




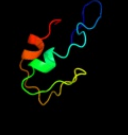






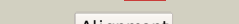

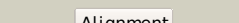

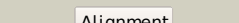



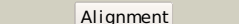
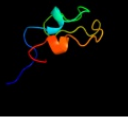












| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c1hfeL_ |  Alignment |  | 98.4 | 18 | PDB header: hydrogenase Chain: L: PDB Molecule: protein (fe-only hydrogenase (e.c.1.18.99.1) PDBTitle: 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans |
| 2 | c1gx7A_ |  Alignment |  | 98.2 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase |
| 3 | d2fug91 |  Alignment |  | 98.2 | 34 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 4 | c2fugG_ |  Alignment |  | 98.2 | 34 | 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 |
| 5 | c2ivfB_ |  Alignment |  | 98.1 | 44 | PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 6 | c2zvsB_ |  Alignment |  | 98.0 | 32 | PDB header: electron transport Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfh1; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli |
| 7 | d1rgva_ |  Alignment |  | 98.0 | 34 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 8 | c2fgoA_ |  Alignment |  | 98.0 | 32 | PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa |
| 9 | d7fd1a_ |  Alignment |  | 97.9 | 30 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 10 | c1gthD_ |  Alignment |  | 97.9 | 35 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil |
| 11 | d1y5ib1 |  Alignment |  | 97.9 | 38 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|--|
| 12 | d2c42a5 | Alignment |  | 97.7 | 23 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 13 | d1blua_ | Alignment |  | 97.7 | 34 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 14 | c1kqfB_ | Alignment |  | 97.7 | 38 | PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli |
| 15 | d1fcaa_ | Alignment |  | 97.7 | 41 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 16 | d1clfa_ | Alignment |  | 97.7 | 36 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 17 | d3c8ya3 | Alignment |  | 97.6 | 17 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 18 | d1jb0c_ | Alignment |  | 97.6 | 32 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 19 | d1dura_ | Alignment |  | 97.6 | 39 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 20 | c2gmhA_ | Alignment |  | 97.5 | 19 | 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 |
| 21 | d1kqfb1 | Alignment | not modelled | 97.5 | 41 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 22 | d1hfel2 | Alignment | not modelled | 97.5 | 40 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 23 | d1bc6a_ | Alignment | not modelled | 97.5 | 32 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 24 | c1ti2F_ | Alignment | not modelled | 97.5 | 23 | PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici |
| 25 | d2gmha3 | Alignment | not modelled | 97.4 | 22 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like |
| 26 | c2v4jE_ | Alignment | not modelled | 97.4 | 33 | 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 |
| 27 | d1h98a_ | Alignment | not modelled | 97.4 | 30 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin |
| 28 | c3c7bA_ | Alignment | not modelled | 97.4 | 39 | PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|--|
| | | | | | | PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus |
| 29 | d2fdna_ | Alignment | not modelled | 97.4 | 41 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins |
| 30 | c3c7bE_ | Alignment | not modelled | 97.4 | 37 | PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus |
| 31 | d1jnrb_ | Alignment | not modelled | 97.4 | 42 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 32 | c2v2kB_ | Alignment | not modelled | 97.4 | 28 | PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis |
| 33 | c2c3yA_ | Alignment | not modelled | 97.4 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus |
| 34 | d1xera_ | Alignment | not modelled | 97.3 | 26 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins |
| 35 | c3gyxJ_ | Alignment | not modelled | 97.1 | 44 | PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas |
| 36 | d1gtea5 | Alignment | not modelled | 97.1 | 34 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 37 | c2v4iA_ | Alignment | not modelled | 97.0 | 23 | 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 |
| 38 | c2vpyB_ | Alignment | not modelled | 96.9 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: nrbc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp) |
| 39 | d3c7bb1 | Alignment | not modelled | 96.9 | 32 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 40 | c1c4cA_ | Alignment | not modelled | 96.8 | 11 | 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 |
| 41 | d1te4a_ | Alignment | not modelled | 96.7 | 13 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PBS lyase HEAT-like repeat |
| 42 | d1h0hb_ | Alignment | not modelled | 96.6 | 19 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 43 | d2bs2b1 | Alignment | not modelled | 96.3 | 19 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain |
| 44 | d1kf6b1 | Alignment | not modelled | 96.2 | 19 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain |
| 45 | c3ltjA_ | Alignment | not modelled | 96.2 | 15 | PDB header: protein binding Chain: A: PDB Molecule: alpharep-4; PDBTitle: structure of a new family of artificial alpha helicoidal repeat2 proteins (alpha-rep) based on thermostable heat-like repeats |
| 46 | d1vlfm2 | Alignment | not modelled | 96.1 | 14 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 47 | c2fugC_ | Alignment |  | 96.0 | 25 | 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 |
| 48 | d1nekb1 | Alignment | not modelled | 96.0 | 17 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain |
| 49 | c3l9tA_ | Alignment | not modelled | 95.9 | 14 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein smu.31; PDBTitle: the crystal structure of smu.31 from streptococcus mutans ua159 |
| 50 | d2fug34 | Alignment | not modelled | 95.7 | 22 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 51 | c1nekb_ | Alignment | not modelled | 95.3 | 20 | 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 |
| | | | | | | PDB header: oxidoreductase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 52 | c2b76N_ | Alignment | not modelled | 95.2 | 19 | Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation |
| 53 | c3cf4A_ | Alignment | not modelled | 95.1 | 23 | 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 |
| 54 | c2bs2E_ | Alignment | not modelled | 94.9 | 23 | PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes |
| 55 | dloyza_ | Alignment | not modelled | 94.7 | 11 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PBS lyase HEAT-like repeat |
| 56 | c2h89B_ | Alignment | not modelled | 94.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound |
| 57 | d1vjwa_ | Alignment | not modelled | 92.8 | 19 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 58 | d1ibrb_ | Alignment | not modelled | 92.1 | 19 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 59 | dliqza_ | Alignment | not modelled | 92.0 | 22 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 60 | d1sj1a_ | Alignment | not modelled | 91.9 | 17 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 61 | c3bk7A_ | Alignment | not modelled | 90.8 | 28 | PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi |
| 62 | d2v4jb1 | Alignment | not modelled | 90.2 | 42 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 63 | d1v18a1 | Alignment | not modelled | 89.9 | 24 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 64 | c3nmwA_ | Alignment | not modelled | 88.4 | 19 | PDB header: cell adhesion/cell cycle Chain: A: PDB Molecule: apc variant protein; PDBTitle: crytal structure of armadillo repeats domain of apc |
| 65 | c3ifqB_ | Alignment | not modelled | 87.0 | 15 | PDB header: cell adhesion Chain: B: PDB Molecule: plakoglobin; PDBTitle: interction of plakoglobin and beta-catenin with desmosomal2 cadherins |
| 66 | c1dwlA_ | Alignment | not modelled | 86.8 | 24 | PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation |
| 67 | d1fxra_ | Alignment | not modelled | 86.6 | 17 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin |
| 68 | c1m5nS_ | Alignment | not modelled | 85.2 | 19 | PDB header: protein transport Chain: S: PDB Molecule: importin beta-1 subunit; PDBTitle: crystal structure of heat repeats (1-11) of importin b2 bound to the non-classical nls(67-94) of pthrp |
| 69 | c3c5wA_ | Alignment | not modelled | 84.5 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: pp2a a subunit; PDBTitle: complex between pp2a-specific methyltransferase pme-1 and pp2a core2 enzyme |
| 70 | c3nmzB_ | Alignment | not modelled | 84.0 | 19 | PDB header: cell adhesion/cell cycle Chain: B: PDB Molecule: apc variant protein; PDBTitle: crytal structure of apc complexed with asef |
| 71 | c3l6yA_ | Alignment | not modelled | 83.8 | 6 | PDB header: cell adhesion Chain: A: PDB Molecule: catenin delta-1; PDBTitle: crystal structure of p120 catenin in complex with e-cadherin |
| 72 | d1xm9a1 | Alignment | not modelled | 83.5 | 9 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Plakophilin 1 helical region |
| 73 | c1lshA_ | Alignment | not modelled | 83.0 | 23 | PDB header: lipid binding protein Chain: A: PDB Molecule: lipovitellin (lv-1n, lv-1c); PDBTitle: lipid-protein interactions in lipovitellin |
| 74 | c3b2aA_ | Alignment | not modelled | 82.8 | 10 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the archael heat-like repeats protein ton_19372 from thermococcus onnurineus na1 |
| 75 | d1lsha1 | Alignment | not modelled | 82.5 | 25 | Fold: alpha-alpha superhelix Superfamily: Lipovitellin-phosvitin complex, superhelical domain Family: Lipovitellin-phosvitin complex, superhelical domain |
| 76 | c3somQ_ | Alignment | not modelled | 81.8 | 16 | PDB header: oxidoreductase Chain: O: PDB Molecule: methylmalonic aciduria and homocystinuria type c protein; PDBTitle: crystal structure of human mmachc |
| 77 | d2v4ja1 | Alignment | not modelled | 81.4 | 29 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 78 | c2z6hA_ | Alignment | not modelled | 79.4 | 13 | PDB header: cell adhesion Chain: A: PDB Molecule: catenin beta-1; PDBTitle: crystal structure of beta-catenin armadillo repeat region2 and its c-terminal domain |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 79 | d3c7ba1 | Alignment | not modelled | 79.0 | 48 | Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins |
| 80 | c2vdcl | Alignment | not modelled | 77.5 | 22 | PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications. |
| 81 | c3t7uA | Alignment | not modelled | 77.2 | 17 | PDB header: cell adhesion Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: a new crytal structure of apc-arm |
| 82 | c2z6gA | Alignment | not modelled | 74.9 | 21 | PDB header: cell adhesion Chain: A: PDB Molecule: b-catenin; PDBTitle: crystal structure of a full-length zebrafish beta-catenin |
| 83 | dljdha | Alignment | not modelled | 73.0 | 21 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 84 | d1t06a | Alignment | not modelled | 72.4 | 5 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: BC3264-like |
| 85 | dlxqra1 | Alignment | not modelled | 70.8 | 16 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HspBP1 domain |
| 86 | c2db0B | Alignment | not modelled | 68.9 | 16 | PDB header: protein binding Chain: B: PDB Molecule: 253aa long hypothetical protein; PDBTitle: crystal structure of ph0542 |
| 87 | dlgw5b | Alignment | not modelled | 65.0 | 16 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin adaptor core protein |
| 88 | dlgtea1 | Alignment | not modelled | 59.4 | 29 | Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain |
| 89 | c1xqrA | Alignment | not modelled | 59.1 | 17 | PDB header: chaperone Chain: A: PDB Molecule: hsppb1 protein; PDBTitle: crystal structure of the hsppb1 core domain |
| 90 | c1g8jC | Alignment | not modelled | 58.6 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis |
| 91 | c1w63A | Alignment | not modelled | 57.5 | 15 | PDB header: endocytosis Chain: A: PDB Molecule: adapter-related protein complex 1 gamma 1 PDBTitle: ap1 clathrin adaptor core |
| 92 | c3bctA | Alignment | not modelled | 51.5 | 13 | PDB header: armadillo repeat Chain: A: PDB Molecule: beta-catenin; PDBTitle: the armadillo repeat region from murine beta-catenin |
| 93 | d1b3ua | Alignment | not modelled | 46.1 | 12 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat |
| 94 | c2hcuA | Alignment | not modelled | 45.4 | 50 | PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus2 mutans |
| 95 | c3h5jA | Alignment | not modelled | 41.3 | 33 | PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis |
| 96 | d1yu8x1 | Alignment | not modelled | 41.1 | 19 | Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain |
| 97 | c2jkrL | Alignment | not modelled | 37.6 | 10 | PDB header: endocytosis Chain: L: PDB Molecule: ap-2 complex subunit alpha-2; PDBTitle: ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse |
| 98 | c2k6nA | Alignment | not modelled | 37.6 | 12 | PDB header: structural protein Chain: A: PDB Molecule: supervillin; PDBTitle: solution structure of human supervillin headpiece, minimized2 average |
| 99 | d1unda | Alignment | not modelled | 37.3 | 19 | Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain |
| 100 | d1unca | Alignment | not modelled | 36.4 | 19 | Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain |
| 101 | d2i9ca1 | Alignment | not modelled | 36.4 | 12 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: RPA1889-like |
| 102 | c3q3wB | Alignment | not modelled | 35.9 | 33 | PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni. |
| 103 | c2l1lB | Alignment | not modelled | 35.0 | 12 | PDB header: nuclear protein Chain: B: PDB Molecule: exportin-1; PDBTitle: nmr solution structure of the phi0 pki nes peptide in complex with2 crm1-rangtp |
| 104 | d1yu5x1 | Alignment | not modelled | 34.3 | 19 | Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| 105 | dlee4a_ | Alignment | not modelled | 33.5 | 13 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 106 | c2fugA_ | Alignment | not modelled | 31.8 | 40 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 107 | d1ujsa_ | Alignment | not modelled | 30.3 | 27 | Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain |
| 108 | c1ovxB_ | Alignment | not modelled | 30.3 | 40 | PDB header: metal binding protein Chain: B: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: nmr structure of the e. coli clpx chaperone zinc binding domain dimer |
| 109 | c2l3xA_ | Alignment | not modelled | 29.8 | 31 | PDB header: protein binding Chain: A: PDB Molecule: ablim2 protein; PDBTitle: villin head piece domain of human ablim2 |
| 110 | d2ds5a1 | Alignment | not modelled | 29.5 | 40 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: ClpX chaperone zinc binding domain |
| 111 | c2qk1A_ | Alignment | not modelled | 28.8 | 8 | PDB header: protein binding Chain: A: PDB Molecule: protein stu2; PDBTitle: structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1 |
| 112 | d1qzpa_ | Alignment | not modelled | 28.3 | 31 | Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain |
| 113 | d1ny8a_ | Alignment | not modelled | 28.1 | 12 | Fold: Alpha-lytic protease prodomain-like Superfamily: BolA-like Family: BolA-like |
| 114 | d1sfla_ | Alignment | not modelled | 24.5 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 115 | c2w3cA_ | Alignment | not modelled | 22.5 | 0 | PDB header: transport protein Chain: A: PDB Molecule: general vesicular transport factor p115; PDBTitle: globular head region of the human general vesicular2 transport factor p115 |
| 116 | c2yswB_ | Alignment | not modelled | 22.5 | 26 | PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5 |
| 117 | d2q22a1 | Alignment | not modelled | 22.4 | 12 | Fold: Ava3019-like Superfamily: Ava3019-like Family: Ava3019-like |
| 118 | d1x3zb1 | Alignment | not modelled | 22.1 | 32 | Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain |
| 119 | d1lrva_ | Alignment | not modelled | 20.7 | 16 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Leucine-rich repeat variant |
| 120 | c2c1tA_ | Alignment | not modelled | 20.6 | 13 | PDB header: protein transport/membrane protein Chain: A: PDB Molecule: importin alpha subunit; PDBTitle: structure of the kap60p:nup2 complex |