

# Skinny 63560-63949 HHPred alignments

1. **d1m5xa\_d.95.2.1 (A:) DNA endonuclease I-MsoI {Monomastix sp. ci-1997 [TaxId: 141716]}**  
Probability: 99.88%, E-value: 1e-20, Score: 124.19, Aligned cols: 125, Identities: 20%, Similarity: 0.28, Template\_Neff: 8.9

```
Q ss_pred      chHHhhheeeceEEEEe--CC--C-CCeEEEEEECCCCcCHHHHHHHHHHC--CEEEeC--CCeEEEEeChHH-
Q Q_4283447   2  DLAYLGGFFDGEIVGLYK--SG--G-ESPRLRVQVFQNHGASQDRMLMHEIHDTFG--GTLHDR--GTGYLYSASGSR- 71 (130)
Q Consensus   2  ~~~~l~Gf~D~eG~i~~~~i~~~~~l~~~~i~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l 71 (130)
T Consensus   6  ..+||+||+||+||+||+.. . . . .+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+ 85 (161)
T d1m5xa_     6  EAAFYIAGFLDGDGIYAKLIPRPDYKDIKYQLAISFIQRKDKFPYLQDIYDQLGKGNLRKDRGDGIADYTIIGSTHL 85 (161)
T ss_dssp     HHHHHHHHHHHHEEEEEEEECCTSSSSCEEEEEEEEEEGGGHHHHHHHHHTTSCSEEECCSSSEEEEEEEESHHHH
T ss_pred     cHHHHHHHccceEEEEEEcCCCCcCEEEEEEEcCCHHHHHHHHHHCcCEEEeCCCEEEEEChHH
```

Q ss\_pred HHHHHHHHHHHcccHHHHHHHHHHCCcCCCCcCHHHHHHHHHHHHHHHHHcC  
Q Q\_4283447 72 VDLLTLQRPHLRLKLEQADEALEWRNRTAERFRSRTAEVAYDESAMTRLKELKRA 129 (130)  
Q Consensus 72 ~~~~l~~~~~k~~~~~k~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l 129 (130)  
T Consensus 86 ..+ 140 (161)  
T d1m5xa\_ 86 SIILPDLVPYLRIKKKQANRILHIINLVPQA---QKNPSKFLDLVKIVDDVQNLKRA 140 (161)  
T ss\_dssp HHHHHHTTTCSTTHHHHHHHHHHHHHHH---TCHHHHHHHHHHHHHHHHTSCT  
T ss\_pred HHHHHHchhhccHHHHHHHHHHHHhhc---CCCHHHHHHHHHHHHHHHhhcccC

[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

2. **1AF5\_A I-CREI; ENDONUCLEASE, GROUP I MOBILE INTRON, INTRON HOMING, CHLOROPLAST DNA, LAGLIDAG MOTIF; 3.0A {Chlamydomonas reinhardtii} SCOP: d.95.2.1**  
Probability: 99.86%, E-value: 1.1e-19, Score: 115.57, Aligned cols: 123, Identities: 24%, Similarity: 0.333, Template\_Neff: 10

```
Q ss_pred      chHHhhheeeceEEEEeC---CCCCeEEEEEECCCCcCHHHHHHHHHHC--CEEEeCCeEEEEeChHH--HHH
Q Q_4283447   2  DLAYLGGFFDGEIVGLYK--S---GGESPRLRVQVFQNHGASQDRMLMHEIHDTFG--GTLHDRGTGYLYSASGSR-VDLL 75 (130)
Q Consensus   2  ~~~~l~Gf~D~eG~i~~~~i~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l 75 (130)
T Consensus   6  +..+||+||+||+||+||+.. . . . .+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+..+ 85 (135)
T 1AF5_A      6  FLLYLAFVFDGDSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLGKLVDEIGVG YVRDRGSVSDYILSEIKPLHNF 85 (135)
T ss_dssp     SHHHHHHHHSCEEEEEECCSSSSSCEEEEEEECCBGGGGHHHHHHHHHCSCCEEEETEEEECCSHHHHHHHH
T ss_pred     HHHHHHHhccCeEEEEEEcCCCCcCEEEEEEEcCccHHHHHHHHHCCEEEeCCeEEEEcChHHHHHHH
```

Q ss\_pred HHHHHHcccHHHHHHHHHHcCccccCCCHHHHHHHHHHHHHHHHH  
Q Q\_4283447 76 TQLRPHRLRLKLEQADEALEWRNRTAERFRSRTAEVAYDESAMTRLKELKR 127 (130)  
Q Consensus 76 ~~~~k~~~~~k~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l 127 (130)  
T Consensus 86 +.. 134 (135)  
T 1AF5\_A 86 TQLQPFLKQLKQKANLVKIIQPLPS---AKESPDKFLEVCTWVDQIAALND 134 (135)  
T ss\_dssp HHGGCSSSHHHHHHHHTSccc-----cCTTCHHHHTCSCSC  
T ss\_pred HHHHHHcccHHHHHHHHHHc---cCCHHHHHHHHHHHHHhhcc

## Variation in LAGLIDAG motif

Table 1.  
Double-motif LAGLIDAG sequence analysis<sup>a</sup>

1	2	3	4	5	6	7	8	9	10
X	L	A	G	L	I	D	A	D	G
			G	x	x	x	G		
X	X	X	A	F	X	X	A	D	A
			G	I			D	E	G
			S	L			G		
			T	W			S		
				Y			T		

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<sup>a</sup>Alignment of the LAGLIDAG and GxxxG motifs with the query pattern (bottom) used to produce a dataset of 131 unique putative double-motif LAGLIDAG proteins representing a total of 262 helices.

Here are a couple of references for LAGLIDADG endonuclease:  
Lucas et al. 2001 doi: 10.1093/nar/29.4.960  
Silva and Belfort 2004 doi: 10.1093/nar/gkh618


## Pham View

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Starterator Report

Gene List w Locus Tags

Details for Pham 9924					
Number	9924				
Color					
Number of Members	4				
Members of Pham 9924					
Gene	Phage	Accession	Notes	Cluster	Length
Forrest_188	Forrest	MZ820093	LAGLIDADG endonuclease	BK	327 bp
Jada_185	Jada	MZ820094	LAGLIDADG endonuclease	BK	327 bp
Pumpnickel_170	Pumpnickel	OK040790	homing endonuclease	Singleton	426 bp
Skinny_Draft_118	Skinny			M	390 bp