Phyre2

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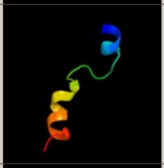
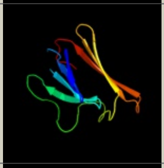
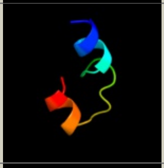
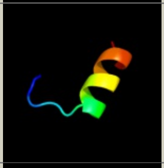
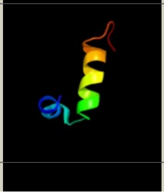
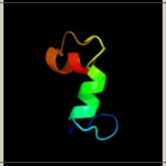
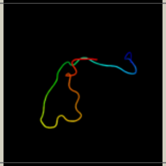
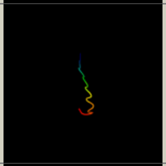
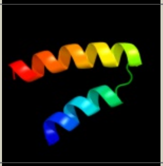
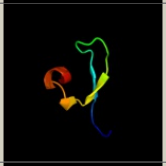
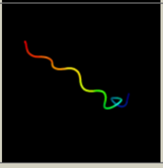
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1txlA_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**metal-binding protein yoda; **PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149
2	d1txla_	Alignment		100.0	100	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YodA
3	d1c8ba_	Alignment		55.3	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
4	c2nvuB_	Alignment		39.0	32	**PDB header:**protein turnover, ligase **Chain:** B: **PDB Molecule:**maltose binding protein/nedd8-activating enzyme **PDBTitle:** structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
5	c2nogA_	Alignment		29.7	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**iswi protein; **PDBTitle:** sant domain structure of xenopus remodeling factor iswi
6	d1nkga3	Alignment		27.3	12	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Rhamnogalacturonase B, RhgB, N-terminal domain
7	c2kkmA_	Alignment		27.2	29	**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
8	d1gjja1	Alignment		24.0	19	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
9	d1h9ea_	Alignment		22.0	19	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
10	d1yovb1	Alignment		17.8	35	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
11	c1x41A_	Alignment		16.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional adaptor 2-like, isoform b; **PDBTitle:** solution structure of the myb-like dna binding domain of2 human transcriptional adaptor 2-like, isoform b

12	c3gznB_	Alignment		15.1	35	**PDB header:**protein binding/ligase **Chain:** B: **PDB Molecule:**nedd8-activating enzyme e1 catalytic subunit; **PDBTitle:** structure of nedd8-activating enzyme in complex with nedd82 and mln4924
13	c2l5qA_	Alignment		12.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of bvu_3817 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr159
14	d1jlxa1	Alignment		12.3	10	**Fold:**beta-Trefoil **Superfamily:**Agglutinin **Family:**Agglutinin
15	d1izna_	Alignment		11.1	25	**Fold:**Subunits of heterodimeric actin filament capping protein Capz **Superfamily:**Subunits of heterodimeric actin filament capping protein Capz **Family:**Capz alpha-1 subunit
16	c3lggA_	Alignment		10.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase cecr1; **PDBTitle:** crystal structure of human adenosine deaminase growth factor,2 adenosine deaminase type 2 (ada2) complexed with transition state3 analogue, coformycin
17	d1q8ca_	Alignment		10.2	19	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Hypothetical protein MG027
18	d1w5ra1	Alignment		10.2	15	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
19	d3deoa1	Alignment		9.4	23	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**Chromo domain
20	d1cmca_	Alignment		9.3	33	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)
21	d1dixa_	Alignment	not modelled	9.2	25	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
22	d1ofcx1	Alignment	not modelled	9.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
23	c2x0lB_	Alignment	not modelled	8.6	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of a neuro-specific splicing variant of2 human histone lysine demethylase lsd1.
24	c2iw5B_	Alignment	not modelled	8.6	19	**PDB header:**oxidoreductase/transcription regulator **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis for corest-dependent demethylation of2 nucleosomes by the human lsd1 histone demethylase
25	c2xajB_	Alignment	not modelled	8.6	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of lsd1-corest in complex with (-)-trans-2 2-phenylcyclopropyl-1-amine
26	c2v1dB_	Alignment	not modelled	8.6	19	**PDB header:**oxidoreductase/repressor **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
27	d1xc5a1	Alignment	not modelled	8.6	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
28	d2cqqa1	Alignment	not modelled	8.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
29	d1mdwa_	Alignment	not modelled	8.4	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Calpain large subunit, catalytic domain (domain II)

30	d1a4ma_	Alignment	not modelled	8.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
31	d1x41a1	Alignment	not modelled	8.1	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
32	d2ijra1	Alignment	not modelled	8.1	19	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
33	d1vmha_	Alignment	not modelled	7.8	57	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
34	d1j0ha1	Alignment	not modelled	7.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
35	d1vmfa_	Alignment	not modelled	7.1	71	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
36	c2kmuA_	Alignment	not modelled	6.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase q4; **PDBTitle:** recql4 amino-terminal domain
37	d1vmja_	Alignment	not modelled	6.8	43	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
38	c2p6cB_	Alignment	not modelled	6.7	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
39	c3oiqB_	Alignment	not modelled	6.7	44	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of yeast telomere protein cdc13 ob1 and the2 catalytic subunit of dna polymerase alpha pol1
40	d1gvia1	Alignment	not modelled	6.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
41	c3efcA_	Alignment	not modelled	6.6	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** crystal structure of yaet periplasmic domain
42	c2cu5C_	Alignment	not modelled	6.5	57	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved hypothetical protein tt1486; **PDBTitle:** crystal structure of the conserved hypothetical protein tt1486 from2 thermus thermophilus hb8
43	c2vzkD_	Alignment	not modelled	6.3	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate n-acetyltransferase 2 beta chain; **PDBTitle:** structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
44	d2ok5a4	Alignment	not modelled	6.2	16	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
45	c1v91A_	Alignment	not modelled	6.2	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-palutoxin it2; **PDBTitle:** solution structure of insectidal toxin delta-paluit2-nh2
46	d2fefa1	Alignment	not modelled	6.1	32	**Fold:**Bromodomain-like **Superfamily:**PA2201 N-terminal domain-like **Family:**PA2201 N-terminal domain-like
47	c3fljA_	Alignment	not modelled	5.9	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein conserved in bacteria with a **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
48	d2soba_	Alignment	not modelled	5.9	11	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
49	c3lnbA_	Alignment	not modelled	5.8	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase family protein; **PDBTitle:** crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
50	d1vpha_	Alignment	not modelled	5.8	43	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
51	c1vraB_	Alignment	not modelled	5.8	4	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
52	d1xcra1	Alignment	not modelled	5.8	31	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**PTD012-like
53	c1ve0A_	Alignment	not modelled	5.7	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein (st2072); **PDBTitle:** crystal structure of uncharacterized protein st2072 from sulfolobus2 tokodaii
54	c3it4B_	Alignment	not modelled	5.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj **PDBTitle:** the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a

55	c3acgA_	Alignment	not modelled	5.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-1,4-endoglucanase; **PDBTitle:** crystal structure of carbohydrate-binding module family 282 from clostridium josui cel5a in complex with cellobiose
56	c2elkA_	Alignment	not modelled	5.4	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**spcc24b10.08c protein; **PDBTitle:** solution structure of the sant domain of fission yeast2 spcc24b10.08c protein
57	c2p6hB_	Alignment	not modelled	5.3	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
58	d2v94a1	Alignment	not modelled	5.2	13	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e