**Table S2. Log-likelihood values and parameter estimates for the *sidJ* gene of *L. pneumophila* using unmodified topology tree of the alleles.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Model | *nP* | *lnL* | Estimates of parameters | LRT P-value | Positively sites |
| M3 (discrete) | 81 | -8714.6954 | p0=0.7795, p1=0.2133, p**2=0.00723**, ω0=0.01729,ω1=0.7069, **ω2=3.7116** | P <10-9 | **58G\*\*\***, 200N\*, 868T\*, 869S\* |
| M0 (one ratio) | 77 | -8863.1637 | ω0=0.1732 | Not Allowed |
| M2a (selection) | 80 | -8717.1477 | p0=0.8370, p1=0.1587, **p2=0.00431**, ω0=0.03499, ω1=1.00000, **ω2=4.5150** | P =0.011129923 | **N/A** |
| M1a (neutral) | 78 | -8721.6458 | p0=0.8375, p1=0.1625ω0=0.03404, ω1=1.0000 | Not Allowed |
| M8a (beta&ω) | 80 | -8718.3447 | p0=0.9844, p=0.03938, q=0.1953**p1=0.0156, ω=2.7132** | P =0.000000637 | **58G\*\*, 200N\*\*,** 868T\***, 869S\*\*** |
| M7 (beta) | 78 | -8732.6114 | p=0.03809, q=0.17020 | Not Allowed |

*P* is the number of parameters in the ω distribution; lnL is the log likelihood; ω is ratio of *dN*/*dS*, LRT P-value indicates the value of chi-square test; Parameters indicating positive selection are presented in bold; Positive selection sites were identified by the Bayes empirical Bayes (BEB) methods under M8 model or by Naive Empirical Bayes (NEB) methods under M3 and M2a models. The posterior probabilities(p)≥0.90, (p)≥0.95 and p≥0.99 are indicated by \*, \*\* and \*\*\*, respectively. Yang *et al.* recommended that results from M8 model were preferred to find sites under positive selection pressure, and it is more robust to recombination which was proved by Maria et al.