

# Katherine A Henzler-Wildman

## List of Publications by Year in descending order

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31  
papers

5,560  
citations

535685

17  
h-index

511568

30  
g-index

41  
all docs

41  
docs citations

41  
times ranked

7429  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-pH structure of EmrE reveals the mechanism of proton-coupled substrate transport. <i>Nature Communications</i> , 2022, 13, 991.	5.8	15
2	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N backbone and side chain chemical shift assignments of the SARS-CoV-2 non-structural protein 7. <i>Biomolecular NMR Assignments</i> , 2021, 15, 73-77.	0.4	6
3	Mapping temperature-dependent conformational change in the voltage-sensing domain of an engineered heat-activated K <sup>+</sup> channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
4	A solid-supported membrane electrophysiology assay for efficient characterization of ion-coupled transport. <i>Journal of Biological Chemistry</i> , 2021, 297, 101220.	1.6	15
5	Structure and dynamics of the drug-bound bacterial transporter EmrE in lipid bilayers. <i>Nature Communications</i> , 2021, 12, 172.	5.8	40
6	Ion-dependent structure, dynamics, and allosteric coupling in a non-selective cation channel. <i>Nature Communications</i> , 2021, 12, 6225.	5.8	13
7	Highly coupled transport can be achieved in free-exchange transport models. <i>Journal of General Physiology</i> , 2020, 152, .	0.9	25
8	NMR Structural Analysis of Isolated Shaker Voltage-Sensing Domain in LPPG Micelles. <i>Biophysical Journal</i> , 2019, 117, 388-398.	0.2	3
9	Identification of an Alternating-Access Dynamics Mutant of EmrE with Impaired Transport. <i>Journal of Molecular Biology</i> , 2019, 431, 2777-2789.	2.0	19
10	A free-exchange mathematical model of EmrE. <i>FASEB Journal</i> , 2019, 33, 656.6.	0.2	0
11	A mass spectrometry based transport assay for studying EmrE transport of unlabeled substrates. <i>Analytical Biochemistry</i> , 2018, 549, 130-135.	1.1	3
12	The C terminus of the bacterial multidrug transporter EmrE couples drug binding to proton release. <i>Journal of Biological Chemistry</i> , 2018, 293, 19137-19147.	1.6	17
13	New free-exchange model of EmrE transport. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10083-E10091.	3.3	50
14	Integrative NMR for biomolecular research. <i>Journal of Biomolecular NMR</i> , 2016, 64, 307-332.	1.6	47
15	Asymmetric protonation of EmrE. <i>Journal of General Physiology</i> , 2015, 146, 445-461.	0.9	46
16	Role of protein dynamics in ion selectivity and allosteric coupling in the NaK channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15366-15371.	3.3	17
17	Red Blood Cell Invasion by <i>Plasmodium vivax</i> : Structural Basis for DBP Engagement of DARC. <i>PLoS Pathogens</i> , 2014, 10, e1003869.	2.1	99
18	Transported Substrate Determines Exchange Rate in the Multidrug Resistance Transporter EmrE. <i>Journal of Biological Chemistry</i> , 2014, 289, 6825-6836.	1.6	43

#	ARTICLE	IF	CITATIONS
19	EmrE dimerization depends on membrane environment. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1817-1822.	1.4	11
20	Blocking Dynamics of the SMR Transporter EmrE Impairs Efflux Activity. <i>Biophysical Journal</i> , 2014, 107, 613-620.	0.2	20
21	Antiparallel EmrE exports drugs by exchanging between asymmetric structures. <i>Nature</i> , 2012, 481, 45-50.	13.7	188
22	Reconstitution of integral membrane proteins into isotropic bicelles with improved sample stability and expanded lipid composition profile. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 814-820.	1.4	61
23	Analyzing conformational changes in the transport cycle of EmrE. <i>Current Opinion in Structural Biology</i> , 2012, 22, 38-43.	2.6	18
24	NMR Structure of the Cathelicidin-Derived Human Antimicrobial Peptide LL-37 in Dodecylphosphocholine Micelles. <i>Biochemistry</i> , 2008, 47, 5565-5572.	1.2	157
25	Nitrogen-14 Solid-State NMR Spectroscopy of Aligned Phospholipid Bilayers to Probe Peptide-Lipid Interaction and Oligomerization of Membrane Associated Peptides. <i>Journal of the American Chemical Society</i> , 2008, 130, 11023-11029.	6.6	46
26	A hierarchy of timescales in protein dynamics is linked to enzyme catalysis. <i>Nature</i> , 2007, 450, 913-916.	13.7	963
27	Intrinsic motions along an enzymatic reaction trajectory. <i>Nature</i> , 2007, 450, 838-844.	13.7	814
28	Dynamic personalities of proteins. <i>Nature</i> , 2007, 450, 964-972.	13.7	2,042
29	Expression and purification of a recombinant LL-37 from <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2006, 1758, 1351-1358.	1.4	71
30	Linkage between dynamics and catalysis in a thermophilic-mesophilic enzyme pair. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 945-949.	3.6	448
31	Perturbation of the Hydrophobic Core of Lipid Bilayers by the Human Antimicrobial Peptide LL-37. <i>Biochemistry</i> , 2004, 43, 8459-8469.	1.2	247