Phyre2

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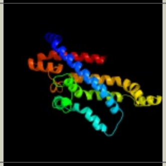
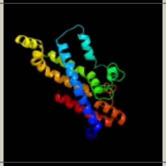
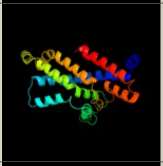
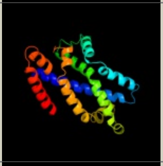
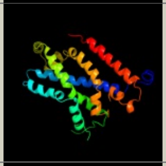
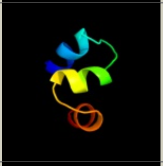
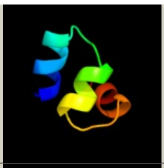
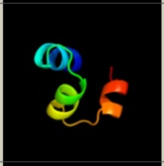
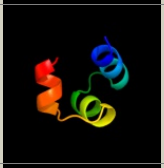
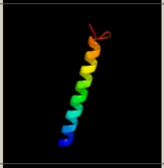
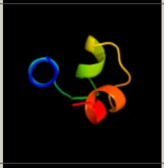
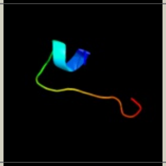
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2onkC_	Alignment		99.9	15	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
2	d2onkc1	Alignment		99.9	15	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	d3d31c1	Alignment		99.9	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	c3d31D_	Alignment		99.9	14	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
5	c2r6gF_	Alignment		99.8	13	**PDB header:**hydrolase/transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** the crystal structure of the e. coli maltose transporter
6	d2r6gf2	Alignment		99.8	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c3fh6F_	Alignment		99.8	12	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
8	d2r6gg1	Alignment		99.7	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d3dhwa1	Alignment		99.7	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	d1ntca_	Alignment		35.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
11	d1umqa_	Alignment		34.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

12	c1umqA_	Alignment		34.0	22	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
13	d1etob_	Alignment		32.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	d1fipa_	Alignment		32.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
15	d1etxa_	Alignment		27.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	c3e7lD_	Alignment		24.1	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
17	c2jwaA_	Alignment		23.1	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
18	d1g2ha_	Alignment		21.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	d2ns0a1	Alignment		18.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
20	c2cw1A_	Alignment		17.8	43	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
21	c2hx6A_	Alignment	not modelled	13.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
22	c2d7dB_	Alignment	not modelled	11.3	15	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**40-mer from uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
23	d1i3ja_	Alignment	not modelled	8.9	10	**Fold:**DNA-binding domain of intron-encoded endonucleases **Superfamily:**DNA-binding domain of intron-encoded endonucleases **Family:**DNA-binding domain of intron-encoded endonucleases
24	c3qkbB_	Alignment	not modelled	8.7	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
25	c3iwcD_	Alignment	not modelled	8.3	35	**PDB header:**lyase **Chain:** D: **PDB Molecule:**s-adenosylmethionine decarboxylase; **PDBTitle:** t. maritima adometdc complex with s-adenosylmethionine2 methyl ester
26	d1st6a6	Alignment	not modelled	8.2	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
27	d2auwa1	Alignment	not modelled	8.0	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
28	d1i1ga1	Alignment	not modelled	7.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain

29	d1x8da1	Alignment	not modelled	7.9	7	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
30	c2kvlA_	Alignment	not modelled	7.8	8	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
31	d1cf7a_	Alignment	not modelled	7.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
32	c1twcF_	Alignment	not modelled	7.5	29	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 23 **PDBTitle:** rna polymerase ii complexed with gtp
33	d1twff_	Alignment	not modelled	7.5	29	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
34	c2lhuA_	Alignment	not modelled	7.4	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
35	d1qkla_	Alignment	not modelled	7.3	29	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
36	c2pmzW_	Alignment	not modelled	7.3	14	**PDB header:**translation, transferase **Chain:** W: **PDB Molecule:**dna-directed rna polymerase subunit k; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
37	c3s1bA_	Alignment	not modelled	7.3	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mini-z; **PDBTitle:** the development of peptide-based tools for the analysis of2 angiogenesis
38	c1ciiA_	Alignment	not modelled	7.2	30	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
39	d2cg4a1	Alignment	not modelled	7.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
40	d3orca_	Alignment	not modelled	7.0	36	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
41	d2cyya1	Alignment	not modelled	7.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
42	c1y2iC_	Alignment	not modelled	7.0	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein s0862; **PDBTitle:** crystal structure of mcsg target apc27401 from shigella2 flexneri
43	d1y2ia_	Alignment	not modelled	7.0	27	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
44	c2ks1B_	Alignment	not modelled	6.9	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
45	d2hqva1	Alignment	not modelled	6.9	8	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**ChuX-like
46	d2obpa1	Alignment	not modelled	6.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ReutB4095-like
47	c2nq2A_	Alignment	not modelled	6.8	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**hypothetical abc transporter permease protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
48	d1se7a_	Alignment	not modelled	6.7	40	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
49	d2cfxa1	Alignment	not modelled	6.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
50	c2qlxA_	Alignment	not modelled	6.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
51	c2qlwA_	Alignment	not modelled	6.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
52	d1vr4a1	Alignment	not modelled	6.4	9	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
53	d1sdia_	Alignment	not modelled	6.4	23	**Fold:**YcfC-like **Superfamily:**YcfC-like **Family:**YcfC-like
54	c2auwB_	Alignment	not modelled	6.4	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
55	c2zihC_	Alignment	not modelled	6.4	6	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 74;

						PDBTitle: crystal structure of yeast vps74
56	d1v54g_	Alignment	not modelled	6.4	12	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
57	d1brwa3	Alignment	not modelled	6.4	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
58	c2i88A_	Alignment	not modelled	6.4	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**colicin-e1; **PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1
59	c2ziiA_	Alignment	not modelled	6.3	6	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 74; **PDBTitle:** crystal structure of yeast vps74-n-term truncation variant
60	d2o3aa1	Alignment	not modelled	6.3	33	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
61	d1o8ca2	Alignment	not modelled	6.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
62	c2kz3A_	Alignment	not modelled	6.3	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
63	d1h6gb1	Alignment	not modelled	6.3	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
64	d2phcb1	Alignment	not modelled	6.2	8	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
65	c2yy8B_	Alignment	not modelled	6.2	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0106 protein ph0461; **PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
66	d2tpta3	Alignment	not modelled	6.2	29	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
67	c1pyuD_	Alignment	not modelled	6.1	31	**PDB header:**lyase **Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain; **PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys
68	c2vn2B_	Alignment	not modelled	6.1	14	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
69	c1piiA_	Alignment	not modelled	6.0	20	**PDB header:**bifunctional(isomerase and synthase) **Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase; **PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
70	c1rkcB_	Alignment	not modelled	6.0	11	**PDB header:**cell adhesion, structural protein **Chain:** B: **PDB Molecule:**talin; **PDBTitle:** human vinculin head (1-258) in complex with talin's2 vinculin binding site 3 (residues 1944-1969)
71	d1jhfa1	Alignment	not modelled	6.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
72	c2gqqB_	Alignment	not modelled	6.0	6	**PDB header:**transcription **Chain:** B: **PDB Molecule:**leucine-responsive regulatory protein; **PDBTitle:** crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
73	c3mmlD_	Alignment	not modelled	5.9	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
74	c3h0gF_	Alignment	not modelled	5.9	27	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
75	c1xwjB_	Alignment	not modelled	5.9	11	**PDB header:**cell adhesion/protein binding **Chain:** B: **PDB Molecule:**talin; **PDBTitle:** vinculin head (1-258) in complex with the talin vinculin2 binding site 3 (1945-1969)
76	d1icha_	Alignment	not modelled	5.9	5	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
77	c1ichA_	Alignment	not modelled	5.9	5	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
78	c2ka1A_	Alignment	not modelled	5.8	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
79	c2ka2B_	Alignment	not modelled	5.8	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints

80	d1a53a_	Alignment	not modelled	5.8	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
81	c2e75E_	Alignment	not modelled	5.8	29	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
82	c1vf5R_	Alignment	not modelled	5.8	29	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
83	c2e74E_	Alignment	not modelled	5.8	29	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
84	c2e76E_	Alignment	not modelled	5.8	29	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
85	d2e74e1	Alignment	not modelled	5.8	29	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
86	c2xa6B_	Alignment	not modelled	5.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**kh domain-containing\,rna-binding\,signal **PDBTitle:** structural basis for homodimerization of the src-associated2 during mitosis, 68 kd protein (sam68) qua1 domain
87	c2ka2A_	Alignment	not modelled	5.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
88	c2ka1B_	Alignment	not modelled	5.7	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
89	c3lpeF_	Alignment	not modelled	5.7	25	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
90	d1nyoa_	Alignment	not modelled	5.7	3	**Fold:**FAS1 domain **Superfamily:**FAS1 domain **Family:**FAS1 domain
91	c2ijlB_	Alignment	not modelled	5.6	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**molybdenum-binding transcriptional repressor; **PDBTitle:** the structure of a putative mode from agrobacterium tumefaciens.
92	d1vf5c3	Alignment	not modelled	5.6	17	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor **Family:**Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor
93	c2zp2B_	Alignment	not modelled	5.5	4	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
94	d1l7va_	Alignment	not modelled	5.5	13	**Fold:**ABC transporter involved in vitamin B12 uptake, BtuC **Superfamily:**ABC transporter involved in vitamin B12 uptake, BtuC **Family:**ABC transporter involved in vitamin B12 uptake, BtuC
95	c2kncA_	Alignment	not modelled	5.5	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
96	c1jd7A_	Alignment	not modelled	5.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
97	c3gebC_	Alignment	not modelled	5.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**eyes absent homolog 2; **PDBTitle:** crystal structure of edeya2
98	c3gk0H_	Alignment	not modelled	5.4	27	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
99	c1vf5E_	Alignment	not modelled	5.4	30	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus