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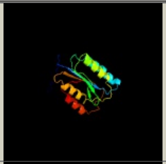
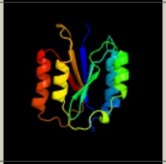
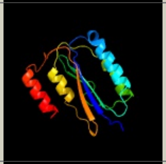
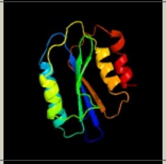
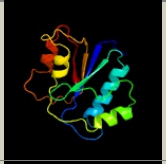
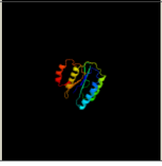
|---|---|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0368c_(-)_445315_446526 |
| Date | Tue Jul 23 14:50:44 BST 2019 |
| Unique Job ID | 9645c9ad7a93a1f1 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c4fx5A_ | Alignment |  | 99.2 | 15 | **PDB header:**blood clotting<br>**Chain:** A: **PDB Molecule:**von willebrand factor type a;<br>**PDBTitle:** von willebrand factor type a from catenulispora acidiphila |
| 2 | c3ibsA_ | Alignment |  | 99.2 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved hypothetical protein batb;<br>**PDBTitle:** crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron |
| 3 | c6fpzA_ | Alignment |  | 99.1 | 14 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**inter-alpha-trypsin inhibitor heavy chain h1;<br>**PDBTitle:** inter-alpha-inhibitor heavy chain 1, d298a |
| 4 | c5iy70_ | Alignment |  | 99.1 | 9 | **PDB header:**transcription, transferase/dna<br>**Chain:** 0: **PDB Molecule:**general transcription factor iih subunit 2;<br>**PDBTitle:** human holo-pic in the open state |
| 5 | c4wfqA_ | Alignment |  | 99.0 | 11 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**suppressor of stem-loop protein 1;<br>**PDBTitle:** crystal structure of tfiih subunit |
| 6 | c2i6sA_ | Alignment |  | 99.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**complement c2a fragment;<br>**PDBTitle:** complement component c2a |
| 7 | d1yvra2 | Alignment |  | 99.0 | 19 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**RoRNP C-terminal domain-like |
| 8 | d2ok5a1 | Alignment |  | 99.0 | 15 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 9 | c1rs0A_ | Alignment |  | 98.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**complement factor b;<br>**PDBTitle:** crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip) |
| 10 | c2x31F_ | Alignment |  | 98.9 | 12 | **PDB header:**ligase<br>**Chain:** F: **PDB Molecule:**magnesium-chelatase 60 kda subunit;<br>**PDBTitle:** modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang |
| 11 | c6o9l6_ | Alignment |  | 98.9 | 10 | **PDB header:**transcription/dna<br>**Chain:** 6: **PDB Molecule:**general transcription factor iih subunit 2;<br>**PDBTitle:** human holo-pic in the closed state |

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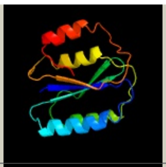
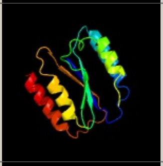
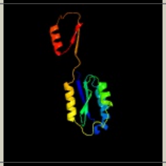
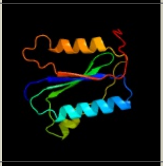
| 12 | c6nmiE_ | Alignment |  | 98.9 | 11 | **PDB header:**transcription<br>**Chain:** E: **PDB Molecule:**general transcription factor iih subunit 2, p44;<br>**PDBTitle:** cryo-em structure of the human tfiih core complex |
| 13 | c2ok5A_ | Alignment |  | 98.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**complement factor b;<br>**PDBTitle:** human complement factor b |
| 14 | c2nvoA_ | Alignment |  | 98.8 | 17 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**ro sixty-related protein, rsr;<br>**PDBTitle:** crystal structure of deinococcus radiodurans ro (rsr) protein |
| 15 | c4rckB_ | Alignment |  | 98.8 | 14 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**hypothetical membrane spanning protein;<br>**PDBTitle:** crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri |
| 16 | c5a8jA_ | Alignment |  | 98.8 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**vwa2;<br>**PDBTitle:** crystal structure of the arnb paralog vwa2 from2 sulfolobus acidocaldarius |
| 17 | c4hqnB_ | Alignment |  | 98.8 | 16 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**sporozoite surface protein 2;<br>**PDBTitle:** crystal structure of manganese-loaded plasmodium vivax trap protein |
| 18 | c4okuA_ | Alignment |  | 98.8 | 15 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**micronemal protein mic2;<br>**PDBTitle:** structure of toxoplasma gondii promic2 |
| 19 | d1v7pc_ | Alignment |  | 98.7 | 14 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 20 | c2xggB_ | Alignment |  | 98.7 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**microneme protein 2;<br>**PDBTitle:** structure of toxoplasma gondii micronemal protein 2 a_i2 domain |
| 21 | c5oqj6_ | Alignment | not modelled | 98.7 | 11 | **PDB header:**transcription<br>**Chain:** 6: **PDB Molecule:**suppressor of stem-loop protein 1;<br>**PDBTitle:** structure of yeast transcription pre-initiation complex with tfiih |
| 22 | c4b4tW_ | Alignment | not modelled | 98.7 | 13 | **PDB header:**hydrolase<br>**Chain:** W: **PDB Molecule:**26s proteasome regulatory subunit rpn10;<br>**PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome |
| 23 | c4cnbA_ | Alignment | not modelled | 98.6 | 17 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**proximal thread matrix protein 1;<br>**PDBTitle:** structure of proximal thread matrix protein 1 (ptmp1) from the2 mussel byssus - crystal form 2 |
| 24 | c2iueA_ | Alignment | not modelled | 98.6 | 12 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**pactolus i-domain;<br>**PDBTitle:** pactolus i-domain: functional switching of the rossmann2 fold |
| 25 | d1jeyb2 | Alignment | not modelled | 98.6 | 12 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Ku80 subunit N-terminal domain |
| 26 | d1jeya2 | Alignment | not modelled | 98.6 | 6 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Ku70 subunit N-terminal domain |
| 27 | d1ck4a_ | Alignment | not modelled | 98.6 | 15 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 28 | c2b2xB_ | Alignment | not modelled | 98.6 | 10 | **PDB header:**immune system<br>**Chain:** B: **PDB Molecule:**integrin alpha-1;<br>**PDBTitle:** vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab |
|  |  |  |  |  |  | **PDB header:**rna binding protein |

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| 29 | c1yvrA_ | Alignment | not modelled | 98.5 | 18 | **Chain:** A: **PDB Molecule:**60-kda ss-a/ro ribonucleoprotein;<br>**PDBTitle:** ro autoantigen |
| 30 | d1pt6a_ | Alignment | not modelled | 98.5 | 16 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 31 | c2x5nA_ | Alignment | not modelled | 98.5 | 10 | **PDB header:**nuclear protein<br>**Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn10;<br>**PDBTitle:** crystal structure of the sprpn10 vwa domain |
| 32 | c3jbrF_ | Alignment | not modelled | 98.5 | 13 | **PDB header:**membrane protein<br>**Chain:** F: **PDB Molecule:**voltage-dependent calcium channel subunit alpha-2/delta-1;<br>**PDBTitle:** cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom |
| 33 | c4hqfA_ | Alignment | not modelled | 98.4 | 16 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**thrombospondin-related anonymous protein, trap;<br>**PDBTitle:** crystal structure of plasmodium falciparum trap, i4 form |
| 34 | d1ijba_ | Alignment | not modelled | 98.4 | 8 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 35 | c5gjqW_ | Alignment | not modelled | 98.4 | 10 | **PDB header:**hydrolase<br>**Chain:** W: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 4;<br>**PDBTitle:** structure of the human 26s proteasome bound to usp14-ubal |
| 36 | c5e6rA_ | Alignment | not modelled | 98.4 | 18 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-l;<br>**PDBTitle:** structures of leukocyte integrin alb2: the ai domain, the headpiece,2 and the pocket for the internal ligand |
| 37 | d1u0oc1 | Alignment | not modelled | 98.4 | 7 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 38 | d1shux_ | Alignment | not modelled | 98.4 | 13 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 39 | c3tw0D_ | Alignment | not modelled | 98.3 | 19 | **PDB header:**cell adhesion<br>**Chain:** D: **PDB Molecule:**cell wall surface anchor family protein;<br>**PDBTitle:** structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae |
| 40 | c3txaA_ | Alignment | not modelled | 98.3 | 20 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**cell wall surface anchor family protein;<br>**PDBTitle:** structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae |
| 41 | c5gjvF_ | Alignment | not modelled | 98.3 | 13 | **PDB header:**membrane protein<br>**Chain:** F: **PDB Molecule:**voltage-dependent calcium channel subunit alpha-2/delta-1;<br>**PDBTitle:** structure of the mammalian voltage-gated calcium channel cav1.12 complex at near atomic resolution |
| 42 | c6bxjA_ | Alignment | not modelled | 98.3 | 14 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**chimera protein of integrin beta-3 and integrin alpha-l;<br>**PDBTitle:** structure of a single-chain beta3 integrin |
| 43 | d1atza_ | Alignment | not modelled | 98.3 | 15 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 44 | d1q0pa_ | Alignment | not modelled | 98.3 | 14 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 45 | c3n2nC_ | Alignment | not modelled | 98.2 | 11 | **PDB header:**toxin receptor<br>**Chain:** C: **PDB Molecule:**anthrax toxin receptor 1;<br>**PDBTitle:** the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain |
| 46 | c3gxbB_ | Alignment | not modelled | 98.2 | 14 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**von willebrand factor;<br>**PDBTitle:** crystal structure of vwf a2 domain |
| 47 | c6bxfA_ | Alignment | not modelled | 98.2 | 17 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**chimera protein of integrin beta-3 and integrin alpha-l;<br>**PDBTitle:** crystal structure of an extended b3 integrin l33 |
| 48 | c4ihkA_ | Alignment | not modelled | 98.0 | 12 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**collagen alpha3(vi);<br>**PDBTitle:** crystal structure of the collagen vi alpha3 n5 domain r1061q |
| 49 | c1jeyB_ | Alignment | not modelled | 98.0 | 11 | **PDB header:**dna binding protein/dna<br>**Chain:** B: **PDB Molecule:**ku80;<br>**PDBTitle:** crystal structure of the ku heterodimer bound to dna |
| 50 | c3ragA_ | Alignment | not modelled | 98.0 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446 |
| 51 | d1n3ya_ | Alignment | not modelled | 98.0 | 12 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 52 | d1mf7a_ | Alignment | not modelled | 97.8 | 11 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 53 | d1mjna_ | Alignment | not modelled | 97.8 | 14 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 54 | c6djpB_ | Alignment | not modelled | 97.6 | 15 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**integrin beta-8;<br>**PDBTitle:** integrin alpha-v beta-8 in complex with the fabs 8b8 and 68 |
| | | | | | | **PDB header:**immune system |

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| 55 | c4um9D_ | Alignment | not modelled | 97.6 | 13 | **Chain:** D: **PDB Molecule:**integrin beta-6;<br>**PDBTitle:** crystal structure of alpha v beta 6 with peptide |
| 56 | c3fcuB_ | Alignment | not modelled | 97.6 | 13 | **PDB header:**cell adhesion/blood clotting<br>**Chain:** B: **PDB Molecule:**integrin beta-3;<br>**PDBTitle:** structure of headpiece of integrin aiibb3 in open conformation |
| 57 | d1pd0a3 | Alignment | not modelled | 97.5 | 11 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Trunk domain of Sec23/24 |
| 58 | c3vi3D_ | Alignment | not modelled | 97.5 | 15 | **PDB header:**cell adhesion/immune system<br>**Chain:** D: **PDB Molecule:**integrin beta-1;<br>**PDBTitle:** crystal structure of alpha5beta1 integrin headpiece (ligand-free form) |
| 59 | d1tyeb2 | Alignment | not modelled | 97.3 | 15 | **Fold:**vWA-like<br>**Superfamily:**vWA-like<br>**Family:**Integrin A (or I) domain |
| 60 | c3v4pB_ | Alignment | not modelled | 97.1 | 15 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**integrin beta-7;<br>**PDBTitle:** crystal structure of a4b7 headpiece complexed with fab act-1 |
| 61 | c1u8cB_ | Alignment | not modelled | 96.5 | 11 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**integrin beta-3;<br>**PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure |
| 62 | c3k6sB_ | Alignment | not modelled | 86.8 | 21 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**integrin beta-2;<br>**PDBTitle:** structure of integrin alphaxbeta2 ectodomain |
| 63 | c3ijeB_ | Alignment | not modelled | 83.0 | 11 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**integrin beta-3;<br>**PDBTitle:** crystal structure of the complete integrin alhavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment |
| 64 | c3k71G_ | Alignment | not modelled | 79.1 | 13 | **PDB header:**cell adhesion<br>**Chain:** G: **PDB Molecule:**integrin alpha-x;<br>**PDBTitle:** structure of integrin alphax beta2 ectodomain |
| 65 | d1o0la_ | Alignment | not modelled | 78.6 | 27 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Bcl-2 inhibitors of programmed cell death<br>**Family:**Bcl-2 inhibitors of programmed cell death |
| 66 | c5f56A_ | Alignment | not modelled | 76.8 | 11 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**single-stranded-dna-specific exonuclease;<br>**PDBTitle:** structure of recj complexed with dna and ssb-ct |
| 67 | c6orbA_ | Alignment | not modelled | 75.6 | 22 | **PDB header:**motor protein<br>**Chain:** A: **PDB Molecule:**midasin;<br>**PDBTitle:** full-length s. pombe mdn1 in the presence of atp and rbin-1 |
| 68 | c5y59B_ | Alignment | not modelled | 75.5 | 9 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**atp-dependent dna helicase ii subunit 2;<br>**PDBTitle:** crystal structure of ku80 and sir4 |
| 69 | c6eesA_ | Alignment | not modelled | 70.9 | 22 | **PDB header:**motor protein<br>**Chain:** A: **PDB Molecule:**midasin;<br>**PDBTitle:** fitted model of s. pombe mdn1 into the cryo-em map obtained in the2 presence of atp and rbin-1 |
| 70 | c2qpuB_ | Alignment | not modelled | 70.5 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme;<br>**PDBTitle:** sugar tongs mutant s378p in complex with acarbose |
| 71 | c5y58D_ | Alignment | not modelled | 69.7 | 12 | **PDB header:**rna binding protein<br>**Chain:** D: **PDB Molecule:**atp-dependent dna helicase ii subunit 2;<br>**PDBTitle:** crystal structure of ku70/80 and tlc1 |
| 72 | c1pd0A_ | Alignment | not modelled | 62.8 | 11 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**protein transport protein sec24;<br>**PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5) |
| 73 | c5y58E_ | Alignment | not modelled | 61.1 | 14 | **PDB header:**rna binding protein<br>**Chain:** E: **PDB Molecule:**atp-dependent dna helicase ii subunit 1;<br>**PDBTitle:** crystal structure of ku70/80 and tlc1 |
| 74 | c1lwhA_ | Alignment | not modelled | 60.6 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase;<br>**PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase |
| 75 | d1zy3a1 | Alignment | not modelled | 60.2 | 26 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Bcl-2 inhibitors of programmed cell death<br>**Family:**Bcl-2 inhibitors of programmed cell death |
| 76 | c3n92A_ | Alignment | not modelled | 57.3 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**alpha-amylase, gh57 family;<br>**PDBTitle:** crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose |
| 77 | c3k8kB_ | Alignment | not modelled | 57.1 | 17 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**alpha-amylase, susg;<br>**PDBTitle:** crystal structure of susg |
| 78 | c3egxB_ | Alignment | not modelled | 56.9 | 10 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**protein transport protein sec24a;<br>**PDBTitle:** crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22b and bound to the transport3 signal sequence of the snare protein bet1 |
| 79 | c6a6iG_ | Alignment | not modelled | 56.2 | 12 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**excision repair cross-complementing rodent repair<br>**PDBTitle:** crystal structure of the winged-helix domain of cockayne syndrome2 group b protein in complex with ubiquitin |
| 80 | c5x7uA_ | Alignment | not modelled | 55.2 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**trehalose synthase;<br>**PDBTitle:** trehalose synthase from thermobaculum terrenum |
| | | | | | | **PDB header:**protein transport |

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| 81 | c3eg9A_ | Alignment | not modelled | 45.5 | 12 | **Chain:** A: **PDB Molecule:**protein transport protein sec23a;<br>**PDBTitle:** crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin |
| 82 | c1jeqA_ | Alignment | not modelled | 44.3 | 8 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**ku70;<br>**PDBTitle:** crystal structure of the ku heterodimer |
| 83 | c2aaaA_ | Alignment | not modelled | 43.7 | 14 | **PDB header:**glycosidase<br>**Chain:** A: **PDB Molecule:**alpha-amylase;<br>**PDBTitle:** calcium binding in alpha-amylases: an x-ray diffraction study at 2.12 angstroms resolution of two enzymes from aspergillus |
| 84 | c3hn7A_ | Alignment | not modelled | 43.6 | 11 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase;<br>**PDBTitle:** crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution |
| 85 | d1r7aa2 | Alignment | not modelled | 43.6 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 86 | d1l5wa_ | Alignment | not modelled | 43.6 | 29 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Oligosaccharide phosphorylase |
| 87 | d1wzla3 | Alignment | not modelled | 42.8 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 88 | c2z1kA_ | Alignment | not modelled | 42.6 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**(neo)pullulanase;<br>**PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8 |
| 89 | d1ygpa_ | Alignment | not modelled | 42.1 | 14 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Oligosaccharide phosphorylase |
| 90 | d2gj4a1 | Alignment | not modelled | 40.7 | 24 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Oligosaccharide phosphorylase |
| 91 | c3ddsB_ | Alignment | not modelled | 40.3 | 24 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**glycogen phosphorylase, liver form;<br>**PDBTitle:** crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261 |
| 92 | c2taaA_ | Alignment | not modelled | 40.2 | 19 | **PDB header:**hydrolase (o-glycosyl)<br>**Chain:** A: **PDB Molecule:**taka-amylase a;<br>**PDBTitle:** structure and possible catalytic residues of taka-amylase a |
| 93 | d2atia1 | Alignment | not modelled | 39.7 | 24 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Oligosaccharide phosphorylase |
| 94 | d1ea9c3 | Alignment | not modelled | 39.5 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 95 | c2wcsA_ | Alignment | not modelled | 38.4 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha amylase, catalytic region;<br>**PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde) |
