Your MKT Results

Comparison Number:	Neutral Region:	Testing Region:	Counts correspond to SITES/CHANGES:
Comparison 1	1 (synonymous)	1 (non-synonymous)	Changes

Genetic code: Universal Code

INPUT SEQUENCES for Region 1:

Number of Sequences for Species 1: 2
Number of Sequences for Species 2: 2

Length of the Alignment: 399
Percentage of gaps within the alignment (excluding end gaps): 0.0%

View Alignment for Region 1
(Sequences were already aligned)

Input Sequences: 120376.1.txt

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	**3**	**5.17**	8.17
Non-Neutral	**0**	**5.05**	5.05
TOTAL	3	10.22	13.22

Estimates:

Neutrality Index (NI) Jukes&Cantor: 0.000
Proportion of adaptive substitutions (α) Jukes&Cantor: 1.000

χ^2 value Jukes&Cantor: 2.398
p-value Jukes&Cantor: 0.121