# Phyre$^2$

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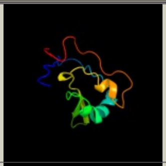
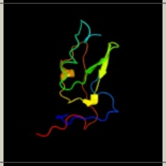
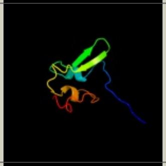
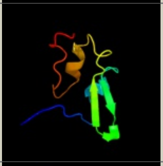
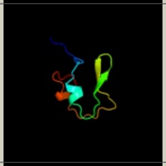
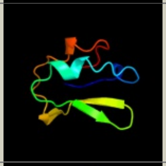
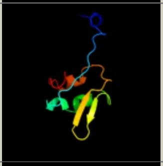
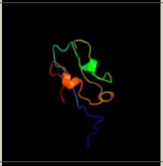
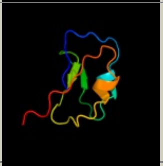
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q46905 |
| Date | Thu Jan 5 12:35:43 GMT 2012 |
| Unique Job ID | 16bb22ac14f6c157 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2gmha3 | Alignment |  | 99.8 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**ETF-QO domain-like |
| 2 | c2gmhA_ | Alignment |  | 99.8 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone<br>**PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone |
| 3 | c2ivfB_ | Alignment |  | 99.4 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit;<br>**PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 4 | c1ti2F_ | Alignment |  | 99.3 | 9 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit;<br>**PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici |
| 5 | d3c7bb1 | Alignment |  | 99.3 | 23 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 6 | d1y5ib1 | Alignment |  | 99.3 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 7 | d7fd1a_ | Alignment |  | 99.3 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |
| 8 | c1gthD_ | Alignment |  | 99.3 | 13 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase;<br>**PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil |
| 9 | d1hfel2 | Alignment |  | 99.2 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 10 | c3gyxJ_ | Alignment |  | 99.2 | 21 | **PDB header:**oxidoreductase<br>**Chain:** J: **PDB Molecule:**adenylylsulfate reductase;<br>**PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas |
| 11 | d1h98a_ | Alignment |  | 99.2 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |

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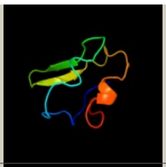
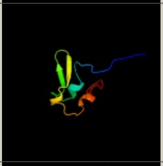
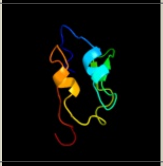
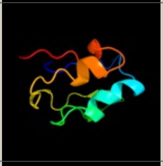
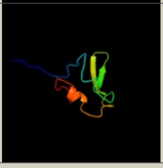
|---|---|---|---|---|---|---|
| 12 | d1bc6a_ | Alignment |  | 99.2 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |
| 13 | c1kqfB_ | Alignment |  | 99.2 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur<br>**PDBTitle:** formate dehydrogenase n from e. coli |
| 14 | d2fug91 | Alignment |  | 99.2 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 15 | c2fugG_ | Alignment |  | 99.2 | 18 | **PDB header:**oxidoreductase<br>**Chain:** G: **PDB Molecule:**nadh-quinone oxidoreductase chain 9;<br>**PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 16 | d1jnrb_ | Alignment |  | 99.1 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 17 | d1kqfb1 | Alignment |  | 99.1 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 18 | d1xera_ | Alignment |  | 99.1 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Archaeal ferredoxins |
| 19 | d1fcaa_ | Alignment |  | 99.1 | 21 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Short-chain ferredoxins |
| 20 | c2vpyB_ | Alignment |  | 99.1 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nrfc protein;<br>**PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp) |
| 21 | d2fdna_ | Alignment | not modelled | 99.1 | 21 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Short-chain ferredoxins |
| 22 | c2v2kB_ | Alignment | not modelled | 99.1 | 20 | **PDB header:**electron transport<br>**Chain:** B: **PDB Molecule:**ferredoxin;<br>**PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis |
| 23 | c1hfeL_ | Alignment | not modelled | 99.1 | 13 | **PDB header:**hydrogenase<br>**Chain:** L: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1)<br>**PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans |
| 24 | c1gx7A_ | Alignment | not modelled | 99.1 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**periplasmic [fe] hydrogenase large subunit;<br>**PDBTitle:** best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase |
| 25 | d1jb0c_ | Alignment | not modelled | 99.0 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |
| 26 | d1clfa_ | Alignment | not modelled | 99.0 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Short-chain ferredoxins |
| 27 | d1dura_ | Alignment | not modelled | 99.0 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Short-chain ferredoxins |
| 28 | c2c3yA_ | Alignment | not modelled | 99.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase;<br>**PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus |

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| 29 | c2zvsB_ | Alignment | not modelled | 98.9 | 19 | **PDB header:**electron transport<br>**Chain:** B: **PDB Molecule:**uncharacterized ferredoxin-like protein yfhl;<br>**PDBTitle:** crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli |
| 30 | c3bk7A_ | Alignment | not modelled | 98.9 | 21 | **PDB header:**hydrolyase/translation<br>**Chain:** A: **PDB Molecule:**abc transporter atp-binding protein;<br>**PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii |
| 31 | d3c8ya3 | Alignment | not modelled | 98.9 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 32 | d1gtea5 | Alignment | not modelled | 98.9 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 33 | d1vlfn2 | Alignment | not modelled | 98.9 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 34 | c2fgoA_ | Alignment | not modelled | 98.8 | 23 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**ferredoxin;<br>**PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa |
| 35 | d1blua_ | Alignment | not modelled | 98.8 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Short-chain ferredoxins |
| 36 | d1h0hb_ | Alignment | not modelled | 98.8 | 7 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 37 | d1rgva_ | Alignment | not modelled | 98.8 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Short-chain ferredoxins |
| 38 | c3c7bE_ | Alignment | not modelled | 98.8 | 23 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta;<br>**PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus |
| 39 | c2v4jE_ | Alignment | not modelled | 98.7 | 20 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit<br>**PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration |
| 40 | d2c42a5 | Alignment | not modelled | 98.7 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 41 | c3c7bA_ | Alignment | not modelled | 98.6 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha;<br>**PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus |
| 42 | d1vjwa_ | Alignment | not modelled | 98.6 | 7 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Single 4Fe-4S cluster ferredoxin |
| 43 | d1iqza_ | Alignment | not modelled | 98.6 | 9 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Single 4Fe-4S cluster ferredoxin |
| 44 | d2fug34 | Alignment | not modelled | 98.6 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 45 | c2v4jA_ | Alignment | not modelled | 98.5 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit<br>**PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration |
| 46 | c1c4cA_ | Alignment | not modelled | 98.5 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase);<br>**PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum |
| 47 | c1dwlA_ | Alignment | not modelled | 98.4 | 14 | **PDB header:**electron transfer<br>**Chain:** A: **PDB Molecule:**ferredoxin i;<br>**PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation |
| 48 | d1sj1a_ | Alignment | not modelled | 98.2 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Single 4Fe-4S cluster ferredoxin |
| 49 | d1fxra_ | Alignment | not modelled | 97.9 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Single 4Fe-4S cluster ferredoxin |
| 50 | d2v4jb1 | Alignment | not modelled | 97.7 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 51 | c2fugC_ | Alignment | not modelled | 97.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3;<br>**PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 52 | d3c7ba1 | Alignment | not modelled | 96.2 | 29 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 53 | d2v4ja1 | Alignment | not modelled | 96.2 | 26 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |

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|---|---|---|---|---|---|---|
| 54 | d1kf6b1 | Alignment | not modelled | 95.4 | 27 | **Fold:**Globin-like<br>**Superfamily:**alpha-helical ferredoxin<br>**Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain |
| 55 | c2b76N_ | Alignment | not modelled | 94.4 | 25 | **PDB header:**oxidoreductase<br>**Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein;<br>**PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation |
| 56 | d2bs2b1 | Alignment | not modelled | 92.4 | 30 | **Fold:**Globin-like<br>**Superfamily:**alpha-helical ferredoxin<br>**Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain |
| 57 | c2bs2E_ | Alignment | not modelled | 89.4 | 35 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b;<br>**PDBTitle:** quinol:fumarate reductase from wolinella succinogenes |
| 58 | c1nekB_ | Alignment | not modelled | 88.2 | 25 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** B: **PDB Molecule:**succinate dehydrogenase iron-sulfur protein;<br>**PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound |
| 59 | d1nekb1 | Alignment | not modelled | 87.3 | 19 | **Fold:**Globin-like<br>**Superfamily:**alpha-helical ferredoxin<br>**Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain |
| 60 | c2h89B_ | Alignment | not modelled | 87.2 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit;<br>**PDBTitle:** avian respiratory complex ii with malonate bound |
| 61 | c3cf4A_ | Alignment | not modelled | 82.1 | 24 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit;<br>**PDBTitle:** structure of the codh component of the m. barkeri acds complex |
| 62 | d1fxda_ | Alignment | not modelled | 80.3 | 21 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Single 4Fe-4S cluster ferredoxin |
| 63 | c2vdcI_ | Alignment | not modelled | 74.8 | 33 | **PDB header:**oxidoreductase<br>**Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain;<br>**PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications. |
| 64 | d1gtea1 | Alignment | not modelled | 22.3 | 29 | **Fold:**Globin-like<br>**Superfamily:**alpha-helical ferredoxin<br>**Family:**Dihydropyrimidine dehydrogenase, N-terminal domain |
| 65 | c2pmzS_ | Alignment | not modelled | 16.3 | 32 | **PDB header:**translation, transferase<br>**Chain:** S: **PDB Molecule:**dna-directed rna polymerase subunit d;<br>**PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus |
| 66 | c1g8jC_ | Alignment | not modelled | 14.6 | 15 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**arsenite oxidase;<br>**PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis |
| 67 | d1g8ka2 | Alignment | not modelled | 11.1 | 17 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 68 | c2qasA_ | Alignment | not modelled | 6.9 | 15 | **PDB header:**hydrolase activator<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of caulobacter crescentus sspb ortholog |
| 69 | d1h6ta1 | Alignment | not modelled | 6.3 | 19 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**Internalin Ig-like domain |
| 70 | d1h6ua1 | Alignment | not modelled | 6.2 | 19 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**Internalin Ig-like domain |
| 71 | c2qazC_ | Alignment | not modelled | 6.2 | 15 | **PDB header:**hydrolase activator<br>**Chain:** C: **PDB Molecule:**sspb protein;<br>**PDBTitle:** structure of c. crescentus sspb ortholog |
| 72 | c2fugA_ | Alignment | not modelled | 6.1 | 33 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase chain 1;<br>**PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 73 | d2omza1 | Alignment | not modelled | 5.7 | 25 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**Internalin Ig-like domain |
| 74 | c2nysA_ | Alignment | not modelled | 5.7 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**agr_c_3712p;<br>**PDBTitle:** x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88. |