Phyre^2

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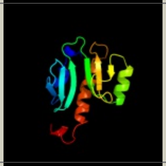
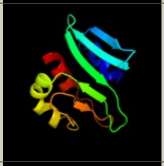
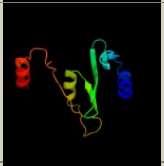
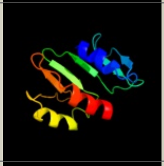
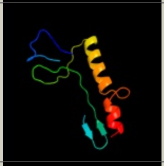
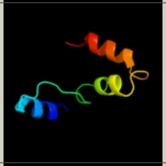
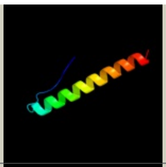
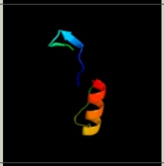
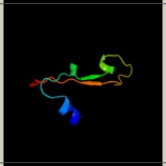
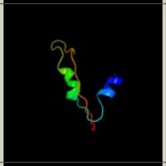
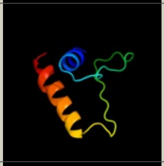
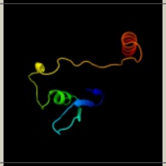
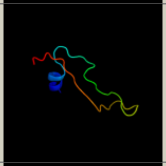
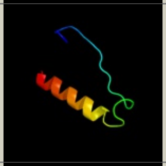
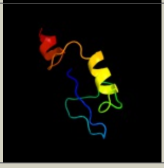
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fkia1	Alignment		100.0	100	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like
2	d2a1va1	Alignment		100.0	33	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like
3	c3h9xB_	Alignment		100.0	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein pspto_3016; **PDBTitle:** crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293
4	d2oc6a1	Alignment		96.9	7	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
5	d2i8da1	Alignment		96.7	9	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
6	c2kl4A_	Alignment		96.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2032 protein; **PDBTitle:** nmr structure of the protein nb7804a
7	d2od0a1	Alignment		95.6	7	**Fold:**Secretion chaperone-like **Superfamily:**YgaC/TfoX-N like **Family:**TfoX N-terminal domain-like
8	c3n0kA_	Alignment		52.4	18	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine protease inhibitor 1; **PDBTitle:** proteinase inhibitor from coprinopsis cinerea
9	c3rpjA_	Alignment		24.5	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**curlin genes transcriptional regulator; **PDBTitle:** structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
10	c3s83A_	Alignment		22.9	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
11	c2raxY_	Alignment		22.8	25	**PDB header:**cell cycle **Chain:** Y: **PDB Molecule:**borealin; **PDBTitle:** crystal structure of borealin (20-78) bound to survivin (1-120)

12	c1ybxA_	Alignment		17.5	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
13	d2gkpa1	Alignment		16.5	24	**Fold:**NMB0488-like **Superfamily:**NMB0488-like **Family:**NMB0488-like
14	d1iica1	Alignment		14.1	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
15	d1iyka1	Alignment		13.7	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
16	c2fyfB_	Alignment		11.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
17	d2j7qa1	Alignment		11.5	11	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**M48USP-like
18	d1rxta1	Alignment		10.6	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
19	d1xx6a1	Alignment		10.6	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
20	d2pstx1	Alignment		10.5	15	**Fold:**MbtH/L9 domain-like **Superfamily:**MbtH-like **Family:**MbtH-like
21	d1pu1a_	Alignment	not modelled	9.9	30	**Fold:**Hypothetical protein MTH677 **Superfamily:**Hypothetical protein MTH677 **Family:**Hypothetical protein MTH677
22	d1o4sa_	Alignment	not modelled	8.7	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
23	d1iwga1	Alignment	not modelled	8.4	23	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
24	d1j98a_	Alignment	not modelled	8.3	25	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
25	d1vjea_	Alignment	not modelled	8.1	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
26	d1lq9a_	Alignment	not modelled	7.7	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Actinorhodin biosynthesis monooxygenase ActVa-Orf6
27	c2khrA_	Alignment	not modelled	7.5	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**protein mbth; **PDBTitle:** solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
28	c2p6fA_	Alignment	not modelled	7.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase; **PDBTitle:** crystal structures of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoyl-coa and inhibitors

29	d1j8ba_	Alignment	not modelled	7.3	16	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
30	c2wuuA_	Alignment	not modelled	7.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-myristoyltransferase; **PDBTitle:** structure of n-myristoyltransferase from l. donovani
31	c1iylC_	Alignment	not modelled	7.1	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**myristoyl-coa:protein n-myristoyltransferase; **PDBTitle:** crystal structure of candida albicans n-myristoyltransferase with non-2 peptidic inhibitor
32	d157la_	Alignment	not modelled	7.0	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
33	c3ouiA_	Alignment	not modelled	7.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**egl nine homolog 1; **PDBTitle:** phd2-r717 with 40787422
34	d2gpfa1	Alignment	not modelled	7.0	14	**Fold:**MbtH/L9 domain-like **Superfamily:**MbtH-like **Family:**MbtH-like
35	d1dxha1	Alignment	not modelled	6.9	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
36	d2f2qa1	Alignment	not modelled	6.7	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
37	c3jvvA_	Alignment	not modelled	6.7	26	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
38	c1ij3A_	Alignment	not modelled	6.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
39	d2glza1	Alignment	not modelled	6.4	12	**Fold:**FwdE/GAPDH domain-like **Superfamily:**FwdE-like **Family:**FwdE-like
40	c2e8mA_	Alignment	not modelled	6.3	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**epidermal growth factor receptor kinase **PDBTitle:** solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
41	d1igna1	Alignment	not modelled	6.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of rap1
42	c1iicA_	Alignment	not modelled	6.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**peptide n-myristoyltransferase; **PDBTitle:** crystal structure of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoylcoa
43	c1wwuA_	Alignment	not modelled	5.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein flj21935; **PDBTitle:** solution structure of the sam_pnt domain of human protein2 flj21935
44	d1ix1a_	Alignment	not modelled	5.8	33	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
45	c2wzlA_	Alignment	not modelled	5.7	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phosphoprotein; **PDBTitle:** the structure of the n-rna binding domain of the mokola2 virus phosphoprotein
46	c1ws1A_	Alignment	not modelled	5.5	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase 1; **PDBTitle:** structure analysis of peptide deformylase from bacillus2 cereus
47	c3qu1B_	Alignment	not modelled	5.5	25	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**peptide deformylase 2; **PDBTitle:** peptide deformylase from vibrio cholerae
48	c1rxtB_	Alignment	not modelled	5.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase 1; **PDBTitle:** crystal structure of human myristoyl-coa:protein n-2 myristoyltransferase.
49	d1nyra3	Alignment	not modelled	5.4	8	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
50	c3iu2B_	Alignment	not modelled	5.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase 1; **PDBTitle:** crystal structure of human type-i n-myristoyltransferase with bound2 myristoyl-coa and inhibitor ddd90096
51	c2w3tA_	Alignment	not modelled	5.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** chloro complex of the ni-form of e.coli deformylase
52	d1vyia_	Alignment	not modelled	5.4	18	**Fold:**Phosphoprotein M1, C-terminal domain **Superfamily:**Phosphoprotein M1, C-terminal domain **Family:**Phosphoprotein M1, C-terminal domain
53	c3oa1B_	Alignment	not modelled	5.3	18	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**phosphoprotein; **PDBTitle:** crystal structure of phosphoprotein/protein p/protein m1 residues 69-2 297 from rabies virus reveals degradation to c-terminal domain only
54	d189la_	Alignment	not modelled	5.2	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme