## Supporting information for: Thermodynamics of the binding of lysozyme to a dendritic polyelectrolyte: Electrostatics vs. hydration

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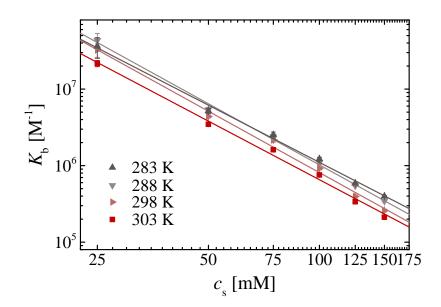


Figure S1: The salt dependence of binding constant for dPGS-Lys interaction at different temperatures. The number of released counterions  $\Delta N_{\rm ci}$  is 2.5±0.1, 2.7±0.1, 2.7±0.1, and 2.5±0.1 for 283 K, 288 K, 298 K, and 303 K, respectively.

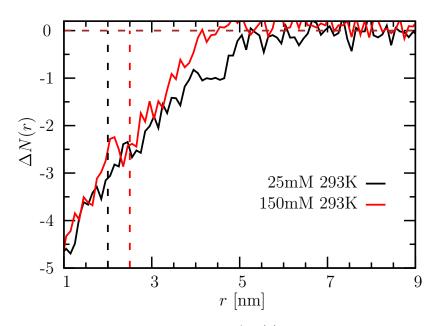


Figure S2: The decrease of condensed counterions  $\Delta N(r)$  on the dPGS surface upon binding with lysozyme according to computer simulations. r denotes the center-of-mass distance between dPGS and the first bound lysozyme. The number of released counterions can be read off at the distance  $r_{\rm b}$  found with the bound state (dashed lines).  $\Delta N(r_{\rm b})$  is 3.0 at  $r_{\rm b}=2.0$  nm, and 2.5 at  $r_{\rm b}=2.5$  nm.

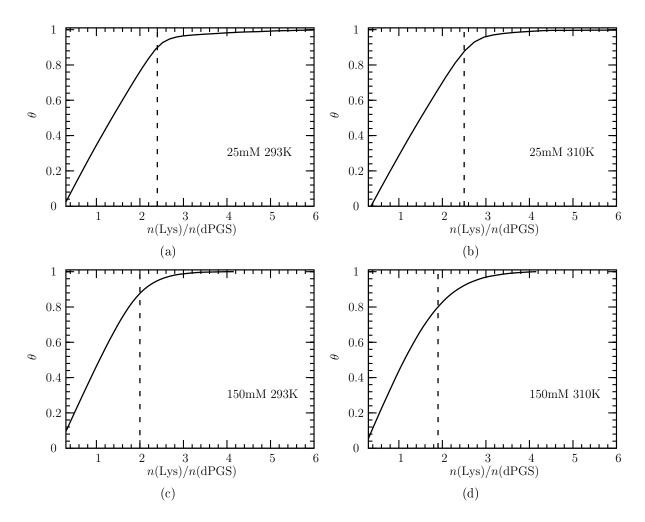


Figure S3: The protein coverage  $\theta$  as a function of the molar ratio n(Lys)/n(dPGS) in ITC measurements at different ionic strengths and temperatures.  $\theta$  are plotted according to previous deviations (see the SI in ref.<sup>S1</sup>). Each dashed line denotes the inflection point (binding number N) in the respective ITC isotherm. The intersection points with  $\theta$  refer to the coverage  $\theta^*$  at the inflection points.

## References

(S1) Xu, X.; Ran, Q.; Dey, P.; Nikam, R.; Haag, R.; Ballauff, M.; Dzubiella, J. Counterionrelease entropy governs the inhibition of serum proteins by polyelectrolyte drugs. *Biomacromolecules* 2018, 19, 409–416.