## Supporting information

## On the parallelism between the mechanisms behind chromatography

## and drug delivery: the role of interactions with stationary phase

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**Figure S1.** Free energy of dimerization of protonated IP molecules obtained from simulation S2. (*Top left*) Free Energy Surface (FES) as a function of the CVs used to enhance the sampling through WTmetaD. (*Top right*) FES error in the space of CVs evaluated as the standard deviation of the time-independent estimator of the free energy in the CVs space. (*Bottom-left*) Free energy difference between dissociated and dimer-like states as a function of simulation time. (*Bottom-right*) Equilibrium probabilities of undissociated and dissociated states.



**Figure S2.** Free energy of dimerization of protonated IP molecules obtained from simulation S3. (*Top left*) Free Energy Surface (FES) as a function of the CVs used to enhance the sampling through WTmetaD. (*Top right*) FES error in the space of CVs evaluated as the standard deviation of the time-independent estimator of the free energy in the CVs space. (*Bottom-left*) Free energy difference between dissociated and dimer-like states as a function of simulation time. (*Bottom-right*) Equilibrium probabilities of undissociated and dissociated states.