



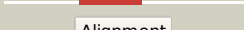

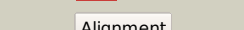



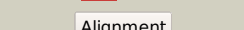



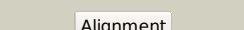



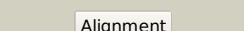

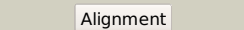





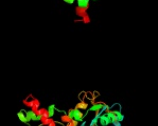
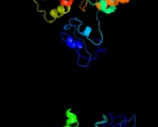
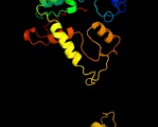
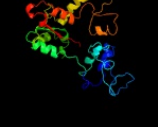
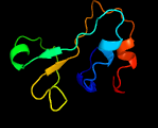


Phyre2

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|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0338c_(-)_403193_405841 |
| Date | Tue Jul 23 14:50:40 BST 2019 |
| Unique Job ID | 2cbbdcbd88909a7b |

Detailed template information

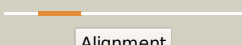
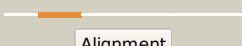
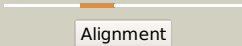
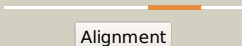


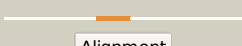





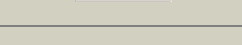
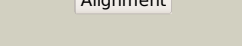
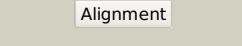
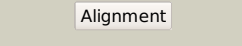
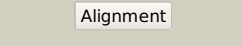
| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c5odhH_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: H: PDB Molecule: heterodisulfide reductase, subunit b; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes |
| 2 | d1y5ic1 |  Alignment |  | 99.9 | 12 | Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain |
| 3 | c5odcC_ |  Alignment |  | 99.7 | 19 | PDB header: oxidoreductase Chain: C: PDB Molecule: heterodisulfide reductase, subunit c; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution |
| 4 | d2bs2b1 |  Alignment |  | 99.4 | 20 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain |
| 5 | c2b76N_ |  Alignment |  | 99.3 | 21 | PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation |
| 6 | c2h89B_ |  Alignment |  | 99.3 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound |
| 7 | c3kwIA_ |  Alignment |  | 99.3 | 10 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from helicobacter pylori |
| 8 | d1nekB1 |  Alignment |  | 99.3 | 18 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain |
| 9 | c2bs2E_ |  Alignment |  | 99.3 | 21 | PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes |
| 10 | c3vrbF_ |  Alignment |  | 99.3 | 18 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: F: PDB Molecule: iron-sulfur subunit of succinate dehydrogenase; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate |
| 11 | c1nekB_ |  Alignment |  | 99.3 | 30 | PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: succinate dehydrogenase iron-sulfur protein; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|--|
| 12 | c5xmjl_ | Alignment |  | 99.2 | 23 | PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas |
| 13 | d1kf6b1 | Alignment |  | 99.2 | 22 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain |
| 14 | c3cf4A_ | Alignment |  | 99.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex |
| 15 | c4p6vA_ | Alignment |  | 98.1 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae |
| 16 | c1hfeL_ | Alignment |  | 98.1 | 18 | PDB header: hydrogenase Chain: L: PDB Molecule: protein (fe-only hydrogenase (e.c.1.18.99.1) PDBTitle: 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans |
| 17 | c1gx7A_ | Alignment |  | 98.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between cytochrome c3 and2 [fe]-hydrogenase |
| 18 | c1c4cA_ | Alignment |  | 98.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: protein (fe-only hydrogenase); PDBTitle: binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum |
| 19 | d2c42a5 | Alignment |  | 97.9 | 18 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 20 | c6fahE_ | Alignment |  | 97.9 | 36 | PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction |
| 21 | c5xf9F_ | Alignment | not modelled | 97.7 | 23 | PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state |
| 22 | c6cipD_ | Alignment | not modelled | 97.4 | 31 | PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpb bound |
| 23 | c5c4iB_ | Alignment | not modelled | 97.4 | 35 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase |
| 24 | c2c3yA_ | Alignment | not modelled | 97.3 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus |
| 25 | d3c8ya3 | Alignment | not modelled | 97.3 | 23 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 26 | c5ldxG_ | Alignment | not modelled | 97.2 | 15 | PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3. |
| 27 | c5ldwG_ | Alignment | not modelled | 97.2 | 15 | PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1 |
| 28 | c5lc5G_ | Alignment | not modelled | 97.2 | 15 | PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2 |
| 29 | c4haaO_ | Alignment | not modelled | 97.2 | 24 | PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c4hea0_ | Alignment | not modelled | 97.2 | 24 | PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus PDB header: oxidoreductase |
| 30 | c6gcsA_ | Alignment | not modelled | 97.2 | 15 | Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 31 | c5t5iG_ | Alignment | not modelled | 97.2 | 33 | PDB header: oxidoreductase Chain: G: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdg; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a |
| 32 | d2fug34 | Alignment | not modelled | 97.2 | 24 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 33 | c6gcsI_ | Alignment | not modelled | 97.1 | 32 | PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 34 | d2fug91 | Alignment | not modelled | 97.1 | 58 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 35 | c2fugG_ | Alignment | not modelled | 97.1 | 58 | PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase chain 9; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 36 | c6cfwN_ | Alignment | not modelled | 97.1 | 31 | PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase |
| 37 | d1kqfc_ | Alignment | not modelled | 97.1 | 18 | Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Formate dehydrogenase N, cytochrome (gamma) subunit |
| 38 | c5lc5I_ | Alignment | not modelled | 97.1 | 26 | PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2 |
| 39 | c5odhG_ | Alignment | not modelled | 97.0 | 37 | PDB header: oxidoreductase Chain: G: PDB Molecule: heterodisulfide reductase, subunit a; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes |
| 40 | d1hfel2 | Alignment | not modelled | 97.0 | 32 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 41 | c6humI_ | Alignment | not modelled | 97.0 | 31 | PDB header: proton transport Chain: I: PDB Molecule: nad(p)h-quinone oxidoreductase subunit i; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus |
| 42 | d1xera_ | Alignment | not modelled | 96.9 | 33 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins |
| 43 | d1gtea5 | Alignment | not modelled | 96.9 | 32 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 44 | d1jb0c_ | Alignment | not modelled | 96.8 | 29 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 45 | c2gmbA_ | Alignment | not modelled | 96.8 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone |
| 46 | c5lnk3_ | Alignment | not modelled | 96.8 | 15 | PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i |
| 47 | c5t5iN_ | Alignment | not modelled | 96.8 | 49 | PDB header: oxidoreductase Chain: N: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdf; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a |
| 48 | c2fugC_ | Alignment | not modelled | 96.7 | 26 | PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 49 | c1gthD_ | Alignment | not modelled | 96.7 | 27 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil |
| 50 | d7fd1a_ | Alignment | not modelled | 96.6 | 31 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 51 | c6btmB_ | Alignment | not modelled | 96.6 | 33 | PDB header: membrane protein Chain: B: PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type) |
| 52 | d1bc6a_ | Alignment | not modelled | 96.6 | 38 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 53 | c2vdcl_ | Alignment | not modelled | 96.5 | 16 | PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications. |
| 54 | c5jcaL_ | Alignment | not modelled | 96.5 | 21 | PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (fnfi)2 from pyrococcus furiosus |
| 55 | d1y5ib1 | Alignment | not modelled | 96.4 | 35 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 56 | c5oc0A | Alignment | not modelled | 96.4 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b561; PDBTitle: structure of e. coli superoxide oxidase |
| 57 | d1clfa | Alignment | not modelled | 96.3 | 53 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 58 | d2fdna | Alignment | not modelled | 96.3 | 52 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 59 | c3zfsB | Alignment | not modelled | 96.0 | 38 | PDB header: oxidoreductase Chain: B: PDB Molecule: f420-reducing hydrogenase, subunit gamma; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate |
| 60 | c4z3zE | Alignment | not modelled | 96.0 | 20 | PDB header: oxidoreductase Chain: E: PDB Molecule: iron-sulfur cluster-binding oxidoreductase, putative PDBTitle: active site complex bambc of benzoyl coenzyme a reductase in complex2 with zinc |
| 61 | c6f0kB | Alignment | not modelled | 96.0 | 18 | PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii |
| 62 | d1fcaa | Alignment | not modelled | 96.0 | 56 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 63 | d1h98a | Alignment | not modelled | 95.9 | 31 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 64 | d1rgva | Alignment | not modelled | 95.8 | 42 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 65 | c4rasC | Alignment | not modelled | 95.8 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, nad-binding/iron-sulfur cluster-binding PDBTitle: reductive dehalogenase structure suggests a mechanism for b12-2 dependent dehalogenation |
| 66 | c2fgoA | Alignment | not modelled | 95.8 | 48 | PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa |
| 67 | c2v2kB | Alignment | not modelled | 95.8 | 34 | PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis |
| 68 | c2ivfB | Alignment | not modelled | 95.8 | 35 | PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 69 | d1dura | Alignment | not modelled | 95.8 | 47 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 70 | c2vpyB | Alignment | not modelled | 95.6 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp) |
| 71 | c3gyxJ | Alignment | not modelled | 95.6 | 35 | PDB header: oxidoreductase Chain: J: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas |
| 72 | d2gmha3 | Alignment | not modelled | 95.5 | 19 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like |
| 73 | c5elmB | Alignment | not modelled | 95.5 | 11 | PDB header: isomerase Chain: B: PDB Molecule: asp/glu_racemase family protein; PDBTitle: crystal structure of l-aspartate/glutamate specific racemase in2 complex with l-glutamate |
| 74 | d1blua | Alignment | not modelled | 95.4 | 48 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 75 | c3ojcD | Alignment | not modelled | 95.4 | 13 | PDB header: isomerase Chain: D: PDB Molecule: putative aspartate/glutamate racemase; PDBTitle: crystal structure of a putative asp/glu racemase from yersinia pestis |
| 76 | c2zvsB | Alignment | not modelled | 95.3 | 37 | PDB header: electron transport Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfhI; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli |
| 77 | d1jnrb | Alignment | not modelled | 95.3 | 29 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 78 | c4yifD | Alignment | not modelled | 95.2 | 15 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase subunit a; PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure |
| 79 | c1kqfB | Alignment | not modelled | 95.1 | 47 | PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: formate dehydrogenase n from e. coli |
| 80 | c5d0bB_ | Alignment | not modelled | 95.0 | 33 | PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop |
| 81 | c4yddF_ | Alignment | not modelled | 94.8 | 36 | PDB header: oxidoreductase Chain: F: PDB Molecule: dmsO reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps |
| 82 | d1vifn2 | Alignment | not modelled | 94.8 | 19 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 83 | c6czaB_ | Alignment | not modelled | 94.6 | 26 | PDB header: oxidoreductase Chain: B: PDB Molecule: 4fe-4s ferredoxin, iron-sulfur binding domain protein; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3 bound to phosphate |
| 84 | c3c7bE_ | Alignment | not modelled | 94.6 | 39 | PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus |
| 85 | c2v4jE_ | Alignment | not modelled | 94.6 | 26 | PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration |
| 86 | c1ti2F_ | Alignment | not modelled | 94.5 | 14 | PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici |
| 87 | c5d6sB_ | Alignment | not modelled | 94.4 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus. |
| 88 | d1kqfb1 | Alignment | not modelled | 94.3 | 40 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 89 | d1h0hb_ | Alignment | not modelled | 94.1 | 27 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 90 | c2zskA_ | Alignment | not modelled | 94.1 | 11 | PDB header: unknown function Chain: A: PDB Molecule: 226aa long hypothetical aspartate racemase; PDBTitle: crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3 |
| 91 | c5ijwA_ | Alignment | not modelled | 93.4 | 12 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction |
| 92 | c4ur1A_ | Alignment | not modelled | 93.2 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: tetrachloroethene reductive dehalogenase catalytic subunit PDBTitle: crystal structure of the pce reductive dehalogenase from s.2 multivorans in complex with dibromoethene |
| 93 | d1iqza_ | Alignment | not modelled | 93.0 | 32 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 94 | c3j16B_ | Alignment | not modelled | 92.9 | 36 | PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners |
| 95 | d1vjwa_ | Alignment | not modelled | 92.9 | 26 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 96 | d3c7bb1 | Alignment | not modelled | 92.5 | 38 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 97 | c1dwA_ | Alignment | not modelled | 92.0 | 29 | PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation |
| 98 | d1sj1a_ | Alignment | not modelled | 92.0 | 25 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 99 | c3c7bA_ | Alignment | not modelled | 91.4 | 42 | PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus |
| 100 | c3bk7A_ | Alignment | not modelled | 91.1 | 30 | PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-i inhibitor protein from2 pyrococcus abyssi |
| 101 | c2v4jA_ | Alignment | not modelled | 89.5 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration |
| 102 | d1gtea1 | Alignment | not modelled | 89.5 | 15 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain |

| | | | | | | |
|-----|-------------------------|---|--------------|------|----|---|
| 103 | c4gd3B_ |  Alignment | not modelled | 88.3 | 9 | PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: ni/fe-hydrogenase 1 b-type cytochrome subunit; PDBTitle: structure of e. coli hydrogenase-1 in complex with cytochrome b |
| 104 | c4gd3A_ |  Alignment | not modelled | 88.3 | 9 | PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: ni/fe-hydrogenase 1 b-type cytochrome subunit; PDBTitle: structure of e. coli hydrogenase-1 in complex with cytochrome b |
| 105 | c4id8A_ |  Alignment | not modelled | 88.0 | 26 | PDB header: electron transport Chain: A: PDB Molecule: putative ferredoxin; PDBTitle: the crystal structure of a [3fe-4s] ferredoxin associated with2 cyp194a4 from r. palustris haa2 |
| 106 | c3uhfB_ |  Alignment | not modelled | 83.6 | 11 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni |
| 107 | c3hfrA_ |  Alignment | not modelled | 83.4 | 17 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes |
| 108 | d1fxra_ |  Alignment | not modelled | 83.0 | 30 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 109 | c5dqrA_ |  Alignment | not modelled | 82.5 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: 7-hydroxymethyl chlorophyll a reductase, chloroplastic; PDBTitle: the crystal structure of arabidopsis 7-hydroxymethyl chlorophyll a2 reductase (hcar) |
| 110 | c2dx7B_ |  Alignment | not modelled | 76.7 | 11 | PDB header: isomerase Chain: B: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid |
| 111 | c5lc5F_ |  Alignment | not modelled | 75.9 | 10 | PDB header: oxidoreductase Chain: F: PDB Molecule: nahd dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class2 |
| 112 | c1b74A_ |  Alignment | not modelled | 73.1 | 16 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus |
| 113 | c5xf9E_ |  Alignment | not modelled | 71.7 | 18 | PDB header: oxidoreductase Chain: E: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state |
| 114 | c3outC_ |  Alignment | not modelled | 69.5 | 16 | PDB header: isomerase Chain: C: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate. |
| 115 | c5xpdA_ |  Alignment | not modelled | 67.2 | 13 | PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog |
| 116 | c2vdcF_ |  Alignment | not modelled | 66.9 | 33 | PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications. |
| 117 | c6mizC_ |  Alignment | not modelled | 66.5 | 14 | PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: human trpm2 ion channel in an adpr-bound state |
| 118 | c2jfoB_ |  Alignment | not modelled | 65.7 | 16 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate |
| 119 | c2ohoA_ |  Alignment | not modelled | 65.7 | 17 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor |
| 120 | c1lm1A_ |  Alignment | not modelled | 64.4 | 33 | PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme |