignment | not modelled | 97.3 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit<br><b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration |
|    |                         |           |              |      |    | <b>PDB header:</b> oxidoreductase                                                                                                                                                                                                                                                                              |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                   |
|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 52 | <a href="#">c3cf4A_</a> | Alignment | not modelled | 97.2 | 19 | <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase alpha subunit;<br><b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex                                                                                                                         |
| 53 | <a href="#">c1nekB_</a> | Alignment | not modelled | 97.1 | 21 | <b>PDB header:</b> oxidoreductase/electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur protein;<br><b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound                                                           |
| 54 | <a href="#">d1kf6b1</a> | Alignment | not modelled | 97.0 | 25 | <b>Fold:</b> Globin-like<br><b>Superfamily:</b> alpha-helical ferredoxin<br><b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain                                                                                                                      |
| 55 | <a href="#">d1nekb1</a> | Alignment | not modelled | 96.9 | 22 | <b>Fold:</b> Globin-like<br><b>Superfamily:</b> alpha-helical ferredoxin<br><b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain                                                                                                                      |
| 56 | <a href="#">c2b76N_</a> | Alignment | not modelled | 96.9 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> N: <b>PDB Molecule:</b> fumarate reductase iron-sulfur protein;<br><b>PDBTitle:</b> e. coli quinol fumarate reductase frda e49q mutation                                                                                                       |
| 57 | <a href="#">c2bs2E_</a> | Alignment | not modelled | 96.9 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> quinol-fumarate reductase iron-sulfur subunit b;<br><b>PDBTitle:</b> quinol:fumarate reductase from wolinetella succinogenes                                                                                           |
| 58 | <a href="#">c2h89B_</a> | Alignment | not modelled | 96.6 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase ip subunit;<br><b>PDBTitle:</b> avian respiratory complex ii with malonate bound                                                                                                               |
| 59 | <a href="#">d2v4jb1</a> | Alignment | not modelled | 92.9 | 26 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                                                             |
| 60 | <a href="#">c2vdcl_</a> | Alignment | not modelled | 89.3 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadh] small chain;<br><b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications. |
| 61 | <a href="#">d1fxda_</a> | Alignment | not modelled | 70.7 | 19 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Single 4Fe-4S cluster ferredoxin                                                                                                                                                                         |
| 62 | <a href="#">d2v4ja1</a> | Alignment | not modelled | 68.9 | 24 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                                                             |
| 63 | <a href="#">d3c7ba1</a> | Alignment | not modelled | 65.4 | 21 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                                                                             |
| 64 | <a href="#">d1gtea1</a> | Alignment | not modelled | 62.8 | 15 | <b>Fold:</b> Globin-like<br><b>Superfamily:</b> alpha-helical ferredoxin<br><b>Family:</b> Dihydropyrimidine dehydrogenase, N-terminal domain                                                                                                                                                     |
| 65 | <a href="#">c2pq4B_</a> | Alignment | not modelled | 17.0 | 30 | <b>PDB header:</b> chaperone/oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic nitrate reductase precursor;<br><b>PDBTitle:</b> nmr solution structure of napd in complex with napa1-352 signal peptide                                                                         |
| 66 | <a href="#">c3gliP_</a> | Alignment | not modelled | 13.7 | 21 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> P: <b>PDB Molecule:</b> dna polymerase iii subunit psi;<br><b>PDBTitle:</b> crystal structure of the e. coli clamp loader bound to2 primer-template dna and psi peptide                                                                       |
| 67 | <a href="#">c2htfA_</a> | Alignment | not modelled | 13.2 | 46 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu;<br><b>PDBTitle:</b> the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain                                                                         |
| 68 | <a href="#">c3gliO_</a> | Alignment | not modelled | 12.7 | 21 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> O: <b>PDB Molecule:</b> dna polymerase iii subunit psi;<br><b>PDBTitle:</b> crystal structure of the e. coli clamp loader bound to2 primer-template dna and psi peptide                                                                       |
| 69 | <a href="#">d1djqa3</a> | Alignment | not modelled | 11.1 | 41 | <b>Fold:</b> Nucleotide-binding domain<br><b>Superfamily:</b> Nucleotide-binding domain<br><b>Family:</b> N-terminal domain of adrenodoxin reductase-like                                                                                                                                         |
| 70 | <a href="#">c2e76D_</a> | Alignment | not modelled | 9.7  | 30 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome b6-f complex iron-sulfur subunit;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus                                                   |
| 71 | <a href="#">c2bpbB_</a> | Alignment | not modelled | 7.7  | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sulfite\cytochrome c oxidoreductase subunit b;<br><b>PDBTitle:</b> sulfite dehydrogenase from starkeya novellia                                                                                                        |
| 72 | <a href="#">c3k30B_</a> | Alignment | not modelled | 7.5  | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase;<br><b>PDBTitle:</b> histamine dehydrogenase from nocardioodes simplex                                                                                                                         |
| 73 | <a href="#">c1n10A_</a> | Alignment | not modelled | 7.3  | 25 | <b>PDB header:</b> allergen<br><b>Chain:</b> A: <b>PDB Molecule:</b> pollen allergen phl p 1;<br><b>PDBTitle:</b> crystal structure of phl p 1, a major timothy grass pollen allergen                                                                                                             |
| 74 | <a href="#">c2fynO_</a> | Alignment | not modelled | 6.9  | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur<br><b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex                                                                  |