

Phyre²

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| Description | P76559 |
| Date | Thu Jan 5 12:24:37 GMT 2012 |
| Unique Job ID | 358b8adb569fc7a1 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|----------|--------------------|----------|------------|--------|---|
| 1 | c3dtl_ | Alignment | | 98.8 | 20 | PDB header: structural genomics, unknown function Chain: I; PDB Molecule: invasion-associated protein b; PDBTitle: crystal structure of invasion associated protein b from bartonella2 henselae |
| 2 | d1jke_a | Alignment | | 30.4 | 12 | Fold: DTD-like Superfamily: DTD-like Family: DTD-like |
| 3 | d2byca1 | Alignment | | 18.5 | 31 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: BLUF domain |
| 4 | c3ko7E_ | Alignment | | 18.5 | 12 | PDB header: hydrolase Chain: E; PDB Molecule: d-tyrosyl-trna(try) deacylase; PDBTitle: dtd from plasmodium falciparum in complex with d-lysine |
| 5 | d1j7ga_ | Alignment | | 17.4 | 12 | Fold: DTD-like Superfamily: DTD-like Family: DTD-like |
| 6 | c2kb2A_ | Alignment | | 16.3 | 13 | PDB header: signaling protein, hydrolase regulator Chain: A; PDB Molecule: blrp1; PDBTitle: blrp1 bluf |
| 7 | d2elca1 | Alignment | | 16.2 | 11 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 8 | c2hfjn_ | Alignment | | 15.8 | 27 | PDB header: electron transport Chain: J; PDB Molecule: synechocystis photoreceptor (slr1694); PDBTitle: crystal structures of the synechocystis photoreceptor slr1694 reveal2 distinct structural states related to signaling |
| 9 | c2okvC_ | Alignment | | 14.2 | 14 | PDB header: hydrolase Chain: C; PDB Molecule: probable d-tyrosyl-trna(try) deacylase 1; PDBTitle: c-myc dna unwinding element binding protein |
| 10 | d2o8ra3 | Alignment | | 14.0 | 25 | Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain |
| 11 | d1x0pa1 | Alignment | | 13.2 | 27 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: BLUF domain |

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|----|-------------------------|--|--------------|------|----|--|
| 12 | d1yra1 | | | 12.0 | 27 | Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: BLUF domain |
| 13 | c2wivE | | | 11.3 | 18 | PDB header: hydrolase Chain: E: PDB Molecule: regulator of nonsense transcripts 2; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 |
| 14 | c2dboA | | | 11.1 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: d-tyrosyl-trna(try) deacylase; PDBTitle: crystal structure of d-tyr-trna(try) deacylase from aquifex aeolicus |
| 15 | d2d32a1 | | | 10.0 | 19 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase |
| 16 | c3nztA | | | 9.9 | 18 | PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase; PDBTitle: 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 from francisella tularensis in complex with amp |
| 17 | d1uo1a1 | | | 9.8 | 22 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 18 | d1brw1 | | | 9.1 | 17 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 19 | c2ov2O | | | 9.0 | 14 | PDB header: protein binding/transferase Chain: O: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4) |
| 20 | d1khda1 | | | 8.8 | 6 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 21 | d1v8gal | | not modelled | 8.7 | 11 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 22 | d1u2ca2 | | not modelled | 7.2 | 29 | Fold: Dystroglycan, domain 2 Superfamily: Dystroglycan, domain 2 Family: Dystroglycan, domain 2 |
| 23 | d2tpta1 | | not modelled | 7.2 | 23 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 24 | c2odbB | | not modelled | 7.2 | 23 | PDB header: protein binding Chain: B: PDB Molecule: serine/threonine-protein kinase pak 6; PDBTitle: the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6) |
| 25 | d1j26a | | not modelled | 6.8 | 22 | Fold: dsRBD-like Superfamily: Peptidyl-tRNA hydrolase domain-like Family: Peptidyl-tRNA hydrolase domain |
| 26 | c2o8rA | | not modelled | 6.7 | 24 | PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from2 porphyromonas gingivalis |
| 27 | c2bs5A | | not modelled | 6.6 | 28 | PDB header: sugar binding protein Chain: A: PDB Molecule: fucose-binding lectin protein; PDBTitle: lectin from ralstonia solanacearum complexed with 2-2 fucosyllactose |
| 28 | d1o17a1 | | not modelled | 6.4 | 8 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |

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|----|-------------------------|-----------|--------------|-----|---|
| | | | | | Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 29 | d1f9fa_ | Alignment | not modelled | 6.4 | 15 Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain |
| 30 | c3In6A_ | Alignment | not modelled | 6.1 | 31 PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae |
| 31 | d1ut9a1 | Alignment | not modelled | 6.1 | 6 Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain |
| 32 | c3In7A_ | Alignment | not modelled | 6.1 | 44 PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida |
| 33 | c1wz5A_ | Alignment | not modelled | 6.0 | 78 PDB header: toxin Chain: A: PDB Molecule: potassium channel blocking toxin 1; PDBTitle: solution structure of pi1-3p |
| 34 | c1f3mB_ | Alignment | not modelled | 6.0 | 21 PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pak-alpha; PDBTitle: crystal structure of human serine/threonine kinase pak1 |
| 35 | c1w8xN_ | Alignment | not modelled | 5.7 | 14 PDB header: virus Chain: N: PDB Molecule: protein p31; PDBTitle: structural analysis of prd1 |
| 36 | c1e0aB_ | Alignment | not modelled | 5.6 | 14 PDB header: signalling protein Chain: B: PDB Molecule: serine/threonine-protein kinase pak-alpha; PDBTitle: cdc42 complexed with the gtpase binding domain of p212 activated kinase |