Phyre^2

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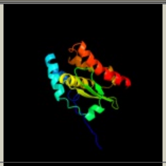
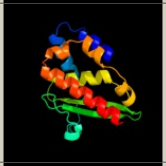
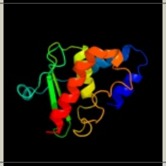
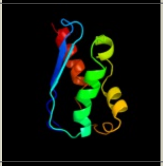
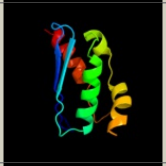
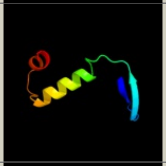
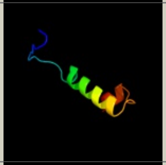
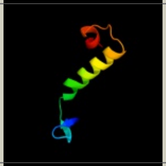
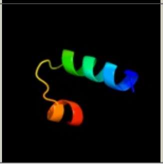
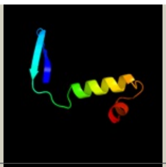
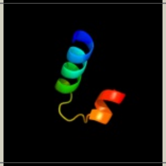
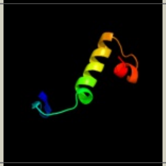
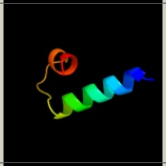
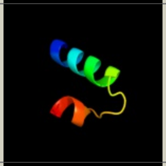
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ni7a_	Alignment		100.0	100	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
2	d1mzga_	Alignment		100.0	33	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
3	c1wloA_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sufe protein; **PDBTitle:** solution structure of the hypothetical protein from thermus2 thermophilus hb8
4	d1r9pa_	Alignment		95.8	22	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
5	d1wfza_	Alignment		91.7	19	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
6	c2z7eB_	Alignment		83.7	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
7	c2iy9A_	Alignment		63.5	25	**PDB header:**toxin **Chain:** A: **PDB Molecule:**suba; **PDBTitle:** crystal structure of the a-subunit of the ab5 toxin from e.2 coli
8	d1gcia_	Alignment		62.8	15	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
9	c2b6nA_	Alignment		62.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteinase k; **PDBTitle:** the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species
10	d1r0re_	Alignment		59.4	20	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
11	c1s2nB_	Alignment		58.8	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular subtilisin-like serine proteinase; **PDBTitle:** crystal strucure of a cold adapted subtilisin-like serine proteinase

12	d2ixta1	Alignment		55.3	20	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
13	c2w2qA_	Alignment		54.4	35	**PDB header:**hydrolase/receptor **Chain:** A: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** pcsk9-deltac d374h mutant bound to wt egf-a of ldlr
14	c3f7oB_	Alignment		53.4	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease; **PDBTitle:** crystal structure of cuticle-degrading protease from paecilomyces2 lilacinus (pl646)
15	c2oxaA_	Alignment		52.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**extracellular serine protease; **PDBTitle:** crystal structure of serine protease of aeromonas sobria
16	d1gnsa_	Alignment		51.3	18	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
17	d1p8ja2	Alignment		50.2	23	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
18	d1to2e_	Alignment		47.6	19	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
19	c2qq4A_	Alignment		47.4	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
20	d1v6ca_	Alignment		45.9	15	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
21	d2id4a2	Alignment	not modelled	45.4	23	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
22	d1pdaa2	Alignment	not modelled	43.9	14	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain **Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
23	c1r64A_	Alignment	not modelled	43.1	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**kexin; **PDBTitle:** the 2.2 a crystal structure of kex2 protease in complex with ac-arg-2 glu-lys-boroarg peptidyl boronic acid inhibitor
24	c1p8jB_	Alignment	not modelled	40.8	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**furin precursor; **PDBTitle:** crystal structure of the proprotein convertase furin
25	c3qfhE_	Alignment	not modelled	40.4	18	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**epidermin leader peptide processing serine protease epip; **PDBTitle:** 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus.
26	d1gtka2	Alignment	not modelled	39.1	14	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain **Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
27	d1bh6a_	Alignment	not modelled	38.7	19	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
						PDB header:hydrolase

28	c3lpcA_	Alignment	not modelled	33.3	35	**Chain:** A: **PDB Molecule:**aprb2; **PDBTitle:** crystal structure of a subtilisin-like protease
29	c3bpsA_	Alignment	not modelled	32.4	35	**PDB header:**hydrolase/lipid transport **Chain:** A: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** pcsk9:egf-a complex
30	d1nexa1	Alignment	not modelled	31.1	26	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
31	d1xjsa_	Alignment	not modelled	27.0	18	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
32	d1fs1b1	Alignment	not modelled	26.9	39	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
33	c2yukA_	Alignment	not modelled	25.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
34	d1fs2b1	Alignment	not modelled	25.5	39	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
35	d1su0b_	Alignment	not modelled	24.8	21	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
36	d2pwaa1	Alignment	not modelled	23.5	23	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
37	d1r6va_	Alignment	not modelled	22.2	23	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
38	d1meea_	Alignment	not modelled	22.0	23	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
39	d2olra2	Alignment	not modelled	18.8	8	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
40	c2ypnA_	Alignment	not modelled	18.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase
41	d2ovra1	Alignment	not modelled	17.8	39	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
42	c3t41B_	Alignment	not modelled	17.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**epidermin leader peptide processing serine protease epip; **PDBTitle:** 1.95 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) s393a mutant from staphylococcus3 aureus
43	d1go4a_	Alignment	not modelled	17.3	12	**Fold:**The spindle assembly checkpoint protein mad2 **Superfamily:**The spindle assembly checkpoint protein mad2 **Family:**The spindle assembly checkpoint protein mad2
44	c3e21A_	Alignment	not modelled	14.7	19	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** crystal structure of faf-1 uba domain
45	d1luca_	Alignment	not modelled	13.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
46	d2hh6a1	Alignment	not modelled	13.8	33	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
47	c3gq2B_	Alignment	not modelled	13.7	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general vesicular transport factor p115; **PDBTitle:** crystal structure of the dimer of the p115 tether globular head domain
48	d1ii2a2	Alignment	not modelled	12.4	20	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
49	c3lysC_	Alignment	not modelled	12.1	17	**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
50	d1dbia_	Alignment	not modelled	11.9	25	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
51	c3i74B_	Alignment	not modelled	10.7	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**subtilisin-like protease; **PDBTitle:** crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
52	c2w0gA_	Alignment	not modelled	10.6	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** hsp90 co-chaperone cdc37
53	c2gjvF_	Alignment	not modelled	10.3	19	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** crystal structure of a protein of unknown function from salmonella2 typhimurium
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein

54	c2hl7A_	Alignment	not modelled	10.1	23	ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
55	d2gjva1	Alignment	not modelled	10.1	19	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**STM4215-like
56	c2w3cA_	Alignment	not modelled	10.1	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general vesicular transport factor p115; **PDBTitle:** globular head region of the human general vesicular2 transport factor p115
57	c2qk1A_	Alignment	not modelled	10.0	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein stu2; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
58	c2kkpA_	Alignment	not modelled	9.8	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
59	c1bq0A_	Alignment	not modelled	9.8	8	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj; **PDBTitle:** j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
60	d1w6ka2	Alignment	not modelled	8.9	17	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpene synthases
61	d1gm5a1	Alignment	not modelled	8.9	22	**Fold:**Four-helical up-and-down bundle **Superfamily:**RecG, N-terminal domain **Family:**RecG, N-terminal domain
62	d1n83a_	Alignment	not modelled	8.6	6	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
63	d1us7b_	Alignment	not modelled	8.5	27	**Fold:**Hsp90 co-chaperone CDC37 **Superfamily:**Hsp90 co-chaperone CDC37 **Family:**Hsp90 co-chaperone CDC37
64	c1us7B_	Alignment	not modelled	8.5	27	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** complex of hsp90 and p50
65	c2kykA_	Alignment	not modelled	8.5	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
66	c3lbdA_	Alignment	not modelled	7.9	7	**PDB header:**nuclear receptor **Chain:** A: **PDB Molecule:**retinoic acid receptor gamma; **PDBTitle:** ligand-binding domain of the human retinoic acid receptor2 gamma bound to 9-cis retinoic acid
67	c3bvoA_	Alignment	not modelled	7.6	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
68	c3dmbA_	Alignment	not modelled	7.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative general stress protein 26 with a pnp-oxidase like **PDBTitle:** crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
69	c2oaxC_	Alignment	not modelled	7.4	29	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mineralocorticoid receptor; **PDBTitle:** crystal structure of the s810l mutant mineralocorticoid2 receptor associated with sc9420
70	c2kvhA_	Alignment	not modelled	7.2	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
71	c2dl0A_	Alignment	not modelled	7.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1
72	d1fpoa1	Alignment	not modelled	7.1	17	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
73	d1x40a1	Alignment	not modelled	7.1	13	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
74	d1xbla_	Alignment	not modelled	6.9	8	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
75	c3eq1A_	Alignment	not modelled	6.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
76	d1coka_	Alignment	not modelled	6.7	27	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
77	c2kg5A_	Alignment	not modelled	6.7	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**arf-gap, rho-gap domain, ank repeat and ph **PDBTitle:** nmr solution structure of arap3-sam
78	d1dd4c_	Alignment	not modelled	6.6	21	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain

						Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
79	d2fiqa1	Alignment	not modelled	6.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
80	d1dd3a1	Alignment	not modelled	6.5	21	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
81	d1pq9a_	Alignment	not modelled	6.4	12	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
82	d1dd4d_	Alignment	not modelled	6.2	21	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
83	d1i36a1	Alignment	not modelled	6.1	20	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Conserved hypothetical protein MTH1747
84	c2kd1A_	Alignment	not modelled	6.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dna integration/recombination/invertion protein; **PDBTitle:** solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
85	c2kw0A_	Alignment	not modelled	6.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
86	d1hdja_	Alignment	not modelled	5.9	9	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
87	d1sgga_	Alignment	not modelled	5.8	13	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
88	d1oxja1	Alignment	not modelled	5.7	7	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
89	c2wwaJ_	Alignment	not modelled	5.7	33	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
90	c3bgdB_	Alignment	not modelled	5.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiopurine s-methyltransferase; **PDBTitle:** thiopurine s-methyltransferase
91	c3zqpB_	Alignment	not modelled	5.5	23	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**terminase small subunit; **PDBTitle:** crystal structure of the small terminase oligomerization2 domain from a spp1-like bacteriophage
92	d1eg3a2	Alignment	not modelled	5.4	60	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
93	c1z5xU_	Alignment	not modelled	5.4	20	**PDB header:**hormone/growth factor receptor **Chain:** U: **PDB Molecule:**ultraspiracle protein (usp) a homologue of rxr; **PDBTitle:** hemipteran ecdysone receptor ligand-binding domain2 complexed with ponasterone a
94	d1thma_	Alignment	not modelled	5.4	25	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
95	c3c18B_	Alignment	not modelled	5.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein; **PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
96	c2eamA_	Alignment	not modelled	5.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative 47 kda protein; **PDBTitle:** solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
97	c2khqA_	Alignment	not modelled	5.3	10	**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
98	c3lccA_	Alignment	not modelled	5.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyl chloride transferase; **PDBTitle:** structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
99	d1r4va_	Alignment	not modelled	5.1	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Bacterial histone-fold protein