


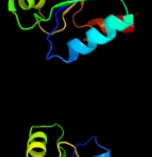
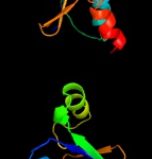
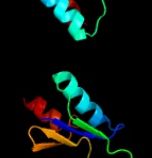
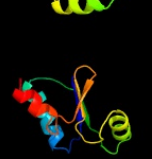
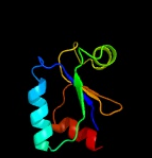
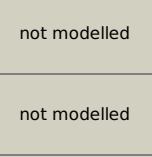


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3053c\_(nrdH)\_3414730\_3414969  
 Date Thu Aug 8 16:20:22 BST 2019  
 Unique Job ID 38bd9bc51da43215

Detailed template information

| #  | Template                | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information   |
|----|-------------------------|--------------------|----------|------------|--------|--|
| 1  | <a href="#">d1h75a_</a> | Alignment          |          | 99.9       | 43     | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase   |
| 2  | <a href="#">d1r7ha_</a> | Alignment          |          | 99.9       | 72     | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase   |
| 3  | <a href="#">c3zija_</a> | Alignment          |          | 99.8       | 26     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin;<br><b>PDBTitle:</b> crystal structure of the thioredoxin-like protein bc3987                               |
| 4  | <a href="#">c3ic4A_</a> | Alignment          |          | 99.8       | 26     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin (grx-1);<br><b>PDBTitle:</b> the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus |
| 5  | <a href="#">c4tr1A_</a> | Alignment          |          | 99.7       | 28     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 3;<br><b>PDBTitle:</b> crystal structure of gsh-bound cgrx2/c15s   |
| 6  | <a href="#">c1nm3B_</a> | Alignment          |          | 99.7       | 21     | <b>PDB header:</b> electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein hi0572;<br><b>PDBTitle:</b> crystal structure of heamophilus influenza hybrid-prx5                          |
| 7  | <a href="#">d1fova_</a> | Alignment          |          | 99.7       | 25     | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase   |
| 8  | <a href="#">c2khpA_</a> | Alignment          |          | 99.7       | 27     | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> solution structure of glutaredoxin from brucella melitensis                       |
| 9  | <a href="#">c3nznA_</a> | Alignment          |          | 99.7       | 26     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> the crystal structure of the glutaredoxin from methanosarcina mazei2 go1              |
| 10 | <a href="#">c3lqcA_</a> | Alignment          |          | 99.7       | 16     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 1;<br><b>PDBTitle:</b> crystal structure of glutaredoxin 1 from francisella tularensis                   |
| 11 | <a href="#">c2kixA_</a> | Alignment          |          | 99.7       | 29     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> solution structure of glutaredoxin from bartonella henselae str.2 houston             |

|    |                         |           |   |      |    |  |
|----|-------------------------|-----------|---|------|----|--|
| 12 | <a href="#">c3qmxA_</a> | Alignment |     | 99.7 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin a;<br><b>PDBTitle:</b> x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a  |
| 13 | <a href="#">d1nm3a1</a> | Alignment |    | 99.7 | 22 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase   |
| 14 | <a href="#">c2mxxA_</a> | Alignment |    | 99.7 | 19 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> mono-cysteine glutaredoxin;<br><b>PDBTitle:</b> nmr structure of the mature form of trypanosoma brucei 1cgrx1  |
| 15 | <a href="#">c2mygA_</a> | Alignment |    | 99.7 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dithiol glutaredoxin 1;<br><b>PDBTitle:</b> solution structure of the dithiolic glutaredoxin 2-c-grx1 from the2 pathogen trypanosoma brucei brucei    |
| 16 | <a href="#">c2e7pC_</a> | Alignment |    | 99.6 | 23 | <b>PDB header:</b> electron transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides                       |
| 17 | <a href="#">c5y4uA_</a> | Alignment |   | 99.6 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-3;<br><b>PDBTitle:</b> crystal structure of grx domain of grx3 from saccharomyces cerevisiae                                   |
| 18 | <a href="#">c3fzaA_</a> | Alignment |  | 99.6 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol                  |
| 19 | <a href="#">c3uiwB_</a> | Alignment |  | 99.6 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin 2;<br><b>PDBTitle:</b> zebrafish grx2 (apo)  |
| 20 | <a href="#">c2lqoA_</a> | Alignment |  | 99.6 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative glutaredoxin rv3198.1/mt3292;<br><b>PDBTitle:</b> mrx1 reduced   |
| 21 | <a href="#">c2ltkA_</a> | Alignment | not modelled  | 99.6 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mono-cysteine glutaredoxin;<br><b>PDBTitle:</b> solution structure of a monomeric truncated mutant of trypanosoma2 brucei 1-c-grx1                    |
| 22 | <a href="#">c1ykaA_</a> | Alignment | not modelled  | 99.6 | 21 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin yhdh;<br><b>PDBTitle:</b> solution structure of grx4, a monothiol glutaredoxin from2 e. coli.                              |
| 23 | <a href="#">c2cq9A_</a> | Alignment | not modelled  | 99.6 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> glrx2 protein;<br><b>PDBTitle:</b> solution structure of rsgi ruh-044, an n-terminal domain of2 glutaredoxin 2 from human cdna |
| 24 | <a href="#">d1wika_</a> | Alignment | not modelled  | 99.6 | 25 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase   |
| 25 | <a href="#">c3h8qB_</a> | Alignment | not modelled  | 99.6 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 3;<br><b>PDBTitle:</b> crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3                               |
| 26 | <a href="#">c4kjeA_</a> | Alignment | not modelled  | 99.6 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> atomic resolution structure of pfgrx1   |
| 27 | <a href="#">c5zvlB_</a> | Alignment | not modelled  | 99.6 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> crystal structure of wheat glutaredoxin   |
| 28 | <a href="#">c2ht9A_</a> | Alignment | not modelled  | 99.6 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-2;<br><b>PDBTitle:</b> the structure of dimeric human glutaredoxin 2   |
|    |                         |           |   |      |    | <b>Fold:</b> Thioredoxin fold  |

|    |                          |           |              |      |    |   |
|----|--------------------------|-----------|--------------|------|----|---|
| 29 | <a href="#">d1legoa_</a> | Alignment | not modelled | 99.6 | 19 | <b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase   |
| 30 | <a href="#">c5gtxA_</a>  | Alignment | not modelled | 99.6 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> buckwheat glutaredoxin;<br><b>PDBTitle:</b> crystal structure of mutated buckwheat glutaredoxin  |
| 31 | <a href="#">c2m80A_</a>  | Alignment | not modelled | 99.6 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-8;<br><b>PDBTitle:</b> solution structure of yeast dithiol glutaredoxin grx8  |
| 32 | <a href="#">c4i2uA_</a>  | Alignment | not modelled | 99.6 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> crystal structure of the reduced glutaredoxin from chlorella2 sorokiniana t-89 in complex with glutathione   |
| 33 | <a href="#">c3zywB_</a>  | Alignment | not modelled | 99.6 | 25 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-3;<br><b>PDBTitle:</b> crystal structure of the first glutaredoxin domain of human2 glutaredoxin 3 (glrx3)   |
| 34 | <a href="#">c3ipzA_</a>  | Alignment | not modelled | 99.5 | 15 | <b>PDB header:</b> electron transport, oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-s14, chloroplastic;<br><b>PDBTitle:</b> crystal structure of arabidopsis monothiol glutaredoxin atgrxcp   |
| 35 | <a href="#">c2hzfA_</a>  | Alignment | not modelled | 99.5 | 26 | <b>PDB header:</b> electron transport, oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1;<br><b>PDBTitle:</b> crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes                                     |
| 36 | <a href="#">d1ktea_</a>  | Alignment | not modelled | 99.5 | 26 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 37 | <a href="#">d1jhba_</a>  | Alignment | not modelled | 99.5 | 26 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 38 | <a href="#">c2wulB_</a>  | Alignment | not modelled | 99.5 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin related protein 5;<br><b>PDBTitle:</b> crystal structure of the human glutaredoxin 5 with bound glutathione2 in an fes cluster  |
| 39 | <a href="#">d1t1va_</a>  | Alignment | not modelled | 99.5 | 28 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> SH3BGR (SH3-binding, glutamic acid-rich protein-like)   |
| 40 | <a href="#">c3l4nA_</a>  | Alignment | not modelled | 99.5 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-6;<br><b>PDBTitle:</b> crystal structure of yeast monothiol glutaredoxin grx6   |
| 41 | <a href="#">c3gx8A_</a>  | Alignment | not modelled | 99.5 | 23 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-5, mitochondrial;<br><b>PDBTitle:</b> structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5   |
| 42 | <a href="#">c2jadA_</a>  | Alignment | not modelled | 99.5 | 17 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> yellow fluorescent protein glutaredoxin fusion protein;<br><b>PDBTitle:</b> yellow fluorescent protein - glutaredoxin fusion protein   |
| 43 | <a href="#">c3d5jB_</a>  | Alignment | not modelled | 99.5 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-2, mitochondrial;<br><b>PDBTitle:</b> structure of yeast grx2-c30s mutant with glutathionyl mixed disulfide   |
| 44 | <a href="#">c2jacA_</a>  | Alignment | not modelled | 99.5 | 18 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1;<br><b>PDBTitle:</b> glutaredoxin grx1p c30s mutant from yeast  |
| 45 | <a href="#">d1abaa_</a>  | Alignment | not modelled | 99.5 | 20 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 46 | <a href="#">c3c1sA_</a>  | Alignment | not modelled | 99.5 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1;<br><b>PDBTitle:</b> crystal structure of grx1 in glutathionylated form   |
| 47 | <a href="#">c2ct6A_</a>  | Alignment | not modelled | 99.3 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-binding glutamic acid-rich-like<br><b>PDBTitle:</b> solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2   |
| 48 | <a href="#">c2kokA_</a>  | Alignment | not modelled | 99.2 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase;<br><b>PDBTitle:</b> solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a. |
| 49 | <a href="#">c1u6tA_</a>  | Alignment | not modelled | 99.2 | 18 | <b>PDB header:</b> protein binding, signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-binding glutamic acid-rich-like<br><b>PDBTitle:</b> crystal structure of the human sh3 binding glutamic-rich2 protein like  |
| 50 | <a href="#">c2mu0A_</a>  | Alignment | not modelled | 99.1 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase;<br><b>PDBTitle:</b> solution structure of a putative arsenate reductase from brucella2 melitensis. seattle structural genomics center for infectious disease3 target braba.00073.a                 |
| 51 | <a href="#">c2m46A_</a>  | Alignment | not modelled | 99.1 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase, putative;<br><b>PDBTitle:</b> solution nmr structure of sac0876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841   |
| 52 | <a href="#">d1ttza_</a>  | Alignment | not modelled | 99.0 | 24 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 53 | <a href="#">c3f0iA_</a>  | Alignment | not modelled | 99.0 | 36 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase;<br><b>PDBTitle:</b> arsenate reductase from vibrio cholerae.   |
| 54 | <a href="#">d1wjka_</a>  | Alignment | not modelled | 99.0 | 11 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
|    |                          |           |              |      |    | <b>Fold:</b> Thioredoxin fold   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 55 | <a href="#">d1rw1a_</a> | Alignment | not modelled | 98.9 | 34 | <b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> ArsC-like  |
| 56 | <a href="#">d1z3ea1</a> | Alignment | not modelled | 98.9 | 23 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> ArsC-like   |
| 57 | <a href="#">c3gkxB_</a> | Alignment | not modelled | 98.8 | 29 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative arsc family related protein;<br><b>PDBTitle:</b> crystal structure of putative arsc family related protein from2 bacteroides fragilis  |
| 58 | <a href="#">c2fgxA_</a> | Alignment | not modelled | 98.8 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative thioredoxin;<br><b>PDBTitle:</b> solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.                                    |
| 59 | <a href="#">c3rdwB_</a> | Alignment | not modelled | 98.8 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative arsenate reductase;<br><b>PDBTitle:</b> putative arsenate reductase from yersinia pestis  |
| 60 | <a href="#">d1z9ha2</a> | Alignment | not modelled | 98.7 | 23 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 61 | <a href="#">c3l78A_</a> | Alignment | not modelled | 98.7 | 23 | <b>PDB header:</b> transcription<br><b>Chain:</b> A; <b>PDB Molecule:</b> regulatory protein spx;<br><b>PDBTitle:</b> the crystal structure of smu.1142c from streptococcus mutans ua159  |
| 62 | <a href="#">d1hyua4</a> | Alignment | not modelled | 98.7 | 15 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> PDI-like  |
| 63 | <a href="#">d1j9ba_</a> | Alignment | not modelled | 98.7 | 18 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> ArsC-like   |
| 64 | <a href="#">d1lloa_</a> | Alignment | not modelled | 98.6 | 23 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 65 | <a href="#">c5w1jA_</a> | Alignment | not modelled | 98.6 | 22 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin glutathione reductase;<br><b>PDBTitle:</b> echinococcus granulosus thioredoxin glutathione reductas (egtgr)   |
| 66 | <a href="#">c3kp8A_</a> | Alignment | not modelled | 98.6 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> vkorc1/thioredoxin domain protein;<br><b>PDBTitle:</b> the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.   |
| 67 | <a href="#">c1z9hB_</a> | Alignment | not modelled | 98.6 | 25 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B; <b>PDB Molecule:</b> membrane-associated prostaglandin e synthase-2;<br><b>PDBTitle:</b> microsomal prostaglandin e synthase type-2  |
| 68 | <a href="#">c3fz4A_</a> | Alignment | not modelled | 98.6 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative arsenate reductase;<br><b>PDBTitle:</b> the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159   |
| 69 | <a href="#">d1k0ma2</a> | Alignment | not modelled | 98.6 | 14 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 70 | <a href="#">d1g7oa2</a> | Alignment | not modelled | 98.5 | 14 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 71 | <a href="#">d1oyja2</a> | Alignment | not modelled | 98.5 | 10 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 72 | <a href="#">c1zypB_</a> | Alignment | not modelled | 98.5 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f;<br><b>PDBTitle:</b> synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf   |
| 73 | <a href="#">c3kp9A_</a> | Alignment | not modelled | 98.5 | 19 | <b>PDB header:</b> blood coagulation,oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> vkorc1/thioredoxin domain protein;<br><b>PDBTitle:</b> structure of a bacterial homolog of vitamin k epoxide reductase   |
| 74 | <a href="#">d1eema2</a> | Alignment | not modelled | 98.5 | 14 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 75 | <a href="#">c3lykA_</a> | Alignment | not modelled | 98.5 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> stringent starvation protein a homolog;<br><b>PDBTitle:</b> structure of stringent starvation protein a homolog from haemophilus2 influenzae  |
| 76 | <a href="#">c4mnnA_</a> | Alignment | not modelled | 98.5 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> glutaredoxin related protein;<br><b>PDBTitle:</b> the crystal structure of sso1120 from sulfolobus solfataricus  |
| 77 | <a href="#">d1nhoa_</a> | Alignment | not modelled | 98.4 | 15 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 78 | <a href="#">c2l6dA_</a> | Alignment | not modelled | 98.4 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin;<br><b>PDBTitle:</b> solution structure of desulfthioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form  |
| 79 | <a href="#">c4kf9A_</a> | Alignment | not modelled | 98.4 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> glutathione s-transferase protein;<br><b>PDBTitle:</b> crystal structure of a glutathione transferase family member from2 ralstonia solanacearum, target efi-501780, with bound gsh coordinated3 to a zinc ion, ordered active site |
| 80 | <a href="#">d1gwca2</a> | Alignment | not modelled | 98.4 | 13 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 81 | <a href="#">c1k0nB_</a> | Alignment | not modelled | 98.4 | 11 | <b>PDB header:</b> metal transport<br><b>Chain:</b> B; <b>PDB Molecule:</b> chloride intracellular channel protein 1;   |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
| 81  | <a href="#">c1k0nB</a>  | Alignment | not modelled | 98.4 | 11 | <b>PDBTitle:</b> chloride intracellular channel 1 (clc1) complexed with glutathione   |
| 82  | <a href="#">c1g7oA</a>  | Alignment | not modelled | 98.4 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 2;<br><b>PDBTitle:</b> nmr solution structure of reduced e. coli glutaredoxin 2   |
| 83  | <a href="#">c4agsA</a>  | Alignment | not modelled | 98.3 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thiol-dependent reductase 1;<br><b>PDBTitle:</b> leishmania tdr1 - a unique trimeric glutathione transferase  |
| 84  | <a href="#">d1j08a2</a> | Alignment | not modelled | 98.3 | 16 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> PDI-like  |
| 85  | <a href="#">c5h29A</a>  | Alignment | not modelled | 98.3 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase/glutathione-related protein;<br><b>PDBTitle:</b> crystal structure of the ntd_n/c domain of alkylhydroperoxide2 reductase ahpf from enterococcus faecalis (v583) |
| 86  | <a href="#">d1e6ba2</a> | Alignment | not modelled | 98.3 | 16 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 87  | <a href="#">c4igjB</a>  | Alignment | not modelled | 98.3 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> maleylacetoacetate isomerase;<br><b>PDBTitle:</b> crystal structure of maleylacetoacetate isomerase from2 anaeromyxobacter dehalogenans 2cp-1, target efi-507175                            |
| 88  | <a href="#">c2aheA</a>  | Alignment | not modelled | 98.3 | 12 | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> chloride intracellular channel protein 4;<br><b>PDBTitle:</b> crystal structure of a soluble form of clc4. intercellular2 chloride ion channel  |
| 89  | <a href="#">d1ljra2</a> | Alignment | not modelled | 98.3 | 11 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 90  | <a href="#">c3ic8D</a>  | Alignment | not modelled | 98.3 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized gst-like proteinprotein;<br><b>PDBTitle:</b> the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a                     |
| 91  | <a href="#">d1a8la2</a> | Alignment | not modelled | 98.3 | 17 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> PDI-like  |
| 92  | <a href="#">c1oyjC</a>  | Alignment | not modelled | 98.3 | 7  | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutathione s-transferase;<br><b>PDBTitle:</b> crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.  |
| 93  | <a href="#">c5y7iB</a>  | Alignment | not modelled | 98.3 | 10 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> chloride intracellular channel protein 2;<br><b>PDBTitle:</b> structure of tilapia fish clc2  |
| 94  | <a href="#">c5g5aC</a>  | Alignment | not modelled | 98.3 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutathione s-transferase u25;<br><b>PDBTitle:</b> glutathione transferase u25 from arabidopsis thaliana in complex with2 glutathione disulfide   |
| 95  | <a href="#">c2n5fA</a>  | Alignment | not modelled | 98.2 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dehydroascorbate reductase family protein;<br><b>PDBTitle:</b> solution structure of the dehydroascorbate reductase 3a from populus2 trichocarpa                                       |
| 96  | <a href="#">c4yamA</a>  | Alignment | not modelled | 98.2 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-etherase;<br><b>PDBTitle:</b> crystal structure of lige-apo form from sphingobium sp. strain syk-6   |
| 97  | <a href="#">c6ghfA</a>  | Alignment | not modelled | 98.2 | 18 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> pvgmgstug;<br><b>PDBTitle:</b> crystal structure of a gst variant  |
| 98  | <a href="#">c3qagA</a>  | Alignment | not modelled | 98.2 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase omega-2;<br><b>PDBTitle:</b> human glutathione transferase o2 with glutathione -new crystal form  |
| 99  | <a href="#">c2v1vA</a>  | Alignment | not modelled | 98.2 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin h isoform 2.;;<br><b>PDBTitle:</b> crystal structure of barley thioredoxin h isoform 2 in partially2 radiation-reduced state   |
| 100 | <a href="#">c5kejA</a>  | Alignment | not modelled | 98.2 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tau class glutathione s-transferase;<br><b>PDBTitle:</b> crystallographic structure of the tau class glutathione s-transferase2 migstu in complex with s-hexyl-glutathione                |
| 101 | <a href="#">c4g10A</a>  | Alignment | not modelled | 98.2 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase homolog;<br><b>PDBTitle:</b> ligg from sphingobium sp. syk-6 is related to the glutathione2 transferase omega class   |
| 102 | <a href="#">c5zfgB</a>  | Alignment | not modelled | 98.2 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase;<br><b>PDBTitle:</b> crystal structure of a diazinon-metabolizing glutathione s-transferase2 in the silkworm, bombyx mori                                       |
| 103 | <a href="#">c1yy7A</a>  | Alignment | not modelled | 98.2 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> stringent starvation protein a;<br><b>PDBTitle:</b> crystal structure of stringent starvation protein a (sspa),2 an rna polymerase-associated transcription factor                      |
| 104 | <a href="#">d1v2aa2</a> | Alignment | not modelled | 98.2 | 13 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Glutathione S-transferase (GST), N-terminal domain  |
| 105 | <a href="#">c4f03A</a>  | Alignment | not modelled | 98.2 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione transferase;<br><b>PDBTitle:</b> crystal structure of the glutathione transferase gte1 from2 phanerochaete chrysosporium  |
| 106 | <a href="#">c1hyuA</a>  | Alignment | not modelled | 98.2 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f;<br><b>PDBTitle:</b> crystal structure of intact ahpf  |
|     |                         |           |              |      |    | <b>PDB header:</b> transferase  |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
| 107 | <a href="#">c4xt0A_</a> | Alignment | not modelled | 98.2 | 14 | <b>Chain:</b> A: <b>PDB Molecule:</b> protein ligf;<br><b>PDBTitle:</b> crystal structure of beta-etherase ligf from sphingobium sp. strain2 syk-6  |
| 108 | <a href="#">c1ljb_</a>  | Alignment | not modelled | 98.1 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase;<br><b>PDBTitle:</b> glutathione transferase (hgst t2-2) from human   |
| 109 | <a href="#">c4pgiA_</a> | Alignment | not modelled | 98.1 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> in2-1 family protein, glutathione transferase lambda3;<br><b>PDBTitle:</b> crystal structure of glutathione transferase lambda3 from populus2 trichocarpa     |
| 110 | <a href="#">d1xfla_</a> | Alignment | not modelled | 98.1 | 15 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 111 | <a href="#">c2v6oA_</a> | Alignment | not modelled | 98.1 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase;<br><b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)                         |
| 112 | <a href="#">d1r26a_</a> | Alignment | not modelled | 98.1 | 21 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 113 | <a href="#">c1gwcC_</a> | Alignment | not modelled | 98.1 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutathione s-transferase tsi-1;<br><b>PDBTitle:</b> the structure of a tau class glutathione s-transferase from wheat,2 active in herbicide detoxification   |
| 114 | <a href="#">d1zmaa1</a> | Alignment | not modelled | 98.1 | 15 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 115 | <a href="#">c2oe0B_</a> | Alignment | not modelled | 98.1 | 19 | <b>PDB header:</b> electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin-3;<br><b>PDBTitle:</b> crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae                                     |
| 116 | <a href="#">d1xwaa_</a> | Alignment | not modelled | 98.1 | 19 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 117 | <a href="#">c5e37A_</a> | Alignment | not modelled | 98.1 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ef-hand domain-containing thioredoxin;<br><b>PDBTitle:</b> redox protein from chlamydomonas reinhardtii  |
| 118 | <a href="#">c4npbA_</a> | Alignment | not modelled | 98.1 | 26 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide isomerase ii;<br><b>PDBTitle:</b> the crystal structure of thiol:disulfide interchange protein ddbc from2 yersinia pestis co92                |
| 119 | <a href="#">c4hojA_</a> | Alignment | not modelled | 98.1 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> regf protein;<br><b>PDBTitle:</b> crystal structure of glutathione transferase homolog from neisseria2 gonorrhoeae, target efi-501841, with bound glutathione |
| 120 | <a href="#">c3fy7B_</a> | Alignment | not modelled | 98.1 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> chloride intracellular channel protein 3;<br><b>PDBTitle:</b> crystal structure of homo sapiens clic3   |