Phyre^2

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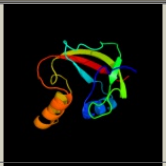
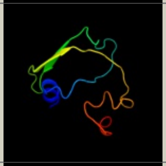
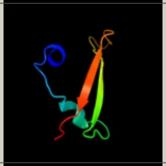
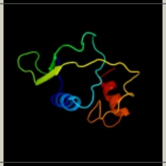
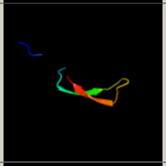
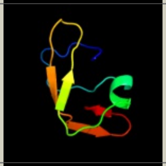
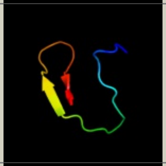
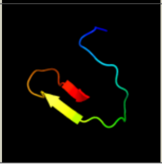
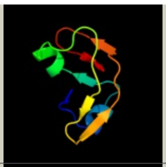
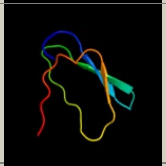
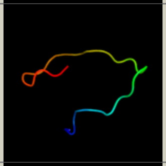
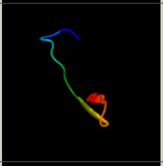
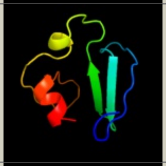
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1te7a_	Alignment		100.0	100	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like
2	c3s9xA_	Alignment		97.0	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asch domain; **PDBTitle:** high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
3	d1t62a_	Alignment		96.9	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical protein EF3133
4	c3iuwA_	Alignment		95.0	23	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**activating signal cointegrator; **PDBTitle:** crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
5	d1xnea_	Alignment		93.7	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
6	d1s04a_	Alignment		87.9	22	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
7	c2e6zA_	Alignment		40.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
8	c2dbkA_	Alignment		34.0	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structures of the sh3 domain of human crk-like2 protein
9	d1nxza1	Alignment		33.5	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
10	c2jw4A_	Alignment		28.6	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** nmr solution structure of the n-terminal sh3 domain of2 human nckalpha
11	c1wxtA_	Alignment		28.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein flj21522; **PDBTitle:** solution structure of the sh3 domain of human hypothetical2 protein flj21522

12	c1vhkA_	Alignment		24.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
13	d1o5ua_	Alignment		23.9	27	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
14	c2i45C_	Alignment		23.8	9	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
15	d1wfwa_	Alignment		23.2	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
16	d1vyva1	Alignment		23.1	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
17	c2xmfA_	Alignment		22.3	19	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**myosin 1e sh3; **PDBTitle:** myosin 1e sh3
18	c2kafA_	Alignment		22.3	31	**PDB header:**viral protein, rna binding protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** solution structure of the sars-unique domain-c from the2 nonstructural protein 3 (nsp3) of the severe acute3 respiratory syndrome coronavirus
19	c3es4B_	Alignment		22.1	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
20	c3bcwB_	Alignment		22.0	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
21	c2eyxA_	Alignment	not modelled	19.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** c-terminal sh3 domain of ct10-regulated kinase
22	c2eqmA_	Alignment	not modelled	19.3	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
23	d1j3ta_	Alignment	not modelled	19.2	15	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
24	d1ep3b1	Alignment	not modelled	19.2	5	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
25	d2p5zx2	Alignment	not modelled	19.1	13	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
26	d1utia_	Alignment	not modelled	18.1	24	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
27	d1t3la1	Alignment	not modelled	17.6	21	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
28	c2ebpA_	Alignment	not modelled	17.4	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sh3 domain from human sam and sh32 domain containing protein 1
						PDB header:protein binding

29	c1zx6A_	Alignment	not modelled	17.4	12	**Chain:** A: **PDB Molecule:**ypr154wp; **PDBTitle:** high-resolution crystal structure of yeast pin3 sh3 domain
30	d1ng2a1	Alignment	not modelled	17.3	32	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
31	c2kgtA_	Alignment	not modelled	16.8	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase 6; **PDBTitle:** solution structure of sh3 domain of ptk6
32	c2cudA_	Alignment	not modelled	16.8	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**src-like-adapter; **PDBTitle:** solution structure of the sh3 domain of the human src-like2 adopter protein (slap)
33	c3myxA_	Alignment	not modelled	16.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pspto_0244; **PDBTitle:** crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
34	c2ct3A_	Alignment	not modelled	16.5	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vinexin; **PDBTitle:** solution structure of the sh3 domain of the vinexin protein
35	c2csqA_	Alignment	not modelled	16.4	32	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**rim binding protein 2; **PDBTitle:** solution structure of the second sh3 domain of human rim-2 binding protein 2
36	d1t0ha_	Alignment	not modelled	16.3	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
37	d1wlpb2	Alignment	not modelled	16.2	31	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
38	d1udla_	Alignment	not modelled	15.3	23	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
39	d1ov3a1	Alignment	not modelled	15.2	32	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
40	c1t0jA_	Alignment	not modelled	15.1	20	**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
41	d1ckaa_	Alignment	not modelled	14.5	32	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
42	c2dl4A_	Alignment	not modelled	14.3	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein stac; **PDBTitle:** solution structure of the first sh3 domain of stac protein
43	c2js0A_	Alignment	not modelled	14.3	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** solution structure of second sh3 domain of adaptor nck
44	c2eczA_	Alignment	not modelled	14.1	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sorbin and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sh3 domain of sorbin and sh32 domain-containing protein 1
45	c2krcA_	Alignment	not modelled	13.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta; **PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
46	c3kw2A_	Alignment	not modelled	13.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
47	d1jo8a_	Alignment	not modelled	13.7	24	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
48	c2ke9A_	Alignment	not modelled	13.4	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**caskin-2; **PDBTitle:** nmr solution structure of the caskin sh3 domain
49	c1zbe1_	Alignment	not modelled	13.2	26	**PDB header:**virus **Chain:** 1: **PDB Molecule:**coat protein vp1; **PDBTitle:** foot-and mouth disease virus serotype a1061
50	d2j01e1	Alignment	not modelled	13.1	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
51	d1qqp1_	Alignment	not modelled	13.1	36	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
52	d1wlfa1	Alignment	not modelled	13.0	10	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
53	c2df6A_	Alignment	not modelled	13.0	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** crystal structure of the sh3 domain of betapix in complex2 with a high affinity peptide from pak2
54	d1ue9a_	Alignment	not modelled	13.0	8	**Fold:**SH3-like barrel **Superfamily:**SH3-domain

						Family:SH3-domain
55	c2bzxA_	Alignment	not modelled	12.9	25	**PDB header:**sh3 domain **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** atomic model of crkl-sh3c monomer
56	c1bf5A_	Alignment	not modelled	12.4	34	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
57	d1sema_	Alignment	not modelled	12.4	28	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
58	c2jxbA_	Alignment	not modelled	12.3	11	**PDB header:**signaling protein complex **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 epsilon chain, **PDBTitle:** structure of cd3epsilon-nck2 first sh3 domain complex
59	c2cubA_	Alignment	not modelled	12.1	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck1
60	c2krnA_	Alignment	not modelled	12.1	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cd2-associated protein; **PDBTitle:** high resolution structure of the second sh3 domain of cd2ap
61	c1g5vA_	Alignment	not modelled	11.9	26	**PDB header:**translation **Chain:** A: **PDB Molecule:**survival motor neuron protein 1; **PDBTitle:** solution structure of the tudor domain of the human smn2 protein
62	c3cgnA_	Alignment	not modelled	11.9	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
63	d1i07a_	Alignment	not modelled	11.8	22	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
64	c2yuoA_	Alignment	not modelled	11.7	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**run and tbc1 domain containing 3; **PDBTitle:** solution structure of the sh3 domain of mouse run and tbc12 domain containing 3
65	d1h8ka_	Alignment	not modelled	11.6	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
66	c2o2oA_	Alignment	not modelled	11.5	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sh3-domain kinase-binding protein 1; **PDBTitle:** solution structure of domain b from human cin85 protein
67	c2egcA_	Alignment	not modelled	11.4	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a; **PDBTitle:** solution structure of the fifth sh3 domain from human2 kiaa0418 protein
68	d1efna_	Alignment	not modelled	11.4	12	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
69	d1uhfa_	Alignment	not modelled	11.4	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
70	d1pwta_	Alignment	not modelled	11.4	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
71	d1yfua1	Alignment	not modelled	11.4	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
72	c2dx1A_	Alignment	not modelled	11.3	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 4; **PDBTitle:** crystal structure of rhogef protein asef
73	d2pyta1	Alignment	not modelled	11.1	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
74	c2pqhA_	Alignment	not modelled	11.0	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin alpha chain, brain; **PDBTitle:** structure of sh3 chimera with a type ii ligand linked to the chain c-2 terminal
75	c1zlmA_	Alignment	not modelled	10.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**osteoclast stimulating factor 1; **PDBTitle:** crystal structure of the sh3 domain of human osteoclast2 stimulating factor
76	d2dp9a1	Alignment	not modelled	10.9	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical protein TTHA0113
77	c2drmB_	Alignment	not modelled	10.8	28	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**acanthamoeba myosin ib; **PDBTitle:** acanthamoeba myosin i sh3 domain bound to acan125
78	c2egaA_	Alignment	not modelled	10.7	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a; **PDBTitle:** solution structure of the first sh3 domain from human2 kiaa0418 protein
79	d1mhna_	Alignment	not modelled	10.6	17	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
80	c1yn8E_	Alignment	not modelled	10.6	16	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**nap1-binding protein 2; **PDBTitle:** sh3 domain of yeast nbp2

81	d1lcka1	Alignment	not modelled	10.6	15	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
82	d1vyua1	Alignment	not modelled	10.5	17	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
83	c1w1fA_	Alignment	not modelled	10.5	15	**PDB header:**sh3-domain **Chain:** A: **PDB Molecule:**tyrosine-protein kinase lyn; **PDBTitle:** sh3 domain of human lyn tyrosine kinase
84	d1gcqa_	Alignment	not modelled	10.4	23	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
85	c1wxbA_	Alignment	not modelled	10.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**epidermal growth factor receptor pathway **PDBTitle:** solution structure of the sh3 domain from human epidermal2 growth factor receptor pathway substrate 8-like protein
86	c2l0aA_	Alignment	not modelled	10.4	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal transducing adapter molecule 1; **PDBTitle:** solution nmr structure of signal transducing adapter molecule 1 stam-12 from homo sapiens, northeast structural genomics consortium target3 hr4479e
87	c1x2qA_	Alignment	not modelled	10.3	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal transducing adapter molecule 2; **PDBTitle:** solution structure of the sh3 domain of the signal2 transducing adaptor molecule 2
88	d2gycb1	Alignment	not modelled	10.3	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
89	c2jmcA_	Alignment	not modelled	10.2	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**spectrin alpha chain, brain and p41 peptide **PDBTitle:** chimer between spc-sh3 and p41
90	d1awwa_	Alignment	not modelled	10.1	8	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
91	d1h5ba_	Alignment	not modelled	10.1	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
92	c3rebD_	Alignment	not modelled	10.0	15	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** hiv-1 nef protein in complex with engineered hck-sh3 domain
93	d1y57a1	Alignment	not modelled	9.9	24	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
94	c2oi3A_	Alignment	not modelled	9.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** nmr structure analysis of the hematopoetic cell kinase sh32 domain complexed with an artificial high affinity ligand3 (pd1)
95	d2zjrb1	Alignment	not modelled	9.7	10	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
96	c2hdeA_	Alignment	not modelled	9.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap18; **PDBTitle:** solution structure of human sap18
97	c3h8uA_	Alignment	not modelled	9.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
98	d1e6ga_	Alignment	not modelled	9.6	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
99	c3nmzD_	Alignment	not modelled	9.6	32	**PDB header:**cell adhesion/cell cycle **Chain:** D: **PDB Molecule:**rho guanine nucleotide exchange factor 4; **PDBTitle:** crytal structure of apc complexed with asef