Phyre2

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Description	P37326
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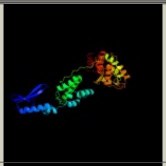
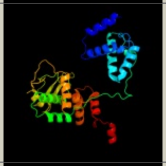
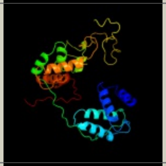
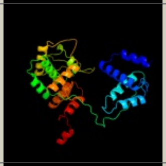
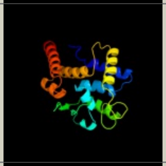
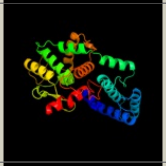
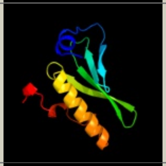
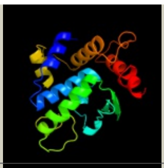
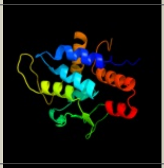
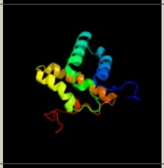
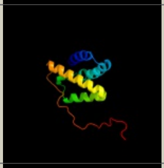
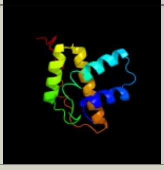
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z1bA_	Alignment		100.0	16	**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
2	d1p7da_	Alignment		99.9	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
3	c1ma7A_	Alignment		99.9	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
4	c2a3vA_	Alignment		99.9	15	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
5	c1crxA_	Alignment		99.9	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
6	c3nkhB_	Alignment		99.9	16	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
7	c1a0pA_	Alignment		99.9	14	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
8	c3ju0A_	Alignment		99.8	37	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
9	c3jtzA_	Alignment		99.8	38	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
10	d1aiha_	Alignment		99.8	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
11	d1f44a2	Alignment		99.7	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	d1a0pa2	Alignment		99.7	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	d1ae9a_	Alignment		99.7	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
14	d5crxb2	Alignment		99.4	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
15	c2kj8A_	Alignment		99.0	98	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
16	c2kj9A_	Alignment		99.0	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
17	c2kkvA_	Alignment		99.0	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
18	c2kiwA_	Alignment		98.9	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**int protein; **PDBTitle:** solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
19	c2kd1A_	Alignment		98.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dna integration/recombination/invertion protein; **PDBTitle:** solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
20	c2khqA_	Alignment		98.7	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
21	c2oxoA_	Alignment	not modelled	98.7	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
22	c2khvA_	Alignment	not modelled	98.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
23	c2kj5A_	Alignment	not modelled	98.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrosospira multiformis,3 northeast structural genomics consortium target nmr46c
24	c3lysC_	Alignment	not modelled	98.7	14	**PDB header:**recombination **Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase; **PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
25	c2kkpA_	Alignment	not modelled	98.6	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
26	c2kobA_	Alignment	not modelled	98.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase;

27	c2keyA_	Alignment	not modelled	98.1	13	**PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
28	c3nrwA_	Alignment	not modelled	97.6	6	**PDB header:**recombination **Chain:** A: **PDB Molecule:**phage integrase/site-specific recombinase; **PDBTitle:** crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
29	c2v6eB_	Alignment	not modelled	97.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
30	c2f4qA_	Alignment	not modelled	93.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
31	d1a0pa1	Alignment	not modelled	93.7	9	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
32	c3igmA_	Alignment	not modelled	87.9	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
33	c2h7fX_	Alignment	not modelled	82.6	16	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
34	d1gcca_	Alignment	not modelled	75.9	18	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
35	d1f44a1	Alignment	not modelled	71.0	13	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
36	c1kjkA_	Alignment	not modelled	69.9	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
37	d1z1ba1	Alignment	not modelled	69.9	28	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
38	d1qu6a2	Alignment	not modelled	52.1	28	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
39	d1x48a1	Alignment	not modelled	48.1	19	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
40	d1a41a_	Alignment	not modelled	45.9	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
41	d1q08a_	Alignment	not modelled	33.3	17	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
42	d1r8da_	Alignment	not modelled	28.6	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
43	c3d6zA_	Alignment	not modelled	28.4	2	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
44	d2gf5a1	Alignment	not modelled	27.1	13	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
45	c2khxA_	Alignment	not modelled	24.8	23	**PDB header:**gene regulation,nuclear protein **Chain:** A: **PDB Molecule:**ribonuclease 3; **PDBTitle:** drosha double-stranded rna binding motif
46	d1r8ea1	Alignment	not modelled	24.0	2	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
47	d1qu6a1	Alignment	not modelled	22.9	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
48	d1x49a1	Alignment	not modelled	20.7	26	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
49	d1uxca_	Alignment	not modelled	18.7	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
50	d1x47a1	Alignment	not modelled	16.9	20	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
51	c3qaoA_	Alignment	not modelled	16.9	13	**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
52	c3hh0C_	Alignment	not modelled	16.7	11	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
						PDB header:gene regulation

53	c3adjA_	Alignment	not modelled	16.5	14	**Chain:** A: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
54	d1o0wa2	Alignment	not modelled	16.0	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
55	c2zhhA_	Alignment	not modelled	15.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
56	c3adiC_	Alignment	not modelled	15.3	18	**PDB header:**gene regulation/rna **Chain:** C: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
57	c2l8nA_	Alignment	not modelled	14.3	4	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
58	c2yt4A_	Alignment	not modelled	13.2	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein dgcr8; **PDBTitle:** crystal structure of human dgcr8 core
59	c2vz4A_	Alignment	not modelled	12.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to2 promoter dna
60	d2auwa1	Alignment	not modelled	12.2	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
61	d1rkta1	Alignment	not modelled	11.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
62	d1uxda_	Alignment	not modelled	11.6	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
63	d1fada_	Alignment	not modelled	10.7	9	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
64	c3ga7A_	Alignment	not modelled	10.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetyl esterase; **PDBTitle:** 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
65	d2b7va1	Alignment	not modelled	10.5	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
66	d1lcda_	Alignment	not modelled	9.6	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
67	c2gf5A_	Alignment	not modelled	9.4	10	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fadd protein; **PDBTitle:** structure of intact fadd (mort1)
68	c2x0lB_	Alignment	not modelled	8.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of a neuro-specific splicing variant of2 human histone lysine demethylase lsd1.
69	c2v1dB_	Alignment	not modelled	8.8	13	**PDB header:**oxidoreductase/repressor **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
70	c2iw5B_	Alignment	not modelled	8.8	13	**PDB header:**oxidoreductase/transcription regulator **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis for corest-dependent demethylation of2 nucleosomes by the human lsd1 histone demethylase
71	c2xajB_	Alignment	not modelled	8.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of lsd1-corest in complex with (-)-trans-2 2-phenylcyclopropyl-1-amine
72	c2lcvA_	Alignment	not modelled	8.4	4	**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
73	d2bjca1	Alignment	not modelled	8.3	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
74	d1qpza1	Alignment	not modelled	7.7	0	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
75	c3gpvA_	Alignment	not modelled	7.6	5	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
76	d2g7la1	Alignment	not modelled	7.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
77	d2b7ta1	Alignment	not modelled	7.5	16	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
78	d2iw5b1	Alignment	not modelled	7.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
79	d2csba1	Alignment	not modelled	7.4	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain

80	c3ol0C_	Alignment	not modelled	7.3	18	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
81	c1yd2A_	Alignment	not modelled	7.3	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrc from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
82	c2eqrA_	Alignment	not modelled	7.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear receptor corepressor 1; **PDBTitle:** solution structure of the first sant domain from human2 nuclear receptor corepressor 1
83	d1xc5a1	Alignment	not modelled	7.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
84	c2k4zA_	Alignment	not modelled	7.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dsrr; **PDBTitle:** solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
85	d1j6xa_	Alignment	not modelled	6.8	18	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
86	c2j8pA_	Alignment	not modelled	6.7	33	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
87	c1qu6A_	Alignment	not modelled	6.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase pkr; **PDBTitle:** structure of the double-stranded rna-binding domain of the2 protein kinase pkr reveals the molecular basis of its3 dsrna-mediated activation
88	d1wi9a_	Alignment	not modelled	6.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
89	d1bb8a_	Alignment	not modelled	6.5	23	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**DNA-binding domain from tn916 integrase
90	c2l3jA_	Alignment	not modelled	6.4	22	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**double-stranded rna-specific editase 1; **PDBTitle:** the solution structure of the adar2 dsrbm-rna complex reveals a2 sequence-specific read out of the minor groove
91	d1vmha_	Alignment	not modelled	6.4	17	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
92	c2ae3A_	Alignment	not modelled	6.3	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
93	d2hsga1	Alignment	not modelled	6.2	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
94	d1vz0a1	Alignment	not modelled	6.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
95	d1zk8a1	Alignment	not modelled	6.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
96	c3lgbB_	Alignment	not modelled	6.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna primase large subunit; **PDBTitle:** crystal structure of the fe-s domain of the yeast dna primase
97	d1j6wa_	Alignment	not modelled	6.1	24	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
98	d1efaa1	Alignment	not modelled	6.1	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
99	d2g39a2	Alignment	not modelled	6.1	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like