Phyre2

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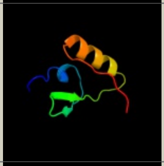
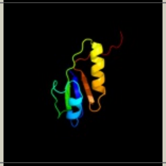
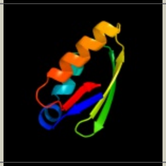
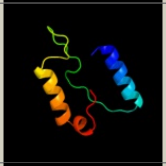
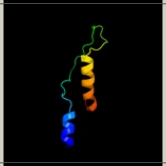
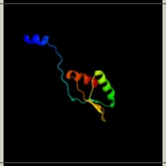
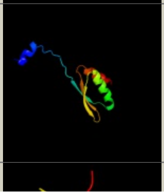
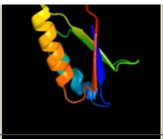
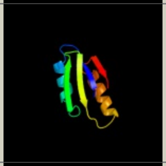
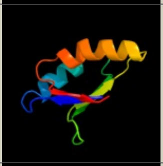
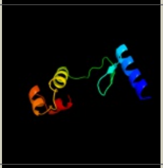
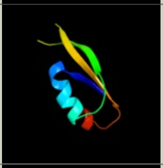
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lfpa_	Alignment		100.0	44	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
2	d1kona_	Alignment		100.0	99	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
3	d1mw7a_	Alignment		100.0	31	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
4	c3k85B_	Alignment		65.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**d-glycero-d-manno-heptose 1-phosphate kinase; **PDBTitle:** crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
5	c2jsxA_	Alignment		62.7	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
6	c3ibwA_	Alignment		62.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
7	c3ke8A_	Alignment		56.3	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
8	d2auna2	Alignment		50.9	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
9	c2zf8A_	Alignment		45.7	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
10	c2cveA_	Alignment		42.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
11	c1vi7A_	Alignment		42.2	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yigz; **PDBTitle:** crystal structure of an hypothetical protein

12	c2e1cA_	Alignment		38.6	11	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
13	d2cyya2	Alignment		37.4	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
14	c2zbcH_	Alignment		36.8	11	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
15	c2f06B_	Alignment		36.4	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
16	d1i1ga2	Alignment		34.5	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
17	d1k47a2	Alignment		34.4	13	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Phosphomevalonate kinase (PMK)
18	c2plyB_	Alignment		33.5	13	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
19	c3bzqA_	Alignment		31.1	22	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
20	d1ub9a_	Alignment		31.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
21	d1sc6a3	Alignment	not modelled	29.1	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
22	d1ewqa2	Alignment	not modelled	27.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
23	d1jr3d2	Alignment	not modelled	27.2	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
24	d1lxja_	Alignment	not modelled	27.0	7	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
25	d1weya_	Alignment	not modelled	26.4	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
26	c2p6tH_	Alignment	not modelled	25.8	7	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
27	c3k2qA_	Alignment	not modelled	25.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
28	c3l7pA_	Alignment	not modelled	25.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii; **PDBTitle:** crystal structure of smu.1657c, putative nitrogen

						regulatory protein2 pii from streptococcus mutans
29	d1lxna_	Alignment	not modelled	25.3	18	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
30	c1fpqA_	Alignment	not modelled	25.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoliquiritigenin 2'-o-methyltransferase; **PDBTitle:** crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
31	c1i1gA_	Alignment	not modelled	25.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
32	c2vsaA_	Alignment	not modelled	24.5	45	**PDB header:**toxin **Chain:** A: **PDB Molecule:**mosquitocidal toxin; **PDBTitle:** structure and mode of action of a mosquitocidal holotoxin
33	d2cg4a2	Alignment	not modelled	24.2	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
34	c2kgrA_	Alignment	not modelled	23.4	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
35	d1kkca2	Alignment	not modelled	23.3	47	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
36	c2epiA_	Alignment	not modelled	22.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0045 protein mj1052; **PDBTitle:** crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannascii (form 2)
37	c2e1aD_	Alignment	not modelled	22.3	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
38	d1kkha2	Alignment	not modelled	22.3	11	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase
39	d1ul3a_	Alignment	not modelled	21.9	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
40	d2nzca1	Alignment	not modelled	21.9	7	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
41	c2csuB_	Alignment	not modelled	21.4	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
42	d1qmha1	Alignment	not modelled	21.1	24	**Fold:**Thioredoxin fold **Superfamily:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain **Family:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain
43	d1cc8a_	Alignment	not modelled	19.9	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
44	d1q5za_	Alignment	not modelled	19.8	22	**Fold:**Invasion protein A (SipA) , C-terminal actin binding domain **Superfamily:**Invasion protein A (SipA) , C-terminal actin binding domain **Family:**Invasion protein A (SipA) , C-terminal actin binding domain
45	c1q5zA_	Alignment	not modelled	19.8	22	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**sipa; **PDBTitle:** crystal structure of the c-terminal actin binding domain of2 salmonella invasion protein a (sipa)
46	c3s01A_	Alignment	not modelled	19.5	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein l; **PDBTitle:** crystal structure of a heterogeneous nuclear ribonucleoprotein l2 (hnrpl) from mus musculus at 2.15 a resolution
47	c3canA_	Alignment	not modelled	19.4	22	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
48	d2iboa1	Alignment	not modelled	19.2	19	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
49	c1zrsB_	Alignment	not modelled	19.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
50	d1zl0a2	Alignment	not modelled	18.7	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
51	c3fiaA_	Alignment	not modelled	18.5	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** crystal structure of the eh 1 domain from human intersectin-2 1 protein. northeast structural genomics consortium target3 hr3646e.
52	d2ev0a2	Alignment	not modelled	18.4	10	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
53	d1ygya3	Alignment	not modelled	18.4	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
						Fold:S-adenosyl-L-methionine-dependent methyltransferases

54	d2ex4a1	Alignment	not modelled	18.3	21	**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
55	d1gtra1	Alignment	not modelled	18.1	13	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain
56	d2q02a1	Alignment	not modelled	17.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
57	d1wb9a2	Alignment	not modelled	17.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
58	d2f06a2	Alignment	not modelled	17.1	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
59	c2e7xA_	Alignment	not modelled	16.9	7	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
60	c3o3nB_	Alignment	not modelled	16.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
61	c2nyiB_	Alignment	not modelled	16.5	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
62	d2f06a1	Alignment	not modelled	16.4	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
63	d1j5ya2	Alignment	not modelled	16.4	15	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
64	d1mwza_	Alignment	not modelled	16.4	23	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
65	d4pfka_	Alignment	not modelled	16.1	35	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
66	c2hw5F_	Alignment	not modelled	15.6	29	**PDB header:**lyase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1
67	d1fima_	Alignment	not modelled	15.4	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
68	c2dhaA_	Alignment	not modelled	15.4	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**flj20171 protein; **PDBTitle:** solution structure of the second rna recognition motif in2 hypothetical protein flj201171
69	d1hwua_	Alignment	not modelled	15.3	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
70	c1ewrA_	Alignment	not modelled	15.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of taq muts
71	d3cx5d2	Alignment	not modelled	14.9	56	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
72	c3fybA_	Alignment	not modelled	14.8	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
73	c2djwF_	Alignment	not modelled	14.8	9	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
74	c2cg4B_	Alignment	not modelled	14.7	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
75	c3g23A_	Alignment	not modelled	14.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ld-carboxypeptidase a; **PDBTitle:** crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
76	d1ppjd2	Alignment	not modelled	13.9	44	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
77	c3ia1A_	Alignment	not modelled	13.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
78	c3lk7A_	Alignment	not modelled	13.8	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanine--d-glutamate ligase; **PDBTitle:** the crystal structure of udp-n-acetylmuramoylalanine-d-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a

79	d2cfxa2	Alignment	not modelled	13.5	6	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
80	d2o35a1	Alignment	not modelled	13.3	33	**Fold:**SMc04008-like **Superfamily:**SMc04008-like **Family:**SMc04008-like
81	c2o35A_	Alignment	not modelled	13.3	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf1244; **PDBTitle:** protein of unknown function (duf1244) from sinorhizobium meliloti
82	c2i38A_	Alignment	not modelled	13.3	22	**PDB header:**rna binding protein/chimera **Chain:** A: **PDB Molecule:**fusion protein consists of immunoglobin g- **PDBTitle:** solution structure of the rrm of srp20
83	c3jz3B_	Alignment	not modelled	13.2	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
84	d1u8sa1	Alignment	not modelled	13.2	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
85	c1b4aA_	Alignment	not modelled	13.0	12	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
86	d2adca1	Alignment	not modelled	12.9	21	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
87	d1lq1a_	Alignment	not modelled	12.7	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**Spo0A
88	d2u1aa_	Alignment	not modelled	12.6	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
89	c1zxxA_	Alignment	not modelled	12.5	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
90	d1gd0a_	Alignment	not modelled	12.3	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
91	c3i4pA_	Alignment	not modelled	12.3	5	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
92	c2d9oA_	Alignment	not modelled	12.2	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**dnaj (hsp40) homolog, subfamily c, member 17; **PDBTitle:** solution structure of rna binding domain in hypothetical2 protein flj10634
93	c1ewqA_	Alignment	not modelled	12.1	22	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution
94	d2g0wa1	Alignment	not modelled	12.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
95	c3thxB_	Alignment	not modelled	11.9	17	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh3; **PDBTitle:** human mutsbeta complexed with an idl of 3 bases (loop3) and adp
96	d1pfka_	Alignment	not modelled	11.8	35	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
97	c3dx5A_	Alignment	not modelled	11.6	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
98	c2pc6C_	Alignment	not modelled	11.6	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
99	c2cfxD_	Alignment	not modelled	11.4	6	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc