Phyre2

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Description	P15070
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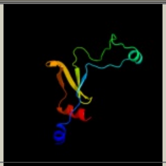
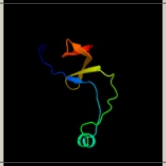
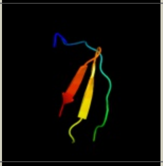
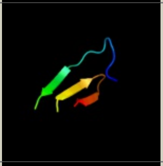
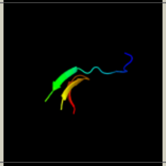
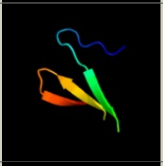
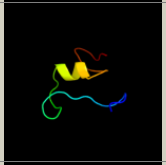
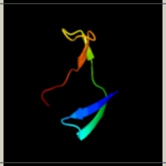
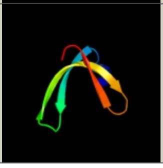
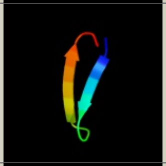
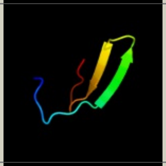
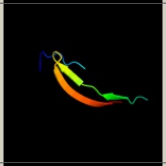
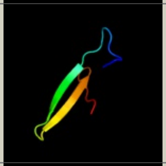
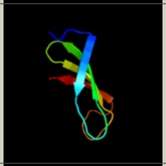
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o6aa_	Alignment		99.9	55	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
2	d1o9ya_	Alignment		99.8	27	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
3	c2k5fA_	Alignment		58.6	29	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferrous iron transport protein a; **PDBTitle:** solution nmr structure of feoa protein from chlorobium2 tepidum. northeast structural genomics consortium target3 ctr121
4	d2gcxa1	Alignment		56.8	23	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
5	c2k5lA_	Alignment		46.5	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**feoa; **PDBTitle:** solution nmr structure of protein feoa from clostridium2 thermocellum, northeast structural genomics consortium3 target cmr17
6	c2k4yA_	Alignment		46.1	23	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**feoa-like protein; **PDBTitle:** nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178
7	c3mhxB_	Alignment		32.6	27	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**putative ferrous iron transport protein a; **PDBTitle:** crystal structure of stenotrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor
8	c2k5iA_	Alignment		32.1	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** solution structure of iron(ii) transport protein a from2 clostridium thermocellum , northeast structural genomics3 consortium (nesg) target vr131
9	c3gt2A_	Alignment		29.5	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
10	d3bwud1	Alignment		26.5	21	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
11	d1m5q1_	Alignment		26.3	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP

12	d1wmxb_	Alignment		24.4	11	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
13	d1zdva1	Alignment		24.0	31	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
14	c3ddyA_	Alignment		23.5	19	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**lumazine protein; **PDBTitle:** structure of lumazine protein, an optical transponder of luminescent2 bacteria
15	d2h3ja1	Alignment		23.3	17	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
16	c2glvA_	Alignment		22.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-acyl carrier protein **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
17	c2e63A_	Alignment		20.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1787 protein; **PDBTitle:** solution structure of the neuz domain in kiaa1787 protein
18	c2fg0B_	Alignment		20.3	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
19	d2evra2	Alignment		20.1	11	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
20	c3e19D_	Alignment		19.2	26	**PDB header:**transcription regulator, metal binding p **Chain:** D: **PDB Molecule:**feoa; **PDBTitle:** crystal structure of iron uptake regulatory protein (feoa) solved by2 sulfur sad in a monoclinic space group
21	d2isba1	Alignment	not modelled	19.0	33	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
22	c2kytA_	Alignment	not modelled	17.9	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
23	d1zdxa1	Alignment	not modelled	17.8	26	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
24	c3pbiA_	Alignment	not modelled	17.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
25	c2xivA_	Alignment	not modelled	15.9	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
26	c1i8dB_	Alignment	not modelled	15.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of riboflavin synthase
27	c3hruA_	Alignment	not modelled	15.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
28	c3cw1D_	Alignment	not modelled	14.9	16	**PDB header:**splicing **Chain:** D: **PDB Molecule:**small nuclear ribonucleoprotein sm d3; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
29	c2gl0A_	Alignment	not modelled	14.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved hypothetical protein;

						PDBTitle: structure of pae2307 in complex with adenosine
30	d1u1za_	Alignment	not modelled	14.7	6	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
31	d1vgga_	Alignment	not modelled	14.6	16	**Fold:**Ta1353-like **Superfamily:**Ta1353-like **Family:**Ta1353-like
32	c2d16B_	Alignment	not modelled	14.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph1918; **PDBTitle:** crystal structure of ph1918 protein from pyrococcus horikoshii ot3
33	c2ekmC_	Alignment	not modelled	14.2	23	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein st1511; **PDBTitle:** structure of st1219 protein from sulfolobus tokodaii
34	c3swnC_	Alignment	not modelled	13.6	10	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**u6 snrna-associated sm-like protein lsm7; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
35	d1i4k1_	Alignment	not modelled	13.2	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
36	d1vyua1	Alignment	not modelled	12.6	6	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
37	c3cw15_	Alignment	not modelled	12.0	19	**PDB header:**splicing **Chain:** 5: **PDB Molecule:**small nuclear ribonucleoprotein g; **PDB Fragment:**residues 1-215; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
38	d2je8a4	Alignment	not modelled	11.8	15	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
39	d1t0ha_	Alignment	not modelled	11.7	12	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
40	c2glwA_	Alignment	not modelled	11.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii
41	d4fiva_	Alignment	not modelled	10.9	27	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
42	c2pn0D_	Alignment	not modelled	10.6	31	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
43	d2as0a1	Alignment	not modelled	10.6	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
44	d1n9ra_	Alignment	not modelled	10.3	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
45	c1b34A_	Alignment	not modelled	10.2	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d1); **PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
46	d1b34a_	Alignment	not modelled	10.2	16	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
47	c3a35B_	Alignment	not modelled	9.9	17	**PDB header:**luminescent protein **Chain:** B: **PDB Molecule:**lumazine protein; **PDBTitle:** crystal structure of lump complexed with riboflavin
48	d2axwa1	Alignment	not modelled	9.7	19	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
49	d1d3ba_	Alignment	not modelled	9.6	16	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
50	c3d37A_	Alignment	not modelled	9.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tail protein, 43 kda; **PDBTitle:** the crystal structure of the tail protein from neisseria meningitidis2 mc58
51	d1t3la1	Alignment	not modelled	9.2	12	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
52	d2fwka1	Alignment	not modelled	8.9	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
53	d1eika_	Alignment	not modelled	8.9	14	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
54	c3f3bA_	Alignment	not modelled	8.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage-like element pbsx protein xkdh; **PDBTitle:** structure of the phage-like element pbsx protein xkdh from2 bacillus subtilus. northeast structural genomics3 consortium target sr352.
55	c1n9sH_	Alignment	not modelled	8.6	13	**PDB header:**translation **Chain:** H: **PDB Molecule:**small nuclear ribonucleoprotein f;

						PDBTitle: crystal structure of yeast smf in spacegroup p43212
56	c1t0jA_	Alignment	not modelled	8.5	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**voltage-gated calcium channel subunit beta2a; **PDBTitle:** crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
57	d1hmja_	Alignment	not modelled	8.4	16	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
58	d1wmxa_	Alignment	not modelled	8.1	8	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
59	d1i8fa_	Alignment	not modelled	8.1	11	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
60	c3fcgB_	Alignment	not modelled	8.1	27	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
61	c3swnA_	Alignment	not modelled	7.7	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
62	d1h641_	Alignment	not modelled	7.6	8	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
63	c1fx7C_	Alignment	not modelled	7.5	6	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
64	c1wruA_	Alignment	not modelled	7.4	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**43 kda tail protein; **PDBTitle:** structure of central hub elucidated by x-ray analysis of gene product2 44; baseplate component of bacteriophage mu
65	c3butA_	Alignment	not modelled	7.3	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
66	d1dzfa2	Alignment	not modelled	7.3	25	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
67	d1d1na_	Alignment	not modelled	7.1	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
68	d1jz8a3	Alignment	not modelled	6.8	17	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
69	c3h41A_	Alignment	not modelled	6.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
70	c3h0gE_	Alignment	not modelled	6.6	25	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
71	c2fwkB_	Alignment	not modelled	6.4	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5; **PDBTitle:** crystal structure of cryptosporidium parvum u6 snrna-associated sm-2 like protein lsm5
72	d2pw9a1	Alignment	not modelled	6.4	25	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**FdhD/NarQ
73	c2fvnA_	Alignment	not modelled	6.3	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein afad; **PDBTitle:** the fibrillar tip complex of the afa/dr adhesins from2 pathogen e. coli displays synergistic binding to 5 1 and v3 3 integrins
74	d1n9sc_	Alignment	not modelled	6.3	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
75	c2dlpA_	Alignment	not modelled	6.2	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**kiaa1783 protein; **PDBTitle:** solution structure of the sh3 domain of human kiaa17832 protein
76	c3cw1Z_	Alignment	not modelled	6.2	22	**PDB header:**splicing **Chain:** Z: **PDB Molecule:**small nuclear ribonucleoprotein f; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
77	d1mgqa_	Alignment	not modelled	6.2	16	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
78	c2yueA_	Alignment	not modelled	6.0	7	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein neuralized; **PDBTitle:** solution structure of the neuz (nhr) domain in neuralized2 from drosophila melanogaster
79	c3swnT_	Alignment	not modelled	6.0	11	**PDB header:**rna binding protein **Chain:** T: **PDB Molecule:**u6 snrna-associated sm-like protein lsm6; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
80	d1jbma_	Alignment	not modelled	5.9	16	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins

						Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
81	d1o91a_	Alignment	not modelled	5.7	17	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
82	c1o91B_	Alignment	not modelled	5.7	17	**PDB header:**collagen **Chain:** B: **PDB Molecule:**collagen alpha 1(viii) chain; **PDBTitle:** crystal structure of a collagen viii nc1 domain trimer
83	d1ljoa_	Alignment	not modelled	5.6	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
84	d1d3bb_	Alignment	not modelled	5.6	8	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
85	c3d6xA_	Alignment	not modelled	5.5	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of campylobacter jejuni fabz
86	d1p9ka_	Alignment	not modelled	5.5	24	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
87	c3dzoA_	Alignment	not modelled	5.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhoptry kinase domain; **PDBTitle:** crystal structure of a rhoptry kinase from toxoplasma gondii
88	d1yq2a3	Alignment	not modelled	5.3	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
89	c3cnrA_	Alignment	not modelled	5.2	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**type iv fimbriae assembly protein; **PDBTitle:** crystal structure of pilz (xac1133) from xanthomonas2 axonopodis pv citri
90	c1zyiA_	Alignment	not modelled	5.2	11	**PDB header:**translation **Chain:** A: **PDB Molecule:**methylosome subunit picln; **PDBTitle:** solution structure of icln, a multifunctional protein2 involved in regulatory mechanisms as different as cell3 volume regulation and rna splicing
91	d2cnda1	Alignment	not modelled	5.2	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
92	d2bmwa1	Alignment	not modelled	5.0	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like