Phyre2

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Description	P67624
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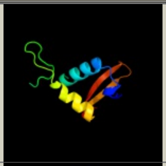
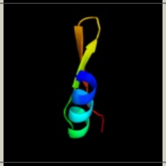
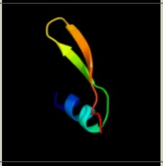
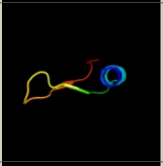
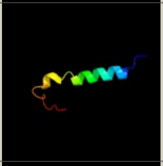
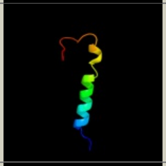
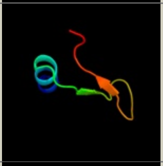
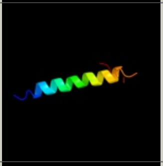
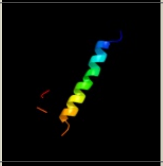
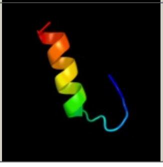
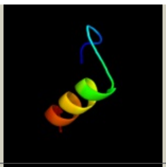
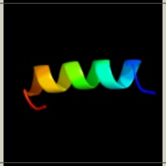
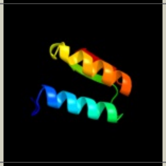
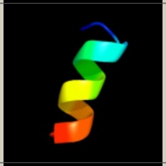
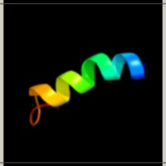
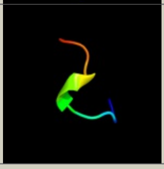
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y0na_	Alignment		100.0	39	**Fold:**YehU-like **Superfamily:**YehU-like **Family:**YehU-like
2	d1g57a_	Alignment		83.2	26	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
3	d1snna_	Alignment		74.3	26	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
4	d1k4ia_	Alignment		68.4	27	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
5	c3mioA_	Alignment		59.6	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
6	c2nysA_	Alignment		54.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**agr_c_3712p; **PDBTitle:** x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88.
7	d2nysa1	Alignment		54.8	25	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**AGR C 3712p-like
8	d1tksa_	Alignment		51.8	23	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
9	c2qasA_	Alignment		43.1	9	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of caulobacter crescentus sspb ortholog
10	c2qazC_	Alignment		40.8	9	**PDB header:**hydrolase activator **Chain:** C: **PDB Molecule:**sspb protein; **PDBTitle:** structure of c. crescentus sspb ortholog
11	d1k3ea_	Alignment		35.4	48	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone

12	c3epuB_	Alignment		30.0	32	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**stm2138 virulence chaperone; **PDBTitle:** crystal structure of stm2138, a novel virulence chaperone in2 salmonella
13	c2dalA_	Alignment		19.3	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein kiaa0794; **PDBTitle:** solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
14	d1ux8a_	Alignment		19.1	30	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
15	c2yr1B_	Alignment		18.0	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
16	d2csba1	Alignment		17.3	54	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
17	d1f7ua3	Alignment		17.0	32	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain **Family:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
18	c2ig3A_	Alignment		17.0	20	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**group iii truncated haemoglobin; **PDBTitle:** crystal structure of group iii truncated hemoglobin from campylobacter2 jejuni
19	c1vyuB_	Alignment		13.4	8	**PDB header:**ion transport **Chain:** B: **PDB Molecule:**calcium channel beta-3 subunit; **PDBTitle:** beta3 subunit of voltage-gated ca2+-channel
20	c3nrtC_	Alignment		12.2	36	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative ryanodine receptor; **PDBTitle:** the crystal strucutre of putative ryanodine receptor from bacteroides2 thetaiotaomicron vpi-5482
21	d2c1ia1	Alignment	not modelled	11.4	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
22	c3rqrA_	Alignment	not modelled	10.9	25	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of the ryr domain of the rabbit ryanodine receptor
23	c2l57A_	Alignment	not modelled	10.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
24	d1iaza_	Alignment	not modelled	10.4	28	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Anemone pore-forming cytolysin
25	d1ttwa_	Alignment	not modelled	9.4	26	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
26	d1f1sa3	Alignment	not modelled	9.1	6	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
27	d1gwya_	Alignment	not modelled	9.1	22	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Anemone pore-forming cytolysin
28	c3rhtB_	Alignment	not modelled	8.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**(gatase1)-like protein; **PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
						Fold:RING/U-box

29	d1t1ha_	Alignment	not modelled	7.9	25	**Superfamily:**RING/U-box **Family:**U-box
30	c2kkmA_	Alignment	not modelled	7.9	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation machinery-associated protein 16; **PDBTitle:** solution nmr structure of yeast protein yor252w [residues2 38-178]: northeast structural genomics consortium target3 yt654
31	d1n7oa2	Alignment	not modelled	7.8	11	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
32	d1zata2	Alignment	not modelled	7.6	13	**Fold:**L,D-transpeptidase pre-catalytic domain-like **Superfamily:**L,D-transpeptidase pre-catalytic domain-like **Family:**L,D-transpeptidase pre-catalytic domain-like
33	c3o85A_	Alignment	not modelled	6.7	29	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**ribosomal protein l7ae; **PDBTitle:** giardia lamblia 15.5kd rna binding protein
34	c3pkzK_	Alignment	not modelled	6.7	16	**PDB header:**recombination **Chain:** K: **PDB Molecule:**recombinase sin; **PDBTitle:** structural basis for catalytic activation of a serine recombinase
35	d1d8wa_	Alignment	not modelled	6.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**L-rhamnose isomerase
36	d1wmha_	Alignment	not modelled	6.2	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
37	d1j75a_	Alignment	not modelled	5.9	45	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
38	d1ixrc1	Alignment	not modelled	5.6	39	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
39	d1ueab_	Alignment	not modelled	5.4	25	**Fold:**OB-fold **Superfamily:**TIMP-like **Family:**Tissue inhibitor of metalloproteinases, TIMP
40	d2ozba1	Alignment	not modelled	5.4	12	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
41	c3uowB_	Alignment	not modelled	5.3	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
42	c2cb1A_	Alignment	not modelled	5.3	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
43	c1fqvK_	Alignment	not modelled	5.2	25	**PDB header:**ligase **Chain:** K: **PDB Molecule:**skp2; **PDBTitle:** insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex