Phyre^2

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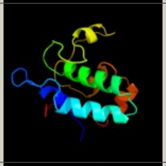
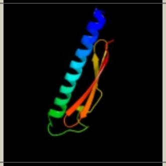
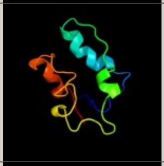
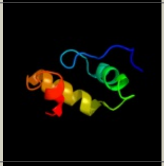
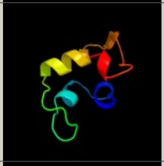
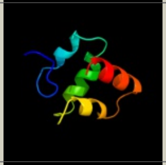
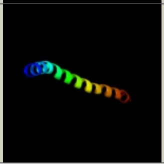
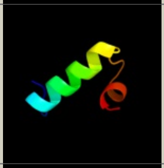
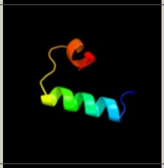
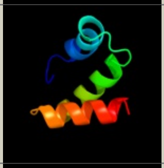
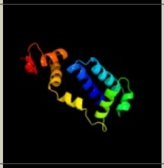
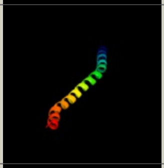
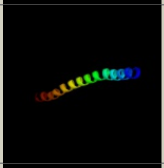
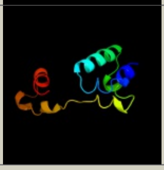
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ci0K_	Alignment		100.0	35	**PDB header:** protein transport **Chain:** K: **PDB Molecule:** pseudopilin gspk; **PDBTitle:** the crystal structure of the gspk-gspi-gspj complex from2 enterotoxigenic escherichia coli type 2 secretion system
2	d3ci0k2	Alignment		100.0	38	**Fold:** SAM domain-like **Superfamily:** GspK insert domain-like **Family:** GspK insert domain-like
3	d3ci0k3	Alignment		99.6	28	**Fold:** Pili subunits **Superfamily:** Pili subunits **Family:** GspK pilin-like domain
4	d3ci0k1	Alignment		99.0	40	**Fold:** SAM domain-like **Superfamily:** GspK insert domain-like **Family:** GspK insert domain-like
5	d2duya1	Alignment		97.2	24	**Fold:** SAM domain-like **Superfamily:** RuvA domain 2-like **Family:** ComEA-like
6	d2edua1	Alignment		96.4	20	**Fold:** SAM domain-like **Superfamily:** RuvA domain 2-like **Family:** ComEA-like
7	d3bzka1	Alignment		96.2	24	**Fold:** SAM domain-like **Superfamily:** RuvA domain 2-like **Family:** Tex HhH-containing domain-like
8	c1s5lu_	Alignment		95.9	21	**PDB header:** photosynthesis **Chain:** U: **PDB Molecule:** photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
9	d2axtu1	Alignment		95.7	22	**Fold:** SAM domain-like **Superfamily:** PsbU/PolX domain-like **Family:** PsbU-like
10	c2oceA_	Alignment		79.7	14	**PDB header:** structural genomics, unknown function **Chain:** A: **PDB Molecule:** hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
11	c3sokB_	Alignment		73.5	18	**PDB header:** cell adhesion **Chain:** B: **PDB Molecule:** fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima

12	c2i5hA_	Alignment		66.1	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1531; **PDBTitle:** crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
13	d2i5ha1	Alignment		66.1	7	**Fold:**AF1531-like **Superfamily:**AF1531-like **Family:**AF1531-like
14	c3f2cA_	Alignment		60.5	10	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
15	d1wg8a1	Alignment		57.0	19	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
16	c8iczA_	Alignment		50.6	12	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7)); **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
17	d2pila_	Alignment		49.3	16	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
18	d1oqwa_	Alignment		41.4	14	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
19	c3e0dA_	Alignment		38.9	32	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
20	d1u5ta1	Alignment		38.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
21	c1wg8B_	Alignment	not modelled	37.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted s-adenosylmethionine-dependent **PDBTitle:** crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
22	d2bgwa1	Alignment	not modelled	35.1	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
23	d2e1fa1	Alignment	not modelled	31.8	21	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
24	c2bcuA_	Alignment	not modelled	31.0	15	**PDB header:**transferase, lyase/dna **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
25	c2kp7A_	Alignment	not modelled	29.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
26	d1ej5a_	Alignment	not modelled	27.1	31	**Fold:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Superfamily:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Family:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
27	c2jd3B_	Alignment	not modelled	26.8	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**stbb protein; **PDBTitle:** parr from plasmid pb171
28	d1dgsa1	Alignment	not modelled	26.4	15	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like

						Family:NAD+-dependent DNA ligase, domain 3
29	c2ihmA_	Alignment	not modelled	24.9	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
30	d1x2ia1	Alignment	not modelled	24.5	25	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
31	d2fmpa1	Alignment	not modelled	21.3	8	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
32	c1kdhA_	Alignment	not modelled	19.6	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short **PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
33	d1kfta_	Alignment	not modelled	19.0	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
34	c1kftA_	Alignment	not modelled	19.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
35	d2a1jb1	Alignment	not modelled	17.9	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
36	c1dgrW_	Alignment	not modelled	17.2	9	**PDB header:**plant protein **Chain:** W: **PDB Molecule:**canavalin; **PDBTitle:** refined crystal structure of canavalin from jack bean
37	c1u5tA_	Alignment	not modelled	16.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
38	c2hnhA_	Alignment	not modelled	15.4	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
39	d1unca_	Alignment	not modelled	15.1	18	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
40	c2x49A_	Alignment	not modelled	14.6	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**invasion protein inva; **PDBTitle:** crystal structure of the c-terminal domain of inva
41	c3s7eB_	Alignment	not modelled	14.6	6	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
42	d1dk2a_	Alignment	not modelled	14.1	8	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
43	c3al0B_	Alignment	not modelled	13.7	15	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
44	d1pzna1	Alignment	not modelled	12.4	25	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
45	c3psiA_	Alignment	not modelled	12.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
46	d1yu8x1	Alignment	not modelled	12.0	14	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
47	c2rhfA_	Alignment	not modelled	11.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase recq; **PDBTitle:** d. radiodurans recq hrdc domain 3
48	d2bcqa1	Alignment	not modelled	11.2	18	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
49	c2ql5A_	Alignment	not modelled	11.1	42	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of caspase-7 with inhibitor ac-dmqd-cho
50	c1i51A_	Alignment	not modelled	11.1	42	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7 subunit p20; **PDBTitle:** crystal structure of caspase-7 complexed with xiap
51	d2p6ra2	Alignment	not modelled	10.8	19	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
52	d1d8ba_	Alignment	not modelled	10.7	4	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
53	c3iuoA_	Alignment	not modelled	10.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase recq; **PDBTitle:** the crystal structure of the c-terminal domain of the atp-dependent2 dna helicase recq from porphyromonas gingivalis to 1.6a
54	d1unda_	Alignment	not modelled	10.5	18	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain

55	c2eaaB_	Alignment	not modelled	10.4	9	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
56	c3kscD_	Alignment	not modelled	10.0	31	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
57	c3edqC_	Alignment	not modelled	9.9	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**caspase-3; **PDBTitle:** crystal structure of caspase-3 with inhibitor ac-ldesd-cho
58	c3c3vA_	Alignment	not modelled	9.8	19	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
59	d1nzpa_	Alignment	not modelled	9.8	17	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
60	c3psfA_	Alignment	not modelled	9.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
61	d2jxca1	Alignment	not modelled	9.3	10	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
62	d1jmsa1	Alignment	not modelled	9.2	4	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
63	c2g5iB_	Alignment	not modelled	8.8	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
64	c1i3oC_	Alignment	not modelled	8.6	18	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**caspase 3; **PDBTitle:** crystal structure of the complex of xiap-bir2 and caspase 3
65	d2i1qa1	Alignment	not modelled	8.5	35	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
66	d1wuda1	Alignment	not modelled	8.0	16	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
67	c3pc3A_	Alignment	not modelled	7.9	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
68	c2rrdA_	Alignment	not modelled	7.8	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hrdc domain from bloom syndrome protein; **PDBTitle:** structure of hrdc domain from human bloom syndrome protein, blm
69	c3sirD_	Alignment	not modelled	7.8	42	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice
70	d1wgla_	Alignment	not modelled	7.8	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
71	c2voyB_	Alignment	not modelled	7.7	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
72	c1uijA_	Alignment	not modelled	7.6	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
73	c1qdul_	Alignment	not modelled	7.4	36	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**caspase-8 alpha-chain; **PDBTitle:** crystal structure of the complex of caspase-8 with the tripeptide2 ketone inhibitor zevd-dcbmk
74	c2funB_	Alignment	not modelled	7.4	42	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-8; **PDBTitle:** alternative p35-caspase-8 complex
75	c2cauA_	Alignment	not modelled	7.3	9	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
76	d1uija2	Alignment	not modelled	7.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
77	c1pyoA_	Alignment	not modelled	7.2	36	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-2; **PDBTitle:** crystal structure of human caspase-2 in complex with acetyl-leu-asp-2 glu-ser-asp-cho
78	c3a5iB_	Alignment	not modelled	7.1	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha
79	d1vzva_	Alignment	not modelled	7.0	38	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
80	c1wtjB_	Alignment	not modelled	6.9	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
						PDB header:protein transport

81	c3mydA_	Alignment	not modelled	6.9	18	**Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha from helicobacter pylori
82	c3i0pA_	Alignment	not modelled	6.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from entamoeba histolytica
83	c2e9qA_	Alignment	not modelled	6.7	16	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
84	c2d5fB_	Alignment	not modelled	6.7	9	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**glycinin a3b4 subunit; **PDBTitle:** crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
85	c3h11A_	Alignment	not modelled	6.6	27	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**casp8 and fadd-like apoptosis regulator; **PDBTitle:** zymogen caspase-8:c-flipl protease domain complex
86	d1u9la_	Alignment	not modelled	6.6	30	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**NusA extra C-terminal domains
87	c3sipC_	Alignment	not modelled	6.6	42	**PDB header:**hydrolase/ligase/hydrolase **Chain:** C: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice and diap1-bir1 complex
88	d1luia_	Alignment	not modelled	6.5	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
89	d1m6ya1	Alignment	not modelled	6.5	20	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
90	c2g8yB_	Alignment	not modelled	6.3	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
91	c3kglB_	Alignment	not modelled	6.3	16	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
92	d1rvga_	Alignment	not modelled	6.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
93	c2nn3D_	Alignment	not modelled	6.2	42	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase-1; **PDBTitle:** structure of pro-sf-caspase-1
94	d1b22a_	Alignment	not modelled	6.2	16	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
95	c1b22A_	Alignment	not modelled	6.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
96	d1uika2	Alignment	not modelled	6.1	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
97	c3nn4C_	Alignment	not modelled	6.1	37	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorite dismutase; **PDBTitle:** structure of chlorite dismutase from candidatus nitrospira defluvii2 r173k mutant
98	c2k42A_	Alignment	not modelled	6.1	37	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
99	c3p45I_	Alignment	not modelled	6.1	45	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**caspase-6; **PDBTitle:** crystal structure of apo-caspase-6 at physiological ph