Phyre2

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Description	P0AEZ7
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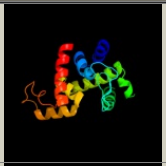
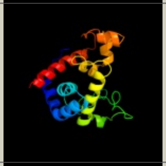
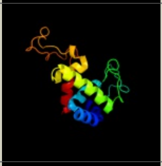
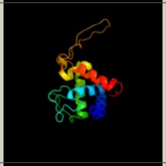
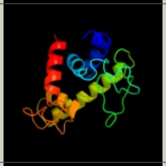
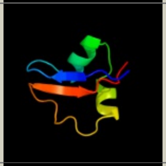
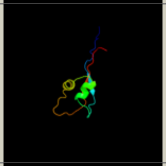
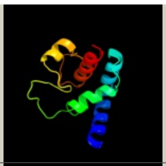
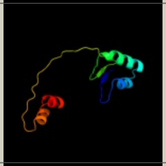
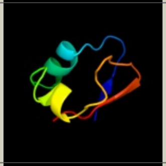
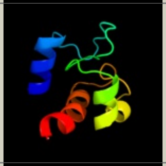
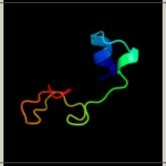
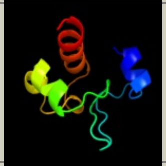
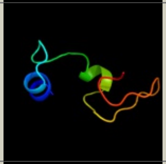
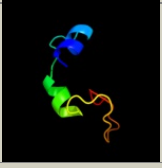
Unique Job ID	18694f5534592bc9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1slyA_	Alignment		100.0	22	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
2	c2y8pA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a; **PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
3	d1qsaa2	Alignment		100.0	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
4	d1gbsa_	Alignment		99.9	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
5	c3mgwA_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
6	c3gxkB_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9
7	c2l9yA_	Alignment		99.5	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
8	d1e0ga_	Alignment		99.4	100	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
9	c2djpA_	Alignment		99.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
10	d1y7ma2	Alignment		99.2	27	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
11	c3bkhA_	Alignment		98.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144

12	d1qusa_	Alignment		98.6	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
13	c2gu1A_	Alignment		98.5	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
14	c1y7mB_	Alignment		98.2	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
15	c1xsfA_	Alignment		96.8	13	**PDB header:**cell cycle, hydrolase **Chain:** A: **PDB Molecule:**probable resuscitation-promoting factor rpfb; **PDBTitle:** solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis
16	d1xsfa1	Alignment		96.5	13	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
17	c2fbdB_	Alignment		95.3	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lysozyme 1; **PDBTitle:** the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
18	c3eo5A_	Alignment		95.3	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
19	d1iiza_	Alignment		94.9	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
20	d1gd6a_	Alignment		94.6	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
21	c3ct5A_	Alignment	not modelled	94.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
22	d2vb1a1	Alignment	not modelled	94.4	33	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
23	d1hhla_	Alignment	not modelled	94.3	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
24	d1ghla_	Alignment	not modelled	94.2	33	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
25	d1jsea_	Alignment	not modelled	93.9	35	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
26	c2goiC_	Alignment	not modelled	93.6	28	**PDB header:**cell adhesion, sugar binding protein **Chain:** C: **PDB Molecule:**sperm lysozyme-like protein 1; **PDBTitle:** crystal structure of mouse sperm c-type lysozyme-like2 protein 1
27	c2z2fA_	Alignment	not modelled	93.5	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme c-2; **PDBTitle:** x-ray crystal structure of bovine stomach lysozyme
28	d1juga_	Alignment	not modelled	93.2	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
29	d1qqya_	Alignment	not modelled	93.1	33	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like

						Family:C-type lysozyme
30	d1lmqa_	Alignment	not modelled	92.8	35	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
31	d1ivma_	Alignment	not modelled	92.7	33	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
32	d1lsga1	Alignment	not modelled	92.2	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
33	d2nwdx1	Alignment	not modelled	91.8	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
34	d1fkqa_	Alignment	not modelled	88.1	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
35	d1b9oa_	Alignment	not modelled	86.5	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
36	d1yroa1	Alignment	not modelled	85.6	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
37	c2zycA_	Alignment	not modelled	85.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
38	d1hfxa_	Alignment	not modelled	84.9	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
39	d1f6sa_	Alignment	not modelled	84.1	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
40	c3csqC_	Alignment	not modelled	83.5	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
41	d2eqla_	Alignment	not modelled	82.9	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
42	c3fi7A_	Alignment	not modelled	82.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
43	d1alca_	Alignment	not modelled	82.2	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
44	c2kpjA_	Alignment	not modelled	77.2	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
45	d2icta1	Alignment	not modelled	71.7	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
46	d2jn6a1	Alignment	not modelled	68.6	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
47	d2ofya1	Alignment	not modelled	67.1	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
48	c2elhA_	Alignment	not modelled	65.1	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
49	c2bnoA_	Alignment	not modelled	62.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
50	d1y0pa3	Alignment	not modelled	62.8	26	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
51	d1r69a_	Alignment	not modelled	60.4	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
52	d1sq8a_	Alignment	not modelled	57.9	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
53	c2lfcA_	Alignment	not modelled	57.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
54	c3bs3A_	Alignment	not modelled	57.3	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
						Fold:lambda repressor-like DNA-binding domains

55	d1b0na2	Alignment	not modelled	56.7	22	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
56	c2rn7A_	Alignment	not modelled	53.4	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
57	d1d4ca3	Alignment	not modelled	53.1	22	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
58	c3t76A_	Alignment	not modelled	52.8	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
59	c3cecA_	Alignment	not modelled	51.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system; **PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
60	c1rr7A_	Alignment	not modelled	50.6	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
61	d1rr7a_	Alignment	not modelled	50.6	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
62	d2croa_	Alignment	not modelled	50.6	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
63	c1y9qA_	Alignment	not modelled	48.3	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
64	c3b7hA_	Alignment	not modelled	48.0	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
65	d1k78a1	Alignment	not modelled	46.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
66	d6paxa1	Alignment	not modelled	45.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
67	d1y7ya1	Alignment	not modelled	44.7	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
68	c2k53A_	Alignment	not modelled	44.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
69	c3op9A_	Alignment	not modelled	41.5	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
70	d1bw6a_	Alignment	not modelled	40.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
71	d1y9qa1	Alignment	not modelled	37.8	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
72	d1utxa_	Alignment	not modelled	37.5	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
73	d1qo8a3	Alignment	not modelled	37.3	30	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
74	c2bkiA_	Alignment	not modelled	35.9	16	**PDB header:**motor protein/metal-binding protein **Chain:** A: **PDB Molecule:**unconventional myosin; **PDBTitle:** myosin vi nucleotide-free (mdinsert2-iq) crystal structure
75	c3ivpD_	Alignment	not modelled	34.5	13	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein; **PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
76	c3omtA_	Alignment	not modelled	34.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
77	c1b0nA_	Alignment	not modelled	34.1	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
78	c3mlfC_	Alignment	not modelled	33.6	24	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
79	c2z99A_	Alignment	not modelled	30.2	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis

80	c3kxaD_	Alignment	not modelled	29.3	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
81	c2ewtA_	Alignment	not modelled	28.8	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
82	d1adra_	Alignment	not modelled	28.4	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
83	d1hlva1	Alignment	not modelled	27.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
84	c2b39B_	Alignment	not modelled	27.3	18	**PDB header:**immune system **Chain:** B: **PDB Molecule:**c3; **PDBTitle:** structure of mammalian c3 with an intact thioester at 3a resolution
85	d1pdnc_	Alignment	not modelled	26.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
86	c2k5eA_	Alignment	not modelled	25.7	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
87	c3qaoA_	Alignment	not modelled	25.6	28	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**merr-like transcriptional regulator; **PDBTitle:** the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
88	d1nera_	Alignment	not modelled	25.5	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
89	d1a9xa1	Alignment	not modelled	25.1	18	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
90	c3clcC_	Alignment	not modelled	24.6	29	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
91	c2gm4B_	Alignment	not modelled	24.5	22	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
92	d1d5ya1	Alignment	not modelled	24.3	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
93	c1t6sB_	Alignment	not modelled	22.0	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
94	d1lmb3_	Alignment	not modelled	21.9	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
95	d2phcb1	Alignment	not modelled	21.8	24	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
96	c3f52A_	Alignment	not modelled	21.2	30	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
97	d1whza_	Alignment	not modelled	20.9	11	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
98	d1mnda2	Alignment	not modelled	20.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
99	c3hefB_	Alignment	not modelled	20.8	38	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
100	d2obpa1	Alignment	not modelled	20.7	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ReutB4095-like
101	c2lcvA_	Alignment	not modelled	20.6	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation