

Michael J Harms

List of Publications by Year in descending order

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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	Identification and Characterization of Zebrafish Tlr4 Coreceptor Md-2. <i>Journal of Immunology</i> , 2021, 206, 1046-1057.	0.8	19
2	Exploring the Evolutionary History of Kinetic Stability in the $\hat{\pm}$ -Lytic Protease Family. <i>Biochemistry</i> , 2021, 60, 170-181.	2.5	2
3	Were Ancestral Proteins Less Specific?. <i>Molecular Biology and Evolution</i> , 2021, 38, 2227-2239.	8.9	8
4	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
5	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
6	Ensemble epistasis: thermodynamic origins of nonadditivity between mutations. <i>Genetics</i> , 2021, 219, .	2.9	13
7	Inferring a complete genotype-phenotype map from a small number of measured phenotypes. <i>PLoS Computational Biology</i> , 2020, 16, e1008243.	3.2	10
8	Learning peptide recognition rules for a $\langle \text{sc} \rangle \text{low} \hat{\epsilon} \text{specificity} \langle / \text{sc} \rangle$ protein. <i>Protein Science</i> , 2020, 29, 2259-2273.	7.6	4
9	Evolution of multifunctionality through a pleiotropic substitution in the innate immune protein S100A9. <i>ELife</i> , 2020, 9, .	6.0	16
10	Tracing the evolution of novel features of human Toll-like receptor 4. <i>Protein Science</i> , 2019, 28, 1350-1358.	7.6	8
11	<i><i>pytc</i></i> : Open-Source Python Software for Global Analyses of Isothermal Titration Calorimetry Data. <i>Biochemistry</i> , 2018, 57, 2578-2583.	2.5	26
12	Conservation of Specificity in Two Low-Specificity Proteins. <i>Biochemistry</i> , 2018, 57, 684-695.	2.5	16
13	Enzymes emerge by upcycling. <i>Nature Chemical Biology</i> , 2018, 14, 526-527.	8.0	5
14	Coevolution of the Toll-Like Receptor 4 Complex with Calgranulins and Lipopolysaccharide. <i>Frontiers in Immunology</i> , 2018, 9, 304.	4.8	20
15	Robustness of Reconstructed Ancestral Protein Functions to Statistical Uncertainty. <i>Molecular Biology and Evolution</i> , 2017, 34, msw223.	8.9	80
16	Detecting High-Order Epistasis in Nonlinear Genotype-Phenotype Maps. <i>Genetics</i> , 2017, 205, 1079-1088.	2.9	120
17	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
18	Human S100A5 binds Ca ²⁺ and Cu ²⁺ independently. <i>BMC Biophysics</i> , 2017, 10, 8.	4.4	10

#	ARTICLE	IF	CITATIONS
19	High-order epistasis shapes evolutionary trajectories. <i>PLoS Computational Biology</i> , 2017, 13, e1005541.	3.2	97
20	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
21	The thermostability and specificity of ancient proteins. <i>Current Opinion in Structural Biology</i> , 2016, 38, 37-43.	5.7	106
22	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
23	Thermodynamic System Drift in Protein Evolution. <i>PLoS Biology</i> , 2014, 12, e1001994.	5.6	78
24	Historical contingency and its biophysical basis in glucocorticoid receptor evolution. <i>Nature</i> , 2014, 512, 203-207.	27.8	132
25	Evolutionary biochemistry: revealing the historical and physical causes of protein properties. <i>Nature Reviews Genetics</i> , 2013, 14, 559-571.	16.3	305
26	Resurrection of an Urbilaterian U1A/U2B ³ /SNF Protein. <i>Journal of Molecular Biology</i> , 2013, 425, 3846-3862.	4.2	17
27	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
28	Evolution of Minimal Specificity and Promiscuity in Steroid Hormone Receptors. <i>PLoS Genetics</i> , 2012, 8, e1003072.	3.5	105
29	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
30	Analyzing protein structure and function using ancestral gene reconstruction. <i>Current Opinion in Structural Biology</i> , 2010, 20, 360-366.	5.7	176
31	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
32	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
33	A buried lysine that titrates with a normal p <i>K</i> _a : Role of conformational flexibility at the protein-water interface as a determinant of p <i>K</i> _a values. <i>Protein Science</i> , 2008, 17, 833-845.	7.6	72
34	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
35	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