Phyre2

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Description	P09162
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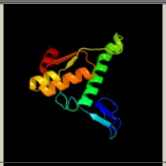
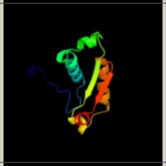
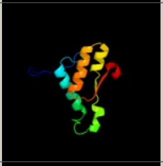
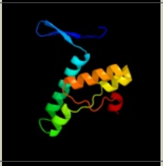
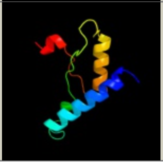
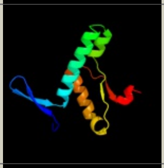
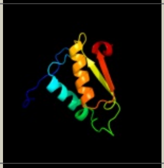
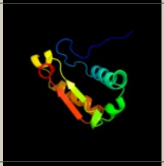
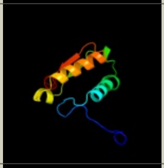
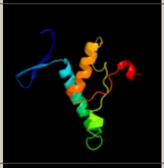
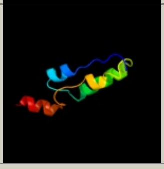
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jcea1	Alignment		98.8	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
2	c3h1qB_	Alignment		97.5	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
3	c1o1f4_	Alignment		97.0	6	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
4	d1bupa1	Alignment		96.8	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
5	c1jcgA_	Alignment		96.8	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
6	d2e8aa1	Alignment		96.8	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
7	c3dwlB_	Alignment		96.1	7	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**actin-related protein 3; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
8	c2p9lA_	Alignment		95.9	4	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
9	c3qb0C_	Alignment		95.6	12	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**actin-related protein 4; **PDBTitle:** crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
10	c2v7yA_	Alignment		94.8	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein dnak; **PDBTitle:** crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
11	d1dkgd1	Alignment		93.8	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70

12	c2khoA_	Alignment		91.8	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 70; **PDBTitle:** nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
13	c3d2fC_	Alignment		91.1	8	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
14	d2hf3a1	Alignment		87.4	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
15	d2fxua1	Alignment		86.7	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
16	d1yaga1	Alignment		86.0	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
17	d1c0fa1	Alignment		73.9	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
18	c2v7zA_	Alignment		73.0	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock cognate 71 kda protein; **PDBTitle:** crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
19	c3iucC_	Alignment		64.3	13	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70kda protein 5 (glucose-regulated **PDBTitle:** crystal structure of the human 70kda heat shock protein2 5 (bip/grp78) atpase domain in complex with adp
20	d1dn1a_	Alignment		58.7	19	**Fold:**Sec1/munc18-like (SM) proteins **Superfamily:**Sec1/munc18-like (SM) proteins **Family:**Sec1/munc18-like (SM) proteins
21	c1dkgD_	Alignment	not modelled	57.9	13	**PDB header:**complex (hsp24/hsp70) **Chain:** D: **PDB Molecule:**molecular chaperone dnak; **PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
22	c1hpmA_	Alignment	not modelled	54.2	11	**PDB header:**hydrolase (acting on acid anhydrides) **Chain:** A: **PDB Molecule:**44k atpase fragment (n-terminal) of 7o kd heat- **PDBTitle:** how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
23	d1k8ka1	Alignment	not modelled	49.2	5	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
24	d1epua_	Alignment	not modelled	33.3	21	**Fold:**Sec1/munc18-like (SM) proteins **Superfamily:**Sec1/munc18-like (SM) proteins **Family:**Sec1/munc18-like (SM) proteins
25	c2xheA_	Alignment	not modelled	27.6	14	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**unc18; **PDBTitle:** crystal structure of the unc18-syntaxin 1 complex from monosiga2 brevicollis
26	c1xofA_	Alignment	not modelled	19.5	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**bbahett1; **PDBTitle:** heterooligomeric beta beta alpha miniprotein
27	c1bmtB_	Alignment	not modelled	17.8	15	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
28	d1sqsa_	Alignment	not modelled	15.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951

29	d1mqsa_	Alignment	not modelled	14.6	13	**Fold:**Sec1/munc18-like (SM) proteins **Superfamily:**Sec1/munc18-like (SM) proteins **Family:**Sec1/munc18-like (SM) proteins
30	c2kk4A_	Alignment	not modelled	14.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_2094; **PDBTitle:** solution nmr structure of protein af2094 from archaeoglobus2 fulgidus. northeast structural genomics consotium (nesg)3 target gt2
31	c2pjxB_	Alignment	not modelled	11.9	15	**PDB header:**endocytosis/exocytosis **Chain:** B: **PDB Molecule:**syntaxin-binding protein 3; **PDBTitle:** crystal structure of the munc18c/syntaxin4 n-peptide complex
32	d1wdea_	Alignment	not modelled	11.3	27	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
33	d1xsza2	Alignment	not modelled	10.2	7	**Fold:**TBP-like **Superfamily:**RalF, C-terminal domain **Family:**RalF, C-terminal domain
34	c2phjA_	Alignment	not modelled	10.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of sure protein from aquifex aeolicus
35	d1mixa2	Alignment	not modelled	9.7	19	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
36	d1vhka2	Alignment	not modelled	9.3	33	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
37	d3d37a2	Alignment	not modelled	9.0	11	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
38	c3itqB_	Alignment	not modelled	8.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prolyl 4-hydroxylase, alpha subunit domain protein; **PDBTitle:** crystal structure of a prolyl 4-hydroxylase from bacillus anthracis
39	c3cq9C_	Alignment	not modelled	8.7	7	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uncharacterized protein lp_1622; **PDBTitle:** crystal structure of the lp_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114
40	d1omwa2	Alignment	not modelled	8.5	18	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
41	d1gyxa_	Alignment	not modelled	7.9	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
42	c2wj8N_	Alignment	not modelled	7.5	29	**PDB header:**rna binding protein/rna **Chain:** N: **PDB Molecule:**nucleoprotein; **PDBTitle:** respiratory syncitial virus ribonucleoprotein
43	c3lmmA_	Alignment	not modelled	7.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
44	c3kw2A_	Alignment	not modelled	6.5	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
45	c1mszA_	Alignment	not modelled	6.4	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein smubp-2; **PDBTitle:** solution structure of the r3h domain from human smubp-2
46	d1msza_	Alignment	not modelled	6.4	15	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
47	d1cqxa3	Alignment	not modelled	6.1	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
48	d2dw4a1	Alignment	not modelled	6.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
49	c2pihA_	Alignment	not modelled	6.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ymca; **PDBTitle:** crystal structure of protein ymca from bacillus subtilis,2 northeast structural genomics target sr375
50	d2piha1	Alignment	not modelled	6.1	17	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YmcA-like
51	d2bz2a1	Alignment	not modelled	5.9	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
52	d1gph11	Alignment	not modelled	5.9	9	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
53	c2rm4A_	Alignment	not modelled	5.7	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cg6311-pb; **PDBTitle:** solution structure of the lsm domain of dm edc3 (enhancer2 of decapping 3)
54	d2nu7a1	Alignment	not modelled	5.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain

55	c3bt6B_	 Alignment	not modelled	5.4	18	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**influenza b hemagglutinin (ha); **PDBTitle:** crystal structure of influenza b virus hemagglutinin
56	c3melC_	 Alignment	not modelled	5.3	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase family protein; **PDBTitle:** crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150