

Table S3. Evaluation of the evolutionary selective pressure acting on ENDOV. Ratio of amino acid replacing (K_a) and silent (K_s) mutation rates for pairwise comparisons of the endonuclease V core regions and C-terminal tails from mouse (GenBank [1] identifier NM_001164636), rat (Ensembl [2] transcript ENSRNOT0000054986) and hamster (XM_003496871) *ENDO V*. These species were selected for analysis because the mRNAs are processed by identical splicing of the same nine exons in the three rodents, simplifying analysis. K_s is the number of synonymous substitutions per synonymous site and K_a is the number of amino acid changing substitutions per non-synonymous site [3]. The calculation of the K_a/K_s ratio is a powerful tool for evaluating evolutionary selective pressure, with $K_a/K_s < 1$ indicating purifying (negative) selection, while $K_a/K_s \sim 1$ is indicating neutral evolution of the protein segment.

	K_a/K_s^a	
	<i>Mm</i> ENDOV core	<i>Rn</i> ENDOV core
<i>Rn</i> ENDOV core	0.129 (0.123)	
<i>Cg</i> ENDOV core	0.233 (0.230)	0.214 (0.210)

	K_a/K_s^b	
	<i>Mm</i> ENDOV C-term	<i>Rn</i> ENDOV C-term
<i>Rn</i> ENDOV C-term	1.424 (1.457)	
<i>Cg</i> ENDOV C-term	1.087 (1.137)	1.752 (1.880)

^a K_a/K_s ratios for pairwise comparisons of ENDOV from mouse (*Mm*), rat (*Rn*), and Chinese hamster (*Cg*) for the core region (residues 1-250) calculated according to the model of Goldman and Yang [4] and the model averaging method of Zhang *et al.* (in parenthesis) [5] with the KaKs_Calculator [6].

^b K_a/K_s ratios for pairwise comparisons of the C-terminal segments (codon 251 – stop) of ENDOV for the three rodents calculated as described above. Sites corresponding to insertions/deletions were removed.

Supporting Table S3 Reference List

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2. Flicek P, Amode MR, Barrell D, Beal K, Brent S, *et al.* (2012) Ensembl 2012. Nucleic Acids Res 40: D84-D90.

3. Hurst LD (2002) The *Ka/Ks* ratio: diagnosing the form of sequence evolution. *Trends Genet* 18: 486-487.
4. Goldman N and Yang Z (1994) A codon-based model of nucleotide substitution for protein-coding DNA sequences. *Mol Biol Evol* 11: 725-736.
5. Zhang Z, Li J, Zhao XQ, Wang J, Wong GK, Yu J (2006) KaKs_Calculator: calculating *Ka* and *Ks* through model selection and model averaging. *Genomics Proteomics Bioinformatics* 4: 259-263.
6. Wang D, Zhang Y, Zhang Z, Zhu J, Yu J (2010) KaKs_Calculator 2.0: a toolkit incorporating gamma-series methods and sliding window strategies. *Genomics Proteomics Bioinformatics* 8: 77-80.