Phyre2

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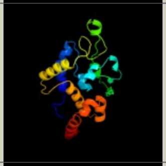
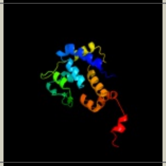
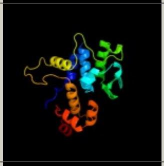
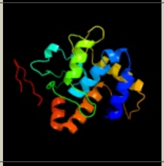
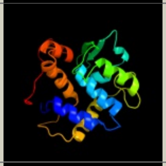
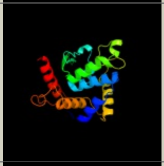
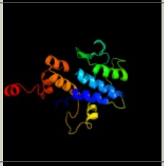
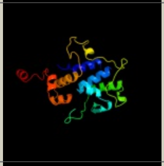
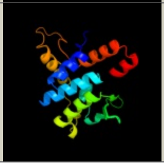
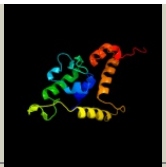
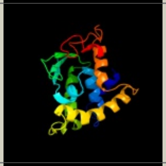
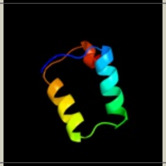
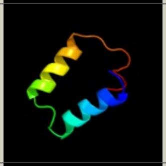
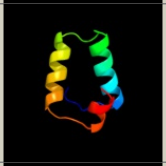
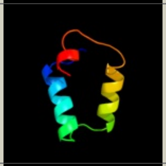
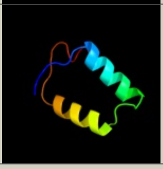
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a0pa2	Alignment		99.9	25	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
2	c3nkhB_	Alignment		99.9	19	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
3	d1aiha_	Alignment		99.9	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
4	d1f44a2	Alignment		99.9	10	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
5	d1ae9a_	Alignment		99.9	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
6	c1z1bA_	Alignment		99.9	20	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a lambda integrase dimer bound to a2 coc' core site
7	d1p7da_	Alignment		99.8	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
8	c1a0pA_	Alignment		99.8	23	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
9	c1ma7A_	Alignment		99.8	13	**PDB header:**hydrolase, ligase/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
10	c1crxA_	Alignment		99.8	15	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
11	d5crxb2	Alignment		99.8	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	c2a3vA_	Alignment		99.6	27	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
13	c2v6eB_	Alignment		97.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
14	c2f4qA_	Alignment		91.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
15	c2h7fX_	Alignment		83.6	14	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
16	d1khda1	Alignment		72.2	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
17	d1uoua1	Alignment		62.2	26	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
18	d1v8ga1	Alignment		61.0	22	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
19	d2tpta1	Alignment		56.1	14	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
20	d1brwa1	Alignment		50.7	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
21	d1o17a1	Alignment	not modelled	43.0	22	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
22	c2dsjA_	Alignment	not modelled	40.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
23	d1s7oa_	Alignment	not modelled	36.8	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
24	c2j0fC_	Alignment	not modelled	35.8	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
25	c1v8gB_	Alignment	not modelled	35.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
26	c3h5qA_	Alignment	not modelled	35.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
27	c1otpA_	Alignment	not modelled	31.1	14	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
						PDB header:transferase

28	c1brwB_	Alignment	not modelled	30.4	21	**Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
29	c1vquB_	Alignment	not modelled	27.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
30	d1xsva_	Alignment	not modelled	27.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
31	d1a41a_	Alignment	not modelled	26.7	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
32	c2bpqB_	Alignment	not modelled	26.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
33	c2b9sA_	Alignment	not modelled	23.2	12	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
34	c1khdD_	Alignment	not modelled	20.2	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
35	d1rr8c1	Alignment	not modelled	20.2	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
36	d2elca1	Alignment	not modelled	17.2	23	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
37	c1o17A_	Alignment	not modelled	16.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
38	d2auwa1	Alignment	not modelled	16.7	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
39	d1e3oc1	Alignment	not modelled	16.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
40	d1f43a_	Alignment	not modelled	14.7	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
41	d1hdpa_	Alignment	not modelled	14.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
42	c2f9jP_	Alignment	not modelled	14.3	36	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
43	c3mzyA_	Alignment	not modelled	14.1	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
44	c2o8xA_	Alignment	not modelled	13.8	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
45	d2ecba1	Alignment	not modelled	13.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
46	d1yu5x1	Alignment	not modelled	13.5	20	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
47	c3narA_	Alignment	not modelled	13.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
48	d1zara1	Alignment	not modelled	13.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rio2 serine protein kinase N-terminal domain
49	d1hmja_	Alignment	not modelled	13.3	10	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
50	c2l9rA_	Alignment	not modelled	13.2	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
51	d1k4ta2	Alignment	not modelled	13.1	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
52	d1qzpa_	Alignment	not modelled	12.9	13	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
						PDB header:dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3;

53	c2da5A_	Alignment	not modelled	12.5	16	**PDBTitle:** solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
54	c1p4eB_	Alignment	not modelled	12.5	12	**PDB header:**dna binding protein/recombination/dna **Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
55	c2k6nA_	Alignment	not modelled	12.4	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**supervillin; **PDBTitle:** solution structure of human supervillin headpiece, minimized2 average
56	d1p4ea2	Alignment	not modelled	12.2	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
57	d1xg1a1	Alignment	not modelled	12.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of telomeric protein
58	d1gt0c1	Alignment	not modelled	12.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
59	d1ujsa_	Alignment	not modelled	11.9	20	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
60	d1ijwc_	Alignment	not modelled	11.7	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
61	d1dzfa2	Alignment	not modelled	11.5	11	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
62	d1fjlb_	Alignment	not modelled	11.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
63	c2l3xA_	Alignment	not modelled	10.8	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ablim2 protein; **PDBTitle:** villin head piece domain of human ablim2
64	d2hsga1	Alignment	not modelled	10.7	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
65	d2cqxa1	Alignment	not modelled	10.5	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
66	d1w0ta_	Alignment	not modelled	10.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of telomeric protein
67	d1eika_	Alignment	not modelled	10.1	8	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
68	d1octc1	Alignment	not modelled	9.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
69	c3h0gE_	Alignment	not modelled	9.6	15	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
70	d1sfka_	Alignment	not modelled	9.3	10	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
71	d1ocpa_	Alignment	not modelled	9.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
72	c2dmsA_	Alignment	not modelled	8.5	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
73	d1au7a1	Alignment	not modelled	8.5	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
74	d1jhfa1	Alignment	not modelled	8.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
75	d1bw5a_	Alignment	not modelled	7.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
76	d1ahdp_	Alignment	not modelled	7.8	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
77	d1s7ea1	Alignment	not modelled	7.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
78	d2ecca1	Alignment	not modelled	7.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
79	d2e1oa1	Alignment	not modelled	7.3	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
80	d1ig7a_	Alignment	not modelled	7.1	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain

81	d1sfkb_	Alignment	not modelled	7.1	4	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
82	c2cg5A_	Alignment	not modelled	6.9	20	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**l-aminoadipate-semialdehyde dehydrogenase- **PDBTitle:** structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic3 acyl carrier protein and coenzyme a
83	c3hugA_	Alignment	not modelled	6.9	15	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
84	c2nogA_	Alignment	not modelled	6.9	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**iswi protein; **PDBTitle:** sant domain structure of xenopus remodeling factor iswi
85	c2dn0A_	Alignment	not modelled	6.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of human2 zinc fingers and homeoboxes protein 3
86	d1b33a_	Alignment	not modelled	6.6	22	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
87	d1efaa1	Alignment	not modelled	6.5	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
88	d1w0ua_	Alignment	not modelled	6.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of telomeric protein
89	d1vnda_	Alignment	not modelled	6.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
90	d1p7ia_	Alignment	not modelled	6.1	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
91	c2dmqA_	Alignment	not modelled	6.1	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**lim/homeobox protein lhx9; **PDBTitle:** solution structure of the homeobox domain of lim/homeobox2 protein lhx9
92	c3jstA_	Alignment	not modelled	5.9	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of transcriptional coactivator/pterin dehydratase2 from brucella melitensis
93	d1yz8p1	Alignment	not modelled	5.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
94	c1y1yE_	Alignment	not modelled	5.9	15	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 27 **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
95	d1eyxa_	Alignment	not modelled	5.9	6	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
96	c2l4dA_	Alignment	not modelled	5.7	27	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
97	d1fjla_	Alignment	not modelled	5.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	d1h1oa1	Alignment	not modelled	5.6	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
99	d1cpcb_	Alignment	not modelled	5.6	22	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins