



Standard & Generalized

# McDonald-Kreitman Test



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## Your MKT Results

Comparison Number:	Neutral Region:	Testing Region:	<u>Counts correspond to SITES/CHANGES:</u>
<a href="#">Comparison 1</a>	1 (synonymous)	1 (non-synonymous)	Changes

**Genetic code:** Universal Code

### INPUT SEQUENCES for Region 1:

Number of Sequences for Species 1: 4

Number of Sequences for Species 2: 2

Length of the Alignment: 399

Percentage of gaps within the alignment (excluding end gaps): -15.0 %

### View Alignment for Region 1

(Sequences have the same order as input. Alignments generated by muscle)

FASTA format: [120628.1.fas](#)

Alignment from species 1: [120628.1.1.txt](#)

Alignment from species 2: [120628.1.2.txt](#)

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**SEE RESULTS:** ☐ Divergence corrected by Jukes&Cantor ☒ Without any correction for divergence

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### Comparison 1:

**NEUTRAL REGION: 1 (synonymous)**

**TESTING REGION: 1 (non-synonymous)**

**CHANGES**

### Contingency table:

	Polymorphism	Divergence	TOTAL
Neutral	0		0
Non-Neutral	0		0
TOTAL	0	0	0

### Estimates:

Neutrality Index (NI): NULL

Proportion of adaptive substitutions ( $\alpha$ ): NULL

$\chi^2$  value: NULL

p-value: NULL

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