

# Oliver F Lange

## List of Publications by Citations

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38  
papers

5,346  
citations

27  
h-index

38  
g-index

38  
ext. papers

6,020  
ext. citations

8.1  
avg, IF

5.07  
L-index

#	Paper	IF	Citations
38	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. <i>Methods in Enzymology</i> , <b>2011</b> , 487, 545-74	1.7	1216
37	Recognition dynamics up to microseconds revealed from an RDC-derived ubiquitin ensemble in solution. <i>Science</i> , <b>2008</b> , 320, 1471-5	33.3	872
36	Consistent blind protein structure generation from NMR chemical shift data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 4685-90	11.5	665
35	Structure prediction for CASP8 with all-atom refinement using Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 77 Suppl 9, 89-99	4.2	342
34	Generalized correlation for biomolecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 62, 1053-61	4.2	278
33	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. <i>Nature</i> , <b>2011</b> , 477, 111-4	50.4	225
32	NMR structure determination for larger proteins using backbone-only data. <i>Science</i> , <b>2010</b> , 327, 1014-8	33.3	220
31	Scrutinizing molecular mechanics force fields on the submicrosecond timescale with NMR data. <i>Biophysical Journal</i> , <b>2010</b> , 99, 647-55	2.9	175
30	Determination of solution structures of proteins up to 40 kDa using CS-Rosetta with sparse NMR data from deuterated samples. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 10873-8	11.5	151
29	Full correlation analysis of conformational protein dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 1294-312	4.2	108
28	Stereochemistry of sagittamide A from residual dipolar coupling enhanced NMR. <i>Journal of the American Chemical Society</i> , <b>2007</b> , 129, 15114-5	16.4	96
27	Self-consistent residual dipolar coupling based model-free analysis for the robust determination of nanosecond to microsecond protein dynamics. <i>Journal of Biomolecular NMR</i> , <b>2008</b> , 41, 139-55	3	90
26	Collective Langevin dynamics of conformational motions in proteins. <i>Journal of Chemical Physics</i> , <b>2006</b> , 124, 214903	3.9	89
25	Can principal components yield a dimension reduced description of protein dynamics on long time scales?. <i>Journal of Physical Chemistry B</i> , <b>2006</b> , 110, 22842-52	3.4	78
24	Blind testing of routine, fully automated determination of protein structures from NMR data. <i>Structure</i> , <b>2012</b> , 20, 227-36	5.2	64
23	A mechanism for the auto-inhibition of hyperpolarization-activated cyclic nucleotide-gated (HCN) channel opening and its relief by cAMP. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 22205-20	5.4	57
22	Resolution-adapted recombination of structural features significantly improves sampling in restraint-guided structure calculation. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 884-95	4.2	57

21	Determination of the structures of symmetric protein oligomers from NMR chemical shifts and residual dipolar couplings. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 6288-98	16.4	55
20	Kinetics of conformational sampling in ubiquitin. <i>Angewandte Chemie - International Edition</i> , <b>2011</b> , 50, 11437-40	16.4	54
19	Estimating absolute configurational entropies of macromolecules: the minimally coupled subspace approach. <i>PLoS ONE</i> , <b>2010</b> , 5, e9179	3.7	53
18	Flooding in GROMACS: accelerated barrier crossings in molecular dynamics. <i>Journal of Computational Chemistry</i> , <b>2006</b> , 27, 1693-702	3.5	53
17	Structure of the BamC two-domain protein obtained by Rosetta with a limited NMR data set. <i>Journal of Molecular Biology</i> , <b>2011</b> , 411, 83-95	6.5	39
16	Evaluation and optimization of discrete state models of protein folding. <i>Journal of Physical Chemistry B</i> , <b>2012</b> , 116, 11405-13	3.4	37
15	Prediction of structures of zinc-binding proteins through explicit modeling of metal coordination geometry. <i>Protein Science</i> , <b>2010</b> , 19, 494-506	6.3	36
14	Improved chemical shift based fragment selection for CS-Rosetta using Rosetta3 fragment picker. <i>Journal of Biomolecular NMR</i> , <b>2013</b> , 57, 117-27	3	34
13	Residual dipolar couplings as a tool to study molecular recognition of ubiquitin. <i>Biochemical Society Transactions</i> , <b>2008</b> , 36, 1433-7	5.1	34
12	A hybrid NMR/SAXS-based approach for discriminating oligomeric protein interfaces using Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 309-17	4.2	30
11	Molecular dynamics simulations of protein G challenge NMR-derived correlated backbone motions. <i>Angewandte Chemie - International Edition</i> , <b>2005</b> , 44, 3394-9	16.4	24
10	Improving 3D structure prediction from chemical shift data. <i>Journal of Biomolecular NMR</i> , <b>2013</b> , 57, 27-35		23
9	Robust and highly accurate automatic NOESY assignment and structure determination with Rosetta. <i>Journal of Biomolecular NMR</i> , <b>2014</b> , 59, 135-45	3	22
8	Adaptive anisotropic kernels for nonparametric estimation of absolute configurational entropies in high-dimensional configuration spaces. <i>Physical Review E</i> , <b>2009</b> , 80, 011913	2.4	19
7	Combining Evolutionary Information and an Iterative Sampling Strategy for Accurate Protein Structure Prediction. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004661	5	15
6	Automatic NOESY assignment in CS-RASREC-Rosetta. <i>Journal of Biomolecular NMR</i> , <b>2014</b> , 59, 147-59	3	11
5	A Framework to Simplify Combined Sampling Strategies in Rosetta. <i>PLoS ONE</i> , <b>2015</b> , 10, e0138220	3.7	10
4	Kinetics of Conformational Sampling in Ubiquitin. <i>Angewandte Chemie</i> , <b>2011</b> , 123, 11639-11642	3.6	6

3	Systematic evaluation of CS-Rosetta for membrane protein structure prediction with sparse NOE restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2017</b> , 85, 812-826	4.2	4
2	Regulatory Implications of Non-Trivial Splicing: Isoform 3 of Rab1A Shows Enhanced Basal Activity and Is Not Controlled by Accessory Proteins. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 1544-57	6.5	3
1	Molecular Dynamics Simulations of Protein G Challenge NMR-Derived Correlated Backbone Motions. <i>Angewandte Chemie</i> , <b>2005</b> , 117, 3460-3465	3.6	1