| *Enzyme* | *Energy terms (kcal.mol* -1*)* |
| --- | --- |
| *E. coli* dimer | *∆HMM* | -203.5 (50.1) | *∆Gsolv* | 97.9 (19.7) | *∆Gbind* | -125.8 (36.2) |
| *∆HCoulomb* | -76.2 (45.8) | *∆Gsolv-pol* | 113.6 (20.0) |  |  |
| *∆HvdW* | -127.3 (12.5) | *∆Gsolv-np* | -15.8 (1.2) |  |  |
|  |  |  |  |  |  |  |
| MR*SA* | *∆HMM* | -431.0 (110.5) | *∆Gsolv* | 121.1 (25.5) | *∆Gbind* | -309.9 (120.7) |
| *∆HCoulomb* | -302.1 (110.4) | *∆Gsolv-pol* | 138.3 (26.1) |  |  |
| *∆HvdW* | -128.9 (19.2) | *∆Gsolv-np* | -17.2 (1.4) |  |  |

**Table S1.** Binding energies and their components at the beginning of the simulations. Values are averaged over two simulations for each enzyme. Standard deviations are given in brackets.