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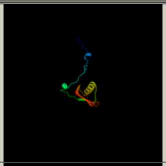
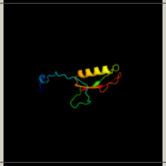
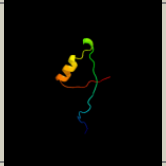
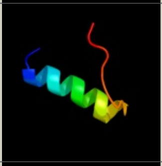
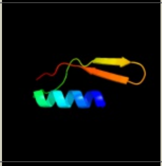
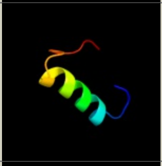
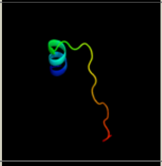
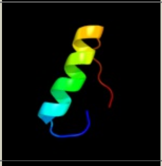
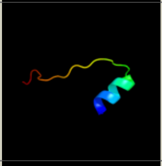
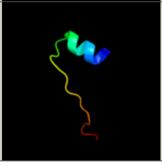
| Description | P0AF82 |
| Date | Thu Jan 5 11:25:33 GMT 2012 |
| Unique Job ID | 484cf8f11c821841 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2jnaa1 | Alignment |  | 100.0 | 33 | **Fold:**Dodecin subunit-like<br>**Superfamily:**YdgH-like<br>**Family:**YdgH-like |
| 2 | d2noca1 | Alignment |  | 99.9 | 24 | **Fold:**Dodecin subunit-like<br>**Superfamily:**YdgH-like<br>**Family:**YdgH-like |
| 3 | c2k4qA_ | Alignment |  | 41.8 | 19 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**major tail protein v;<br>**PDBTitle:** the solution structure of gpv, the major tail protein from2 bacteriophage lambda |
| 4 | c3b9nB_ | Alignment |  | 30.4 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**alkane monoxygenase;<br>**PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada) |
| 5 | c3qkbB_ | Alignment |  | 27.7 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution |
| 6 | c3sdoB_ | Alignment |  | 23.1 | 23 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase;<br>**PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei |
| 7 | c1hl8B_ | Alignment |  | 21.3 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase;<br>**PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase |
| 8 | d1luca_ | Alignment |  | 21.0 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**Bacterial luciferase (alkanal monooxygenase) |
| 9 | c3eypB_ | Alignment |  | 17.3 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase;<br>**PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron |
| 10 | d2hqsa2 | Alignment |  | 16.3 | 16 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**TolB, N-terminal domain<br>**Family:**TolB, N-terminal domain |
| 11 | c3mo4B_ | Alignment |  | 15.9 | 8 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase;<br>**PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697 |

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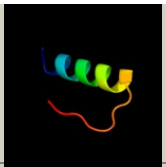
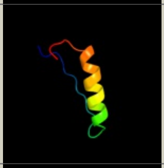
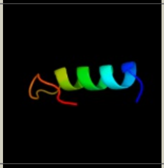
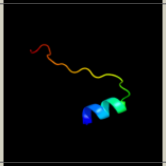
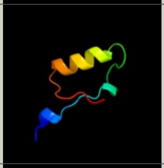
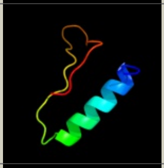
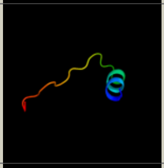
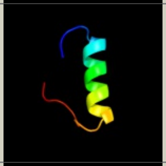
| 12 | d1lucb_ | Alignment |  | 14.4 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**Bacterial luciferase (alkanal monooxygenase) |
| 13 | d3etja1 | Alignment |  | 14.3 | 6 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Rudiment single hybrid motif<br>**Family:**BC C-terminal domain-like |
| 14 | c1z69D_ | Alignment |  | 12.3 | 17 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**coenzyme f420-dependent n(5),n(10)-<br>**PDBTitle:** crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420 |
| 15 | d1hl9a2 | Alignment |  | 11.2 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Putative alpha-L-fucosidase, catalytic domain |
| 16 | d1tqxa_ | Alignment |  | 10.5 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 17 | c1kqfB_ | Alignment |  | 10.4 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur<br>**PDBTitle:** formate dehydrogenase n from e. coli |
| 18 | c2wvsD_ | Alignment |  | 10.0 | 25 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**alpha-l-fucosidase;<br>**PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant |
| 19 | d1tvla_ | Alignment |  | 9.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**Ssud-like monoxygenases |
| 20 | c1tvlA_ | Alignment |  | 9.7 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein ytnj;<br>**PDBTitle:** structure of ytnj from bacillus subtilis |
| 21 | c2i7gA_ | Alignment | not modelled | 8.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**monooxygenase;<br>**PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens |
| 22 | d1wu7a1 | Alignment | not modelled | 8.0 | 22 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 23 | d1nqka_ | Alignment | not modelled | 7.8 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**Ssud-like monoxygenases |
| 24 | c2k38A_ | Alignment | not modelled | 7.7 | 44 | **PDB header:**antimicrobial protein<br>**Chain:** A: **PDB Molecule:**cupiennin-1a;<br>**PDBTitle:** cupiennin 1a, nmr, minimized average structure |
| 25 | c3ne8A_ | Alignment | not modelled | 7.5 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase;<br>**PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1 |
| 26 | d2fiqa1 | Alignment | not modelled | 7.4 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**GatZ-like |
| 27 | c3ir9A_ | Alignment | not modelled | 7.0 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1;<br>**PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei. |
| 28 | d2g39a1 | Alignment | not modelled | 6.8 | 26 | **Fold:**NagB/RpiA/CoA transferase-like<br>**Superfamily:**NagB/RpiA/CoA transferase-like<br>**Family:**CoA transferase alpha subunit-like |
| | | | | | | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; |

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| 29 | c3gzaB_ | Alignment | not modelled | 6.5 | 13 | **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution |
| 30 | d1f07a_ | Alignment | not modelled | 6.3 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**F420 dependent oxidoreductases |
| 31 | d1kjqa1 | Alignment | not modelled | 6.3 | 12 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Rudiment single hybrid motif<br>**Family:**BC C-terminal domain-like |
| 32 | c3raoB_ | Alignment | not modelled | 6.2 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative luciferase-like monooxygenase;<br>**PDBTitle:** crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987. |
| 33 | c2cokA_ | Alignment | not modelled | 6.2 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1;<br>**PDBTitle:** solution structure of brct domain of poly(adp-ribose)2 polymerase-1 |
| 34 | c3no4A_ | Alignment | not modelled | 6.0 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**creatinine amidohydrolase;<br>**PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution |
| 35 | c2jz7A_ | Alignment | not modelled | 5.7 | 17 | **PDB header:**selenium-binding protein<br>**Chain:** A: **PDB Molecule:**selenium binding protein;<br>**PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii |
| 36 | d1rhca_ | Alignment | not modelled | 5.4 | 9 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**F420 dependent oxidoreductases |