Phyre^2

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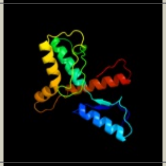
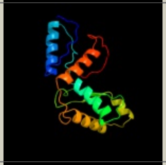
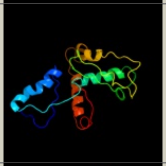
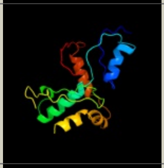
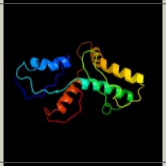
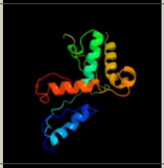
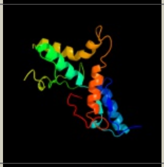
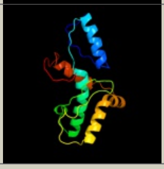
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1smkD_	Alignment		100.0	64	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase, glyoxysomal; **PDBTitle:** mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
2	c1sevA_	Alignment		100.0	64	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase, glyoxysomal precursor; **PDBTitle:** mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
3	c1mldA_	Alignment		100.0	65	**PDB header:**oxidoreductase(nad(a)-choh(d)) **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
4	c2dfdD_	Alignment		100.0	64	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of human malate dehydrogenase type 2
5	c2pwzG_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the apo form of e.coli malate dehydrogenase
6	c1hyhA_	Alignment		100.0	21	**PDB header:**oxidoreductase (choh(d)-nad+(a)) **Chain:** A: **PDB Molecule:**l-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
7	c2d4aC_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of the malate dehydrogenase from aeropyrum pernix
8	c1gv1D_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
9	c3dl2A_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme e2 variant 3; **PDBTitle:** hexagonal structure of the ldh domain of human ubiquitin-2 conjugating enzyme e2-like isoform a
10	c1y6jA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** l-lactate dehydrogenase from clostridium thermocellum cth-1135
11	c1ur5C_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface

12	c1ojuA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
13	c3nepX_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
14	c1ldbA_	Alignment		100.0	23	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**apo-l-lactate dehydrogenase; **PDBTitle:** structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase
15	c1pzfD_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** t.gondii ldh1 ternary complex with apad+ and oxalate
16	c2e37B_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** structure of tt0471 protein from thermus thermophilus
17	c1ez4B_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
18	c3gviB_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
19	c3fi9B_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
20	c1u4sA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
21	c1b8vA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** malate dehydrogenase from aquaspirillum arcticum
22	c3pqeD_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
23	c3p7mC_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4
24	c7mdhA_	Alignment	not modelled	100.0	24	**PDB header:**chloroplastic malate dehydrogenase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
25	c1hygA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate/malate dehydrogenase; **PDBTitle:** crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
26	c5mdhB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and tnad at 2.4 angstroms resolution
27	c2v65A_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase a chain; **PDBTitle:** apo ldh from the psychrophile c. gunnari
28	c2hjrK_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2

						dehydrogenase
29	c2fnzA_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
30	c1lldA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase(choh (d)-nad (a)) **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
31	c8ldhA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**m4 apo-lactate dehydrogenase; **PDBTitle:** refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
32	c2v6bB_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
33	c3d0oA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase 1; **PDBTitle:** crystal structure of lactate dehydrogenase from2 staphylococcus aureus
34	c3tl2A_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.
35	c1a5zA_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh)
36	c1wziA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
37	c2ldxA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**apo-lactate dehydrogenase; **PDBTitle:** characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4
38	c1llcA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** structure determination of the allosteric l-lactate dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution
39	c2hlpB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the e267r mutant of a halophilic2 malate dehydrogenase in the apo form
40	d2cmda2	Alignment	not modelled	100.0	100	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
41	d1mlda2	Alignment	not modelled	100.0	65	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
42	d1ez4a2	Alignment	not modelled	99.9	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
43	d1pzga2	Alignment	not modelled	99.9	30	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
44	d1oc4a2	Alignment	not modelled	99.9	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
45	d1i0za2	Alignment	not modelled	99.9	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
46	d9ldta2	Alignment	not modelled	99.9	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
47	d1o6za2	Alignment	not modelled	99.9	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
48	d1llda2	Alignment	not modelled	99.9	20	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
49	d1i10a2	Alignment	not modelled	99.9	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
50	d1guza2	Alignment	not modelled	99.9	26	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
51	d1hyha2	Alignment	not modelled	99.9	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
52	d1uxja2	Alignment	not modelled	99.9	28	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
53	d1ldna2	Alignment	not modelled	99.9	24	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
54	d1gv0a2	Alignment	not modelled	99.9	26	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain

55	d1a5za2	Alignment	not modelled	99.9	30	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
56	d1t2da2	Alignment	not modelled	99.9	20	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
57	d1ldma2	Alignment	not modelled	99.9	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
58	d1y6ja2	Alignment	not modelled	99.9	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
59	d2ldxa2	Alignment	not modelled	99.9	24	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
60	d1ojua2	Alignment	not modelled	99.9	16	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
61	d1llca2	Alignment	not modelled	99.9	27	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
62	d5mdha2	Alignment	not modelled	99.9	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
63	d1civa2	Alignment	not modelled	99.9	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
64	d1y7ta2	Alignment	not modelled	99.9	22	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
65	d7mdha2	Alignment	not modelled	99.9	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
66	d1hyea2	Alignment	not modelled	99.8	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
67	d1b8pa2	Alignment	not modelled	99.8	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
68	c1s6yA_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** 2.3a crystal structure of phospho-beta-glucosidase
69	c1up6F_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** structure of the 6-phospho-beta glucosidase from thermotoga2 maritima at 2.55 angstrom resolution in the tetragonal form3 with manganese, nad+ and glucose-6-phosphate
70	c3fefB_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glucosidase lpld; **PDBTitle:** crystal structure of putative glucosidase lpld from2 bacillus subtilis
71	c1u8xX_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**maltose-6'-phosphate glucosidase; **PDBTitle:** crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
72	c1obbB_	Alignment	not modelled	98.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
73	c1vjtA_	Alignment	not modelled	97.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
74	d1f7ua3	Alignment	not modelled	42.7	22	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain **Family:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
75	c2l9bB_	Alignment	not modelled	27.6	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mrna 3'-end-processing protein rna14; **PDBTitle:** heterodimer between rna14p monkeytail domain and rna15p hinge domain2 of the yeast cf ia complex
76	c3bd1B_	Alignment	not modelled	23.3	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
77	c2bsjB_	Alignment	not modelled	19.7	26	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein syct; **PDBTitle:** native crystal structure of the type iii secretion2 chaperone syct from yersinia enterocolitica
78	c2kpjA_	Alignment	not modelled	18.2	9	**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
79	c3cecA_	Alignment	not modelled	17.4	12	**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
						Fold:lambda repressor-like DNA-binding domains

80	d1llib_	Alignment	not modelled	16.1	9	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
81	c3omtA_	Alignment	not modelled	15.2	14	**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.
82	d3pmga3	Alignment	not modelled	14.5	17	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
83	d1b0na2	Alignment	not modelled	14.3	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
84	c1b0nA_	Alignment	not modelled	14.2	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
85	c3t5sA_	Alignment	not modelled	13.8	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor; **PDBTitle:** structure of macrophage migration inhibitory factor from giardia2 lamblia
86	d2b5aa1	Alignment	not modelled	13.6	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
87	c3op9A_	Alignment	not modelled	13.4	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
88	c3trbA_	Alignment	not modelled	13.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
89	d1utxa_	Alignment	not modelled	12.9	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
90	c2cgkB_	Alignment	not modelled	12.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-rhamnulose kinase; **PDBTitle:** crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
91	d2icta1	Alignment	not modelled	12.3	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
92	c3clcC_	Alignment	not modelled	11.8	10	**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
93	d1rzsa_	Alignment	not modelled	11.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
94	d2gx8a1	Alignment	not modelled	11.1	27	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
95	c2vi6F_	Alignment	not modelled	11.0	5	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
96	d1wh9a_	Alignment	not modelled	10.8	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
97	c3b7hA_	Alignment	not modelled	10.7	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
98	c1sb7A_	Alignment	not modelled	10.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase d; **PDBTitle:** crystal structure of the e.coli pseudouridine synthase trud
99	c2gx8B_	Alignment	not modelled	10.0	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3