Oliver F Lange

List of Publications by Year
in descending order

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36 papers	6,442 citations	201575 27 h-index	315616 38 g-index
38 all docs	38 docs citations	38 times ranked	8320 citing authors

#	Article	IF	Citations
1	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	0.4	1,620
2	Recognition Dynamics Up to Microseconds Revealed from an RDC-Derived Ubiquitin Ensemble in Solution. Science, 2008, 320, 1471-1475.	6.0	963
3	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, 4685-4690.	3.3	776
4	Structure prediction for CASP8 with allâ€atom refinement using Rosetta. Proteins: Structure, Function and Bioinformatics, 2009, 77, 89-99.	1.5	425
5	Generalized correlation for biomolecular dynamics. Proteins: Structure, Function and Bioinformatics, 2005, 62, 1053-1061.	1.5	380
6	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. Nature, 2011, 477, 111-114.	13.7	265
7	NMR Structure Determination for Larger Proteins Using Backbone-Only Data. Science, 2010, 327, 1014-1018.	6.0	245
8	Scrutinizing Molecular Mechanics Force Fields on the Submicrosecond Timescale with NMR Data. Biophysical Journal, 2010, 99, 647-655.	0.2	192
9	Determination of solution structures of proteins up to 40ÂkDa 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, 10873-10878.	3.3	188
10	Full correlation analysis of conformational protein dynamics. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1294-1312.	1.5	122
11	Collective Langevin dynamics of conformational motions in proteins. Journal of Chemical Physics, 2006, 124, 214903.	1.2	114
12	Stereochemistry of Sagittamide A from Residual Dipolar Coupling Enhanced NMR. Journal of the American Chemical Society, 2007, 129, 15114-15115.	6.6	106
13	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, 139-155.	1.6	100
14	Can Principal Components Yield a Dimension Reduced Description of Protein Dynamics on Long Time Scales?. Journal of Physical Chemistry B, 2006, 110, 22842-22852.	1.2	91
15	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
16	Resolutionâ€adapted recombination of structural features significantly improves sampling in restraintâ€guided structure calculation. Proteins: Structure, Function and Bioinformatics, 2012, 80, 884-895.	1.5	69
17	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, 22205-22220.	1.6	67
18	Determination of the Structures of Symmetric Protein Oligomers from NMR Chemical Shifts and Residual Dipolar Couplings. Journal of the American Chemical Society, 2011, 133, 6288-6298.	6.6	65

#	Article	IF	Citations
19	Flooding inGROMACS: Accelerated barrier crossings in molecular dynamics. Journal of Computational Chemistry, 2006, 27, 1693-1702.	1.5	63
20	Kinetics of Conformational Sampling in Ubiquitin. Angewandte Chemie - International Edition, 2011, 50, 11437-11440.	7.2	59
21	Estimating Absolute Configurational Entropies of Macromolecules: The Minimally Coupled Subspace Approach. PLoS ONE, 2010, 5, e9179.	1.1	57
22	Structure of the BamC Two-Domain Protein Obtained by Rosetta with a Limited NMR Data Set. Journal of Molecular Biology, 2011, 411, 83-95.	2.0	47
23	Prediction of structures of zincâ€binding proteins through explicit modeling of metal coordination geometry. Protein Science, 2010, 19, 494-506.	3.1	44
24	Evaluation and Optimization of Discrete State Models of Protein Folding. Journal of Physical Chemistry B, 2012, 116, 11405-11413.	1.2	44
25	Improved chemical shift based fragment selection for CS-Rosetta using Rosetta3 fragment picker. Journal of Biomolecular NMR, 2013, 57, 117-127.	1.6	38
26	Residual dipolar couplings as a tool to study molecular recognition of ubiquitin. Biochemical Society Transactions, 2008, 36, 1433-1437.	1.6	36
27	A hybrid NMR/SAXSâ€based approach for discriminating oligomeric protein interfaces using ‹scp›R‹/scp›osetta. Proteins: Structure, Function and Bioinformatics, 2015, 83, 309-317.	1.5	33
28	Molecular Dynamics Simulations of Protein G Challenge NMR-Derived Correlated Backbone Motions. Angewandte Chemie - International Edition, 2005, 44, 3394-3399.	7.2	25
29	Improving 3D structure prediction from chemical shift data. Journal of Biomolecular NMR, 2013, 57, 27-35.	1.6	25
30	Robust and highly accurate automatic NOESY assignment and structure determination with Rosetta. Journal of Biomolecular NMR, 2014, 59, 135-145.	1.6	23
31	Adaptive anisotropic kernels for nonparametric estimation of absolute configurational entropies in high-dimensional configuration spaces. Physical Review E, 2009, 80, 011913.	0.8	21
32	Combining Evolutionary Information and an Iterative Sampling Strategy for Accurate Protein Structure Prediction. PLoS Computational Biology, 2015, 11, e1004661.	1.5	17
33	Automatic NOESY assignment in CS-RASREC-Rosetta. Journal of Biomolecular NMR, 2014, 59, 147-159.	1.6	15
34	A Framework to Simplify Combined Sampling Strategies in Rosetta. PLoS ONE, 2015, 10, e0138220.	1.1	10
35	Systematic evaluation of CS-Rosetta for membrane protein structure prediction with sparse NOE restraints. Proteins: Structure, Function and Bioinformatics, 2017, 85, 812-826.	1.5	8
36	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, 1544-1557.	2.0	5