Phyre^2

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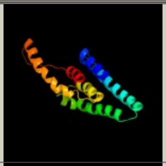
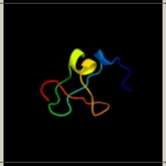
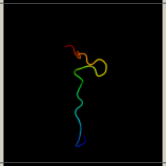
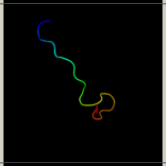
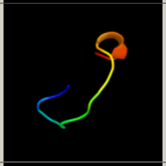
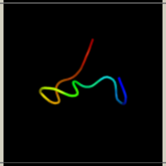
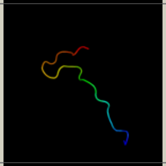
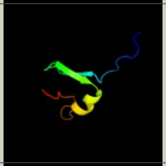
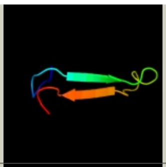
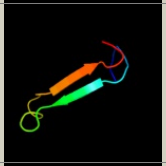
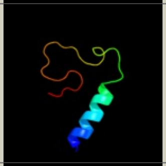
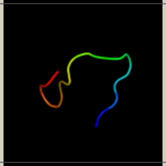
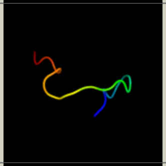
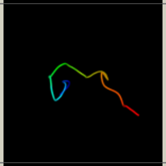
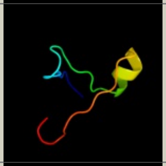
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3s0xB_	Alignment		98.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase a24b, flak domain protein; **PDBTitle:** the crystal structure of gxgd membrane protease flak
2	c2k5cA_	Alignment		80.8	6	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
3	c3py7A_	Alignment		80.8	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,paxillin ld1,protein e6 **PDBTitle:** crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
4	c2owoA_	Alignment		64.3	4	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
5	c1v9pB_	Alignment		63.6	0	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
6	d1dgsa1	Alignment		62.3	0	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
7	d1pfva3	Alignment		60.0	7	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
8	c2lcqA_	Alignment		55.3	7	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
9	c1dgsB_	Alignment		54.4	4	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
10	d1vd4a_	Alignment		53.9	5	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
11	d2fk4a1	Alignment		53.0	10	**Fold:**E6 C-terminal domain-like **Superfamily:**E6 C-terminal domain-like **Family:**E6 C-terminal domain-like

12	d2jnea1	Alignment		48.2	14	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
13	c2jneA_	Alignment		48.2	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
14	d2fiya1	Alignment		45.8	13	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
15	d2gnra1	Alignment		44.2	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
16	d2baya1	Alignment		43.9	6	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
17	c2xeuA_	Alignment		43.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein 4; **PDBTitle:** ring domain
18	d1faqa_	Alignment		41.0	21	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
19	c3pfqA_	Alignment		38.2	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
20	d1rmda2	Alignment		37.5	8	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
21	c2kr6A_	Alignment	not modelled	36.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**presenilin-1; **PDBTitle:** solution structure of presenilin-1 ctf subunit
22	d2ctda2	Alignment	not modelled	36.0	22	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
23	c3lrqB_	Alignment	not modelled	35.6	5	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase trim37; **PDBTitle:** crystal structure of the u-box domain of human ubiquitin-2 protein ligase (e3), northeast structural genomics3 consortium target hr4604d.
24	c2f42A_	Alignment	not modelled	34.6	5	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
25	c2jmdA_	Alignment	not modelled	33.1	5	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of human traf6
26	d1iyca_	Alignment	not modelled	31.5	21	**Fold:**Invertebrate chitin-binding proteins **Superfamily:**Invertebrate chitin-binding proteins **Family:**Antifungal peptide scarabaecin
27	c3cngC_	Alignment	not modelled	31.3	0	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
28	d2cu8a1	Alignment	not modelled	28.8	10	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain

29	c3ky9B_	Alignment	not modelled	28.8	4	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
30	c2eciA_	Alignment	not modelled	28.7	5	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of the human tnf2 receptor-associated factor 6 protein
31	d1vfya_	Alignment	not modelled	28.5	19	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
32	d1kbea_	Alignment	not modelled	28.3	17	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
33	c2db6A_	Alignment	not modelled	28.2	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 and cysteine rich domain 3; **PDBTitle:** solution structure of rsgi ruh-051, a c1 domain of stac32 from human cdna
34	d1dvpa2	Alignment	not modelled	28.2	9	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
35	d1s5pa_	Alignment	not modelled	28.2	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
36	c2jrpA_	Alignment	not modelled	28.2	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
37	c3llkA_	Alignment	not modelled	28.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase 1; **PDBTitle:** sulfhydryl oxidase fragment of human qsox1
38	d2csha2	Alignment	not modelled	27.9	18	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
39	c2klxA_	Alignment	not modelled	27.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
40	d1jm7a_	Alignment	not modelled	26.2	0	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
41	c2i5oA_	Alignment	not modelled	25.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
42	d2cona1	Alignment	not modelled	25.5	18	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
43	d2ct1a1	Alignment	not modelled	25.1	10	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
44	d1dsva_	Alignment	not modelled	25.0	29	**Fold:**Retrovirus zinc finger-like domains **Superfamily:**Retrovirus zinc finger-like domains **Family:**Retrovirus zinc finger-like domains
45	c3zyqA_	Alignment	not modelled	24.5	7	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
46	d2c2la2	Alignment	not modelled	24.1	5	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
47	c3odeA_	Alignment	not modelled	23.4	7	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** human parp-1 zinc finger 2 (zn2) bound to dna
48	d1ptqa_	Alignment	not modelled	23.3	3	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
49	d2vrda1	Alignment	not modelled	22.3	0	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
50	c1dvpA_	Alignment	not modelled	21.9	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
51	c1rfhA_	Alignment	not modelled	21.1	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ras association (ralgds/af-6) domain family 5; **PDBTitle:** solution structure of the c1 domain of nore1, a novel ras2 effector
52	d2jnya1	Alignment	not modelled	21.0	0	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
53	d1x4ka1	Alignment	not modelled	20.9	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
						Fold: Voltage-gated potassium channels

