

List of Publications

Dr. Jožica Dolenc

2016

van Gunsteren WF, Allison JR, Daura X, Dolenc J, Hansen N, Mark AE, Oostenbrink C, Rusu VH, Smith LJ.

Deriving structural information from experimentally measured data on biomolecules.
Angew. Chem. Int. Ed. 2016; 55:2-23.

Smith LJ, Rought Whitta G, Dolenc J, Wang D, van Gunsteren WF.

A molecular dynamics simulation investigation of the relative stability of the cyclic peptide octreotide and its deprotonated and its (CF₃)-Trp substituted analogs in different solvents.

Bioorg. Med. Chem. 2016; 24:4936-4948.

Horta BAC, Merz PT, Fuchs PFJ, Dolenc J, Riniker S, Hünenberger PH.

A GROMOS-compatible force field for small organic molecules in the condensed phase: the 2016H66 parameter set.

J. Chem. Theory Comput. 2016; 12: 3825-3850.

Dolenc J, Meier BH, Rusu VH, van Gunsteren WF.

Investigation of the structural preference and flexibility of the loop residues in amyloid fibrils of the HET-s prion.

Phys. Chem. Chem. Phys. 2016; 18:5860-5866.

Dolenc J, Renn O.

Vermittlung von Informatonskompetenz à la carte im Informationszentrum Chemie | Biologie | Pharmazie der ETH Zürich.

Bibliothek - Forschung und Praxis. 2016; 40:78-82.

2015

Torbееv V, Ebert MO, Dolenc J, Hilvert, D.

Substitution of proline32 by α -methylproline preorganizes β 2-microglobulin for oligomerization but not for aggregation into amyloids.

J. Am. Chem. Soc. 2015; 137:2524-2535.

2014

Bachmann SJ, Lin Z, Stafforst T, van Gunsteren WF, Dolenc J.

On the sensitivity of peptide nucleic acid duplex formation and crystal dissolution to a

variation of force-field parameters.
J. Chem. Theor. Comp. 2014; 10:391-400.

2013

Pechlaner M, Sigel RKO, van Gunsteren WF, Dolenc J.
Structure and conformational dynamics of the domain 5 RNA hairpin of a bacterial group II intron revealed by solution NMR and molecular dynamics simulations.
Biochemistry. 2013; 52:7099-7113.

Bachmann SJ, Dolenc J, van Gunsteren WF.
On the use of one-step perturbation to investigate the dependence of different properties of liquid water upon a variation of model parameters from a single simulation.
Mol. Phys. 2013; 111:2334-2344.

Wang D, Böckmann A, Dolenc J, Meier BH, van Gunsteren WF.
On the behavior of water at subfreezing temperatures in a protein crystal: evidence of higher mobility than in bulk water
J. Phys. Chem. B. 2013; 117:11433-11447.

Choutko A, Eichenberger AP, van Gunsteren WF, Dolenc J.
Exploration of swapping enzymatic function between two proteins: a simulation study of chorismate mutase and isochorismate pyruvate lyase.
Protein Sci. 2013; 22:809-822.

Meier K, Choutko A, Dolenc J, Eichenberger AP, Riniker S, van Gunsteren WF.
Multi-resolution simulation of biomolecular systems: a review of methodological issues.
Angew. Chem. Int. Ed. 2013; 52:2820-2834.

2012

Missimer JH, Steinmetz MO, van Gunsteren WF, Dolenc J.
Influence of 63Ser phosphorylation and dephosphorylation on the structure of the stathmin helical nucleation sequence: A molecular dynamics study.
Biochemistry. 2012; 51:8455-8463.

Wang D, Freitag F, Gattin Z, Haberkern H, Jaun B, Siwko M, Vyas R, van Gunsteren WF, Dolenc J.
Validation of the GROMOS 54A7 force field regarding mixed α/β peptide molecules.
Helvetica Chimica Acta. 2012; 95:2562-2577.

Allison J, Hertig S, Missimer JH, Smith L, Steinmetz MO, Dolenc J.
Probing the structure and dynamics of proteins by combining molecular dynamics simulations and experimental NMR data.
J. Chem. Theory. Comput. 2012; 8:3430-3444.

Hansen N, Dolenc J, Knecht M, Riniker S, van Gunsteren WF.
Assessment of enveloping distribution sampling to calculate relative free enthalpies of binding for eight netropsin-DNA duplex complexes in aqueous solution.
J. Comput. Chem. 2012; 33:640-651.

van Gunsteren WF, Dolenc J.
Thirty-five years of biomolecular simulation: development of methodology, force fields, software.
Molecular Simulation. 2012; 38:1271-1281.

2011

Dolenc J, Riniker S, Gaspari R, Daura X, van Gunsteren WF.
Free energy calculations offer insights into the influence of receptor flexibility on ligand-receptor binding affinities.
J. Comput. Aided Mol. Des. 2011; 25:709-716.

Eichenberger AP, Allison JR, Dolenc J, Geerke DP, Horta BAC, Meier K, Oostenbrink C, Schmid N, Steiner D, Wang D, van Gunsteren WF.
The GROMOS++ software for the analysis of biomolecular simulation trajectories.
J. Chem. Theory. Comput. 2011; 7:3379-3390.

Schmid N, Allison JR, Dolenc J, Eichenberger AP, Kunz APE, van Gunsteren WF.
Biomolecular structure refinement using the GROMOS simulation software.
J. Biomol. NMR 2011; 51:265-281.

2010

Dolenc J, Missimer JH, Steinmetz MO, van Gunsteren WF.
Methods of NMR structure refinement: molecular dynamics simulations improve the agreement with measured NMR data of a C-terminal peptide of GCN4-p1.
J. Biomol. NMR. 2010; 47:221-235.

Missimer JH, Dolenc J, Steinmetz MO, van Gunsteren WF.
Exploring the trigger sequence of the GCN4 coiled-coil: Biased molecular dynamics resolves apparent inconsistencies in NMR measurements.
Protein Sci. 2010; 19:2462-2474.

2008

Dolenc J, Baron R, Missimer JH, Steinmetz MO, van Gunsteren WF.
Exploring the conserved water site and hydration of a coiled-coil trimerisation motif: A MD simulation study.
ChemBioChem. 2008; 9:1749-1756.

van Gunsteren WF, Dolenc J.
Biomolecular simulation: historical picture and future perspectives.
Biochem. Soc. Trans. 2008; 36:11-15.

van Gunsteren WF, Dolenc J, Mark AE.
Molecular simulation as an aid to experimentalists.
Curr. Opin. Struct. Biol. 2008; **18**:149-153.

2006

Vlachy N, Dolenc J, Jerman B, Kogej K.
Influence of stereoregularity of the polymer chain on interactions with surfactants: binding of cetylpyridinium chloride by isotactic and atactic poly(methacrylic acid).
J. Phys. Chem. B. 2006; 110:9061-9071.

Dolenc J, Baron R, Oostenbrink C, Koller J, van Gunsteren WF.
Configurational entropy change of netropsin and distamycin upon DNA minor-groove binding.
Biophys. J. 2006; 91:1460-1470.

Dolenc J, Koller J.
An improved semiempirical MO PM3 method for hydrogen bonded systems.
Acta Chim. Slov. 2006; 53:229-237.

2005

Dolenc J, Borštnik U, Hodošek M, Koller J, Janežič D.
An ab initio QM/MM study of the conformational stability of the complexes formed by netropsin and DNA. The importance of van der Waals interactions and hydrogen bonding.
J. Mol. Struct: THEOCHEM. 2005; 718:77-85.

Dolenc J, Oostenbrink C, Koller J, van Gunsteren WF.
Molecular dynamics simulations and free energy calculations of netropsin and distamycin binding to an AAAAA DNA binding site.
Nucleic Acids Res. 2005; 33:725-733.