| 96 | d1avaa2 | Alignment | not modelled | 37.9 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 97 | c4bqeA_ | Alignment | not modelled | 37.6 | 24 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**alpha-glucan phosphorylase 2,4-glucan phosphorylase;<br>**PDBTitle:** arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2) |
| 98 | c5lrbB_ | Alignment | not modelled | 36.6 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**alpha-1,4 glucan phosphorylase;<br>**PDBTitle:** plastidial phosphorylase from barley in complex with acarbose |
| 99 | c5ot1A_ | Alignment | not modelled | 36.2 | 11 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**pullulanase type ii, gh13 family;<br>**PDBTitle:** the type iii pullulan hydrolase from thermococcus kodakarensis |
| 100 | c4aeeA_ | Alignment | not modelled | 35.4 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha amylase, catalytic region;<br>**PDBTitle:** crystal structure of maltogenic amylase from s.marinus |
| 101 | d1hlva2 | Alignment | not modelled | 34.0 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Centromere-binding |
| 102 | d1ht6a2 | Alignment | not modelled | 33.3 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 103 | d1lwha2 | Alignment | not modelled | 33.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 104 | c2gdvA_ | Alignment | not modelled | 32.8 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sucrose phosphorylase;<br>**PDBTitle:** sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose |
| 105 | d1qhoa4 | Alignment | not modelled | 32.0 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 106 | d2ewca1 | Alignment | not modelled | 31.9 | 15 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**YjgF-like<br>**Family:**YjgF/L-PSP |
| 107 | c1tcmB_ | Alignment | not modelled | 31.8 | 12 | **PDB header:**glycosyltransferase<br>**Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase;<br>**PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from |

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|---|---|---|---|---|---|---|
| | | | | | | bacillus2 circulans strain 251 |
| 108 | d1a7ja_ | Alignment | not modelled | 31.2 | 12 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Phosphoribulokinase/pantothenate kinase |
| 109 | d1jwya1 | Alignment | not modelled | 30.8 | 14 | **Fold:**SH3-like barrel<br>**Superfamily:**Myosin S1 fragment, N-terminal domain<br>**Family:**Myosin S1 fragment, N-terminal domain |
| 110 | d1eh9a3 | Alignment | not modelled | 29.8 | 7 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 111 | c5m99A_ | Alignment | not modelled | 28.8 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-amylase;<br>**PDBTitle:** functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization |
| 112 | c3nbxX_ | Alignment | not modelled | 27.4 | 16 | **PDB header:**hydrolase<br>**Chain:** X: **PDB Molecule:**atpase rava;<br>**PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp |
| 113 | c5wu7A_ | Alignment | not modelled | 27.1 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of gh57-type branching enzyme from hyperthermophilic2 archaeon pyrococcus horikoshii |
| 114 | c5hp8C_ | Alignment | not modelled | 27.1 | 15 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**reactive intermediate deaminase a, chloroplastic;<br>**PDBTitle:** crystal structures of rida in complex with pyruvate |
| 115 | c3e0dA_ | Alignment | not modelled | 27.0 | 18 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha;<br>**PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit |
| 116 | c3gtzA_ | Alignment | not modelled | 26.9 | 8 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative translation initiation inhibitor;<br>**PDBTitle:** crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium |
| 117 | c1m2oA_ | Alignment | not modelled | 25.8 | 12 | **PDB header:**protein transport/signaling protein<br>**Chain:** A: **PDB Molecule:**protein transport protein sec23;<br>**PDBTitle:** crystal structure of the sec23-sar1 complex |
| 118 | c3quwA_ | Alignment | not modelled | 25.5 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**protein mmf1;<br>**PDBTitle:** crystal structure of yeast mmf1 |
| 119 | c5lewA_ | Alignment | not modelled | 25.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha;<br>**PDBTitle:** dna polymerase |
| 120 | d5easa1 | Alignment | not modelled | 24.8 | 29 | **Fold:**alpha/alpha toroid<br>**Superfamily:**Terpenoid cyclases/Protein prenyltransferases<br>**Family:**Terpenoid cyclase N-terminal domain |