Oliver F Lange

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Systematic evaluation of CS-Rosetta for membrane protein structure prediction with sparse NOE restraints. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 812-826	4.2	4
37	Regulatory Implications of Non-Trivial Splicing: Isoform 3 of Rab1A Shows Enhanced Basal Activity and Is Not Controlled by Accessory Proteins. *Journal of Molecular Biology*, **2016**, 428, 1544-57	6.5	3
36	A hybrid NMR/SAXS-based approach for discriminating oligomeric protein interfaces using Rosetta. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 309-17	4.2	30
35	Combining Evolutionary Information and an Iterative Sampling Strategy for Accurate Protein Structure Prediction. *PLoS Computational Biology*, **2015**, 11, e1004661	5	15
34	A Framework to Simplify Combined Sampling Strategies in Rosetta. *PLoS ONE*, **2015**, 10, e0138220	3.7	10
33	A mechanism for the auto-inhibition of hyperpolarization-activated cyclic nucleotide-gated (HCN) channel opening and its relief by cAMP. *Journal of Biological Chemistry*, **2014**, 289, 22205-20	5.4	57
32	Robust and highly accurate automatic NOESY assignment and structure determination with Rosetta. *Journal of Biomolecular NMR*, **2014**, 59, 135-45	3	22
31	Automatic NOESY assignment in CS-RASREC-Rosetta. *Journal of Biomolecular NMR*, **2014**, 59, 147-59	3	11
30	Improving 3D structure prediction from chemical shift data. *Journal of Biomolecular NMR*, **2013**, 57, 27-35	3	23
29	Improved chemical shift based fragment selection for CS-Rosetta using Rosetta3 fragment picker. *Journal of Biomolecular NMR*, **2013**, 57, 117-27	3	34
28	Blind testing of routine, fully automated determination of protein structures from NMR data. *Structure*, **2012**, 20, 227-36	5.2	64
27	Evaluation and optimization of discrete state models of protein folding. *Journal of Physical Chemistry B*, **2012**, 116, 11405-13	3.4	37
26	Resolution-adapted recombination of structural features significantly improves sampling in restraint-guided structure calculation. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 884-95	4.2	57
25	Determination of solution structures of proteins up to 40 kDa using CS-Rosetta with sparse NMR data from deuterated samples. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 10873-8	11.5	151
24	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. *Methods in Enzymology*, **2011**, 487, 545-74	1.7	1216
23	Structure of the BamC two-domain protein obtained by Rosetta with a limited NMR data set. *Journal of Molecular Biology*, **2011**, 411, 83-95	6.5	39
22	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. *Nature*, **2011**, 477, 111-4	50.4	225

21	Kinetics of Conformational Sampling in Ubiquitin. *Angewandte Chemie*, **2011**, 123, 11639-11642	3.6	6
20	Kinetics of conformational sampling in ubiquitin. *Angewandte Chemie - International Edition*, **2011**, 50, 11437-40	16.4	54
19	Determination of the structures of symmetric protein oligomers from NMR chemical shifts and residual dipolar couplings. *Journal of the American Chemical Society*, **2011**, 133, 6288-98	16.4	55
18	Estimating absolute configurational entropies of macromolecules: the minimally coupled subspace approach. *PLoS ONE*, **2010**, 5, e9179	3.7	53
17	NMR structure determination for larger proteins using backbone-only data. *Science*, **2010**, 327, 1014-8	33.3	220
16	Scrutinizing molecular mechanics force fields on the submicrosecond timescale with NMR data. *Biophysical Journal*, **2010**, 99, 647-55	2.9	175
15	Prediction of structures of zinc-binding proteins through explicit modeling of metal coordination geometry. *Protein Science*, **2010**, 19, 494-506	6.3	36
14	Adaptive anisotropic kernels for nonparametric estimation of absolute configurational entropies in high-dimensional configuration spaces. *Physical Review E*, **2009**, 80, 011913	2.4	19
13	Structure prediction for CASP8 with all-atom refinement using Rosetta. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 89-99	4.2	342
12	Recognition dynamics up to microseconds revealed from an RDC-derived ubiquitin ensemble in solution. *Science*, **2008**, 320, 1471-5	33.3	872
11	Residual dipolar couplings as a tool to study molecular recognition of ubiquitin. *Biochemical Society Transactions*, **2008**, 36, 1433-7	5.1	34
10	Consistent blind protein structure generation from NMR chemical shift data. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 4685-90	11.5	665
9	Full correlation analysis of conformational protein dynamics. *Proteins: Structure, Function and Bioinformatics*, **2008**, 70, 1294-312	4.2	108
8	Self-consistent residual dipolar coupling based model-free analysis for the robust determination of nanosecond to microsecond protein dynamics. *Journal of Biomolecular NMR*, **2008**, 41, 139-55	3	90
7	Stereochemistry of sagittamide A from residual dipolar coupling enhanced NMR. *Journal of the American Chemical Society*, **2007**, 129, 15114-5	16.4	96
6	Flooding in GROMACS: accelerated barrier crossings in molecular dynamics. *Journal of Computational Chemistry*, **2006**, 27, 1693-702	3.5	53
5	Collective Langevin dynamics of conformational motions in proteins. *Journal of Chemical Physics*, **2006**, 124, 214903	3.9	89
4	Can principal components yield a dimension reduced description of protein dynamics on long time scales?. *Journal of Physical Chemistry B*, **2006**, 110, 22842-52	3.4	78

3	Generalized correlation for biomolecular dynamics. *Proteins: Structure, Function and Bioinformatics*, **2006**, 62, 1053-61	4.2	278
2	Molecular dynamics simulations of protein G challenge NMR-derived correlated backbone motions. *Angewandte Chemie - International Edition*, **2005**, 44, 3394-9	16.4	24
1	Molecular Dynamics Simulations of Protein G Challenge NMR-Derived Correlated Backbone Motions. *Angewandte Chemie*, **2005**, 117, 3460-3465	3.6	1