

Michael J Harms

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

2,308
citations

394421

19
h-index

361022

35
g-index

46
all docs

46
docs citations

46
times ranked

2850
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary biochemistry: revealing the historical and physical causes of protein properties. <i>Nature Reviews Genetics</i> , 2013, 14, 559-571.	16.3	305
2	Protein Evolution by Molecular Tinkering: Diversification of the Nuclear Receptor Superfamily from a Ligand-Dependent Ancestor. <i>PLoS Biology</i> , 2010, 8, e1000497.	5.6	202
3	Analyzing protein structure and function using ancestral gene reconstruction. <i>Current Opinion in Structural Biology</i> , 2010, 20, 360-366.	5.7	176
4	Arginine residues at internal positions in a protein are always charged. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18954-18959.	7.1	136
5	How sequence defines structure: A crystallographic map of DNA structure and conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7157-7162.	7.1	133
6	Historical contingency and its biophysical basis in glucocorticoid receptor evolution. <i>Nature</i> , 2014, 512, 203-207.	27.8	132
7	The pKa Values of Acidic and Basic Residues Buried at the Same Internal Location in a Protein Are Governed by Different Factors. <i>Journal of Molecular Biology</i> , 2009, 389, 34-47.	4.2	120
8	Detecting High-Order Epistasis in Nonlinear Genotype-Phenotype Maps. <i>Genetics</i> , 2017, 205, 1079-1088.	2.9	120
9	The thermostability and specificity of ancient proteins. <i>Current Opinion in Structural Biology</i> , 2016, 38, 37-43.	5.7	106
10	Evolution of Minimal Specificity and Promiscuity in Steroid Hormone Receptors. <i>PLoS Genetics</i> , 2012, 8, e1003072.	3.5	105
11	High-order epistasis shapes evolutionary trajectories. <i>PLoS Computational Biology</i> , 2017, 13, e1005541.	3.2	97
12	Robustness of Reconstructed Ancestral Protein Functions to Statistical Uncertainty. <i>Molecular Biology and Evolution</i> , 2017, 34, msw223.	8.9	80
13	Thermodynamic System Drift in Protein Evolution. <i>PLoS Biology</i> , 2014, 12, e1001994.	5.6	78
14	A buried lysine that titrates with a normal pK_a : Role of conformational flexibility at the protein-water interface as a determinant of pK_a values. <i>Protein Science</i> , 2008, 17, 833-845.	7.6	72
15	Molecular ensembles make evolution unpredictable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11938-11943.	7.1	66
16	Biophysical mechanisms for large-effect mutations in the evolution of steroid hormone receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11475-11480.	7.1	61
17	Multiple Evolutionary Origins of Ubiquitous Cu^{2+} and Zn^{2+} Binding in the S100 Protein Family. <i>PLoS ONE</i> , 2016, 11, e0164740.	2.5	44
18	Evolutionary trend toward kinetic stability in the folding trajectory of RNases H. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13045-13050.	7.1	37

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19	Laser light-scattering evidence for an altered association of β 1-crystallin deamidated in the connecting peptide. <i>Protein Science</i> , 2004, 13, 678-686.	7.6	35
20	<i>pytc</i> : Open-Source Python Software for Global Analyses of Isothermal Titration Calorimetry Data. <i>Biochemistry</i> , 2018, 57, 2578-2583.	2.5	26
21	Coevolution of the Toll-Like Receptor 4 Complex with Calgranulins and Lipopolysaccharide. <i>Frontiers in Immunology</i> , 2018, 9, 304.	4.8	20
22	Identification and Characterization of Zebrafish Tlr4 Coreceptor Md-2. <i>Journal of Immunology</i> , 2021, 206, 1046-1057.	0.8	19
23	Resurrection of an Urbilaterian U1A/U2B β /SNF Protein. <i>Journal of Molecular Biology</i> , 2013, 425, 3846-3862.	4.2	17
24	Conservation of Specificity in Two Low-Specificity Proteins. <i>Biochemistry</i> , 2018, 57, 684-695.	2.5	16
25	Evolution of multifunctionality through a pleiotropic substitution in the innate immune protein S100A9. <i>ELife</i> , 2020, 9, .	6.0	16
26	Ensemble epistasis: thermodynamic origins of nonadditivity between mutations. <i>Genetics</i> , 2021, 219, .	2.9	13
27	Human S100A5 binds Ca ²⁺ and Cu ²⁺ independently. <i>BMC Biophysics</i> , 2017, 10, 8.	4.4	10
28	Inferring a complete genotype-phenotype map from a small number of measured phenotypes. <i>PLoS Computational Biology</i> , 2020, 16, e1008243.	3.2	10
29	A conserved folding nucleus sculpts the free energy landscape of bacterial and archaeal orthologs from a divergent TIM barrel family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
30	Tracing the evolution of novel features of human Toll-like receptor 4. <i>Protein Science</i> , 2019, 28, 1350-1358.	7.6	8
31	Were Ancestral Proteins Less Specific?. <i>Molecular Biology and Evolution</i> , 2021, 38, 2227-2239.	8.9	8
32	Enzymes emerge by upcycling. <i>Nature Chemical Biology</i> , 2018, 14, 526-527.	8.0	5
33	Learning peptide recognition rules for a low-specificity protein. <i>Protein Science</i> , 2020, 29, 2259-2273.	7.6	4
34	Evolutionary Conservation of Structural and Functional Coupling between the BRM AT-Hook and Bromodomain. <i>Journal of Molecular Biology</i> , 2021, 433, 166845.	4.2	4
35	Exploring the Evolutionary History of Kinetic Stability in the β -Lytic Protease Family. <i>Biochemistry</i> , 2021, 60, 170-181.	2.5	2