Computational studies of influenza hemagglutinin

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List of publications

1. Boonstra S, Onck PR, van der Giessen E. 2016. CHARMM TIP3P water model suppresses peptide folding by solvating the unfolded state. *J. Phys. Chem. B* 120:3692–3698.

2. Blijleven JS, Boonstra S, Onck PR, van der Giessen E, van Oijen AM. 2016. Mechanisms of influenza viral membrane fusion. *Semin. Cell Dev. Biol.* 60:78–88.

3. Boonstra S, Onck PR, van der Giessen E. 2017. Computation of hemagglutinin free energy difference by the confinement method. *J. Phys. Chem. B* Accepted.

4. Boonstra S, Blijleven JS, Roos WH, Onck PR, van der Giessen E, van Oijen AM. Hemagglutinin-mediated membrane fusion: A biophysical perspective. *Annu. Rev. Biophys.* Submitted.

5. Boonstra S, Blijleven JS, Ivanovic T, Onck PR, van Oijen AM, van der Giessen E. Critical interactions in the globular bottom of influenza hemagglutinin. In preparation.