

Table 2. Log-likelihood values and parameter estimates (ω , p , and n) for *pro*, *rt* and *env* in each twin.
 LnL = Likelihood values; ω = estimate of dN/dS (ω_{M2} and ω_{M8}); p = proportion of sites under diversifying selection (p_{M2} and p_{M8});
 PSS = number of positively selected sites with a posterior probability > 0.95 (PSS_{M2} and PSS_{M8}). All comparisons between
 nested models (M1 vs M2, and M7 vs M8) were significant.

	Genes	LnL _{M1}	LnL _{M2}	ω_{M2}	p_{M2}	PSS _{M2}	LnL _{M7}	LnL _{M8}	ω_{M8}	p_{M8}	PSS _{M8}
Twin A	<i>pro</i>	-634.3	-634.3	1	0	0	-634.3	-634.2	1	0	0
	<i>rt</i>	-1098	-1098	1	0	0	-1097.9	-1097.9	1	0	0
	<i>env</i>	-3552.5	-3526.5	3.6	0.19	11	-3553.4	-3526.6	3.3	0.25	13
Twin B	<i>pro</i>	-666.7	-666.7	1	0	0	-666.7	-666.7	1	0	0
	<i>rt</i>	-1444	-1441.8	5.8	0.02	1	-1444.1	-1441.7	5.4	0.02	1
	<i>env</i>	-3040.5	-3039.4	1	0	0	-3041	-3039.4	1	0	0