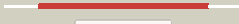
































# Phyre2

|                  |                                  |
|------------------|----------------------------------|
| Email            | mdejesus@rockefeller.edu         |
| Description      | RVBD1461 (-<br>)_1646995_1649535 |
| Date             | Fri Aug 2 13:30:04 BST<br>2019   |
| Unique Job<br>ID | 96a768f87178465e                 |

Detailed template  
information

| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                      |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c5awfA_</a> |  Alignment   |    | 100.0      | 50     | <b>PDB header:</b> transport protein/protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> fes cluster assembly protein sufb;<br><b>PDBTitle:</b> crystal structure of sufb-sufc-sufd complex from escherichia coli                    |
| 2  | <a href="#">c4dn7B_</a> |  Alignment   |    | 100.0      | 28     | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp-binding protein;<br><b>PDBTitle:</b> crystal structure of putative abc transporter, atp-binding protein2 from methanosarcina mazei go1 |
| 3  | <a href="#">d1vh4a_</a> |  Alignment   |    | 100.0      | 19     | <b>Fold:</b> Single-stranded right-handed beta-helix<br><b>Superfamily:</b> Stabilizer of iron transporter SufD<br><b>Family:</b> Stabilizer of iron transporter SufD                                                                     |
| 4  | <a href="#">c1vdeA_</a> |  Alignment   |    | 100.0      | 20     | <b>PDB header:</b> endonuclease<br><b>Chain:</b> A: <b>PDB Molecule:</b> pi-scei;<br><b>PDBTitle:</b> pi-scei, a homing endonuclease with protein splicing2 activity                                                                      |
| 5  | <a href="#">c2cw8A_</a> |  Alignment |  | 100.0      | 30     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease pi-pkoi;<br><b>PDBTitle:</b> crystal structure of intein homing endonuclease ii                                                                        |
| 6  | <a href="#">c1dq3A_</a> |  Alignment |  | 100.0      | 15     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease;<br><b>PDBTitle:</b> crystal structure of an archaeal intein-encoded homing2 endonuclease pi-pfui                                                      |
| 7  | <a href="#">c2jmzA_</a> |  Alignment |  | 99.7       | 34     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mj0781;<br><b>PDBTitle:</b> solution structure of a kba intein precursor from2 methanococcus jannaschii                                 |
| 8  | <a href="#">c1b24A_</a> |  Alignment |  | 99.7       | 12     | <b>PDB header:</b> intron-encoded<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (i-dmoi);<br><b>PDBTitle:</b> i-dmoi, intron-encoded endonuclease                                                                                      |
| 9  | <a href="#">d1mi8a_</a> |  Alignment |  | 99.6       | 26     | <b>Fold:</b> Hedgehog/intein (Hint) domain<br><b>Superfamily:</b> Hedgehog/intein (Hint) domain<br><b>Family:</b> Intein (protein splicing domain)                                                                                        |
| 10 | <a href="#">c4o1rA_</a> |  Alignment |  | 99.6       | 31     | <b>PDB header:</b> splicing<br><b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase;<br><b>PDBTitle:</b> crystal structure of npudnab intein                                                                                    |
| 11 | <a href="#">d1am2a_</a> |  Alignment |  | 99.6       | 27     | <b>Fold:</b> Hedgehog/intein (Hint) domain<br><b>Superfamily:</b> Hedgehog/intein (Hint) domain<br><b>Family:</b> Intein (protein splicing domain)                                                                                        |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                      |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c2in0A_</a> | Alignment |    | 99.5 | 36 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease pi-mtui;<br><b>PDBTitle:</b> crystal structure of mtu reca intein splicing domain                                                                 |
| 13 | <a href="#">c2imzA_</a> | Alignment |    | 99.5 | 31 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease pi-mtui;<br><b>PDBTitle:</b> crystal structure of mtu reca intein splicing domain                                                                 |
| 14 | <a href="#">c1zd7B_</a> | Alignment |    | 99.5 | 29 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii alpha subunit;<br><b>PDBTitle:</b> 1.7 angstrom crystal structure of post-splicing form of a dnae intein2 from synechocystis sp. pcc 6803 |
| 15 | <a href="#">c2lcjA_</a> | Alignment |    | 99.5 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pab polc intein;<br><b>PDBTitle:</b> solution nmr structure of pab polii intein                                                                                |
| 16 | <a href="#">c4o1sB_</a> | Alignment |    | 99.5 | 32 | <b>PDB header:</b> splicing<br><b>Chain:</b> B: <b>PDB Molecule:</b> v-type atp synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of tvovma intein                                                                         |
| 17 | <a href="#">c5o9jB_</a> | Alignment |    | 99.4 | 28 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcription initiation factor iib,transcription<br><b>PDBTitle:</b> crystal structure of transcription factor iib mja mini-intein                            |
| 18 | <a href="#">c2keqA_</a> | Alignment |  | 99.4 | 29 | <b>PDB header:</b> splicing<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii alpha subunit, nucleic acid<br><b>PDBTitle:</b> solution structure of dnae intein from nostoc punctiforme                                    |
| 19 | <a href="#">c4e2uA_</a> | Alignment |  | 99.4 | 28 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> pho rada intein;<br><b>PDBTitle:</b> crystal structures of radamin intein from pyrococcus horikoshii                                                    |
| 20 | <a href="#">c2lwyA_</a> | Alignment |  | 99.4 | 34 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacterial intein-like domain;<br><b>PDBTitle:</b> solution structure of bacterial intein-like domain from clostridium2 thermocellum                     |
| 21 | <a href="#">d1dq3a1</a> | Alignment | not modelled                                                                        | 99.3 | 39 | <b>Fold:</b> Hedgehog/intein (Hint) domain<br><b>Superfamily:</b> Hedgehog/intein (Hint) domain<br><b>Family:</b> Intein (protein splicing domain)                                                                                   |
| 22 | <a href="#">d1jvaa1</a> | Alignment | not modelled                                                                        | 99.3 | 23 | <b>Fold:</b> Hedgehog/intein (Hint) domain<br><b>Superfamily:</b> Hedgehog/intein (Hint) domain<br><b>Family:</b> Intein (protein splicing domain)                                                                                   |
| 23 | <a href="#">d1gppa_</a> | Alignment | not modelled                                                                        | 99.3 | 24 | <b>Fold:</b> Hedgehog/intein (Hint) domain<br><b>Superfamily:</b> Hedgehog/intein (Hint) domain<br><b>Family:</b> Intein (protein splicing domain)                                                                                   |
| 24 | <a href="#">d1at0a_</a> | Alignment | not modelled                                                                        | 99.3 | 16 | <b>Fold:</b> Hedgehog/intein (Hint) domain<br><b>Superfamily:</b> Hedgehog/intein (Hint) domain<br><b>Family:</b> Hedgehog C-terminal (Hog) autoprocessing domain                                                                    |
| 25 | <a href="#">c6bs8C_</a> | Alignment | not modelled                                                                        | 99.2 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> replicative dna helicase;<br><b>PDBTitle:</b> the class 3 dnab intein from mycobacterium smegmatis                                                             |
| 26 | <a href="#">d1jvaa3</a> | Alignment | not modelled                                                                        | 99.2 | 16 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Intein endonuclease                                                                                                              |
| 27 | <a href="#">c5ol5B_</a> | Alignment | not modelled                                                                        | 99.0 | 19 | <b>PDB header:</b> splicing<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit alpha,dna polymerase iii subunit<br><b>PDBTitle:</b> crystal structure of an inactivated ssp siclopps intein with cfahpq2 extein     |
| 28 | <a href="#">d1dq3a4</a> | Alignment | not modelled                                                                        | 98.9 | 9  | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Intein endonuclease                                                                                                              |
|    |                         |           |                                                                                     |      |    | <b>Fold:</b> AXH domain                                                                                                                                                                                                              |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                    |
|----|-------------------------|-----------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">d1oa8a_</a> | Alignment | not modelled | 98.6 | 21 | <b>Superfamily:</b> AXH domain<br><b>Family:</b> AXH domain                                                                                                                                                                                                                        |
| 30 | <a href="#">c3hyiA_</a> | Alignment | not modelled | 98.1 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein duf199/whia;<br><b>PDBTitle:</b> crystal structure of full-length duf199/whia from <i>thermatoga maritima</i>                                                                          |
| 31 | <a href="#">c5ol7A_</a> | Alignment | not modelled | 97.9 | 22 | <b>PDB header:</b> splicing<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed dna polymerase,dna-directed dna polymerase;<br><b>PDBTitle:</b> crystal structure of an inactivated npu siclpps intein with cfahpq2 extein                                                       |
| 32 | <a href="#">c2dchX_</a> | Alignment | not modelled | 97.7 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> X: <b>PDB Molecule:</b> putative homing endonuclease;<br><b>PDBTitle:</b> crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i                                                                               |
| 33 | <a href="#">c3hyjD_</a> | Alignment | not modelled | 97.5 | 12 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> protein duf199/whia;<br><b>PDBTitle:</b> crystal structure of the n-terminal laglidag domain of duf199/whia                                                                                    |
| 34 | <a href="#">c1r7mA_</a> | Alignment | not modelled | 97.3 | 9  | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> intron-encoded endonuclease i-scei;<br><b>PDBTitle:</b> the homing endonuclease i-scei bound to its dna recognition2 region                                                                              |
| 35 | <a href="#">c1v06A_</a> | Alignment | not modelled | 97.0 | 15 | <b>PDB header:</b> dna-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hmg box-containing protein 1;<br><b>PDBTitle:</b> axh domain of the transcription factor hbp1 from <i>m.musculus</i>                                                                               |
| 36 | <a href="#">d1jvaa2</a> | Alignment | not modelled | 97.0 | 20 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Intein endonuclease                                                                                                                                                            |
| 37 | <a href="#">c3mx9A_</a> | Alignment | not modelled | 96.7 | 11 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein scv3v2(g19s);<br><b>PDBTitle:</b> molecular basis of engineered meganuclease targeting of the endogenous2 human rag1 locus                                                                       |
| 38 | <a href="#">c3fd2A_</a> | Alignment | not modelled | 96.1 | 20 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> site-specific dna endonuclease i-msoi;<br><b>PDBTitle:</b> crystal structure of mmsoi/dna complex with calcium                                                                                           |
| 39 | <a href="#">c3mxaA_</a> | Alignment | not modelled | 96.0 | 14 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> scv3v2(g19s);<br><b>PDBTitle:</b> molecular basis of engineered meganuclease targeting of the endogenous2 human rag1 locus                                                                               |
| 40 | <a href="#">c5espA_</a> | Alignment | not modelled | 95.6 | 16 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> i-panmi;<br><b>PDBTitle:</b> crystal structure of laglidag meganuclease i-panmi with coordinated2 calcium ions                                                                                           |
| 41 | <a href="#">c2ab5B_</a> | Alignment | not modelled | 95.2 | 7  | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> smrna maturase;<br><b>PDBTitle:</b> bi3 laglidag maturase                                                                                                                                              |
| 42 | <a href="#">c4efjA_</a> | Alignment | not modelled | 94.9 | 11 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> laglidag endonuclease;<br><b>PDBTitle:</b> crystal structure of i-gzeii laglidag homing endonuclease in complex2 with dna target site                                                                    |
| 43 | <a href="#">c3qqyA_</a> | Alignment | not modelled | 94.8 | 21 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein 3/homing endonuclease-like protein<br><b>PDBTitle:</b> crystal structure of a novel laglidag homing endonuclease, i-onuif2 (from <i>ophiostoma novo-ulmi</i> subsp. <i>americana</i> ) |
| 44 | <a href="#">c4yisA_</a> | Alignment | not modelled | 94.7 | 12 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> meganuclease i-cpami;<br><b>PDBTitle:</b> crystal structure of laglidag meganuclease i-cpami bound to uncleaved2 dna                                                                                     |
| 45 | <a href="#">c2qojZ_</a> | Alignment | not modelled | 94.6 | 9  | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> Z: <b>PDB Molecule:</b> intron-encoded dna endonuclease i-anii;<br><b>PDBTitle:</b> coevolution of a homing endonuclease and its host target sequence                                                                            |
| 46 | <a href="#">d1b24a1</a> | Alignment | not modelled | 94.3 | 16 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                             |
| 47 | <a href="#">c4yitD_</a> | Alignment | not modelled | 94.2 | 21 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> meganuclease i-aabmi;<br><b>PDBTitle:</b> crystal structure of laglidag meganuclease i-aabmi bound to uncleaved2 dna                                                                                     |
| 48 | <a href="#">c1mowG_</a> | Alignment | not modelled | 94.0 | 17 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> G: <b>PDB Molecule:</b> chimera of homing endonuclease i-dmoi and dna endonuclease<br><b>PDBTitle:</b> e-drei                                                                                                                    |
| 49 | <a href="#">d1m5xa_</a> | Alignment | not modelled | 93.7 | 19 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                             |
| 50 | <a href="#">d1r7ma1</a> | Alignment | not modelled | 92.4 | 6  | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                             |
| 51 | <a href="#">c3r7pA_</a> | Alignment | not modelled | 91.9 | 17 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein 3/homing endonuclease-like fusion<br><b>PDBTitle:</b> the crystal structure of i-ltri                                                                                                  |
| 52 | <a href="#">d1t9ia_</a> | Alignment | not modelled | 91.4 | 10 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                             |
| 53 | <a href="#">c5a72B_</a> | Alignment | not modelled | 90.7 | 16 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna endonuclease i-cvui;<br><b>PDBTitle:</b> crystal structure of the homing endonuclease i-cvui in complex2 with its target (sro1.3) in the presence of 2 mm ca                                         |
| 54 | <a href="#">c4loxA_</a> | Alignment | not modelled | 90.1 | 13 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> laglidag homing endonuclease i-smami;<br><b>PDBTitle:</b> crystal structure of the i-smami laglidag homing endonuclease bound2 to cleaved dna                                                            |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                            |
|----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 55 | <a href="#">d1mowa1</a> | Alignment | not modelled | 87.8 | 8  | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                     |
| 56 | <a href="#">d1b24a2</a> | Alignment | not modelled | 87.2 | 15 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                     |
| 57 | <a href="#">d1af5a</a>  | Alignment | not modelled | 86.7 | 7  | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                     |
| 58 | <a href="#">c3e54A</a>  | Alignment | not modelled | 85.6 | 14 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> rrna intron-encoded endonuclease;<br><b>PDBTitle:</b> archaeal intron-encoded homing endonuclease i-vid141i complexed with2 dna                                                                  |
| 59 | <a href="#">c5gkka</a>  | Alignment | not modelled | 83.9 | 10 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative homing endonuclease;<br><b>PDBTitle:</b> crystal structure of a homing endonuclease, i-trnai                                                                                                |
| 60 | <a href="#">d1p8kz1</a> | Alignment | not modelled | 81.9 | 11 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                     |
| 61 | <a href="#">c2dagA</a>  | Alignment | not modelled | 77.8 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 5;<br><b>PDBTitle:</b> solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)                                 |
| 62 | <a href="#">d1p8kz2</a> | Alignment | not modelled | 75.3 | 15 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease                                                                                                                                     |
| 63 | <a href="#">c3fm3B</a>  | Alignment | not modelled | 73.5 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase 2;<br><b>PDBTitle:</b> crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2                                                                  |
| 64 | <a href="#">c4ipaC</a>  | Alignment | not modelled | 71.9 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative curved dna-binding protein;<br><b>PDBTitle:</b> structure of a thermophilic arx1                                                                                                            |
| 65 | <a href="#">c2daiA</a>  | Alignment | not modelled | 71.5 | 26 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin associated domain containing 1;<br><b>PDBTitle:</b> solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadcl) |
| 66 | <a href="#">d1whca</a>  | Alignment | not modelled | 68.9 | 17 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                      |
| 67 | <a href="#">c2ex5B</a>  | Alignment | not modelled | 68.1 | 18 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna endonuclease i-ceui;<br><b>PDBTitle:</b> group i intron-encoded homing endonuclease i-ceui complexed with dna                                                                                |
| 68 | <a href="#">c1yw7A</a>  | Alignment | not modelled | 66.3 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase 2;<br><b>PDBTitle:</b> h-metap2 complexed with a444148                                                                                                                     |
| 69 | <a href="#">c2mroB</a>  | Alignment | not modelled | 64.1 | 19 | <b>PDB header:</b> transport protein/signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna damage-inducible protein 1;<br><b>PDBTitle:</b> structure of the complex of ubiquitin and the uba domain from dna-2 damage-inducible 1 protein (ddi1)                  |
| 70 | <a href="#">c1b6aA</a>  | Alignment | not modelled | 61.9 | 25 | <b>PDB header:</b> angiogenesis inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase;<br><b>PDBTitle:</b> human methionine aminopeptidase 2 complexed with tnp-470                                                                                 |
| 71 | <a href="#">d1veka</a>  | Alignment | not modelled | 61.8 | 15 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                      |
| 72 | <a href="#">c2crnA</a>  | Alignment | not modelled | 61.2 | 19 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubash3a protein;<br><b>PDBTitle:</b> solution structure of the uba domain of human ubash3a2 protein                                                                                              |
| 73 | <a href="#">d1wiva</a>  | Alignment | not modelled | 60.9 | 21 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                      |
| 74 | <a href="#">c2lbcA</a>  | Alignment | not modelled | 56.2 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 13;<br><b>PDBTitle:</b> solution structure of tandem uba of usp13                                                                                              |
| 75 | <a href="#">c2o2ka</a>  | Alignment | not modelled | 55.5 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase;<br><b>PDBTitle:</b> crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n                                                      |
| 76 | <a href="#">d1mska</a>  | Alignment | not modelled | 54.9 | 19 | <b>Fold:</b> Methionine synthase activation domain-like<br><b>Superfamily:</b> Methionine synthase activation domain-like<br><b>Family:</b> Methionine synthase SAM-binding domain                                                                                         |
| 77 | <a href="#">c6dslB</a>  | Alignment | not modelled | 54.3 | 10 | <b>PDB header:</b> splicing<br><b>Chain:</b> B: <b>PDB Molecule:</b> consensus engineered intein catc;<br><b>PDBTitle:</b> consensus engineered intein (cat) with atypical split site                                                                                      |
| 78 | <a href="#">c1dd9A</a>  | Alignment | not modelled | 53.8 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna primase;<br><b>PDBTitle:</b> structure of the dnag catalytic core                                                                                                                              |
| 79 | <a href="#">d1dd9a</a>  | Alignment | not modelled | 53.8 | 26 | <b>Fold:</b> DNA primase core<br><b>Superfamily:</b> DNA primase core<br><b>Family:</b> DNA primase DnaG catalytic core                                                                                                                                                    |
| 80 | <a href="#">c4fukB</a>  | Alignment | not modelled | 53.3 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase;<br><b>PDBTitle:</b> aminopeptidase from trypanosoma brucei                                                                                                                |
| 81 | <a href="#">d1dq3a3</a> | Alignment | not modelled | 50.3 | 11 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Intein endonuclease                                                                                                                                                    |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                        |
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| 82  | <a href="#">c3s6bA_</a> | Alignment | not modelled | 50.1 | 33 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionine aminopeptidase;<br><b>PDBTitle:</b> crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150                                                          |
| 83  | <a href="#">c2higA_</a> | Alignment | not modelled | 48.7 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-1-fructokinase;<br><b>PDBTitle:</b> crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.                                                                     |
| 84  | <a href="#">d2cpwa1</a> | Alignment | not modelled | 47.4 | 21 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                  |
| 85  | <a href="#">c5w34A_</a> | Alignment | not modelled | 45.4 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna primase;<br><b>PDBTitle:</b> crystal structure of the rna polymerase domain (rpd) of mycobacterium2 tuberculosis primase dnag in complex with double-stranded dna3 gaccggaagtgg            |
| 86  | <a href="#">c2cpwA_</a> | Alignment | not modelled | 44.5 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> cbl-interacting protein sts-1 variant;<br><b>PDBTitle:</b> solution structure of rsgi ruh-031, a uba domain from human2 cdna                                         |
| 87  | <a href="#">d1ifya_</a> | Alignment | not modelled | 44.3 | 23 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                  |
| 88  | <a href="#">d2crna1</a> | Alignment | not modelled | 44.1 | 21 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                  |
| 89  | <a href="#">c3zihB_</a> | Alignment | not modelled | 44.1 | 21 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein sepf;<br><b>PDBTitle:</b> bacillus subtilis sepf, c-terminal domain                                                                                                       |
| 90  | <a href="#">c2dakA_</a> | Alignment | not modelled | 43.9 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 5;<br><b>PDBTitle:</b> solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)                            |
| 91  | <a href="#">c1wgzC_</a> | Alignment | not modelled | 42.8 | 27 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> carboxypeptidase 1;<br><b>PDBTitle:</b> crystal structure of carboxypeptidase 1 from thermus thermophilus                                                                                        |
| 92  | <a href="#">c5vazB_</a> | Alignment | not modelled | 42.1 | 35 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna primase;<br><b>PDBTitle:</b> crystal structure of a dna primase domain from pseudomonas aeruginosa                                                                                         |
| 93  | <a href="#">c4b6at_</a> | Alignment | not modelled | 40.8 | 14 | <b>PDB header:</b> ribosome<br><b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein l21-a;<br><b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1                                                                    |
| 94  | <a href="#">d1vega_</a> | Alignment | not modelled | 40.6 | 20 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                  |
| 95  | <a href="#">d1ihma_</a> | Alignment | not modelled | 40.5 | 18 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> Positive stranded ssRNA viruses<br><b>Family:</b> Caliciviridae-like VP                                                                                                     |
| 96  | <a href="#">c3dwcA_</a> | Alignment | not modelled | 39.7 | 38 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> metallocarboxypeptidase;<br><b>PDBTitle:</b> trypanosoma cruzi metallocarboxypeptidase 1                                                                                                         |
| 97  | <a href="#">c5gujA_</a> | Alignment | not modelled | 39.7 | 37 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna primase;<br><b>PDBTitle:</b> crystal structure of the bacillus subtilis dnag rna polymerase domain,2 natural degradation of full length dnag                                               |
| 98  | <a href="#">c1ynxA_</a> | Alignment | not modelled | 39.3 | 20 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication factor-a protein 1;<br><b>PDBTitle:</b> solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)                                    |
| 99  | <a href="#">d1nuia1</a> | Alignment | not modelled | 38.9 | 20 | <b>Fold:</b> DNA primase core<br><b>Superfamily:</b> DNA primase core<br><b>Family:</b> Primase fragment of primase-helicase protein                                                                                                                                   |
| 100 | <a href="#">c1ihmC_</a> | Alignment | not modelled | 38.5 | 18 | <b>PDB header:</b> virus<br><b>Chain:</b> C: <b>PDB Molecule:</b> capsid protein;<br><b>PDBTitle:</b> crystal structure analysis of norwalk virus capsid                                                                                                               |
| 101 | <a href="#">c3p04B_</a> | Alignment | not modelled | 37.9 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized bcr;<br><b>PDBTitle:</b> crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8 |
| 102 | <a href="#">c3mhvC_</a> | Alignment | not modelled | 37.9 | 23 | <b>PDB header:</b> protein transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4;<br><b>PDBTitle:</b> crystal structure of vps4 and vta1                                                                                    |
| 103 | <a href="#">c4ru5C_</a> | Alignment | not modelled | 37.7 | 22 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> tailspike gp27;<br><b>PDBTitle:</b> crystal structure of the pseudomonas phage phi297 tailspike gp61                                                                                                 |
| 104 | <a href="#">c4jrbA_</a> | Alignment | not modelled | 37.5 | 27 | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein;<br><b>PDBTitle:</b> structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion                                                                |
| 105 | <a href="#">c3p04A_</a> | Alignment | not modelled | 37.4 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized bcr;<br><b>PDBTitle:</b> crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8 |
| 106 | <a href="#">c3ic3C_</a> | Alignment | not modelled | 35.7 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative pyruvate dehydrogenase;<br><b>PDBTitle:</b> structure of a putative pyruvate dehydrogenase from the photosynthetic2 bacterium rhodospseudomonas palustris cga009                   |
| 107 | <a href="#">c2q8kA_</a> | Alignment | not modelled | 34.9 | 14 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> proliferation-associated protein 2g4;<br><b>PDBTitle:</b> the crystal structure of ebp1                                                                                                      |
|     |                         |           |              |      |    | <b>PDB header:</b> virus like particle                                                                                                                                                                                                                                 |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                 |
|-----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 108 | <a href="#">c6ou9A_</a> | Alignment | not modelled | 34.6 | 21 | <b>Chain:</b> A: <b>PDB Molecule:</b> major capsid protein;<br><b>PDBTitle:</b> asymmetric focused reconstruction of human norovirus gi.7 houston2 strain vlp asymmetric unit in t=3 symmetry                                                                                   |
| 109 | <a href="#">c2v6cA_</a> | Alignment | not modelled | 34.4 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> proliferation-associated protein 2g4;<br><b>PDBTitle:</b> crystal structure of erbb3 binding protein 1 (ebp1)                                                                               |
| 110 | <a href="#">c6crjC_</a> | Alignment | not modelled | 34.1 | 18 | <b>PDB header:</b> virus<br><b>Chain:</b> C: <b>PDB Molecule:</b> norwalk virus, mnv-1 capsid protein chimera;<br><b>PDBTitle:</b> mouse norovirus model using the crystal structure of mnv p domain and2 the norwalkvirus shell domain                                         |
| 111 | <a href="#">c3jywW_</a> | Alignment | not modelled | 33.8 | 23 | <b>PDB header:</b> ribosome<br><b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein l31(a);<br><b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution                       |
| 112 | <a href="#">c2j376_</a> | Alignment | not modelled | 33.5 | 29 | <b>PDB header:</b> ribosome<br><b>Chain:</b> 6: <b>PDB Molecule:</b> ribosomal protein l31;<br><b>PDBTitle:</b> model of mammalian srp bound to 80s rncs                                                                                                                        |
| 113 | <a href="#">c3e3vA_</a> | Alignment | not modelled | 32.8 | 19 | <b>PDB header:</b> recombination<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein recx;<br><b>PDBTitle:</b> crystal structure of recx from lactobacillus salivarius                                                                                                  |
| 114 | <a href="#">d2z1ca1</a> | Alignment | not modelled | 32.6 | 33 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> HupF/HypC-like<br><b>Family:</b> HupF/HypC-like                                                                                                                                                                                     |
| 115 | <a href="#">c2zkrx_</a> | Alignment | not modelled | 32.6 | 31 | <b>PDB header:</b> ribosomal protein/rna<br><b>Chain:</b> X: <b>PDB Molecule:</b> rna helices;<br><b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 116 | <a href="#">c3izrg_</a> | Alignment | not modelled | 32.2 | 28 | <b>PDB header:</b> ribosome<br><b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l6 (l6e);<br><b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome                           |
| 117 | <a href="#">c2dzoD_</a> | Alignment | not modelled | 31.4 | 22 | <b>PDB header:</b> protein binding<br><b>Chain:</b> D: <b>PDB Molecule:</b> 26s protease regulatory subunit 6b homolog;<br><b>PDBTitle:</b> crystal structure analysis of yeast nas6p complexed with2 the proteasome subunit, rpt3                                              |
| 118 | <a href="#">d1n11a_</a> | Alignment | not modelled | 31.3 | 15 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                                           |
| 119 | <a href="#">c1n11A_</a> | Alignment | not modelled | 31.3 | 15 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin;<br><b>PDBTitle:</b> d34 region of human ankyrin-r and linker                                                                                                                            |
| 120 | <a href="#">c5jhgD_</a> | Alignment | not modelled | 31.2 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> tankyrase-1;<br><b>PDBTitle:</b> arcs 1-3 of human tankyrase-1 bound to a peptide derived from irap                                                                                                     |