Table 1: Results of the evolutionary analyses for positively selected sites for Mx1 in bats. P-values were achieved by performing chi-squared tests on twice the difference of the computed log likelihood values of the models disallowing (M7) or allowing (M8) $dN/dS > 1$. The BEB column lists rapidly evolving sites with a $dN/dS > 1$ and a posterior probability > 0.95, determined by the Bayes Empirical Bayes implemented in `Codeml`. Amino acids refer to *Myotis daubentonii*. Note that INDELs and the stop codon were removed from the alignment prior to evolutionary analysis, so shown positions are based on the **alignment without gaps**. Fragments arising from insignificant breakpoints (adjusted p-value $>$ 0.1) are marked with an asterisk.

Region	**M7 vs M8** (χ^2)	**M7 vs M8** p-value	**% sites with** $\omega > 1$	**avg(ω)**	**M8 BEB** ($PP > 0.95$/ $> \mathbf{0.99}$)
F61					
full (aa 1–649)	82.85	< 0.001	8.06	2.75	L120; D123; R187; A191; S343; R415; **D418**; F421; **R425**; S541; **E544**; S547; **L548**; Q549; **Q550**; **T551**; S552; S553; A555; D556; **T558**
frag1* (aa 1–90)	17.01	< 0.001	38.07	1.92	**A4**; T5; D7; **P9**; **S12**; H13; P14; G18; G23; **L25**; E26; **L28**; **N30**; S31; Q35
frag2* (aa 91–183)	0.39	0.821	NA	NA	NA
frag3* (aa 184–649)	82.48	< 0.001	8.1	3.0	A191; D418; **R425**; E544; S547; **L548**; **Q550**; T551; S552; S553; D556; **T558**
F1X4					
full (aa 1–649)	76.34	< 0.001	7.05	2.79	R187; D418; F421; R425; E544; **L548**; **Q550**; T551; S552; S553; D556; T558
frag1* (aa 1–90)	20.33	< 0.001	31.04	2.12	**A4**; T5; **D7**; **P9**; **S12**; H13; P14; G18; G23; L25; E26; **L28**; **N30**; S31; Q35
frag2* (aa 91–183)	0.09	0.956	NA	NA	NA
frag3* (aa 184–649)	84.88	< 0.001	7.76	3.02	R187; D418; F421; R425; E544; **L548**; **Q550**; T551; **S552**; **S553**; D556; **T558**
F3X4					
full (aa 1–649)	101.39	< 0.001	6.26	3.45	R187; A191; S343; F421; R425; T476; A531; E544; S547; **L548**; **Q550**; T551; S552; **S553**; D556; **T558**
frag1* (aa 1–90)	24.05	< 0.001	21.3	2.76	**A4**; T5; D7; **P9**; A10; **S12**; H13; P14; **G18**; G23; L25; **L28**; N30
frag2* (aa 91–183)	0.19	0.908	NA	NA	NA
frag3* (aa 184–649)	112.69	< 0.001	6.59	3.83	**R187**; A191; **S343**; D418; F421; R425; T476; A531; E544; S547; **L548**; **Q550**; T551; **S552**; **S553**; D556; **T558**