54	d1r3jc_	Alignment	not modelled	20.7	21	**Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
55	d1wfka_	Alignment	not modelled	20.5	8	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
56	d1yfua1	Alignment	not modelled	20.4	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
57	d1tbna_	Alignment	not modelled	20.2	10	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
58	d2pk7a1	Alignment	not modelled	20.1	0	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
59	c3ir9A_	Alignment	not modelled	20.1	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
60	c2j6aA_	Alignment	not modelled	19.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein trm112; **PDBTitle:** crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
61	d2c2vv1	Alignment	not modelled	19.8	5	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
62	c2y43B_	Alignment	not modelled	19.7	5	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18; **PDBTitle:** rad18 ubiquitin ligase ring domain structure
63	d2hf1a1	Alignment	not modelled	19.5	0	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
64	d2gmga1	Alignment	not modelled	19.1	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
65	c3nznA_	Alignment	not modelled	19.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
66	c2ecyA_	Alignment	not modelled	18.9	6	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
67	c2egpA_	Alignment	not modelled	18.7	4	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 34; **PDBTitle:** solution structure of the ring-finger domain from human2 tripartite motif protein 34
68	d2yrka1	Alignment	not modelled	18.5	15	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
69	c2gb5B_	Alignment	not modelled	18.5	0	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
70	c2dmjA_	Alignment	not modelled	18.4	0	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 1; **PDBTitle:** solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
71	c2kreA_	Alignment	not modelled	18.2	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin conjugation factor e4 b; **PDBTitle:** solution structure of e4b/ufd2a u-box domain
72	d1iyma_	Alignment	not modelled	17.7	0	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
73	c2jvyA_	Alignment	not modelled	17.6	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** solution structure of the eda-id-related c417f mutant of2 human nemo zinc finger
74	c3glsC_	Alignment	not modelled	17.6	0	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
75	c1z2qA_	Alignment	not modelled	17.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lm5-1; **PDBTitle:** high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
76	d2dara2	Alignment	not modelled	16.9	5	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
77	d1tdza3	Alignment	not modelled	16.9	0	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
78	d1t1ha_	Alignment	not modelled	16.7	11	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
79	c1jocA_	Alignment	not modelled	16.7	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**early endosomal autoantigen 1; **PDBTitle:** eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
80	d1rutx3	Alignment	not modelled	16.7	7	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain

81	c3mhsE_	Alignment	not modelled	16.6	21	**PDB header:**hydrolase/transcription regulator/protei **Chain:** E: **PDB Molecule:**saga-associated factor 73; **PDBTitle:** structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
82	d1r2za3	Alignment	not modelled	16.4	0	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
83	c2jr6A_	Alignment	not modelled	16.4	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
84	c3htkC_	Alignment	not modelled	16.3	13	**PDB header:**recombination/replication/ligase **Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21; **PDBTitle:** crystal structure of mms21 and smc5 complex
85	d1xx6a2	Alignment	not modelled	16.0	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
86	d1vqo11	Alignment	not modelled	16.0	11	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37e
87	c2e7pC_	Alignment	not modelled	15.9	4	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
88	c2e73A_	Alignment	not modelled	15.7	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c gamma type; **PDBTitle:** solution structure of the phorbol esters/diacylglycerol2 binding domain of protein kinase c gamma
89	d1lkoa2	Alignment	not modelled	15.4	11	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
90	c2zaeB_	Alignment	not modelled	15.3	4	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease p protein component 4; **PDBTitle:** crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
91	c3gkxB_	Alignment	not modelled	15.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
92	c2js4A_	Alignment	not modelled	15.2	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
93	c2h0dB_	Alignment	not modelled	15.2	16	**PDB header:**metal binding protein/ligase **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex
94	c3nw0A_	Alignment	not modelled	15.0	0	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural maintenance of chromosomes element 1 **PDBTitle:** crystal structure of mageg1 and nse1 complex
95	c3i2dA_	Alignment	not modelled	15.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 sumo-protein ligase siz1; **PDBTitle:** crystal structure of s. cerevisiae sumo e3 ligase siz1
96	d1yc5a1	Alignment	not modelled	15.0	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
97	d1imla2	Alignment	not modelled	14.8	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
98	c1v9xA_	Alignment	not modelled	14.7	0	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase; **PDBTitle:** solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1
99	d1q1aa_	Alignment	not modelled	14.7	0	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators