







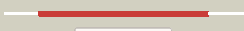


















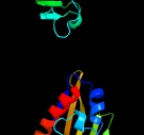
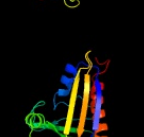

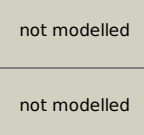


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0857 (-) _953260_953733 |
| Date | Fri Jul 26 01:50:44 BST 2019 |
| Unique Job ID | b5b295eaa3396400 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c5z8oA_ |  Alignment |  | 99.9 | 20 | PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis |
| 2 | c3tfzB_ |  Alignment |  | 99.9 | 16 | PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128 |
| 3 | d2rera1 |  Alignment |  | 99.9 | 20 | Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like |
| 4 | c2kf2A_ |  Alignment |  | 99.9 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: solution nmr structure of of streptomyces coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365 |
| 5 | d2d4ra1 |  Alignment |  | 99.9 | 20 | Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like |
| 6 | d2pcsa1 |  Alignment |  | 99.9 | 9 | Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like |
| 7 | c2le1A_ |  Alignment |  | 99.9 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of tfu_2981 from thermobifida fusca, northeast2 structural genomics consortium target tfr85a |
| 8 | d2ns9a1 |  Alignment |  | 99.9 | 11 | Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like |
| 9 | c4xrwA_ |  Alignment |  | 99.9 | 13 | PDB header: lyase Chain: A: PDB Molecule: bexl; PDBTitle: crystal structure of the di-domain aro/cyc bexl from the be-7585a2 biosynthetic pathway |
| 10 | c3p9vA_ |  Alignment |  | 99.9 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mqr197 |
| 11 | d1t17a_ |  Alignment |  | 99.9 | 12 | Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|---|
| 12 | c5woxA | Alignment |  | 99.8 | 14 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra |
| 13 | d2b79a1 | Alignment |  | 99.8 | 8 | Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like |
| 14 | c4n0gC | Alignment |  | 99.8 | 15 | PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex |
| 15 | c4xrtB | Alignment |  | 99.8 | 9 | PDB header: lyase Chain: B: PDB Molecule: stfq aromatase/cyclase; PDBTitle: crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway |
| 16 | d3cnwa1 | Alignment |  | 99.8 | 10 | Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like |
| 17 | c2m47A | Alignment |  | 99.8 | 9 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein cgl2373; PDBTitle: solution nmr structure of the polyketide_cyc-like protein cgl2372 from2 corynebacterium glutamicum, northeast structural genomics consortium3 target cgr160 |
| 18 | c5vglA | Alignment |  | 99.7 | 10 | PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa |
| 19 | c3p51A | Alignment |  | 99.7 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: three-dimensional structure of protein q2y8n9_nitmu from nitrosospira2 multiformis, northeast structural genomics consortium target nmr118 |
| 20 | c5e4bB | Alignment |  | 99.7 | 12 | PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde |
| 21 | c3qtjA | Alignment | not modelled | 99.7 | 14 | PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal structure of aba receptor pyl10 (apo) |
| 22 | c4oicA | Alignment | not modelled | 99.7 | 7 | PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structural of a soluble protein |
| 23 | c3oquB | Alignment | not modelled | 99.6 | 14 | PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba |
| 24 | c2kczA | Alignment | not modelled | 99.6 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein dr_a0006; PDBTitle: solution nmr structure of the c-terminal domain of protein2 dr_a0006 from deinococcus radiodurans. northeast3 structural genomics consortium target drr147d |
| 25 | c3qszb | Alignment | not modelled | 99.6 | 14 | PDB header: unknown function Chain: B: PDB Molecule: star-related lipid transfer protein; PDBTitle: crystal structure of the star-related lipid transfer protein (fragment2 25-204) from xanthomonas axonopodis at the resolution 2.4a, northeast3 structural genomics consortium target xar342 |
| 26 | c3k90C | Alignment | not modelled | 99.6 | 14 | PDB header: hormone receptor, hydrolase regulator Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: the abscisic acid receptor pyr1 in complex with abscisic acid |
| 27 | c2vq5B | Alignment | not modelled | 99.5 | 10 | PDB header: lyase Chain: B: PDB Molecule: s-norococlaurine synthase; PDBTitle: x-ray structure of norococlaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde |
| 28 | c4r7kA | Alignment | not modelled | 99.5 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein jhp0584; |

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|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c417kA_ | Alignment | not modelled | 99.5 | 13 | PDBTitle: 1.88 angstrom resolution crystal structure of hypothetical protein2 jhp0584 from helicobacter pylori. |
| 29 | c3kixB_ | Alignment | not modelled | 99.5 | 9 | PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3 |
| 30 | d1ifva_ | Alignment | not modelled | 99.5 | 12 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 31 | c2leqA_ | Alignment | not modelled | 99.5 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: chemical shift assignment and solution structure of chr145 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145 |
| 32 | c2r55B_ | Alignment | not modelled | 99.5 | 13 | PDB header: transport protein Chain: B: PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5 |
| 33 | c3p0IC_ | Alignment | not modelled | 99.5 | 18 | PDB header: transport protein Chain: C: PDB Molecule: steroidogenic acute regulatory protein, mitochondrial; PDBTitle: human steroidogenic acute regulatory protein |
| 34 | d1xuva_ | Alignment | not modelled | 99.5 | 10 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 35 | c5ujvA_ | Alignment | not modelled | 99.4 | 8 | PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of fepyr1 in complex with abscisic acid |
| 36 | c3kdiA_ | Alignment | not modelled | 99.4 | 13 | PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2 |
| 37 | d2qpva1 | Alignment | not modelled | 99.4 | 16 | Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like |
| 38 | c2lghA_ | Alignment | not modelled | 99.4 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein aha_2358 from2 aeromonas hydrophila refined with nh rdcs, northeast structural3 genomics consortium target ahr99. |
| 39 | c3c0vC_ | Alignment | not modelled | 99.4 | 9 | PDB header: plant protein Chain: C: PDB Molecule: cytokinin-specific binding protein; PDBTitle: crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12 |
| 40 | c2lf2A_ | Alignment | not modelled | 99.4 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152 |
| 41 | d1icxa_ | Alignment | not modelled | 99.4 | 12 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 42 | c2l9pA_ | Alignment | not modelled | 99.4 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q5hl19 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147 |
| 43 | c2lcgA_ | Alignment | not modelled | 99.4 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115 |
| 44 | c4igyB_ | Alignment | not modelled | 99.4 | 11 | PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form |
| 45 | d1em2a_ | Alignment | not modelled | 99.4 | 11 | Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 46 | c2mouA_ | Alignment | not modelled | 99.4 | 9 | PDB header: transport protein Chain: A: PDB Molecule: star-related lipid transfer protein 6; PDBTitle: solution structure of star-related lipid transfer domain protein 62 (stard6) |
| 47 | d1xfsa_ | Alignment | not modelled | 99.4 | 9 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 48 | c2l8oA_ | Alignment | not modelled | 99.4 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of chr148 from cytophaga hutchinsonii, northeast2 structural genomics consortium target chr148 |
| 49 | d2bk0a1 | Alignment | not modelled | 99.3 | 11 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 50 | d1jssa_ | Alignment | not modelled | 99.3 | 8 | Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 51 | c1jssB_ | Alignment | not modelled | 99.3 | 8 | PDB header: lipid binding protein Chain: B: PDB Molecule: cholesterol-regulated start protein 4; PDBTitle: crystal structure of the mus musculus cholesterol-regulated2 start protein 4 (stard4). |
| 52 | c4rejA_ | Alignment | not modelled | 99.3 | 10 | PDB header: protein binding Chain: A: PDB Molecule: major latex-like protein; PDBTitle: crystal structure of ginseng major latex-like protein 151 (glp) from2 panax ginseng. (crystal-3) |
| 53 | c3pu2G_ | Alignment | not modelled | 99.3 | 14 | PDB header: structure genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics |

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|----|-------------------------|-----------|--------------|------|---|
| | | | | | consortium target rhr263. |
| 54 | d1ln1a_ | Alignment | not modelled | 99.3 | 13 Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 55 | c3uidA_ | Alignment | not modelled | 99.3 | 15 PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis |
| 56 | c2ldkA_ | Alignment | not modelled | 99.3 | 14 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein aaur_3427 from arthrobacter2 aureus, northeast structural genomics consortium target aar96 |
| 57 | d1qmra_ | Alignment | not modelled | 99.3 | 9 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 58 | d1e09a_ | Alignment | not modelled | 99.3 | 14 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 59 | c3otlA_ | Alignment | not modelled | 99.3 | 13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: three-dimensional structure of the putative uncharacterized protein2 from rhizobium leguminosarum at the resolution 1.9a, northeast3 structural genomics consortium target rlr261 |
| 60 | c3rd6A_ | Alignment | not modelled | 99.2 | 14 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ml3558 protein; PDBTitle: crystal structure of ml3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403 |
| 61 | c2k7hA_ | Alignment | not modelled | 99.2 | 14 PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4 |
| 62 | d1fm4a_ | Alignment | not modelled | 99.2 | 10 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 63 | c3q64A_ | Alignment | not modelled | 99.2 | 17 PDB header: structure genomics, unknown function Chain: A: PDB Molecule: ml3774 protein; PDBTitle: x-ray crystal structure of protein ml3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405. |
| 64 | c6gq9A_ | Alignment | not modelled | 99.2 | 10 PDB header: allergen Chain: A: PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401 |
| 65 | c2e3rB_ | Alignment | not modelled | 99.2 | 14 PDB header: lipid transport Chain: B: PDB Molecule: lipid-transfer protein cert; PDBTitle: crystal structure of cert start domain in complex with c18-2 ceramide (p1) |
| 66 | d1xdfa1 | Alignment | not modelled | 99.2 | 16 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 67 | d1z94a1 | Alignment | not modelled | 99.2 | 13 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 68 | c2m89A_ | Alignment | not modelled | 99.2 | 15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea |
| 69 | c3rwsA_ | Alignment | not modelled | 99.2 | 10 PDB header: plant protein Chain: A: PDB Molecule: mtn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin |
| 70 | c2i9yA_ | Alignment | not modelled | 99.2 | 10 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: major latex protein-like protein 28 or mlp-like PDBTitle: solution structure of arabidopsis thaliana protein2 at1g70830, a member of the major latex protein family |
| 71 | c3fo5A_ | Alignment | not modelled | 99.1 | 14 PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11) |
| 72 | c3q6aH_ | Alignment | not modelled | 99.1 | 10 PDB header: structure genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116 |
| 73 | c3q63F_ | Alignment | not modelled | 99.1 | 16 PDB header: structural genomics, unknown function Chain: F: PDB Molecule: ml2253 protein; PDBTitle: x-ray crystal structure of protein ml2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404. |
| 74 | d1xn6a_ | Alignment | not modelled | 99.1 | 15 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 75 | c3ie5A_ | Alignment | not modelled | 99.1 | 11 PDB header: plant protein, biosynthetic protein Chain: A: PDB Molecule: phenolic oxidative coupling protein hyp-1; PDBTitle: crystal structure of hyp-1 protein from hypericum perforatum (st2 john's wort) involved in hypericin biosynthesis |
| 76 | d1txca1 | Alignment | not modelled | 99.0 | 10 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 77 | d2il5a1 | Alignment | not modelled | 99.0 | 13 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| | | | | | Fold: TBP-like |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 78 | d1xn5a_ | Alignment | not modelled | 99.0 | 15 | Superfamily: Bet v1-like Family: AHSA1 domain |
| 79 | c2nn5A_ | Alignment | not modelled | 99.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ef_2215; PDBTitle: structure of conserved protein of unknown function ef2215 from2 enterococcus faecalis |
| 80 | c2lakA_ | Alignment | not modelled | 99.0 | 16 | PDB header: structure genomics, unknown function Chain: A: PDB Molecule: ahsa1-like protein rhe_ch02687; PDBTitle: solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242 |
| 81 | d2k5ga1 | Alignment | not modelled | 98.9 | 16 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 82 | d2nn5a1 | Alignment | not modelled | 98.9 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 83 | d3elia1 | Alignment | not modelled | 98.8 | 14 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 84 | c2kewA_ | Alignment | not modelled | 98.8 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yndb; PDBTitle: the solution structure of bacillus subtilis sr211 start domain by nmr2 spectroscopy |
| 85 | c3oh8A_ | Alignment | not modelled | 98.8 | 9 | PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91 |
| 86 | d1zxfa1 | Alignment | not modelled | 98.8 | 14 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 87 | d2psoa1 | Alignment | not modelled | 98.8 | 15 | Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 88 | c2luzA_ | Alignment | not modelled | 98.6 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: calu16; PDBTitle: solution nmr structure of calu16 from micromonospora echinospora,2 northeast structural genomics consortium (nesg) target mir12 |
| 89 | d1x53a1 | Alignment | not modelled | 98.5 | 10 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 90 | c3ni8A_ | Alignment | not modelled | 98.4 | 13 | PDB header: unknown function Chain: A: PDB Molecule: pf0360w protein; PDBTitle: crystal structure of pf0360w, an hsp90 activator from plasmodium2 falciparum |
| 91 | c5z4eA_ | Alignment | not modelled | 98.3 | 14 | PDB header: biosynthetic protein Chain: A: PDB Molecule: txno9; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09 |
| 92 | c2psoC_ | Alignment | not modelled | 98.0 | 14 | PDB header: structural genomics, unknown function Chain: C: PDB Molecule: star-related lipid transfer protein 13; PDBTitle: human stard13 (dlc2) lipid transfer and protein localization domain |
| 93 | d1vjha_ | Alignment | not modelled | 96.8 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 94 | c5ys0A_ | Alignment | not modelled | 94.1 | 12 | PDB header: transport protein Chain: A: PDB Molecule: membrane-anchored lipid-binding protein ysp2; PDBTitle: crystal structure of the second starkin domain of lam2 in complex with2 ergosterol |
| 95 | c6gqfC_ | Alignment | not modelled | 94.0 | 12 | PDB header: lipid transport Chain: C: PDB Molecule: gram domain-containing protein 1a; PDBTitle: the structure of mouse astera (gramd1a) with 25-hydroxy cholesterol |
| 96 | c5yqiA_ | Alignment | not modelled | 93.4 | 12 | PDB header: transport protein Chain: A: PDB Molecule: membrane-anchored lipid-binding protein ysp2; PDBTitle: crystal structure of the first starkin domain of lam2 |
| 97 | c2ejxA_ | Alignment | not modelled | 92.4 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stk_08120; PDBTitle: crystal structure of the hypothetical protein stk_08120 from2 sulfolobus tokodaii |
| 98 | c5yqiB_ | Alignment | not modelled | 88.6 | 19 | PDB header: transport protein Chain: B: PDB Molecule: membrane-anchored lipid-binding protein lam4; PDBTitle: crystal structure of the first starkin domain of lam4 |
| 99 | d2ffsa1 | Alignment | not modelled | 87.8 | 12 | Fold: TBP-like Superfamily: Bet v1-like Family: PA1206-like |
| 100 | c6bymA_ | Alignment | not modelled | 82.5 | 14 | PDB header: lipid transport Chain: A: PDB Molecule: sterol-binding protein; PDBTitle: crystal structure of the sterol-bound second start domain of yeast2 lam4 |
| 101 | c6gn5A_ | Alignment | not modelled | 60.6 | 11 | PDB header: lipid transport Chain: A: PDB Molecule: gram domain-containing protein 1c; PDBTitle: crystal structure of human gramd1c start domain |
| 102 | c3qrzC_ | Alignment | not modelled | 39.7 | 35 | PDB header: hormone receptor Chain: C: PDB Molecule: abscisic acid receptor pyl5; PDBTitle: crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom |