Phyre2

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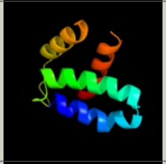
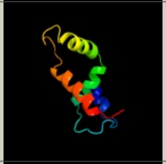
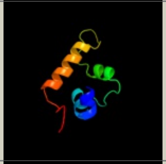
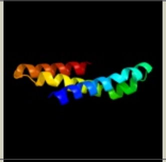
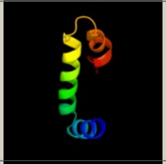
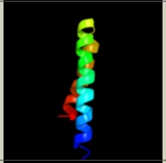
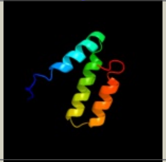
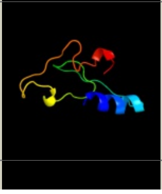
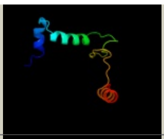
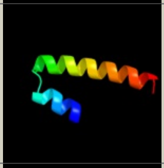
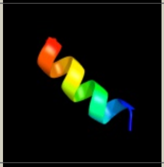
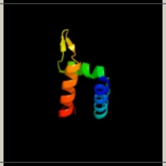
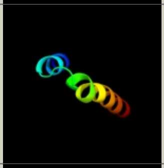
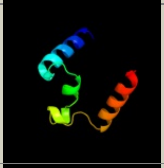
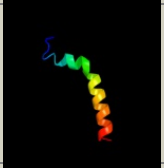
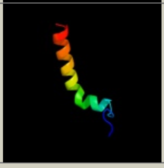
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ld7B_	Alignment		61.6	5	**PDB header:**transcription **Chain:** B: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
2	c2khqA_	Alignment		34.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
3	d1gxya_	Alignment		31.7	10	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Ecto-ART
4	d1puja_	Alignment		31.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
5	c3lysC_	Alignment		30.8	7	**PDB header:**recombination **Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase; **PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
6	c3nkzD_	Alignment		20.6	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**flagellar protein flit; **PDBTitle:** the crystal structure of a flagella protein from yersinia2 enterocolitica subsp. enterocolitica 8081
7	c2oxoA_	Alignment		17.8	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
8	c3zv0A_	Alignment		16.8	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the shq1p-cbf5p complex
9	c2dl1A_	Alignment		16.7	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**spartin; **PDBTitle:** solution structure of the mit domain from human spartin
10	c2rmrA_	Alignment		16.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of msin3a pah1 domain
11	c2x2iB_	Alignment		14.1	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-1,4-glucan lyase isozyme 1; **PDBTitle:** crystal structure of the gracilariopsis lemaneiformis alpha-2 1,4-glucan lyase with acarbose

12	c4a1eF_	Alignment		13.6	25	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl7a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
13	c2v4xA_	Alignment		13.6	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain
14	d1r0va1	Alignment		12.1	14	**Fold:**Restriction endonuclease-like **Superfamily:**tRNA-intron endonuclease catalytic domain-like **Family:**tRNA-intron endonuclease catalytic domain-like
15	c3cnlA_	Alignment		12.0	5	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of gnp-bound ylqf from t. maritima
16	c2kgfA_	Alignment		11.7	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** n-terminal domain of capsid protein from the mason-pfizer2 monkey virus
17	d1sd4a_	Alignment		11.4	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
18	d1t11a2	Alignment		11.3	9	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
19	d1in4a1	Alignment		10.9	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
20	d1p9ya_	Alignment		10.5	16	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
21	c2aaoA_	Alignment	not modelled	10.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calcium-dependent protein kinase, isoform ak1; **PDBTitle:** regulatory apparatus of calcium dependent protein kinase from2 arabidopsis thaliana
22	c2kbrA_	Alignment	not modelled	10.0	12	**PDB header:**structural protein/cell adhesion **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** solution structure of harmonin n terminal domain in complex2 with a internal peptide of cadherin23
23	c3cprB_	Alignment	not modelled	9.6	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
24	d2vbua1	Alignment	not modelled	9.5	36	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
25	d1t07a_	Alignment	not modelled	9.4	9	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
26	d1gkza1	Alignment	not modelled	9.2	13	**Fold:**Bromodomain-like **Superfamily:**alpha-ketoacid dehydrogenase kinase, N-terminal domain **Family:**alpha-ketoacid dehydrogenase kinase, N-terminal domain
27	d1p7da_	Alignment	not modelled	9.2	5	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
28	d1tlha_	Alignment	not modelled	9.1	9	**Fold:**Anti-sigma factor AsiA **Superfamily:**Anti-sigma factor AsiA **Family:**Anti-sigma factor AsiA
						Fold:SH2-like

29	d1nrva_	Alignment	not modelled	9.1	21	**Superfamily:**SH2 domain **Family:**SH2 domain
30	c2c0kB_	Alignment	not modelled	9.1	8	**PDB header:**oxygen transport **Chain:** B: **PDB Molecule:**hemoglobin; **PDBTitle:** the structure of hemoglobin from the botfly gasterophilus2 intestinalis
31	c2dlyA_	Alignment	not modelled	9.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fyn-related kinase; **PDBTitle:** solution structure of the sh2 domain of murine fyn-related2 kinase
32	d1xs8a_	Alignment	not modelled	9.0	36	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
33	c2ekxA_	Alignment	not modelled	8.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic tyrosine-protein kinase bmx; **PDBTitle:** solution structure of the human bmx sh2 domain
34	d1lkka_	Alignment	not modelled	8.6	7	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
35	d1ixrc1	Alignment	not modelled	8.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
36	c1w2wA_	Alignment	not modelled	8.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
37	c3fkkA_	Alignment	not modelled	8.3	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
38	c2rhfA_	Alignment	not modelled	8.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase recq; **PDBTitle:** d. radiodurans recq hrdc domain 3
39	c2kouA_	Alignment	not modelled	8.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dicer-like protein 4; **PDBTitle:** dicer like protein
40	c3knyA_	Alignment	not modelled	7.9	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt_3535; **PDBTitle:** crystal structure of a two domain protein with unknown function2 (bt_3535) from bacteroides thetaiotaomicron vpi-5482 at 2.60 a3 resolution
41	c3lphD_	Alignment	not modelled	7.9	17	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**protein rev; **PDBTitle:** crystal structure of the hiv-1 rev dimer
42	d1g83a2	Alignment	not modelled	7.6	21	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
43	c3a7mA_	Alignment	not modelled	7.6	17	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**flagellar protein flit; **PDBTitle:** structure of flit, the flagellar type iii chaperone for flid
44	c2x7lP_	Alignment	not modelled	7.6	16	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv rev; **PDBTitle:** implications of the hiv-1 rev dimer structure at 3.2a2 resolution for multimeric binding to the rev response3 element
45	d1mila_	Alignment	not modelled	7.6	21	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
46	d1jwoa_	Alignment	not modelled	7.6	14	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
47	c3gxxB_	Alignment	not modelled	7.5	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
48	d1s5qb_	Alignment	not modelled	7.4	12	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
49	d1pica_	Alignment	not modelled	7.3	7	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
50	d1em9a_	Alignment	not modelled	7.3	11	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
51	d2v9va2	Alignment	not modelled	7.2	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
52	d1w53a_	Alignment	not modelled	7.2	16	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Phosphoserine phosphatase RsbU, N-terminal domain
53	c2gsbA_	Alignment	not modelled	7.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ras gtpase-activating protein 1; **PDBTitle:** solution structure of the second sh2 domain of human ras2 gtpase-activating protein 1
54	c2dcrA_	Alignment	not modelled	7.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fes/fps; **PDBTitle:** fully automated solution structure determination of the fes2 sh2 domain
55	d1f54a_	Alignment	not modelled	7.1	4	**Fold:**EF Hand-like **Superfamily:**EF-hand

						Family: Calmodulin-like
56	d1blja_	Alignment	not modelled	7.0	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
57	c2vhdB_	Alignment	not modelled	6.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form
58	d1wz3a1	Alignment	not modelled	6.9	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**APG12-like
59	d1d4ta_	Alignment	not modelled	6.8	7	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
60	d1d1da2	Alignment	not modelled	6.8	11	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
61	c2yqsA_	Alignment	not modelled	6.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
62	c2fa5B_	Alignment	not modelled	6.8	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator marr/emrr family; **PDBTitle:** the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
63	d2qfka1	Alignment	not modelled	6.7	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
64	d2f05a1	Alignment	not modelled	6.7	6	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
65	d1ayaa_	Alignment	not modelled	6.6	21	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
66	c3pm8B_	Alignment	not modelled	6.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calcium-dependent protein kinase 2; **PDBTitle:** cad domain of pff0520w, calcium dependent protein kinase
67	c3a5dG_	Alignment	not modelled	6.6	17	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**v-type atp synthase subunit d; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
68	c3oxpA_	Alignment	not modelled	6.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
69	c3oxpB_	Alignment	not modelled	6.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
70	d1g4yb_	Alignment	not modelled	6.6	19	**Fold:**Small-conductance potassium channel **Superfamily:**Small-conductance potassium channel **Family:**Small-conductance potassium channel
71	d1t5oa_	Alignment	not modelled	6.5	7	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
72	c2lctA_	Alignment	not modelled	6.5	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** solution structure of the vav1 sh2 domain complexed with a syk-derived2 doubly phosphorylated peptide
73	d1cnt1_	Alignment	not modelled	6.5	21	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
74	c3n4dF_	Alignment	not modelled	6.4	26	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
75	c2kj8A_	Alignment	not modelled	6.4	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
76	d1rjaa_	Alignment	not modelled	6.3	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
77	d1opka2	Alignment	not modelled	6.3	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
78	d1a81e2	Alignment	not modelled	6.2	21	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
79	c2ee7A_	Alignment	not modelled	6.2	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sperm flagellar protein 1; **PDBTitle:** solution structure of the ch domain from human sperm2 flagellar protein 1
80	d2c9wa2	Alignment	not modelled	6.2	21	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain

81	d2qmsa1	Alignment	not modelled	6.1	14	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
82	c3g0sA_	Alignment	not modelled	6.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
83	d2fcia1	Alignment	not modelled	6.1	17	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
84	c3noeA_	Alignment	not modelled	6.1	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
85	d1nu9c1	Alignment	not modelled	6.0	35	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Staphylocoagulase **Family:**Staphylocoagulase
86	c3kuqA_	Alignment	not modelled	6.0	17	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**rho gtpase-activating protein 7; **PDBTitle:** crystal structure of the dlc1 rhogap domain
87	d2oq1a2	Alignment	not modelled	5.8	21	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
88	d2shpa3	Alignment	not modelled	5.8	7	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
89	c2dm0A_	Alignment	not modelled	5.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase txk; **PDBTitle:** solution structure of the sh2 domain of human tyrosine-2 protein kinase txk
90	c3lmdA_	Alignment	not modelled	5.7	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**geranylgeranyl pyrophosphate synthase; **PDBTitle:** crystal structure of geranylgeranyl pyrophosphate synthase2 from corynebacterium glutamicum atcc 13032
91	d1zbdb_	Alignment	not modelled	5.7	12	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
92	d1xxxa1	Alignment	not modelled	5.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
93	c3eb2A_	Alignment	not modelled	5.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
94	c3pueA_	Alignment	not modelled	5.7	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
95	d1sfka_	Alignment	not modelled	5.6	22	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
96	c2r8wB_	Alignment	not modelled	5.6	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
97	c2xzmE_	Alignment	not modelled	5.6	32	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein s5 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
98	d2fug11	Alignment	not modelled	5.5	7	**Fold:**Bromodomain-like **Superfamily:**Nqo1C-terminal domain-like **Family:**Nqo1C-terminal domain-like
99	d1rhzb_	Alignment	not modelled	5.5	18	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit