

# Katherine A Henzler-Wildman

## 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.

32  
papers

4,600  
citations

16  
h-index

41  
g-index

41  
ext. papers

5,175  
ext. citations

12.1  
avg, IF

5.57  
L-index

#	Paper	IF	Citations
32	High-pH structure of EmrE reveals the mechanism of proton-coupled substrate transport.. <i>Nature Communications</i> , <b>2022</b> , 13, 991	17.4	1
31	Ion-dependent structure, dynamics, and allosteric coupling in a non-selective cation channel. <i>Nature Communications</i> , <b>2021</b> , 12, 6225	17.4	3
30	Mapping temperature-dependent conformational change in the voltage-sensing domain of an engineered heat-activated K channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	3
29	H, C, and N backbone and side chain chemical shift assignments of the SARS-CoV-2 non-structural protein 7. <i>Biomolecular NMR Assignments</i> , <b>2021</b> , 15, 73-77	0.7	2
28	A solid-supported membrane electrophysiology assay for efficient characterization of ion-coupled transport. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 297, 101220	5.4	1
27	Structure and dynamics of the drug-bound bacterial transporter EmrE in lipid bilayers. <i>Nature Communications</i> , <b>2021</b> , 12, 172	17.4	12
26	Highly coupled transport can be achieved in free-exchange transport models. <i>Journal of General Physiology</i> , <b>2020</b> , 152,	3.4	11
25	Identification of an Alternating-Access Dynamics Mutant of EmrE with Impaired Transport. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 2777-2789	6.5	11
24	NMR Structural Analysis of Isolated Shaker Voltage-Sensing Domain in LPPG Micelles. <i>Biophysical Journal</i> , <b>2019</b> , 117, 388-398	2.9	3
23	A free-exchange mathematical model of EmrE. <i>FASEB Journal</i> , <b>2019</b> , 33, 656.6	0.9	
22	A mass spectrometry based transport assay for studying EmrE transport of unlabeled substrates. <i>Analytical Biochemistry</i> , <b>2018</b> , 549, 130-135	3.1	2
21	The C terminus of the bacterial multidrug transporter EmrE couples drug binding to proton release. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 19137-19147	5.4	9
20	New free-exchange model of EmrE transport. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E10083-E10091	11.5	30
19	Integrative NMR for biomolecular research. <i>Journal of Biomolecular NMR</i> , <b>2016</b> , 64, 307-32	3	36
18	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> , <b>2015</b> , 112, 15366-71	11.5	12
17	Asymmetric protonation of EmrE. <i>Journal of General Physiology</i> , <b>2015</b> , 146, 445-61	3.4	26
16	Blocking dynamics of the SMR transporter EmrE impairs efflux activity. <i>Biophysical Journal</i> , <b>2014</b> , 107, 613-620	2.9	16

15	Red blood cell invasion by Plasmodium vivax: structural basis for DBP engagement of DARC. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1003869	7.6	65
14	Transported substrate determines exchange rate in the multidrug resistance transporter EmrE. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 6825-6836	5.4	31
13	EmrE dimerization depends on membrane environment. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2014</b> , 1838, 1817-22	3.8	10
12	Analyzing conformational changes in the transport cycle of EmrE. <i>Current Opinion in Structural Biology</i> , <b>2012</b> , 22, 38-43	8.1	14
11	Reconstitution of integral membrane proteins into isotropic bicelles with improved sample stability and expanded lipid composition profile. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2012</b> , 1818, 814-20	3.8	50
10	Antiparallel EmrE exports drugs by exchanging between asymmetric structures. <i>Nature</i> , <b>2011</b> , 481, 45-50	50.4	159
9	NMR structure of the cathelicidin-derived human antimicrobial peptide LL-37 in dodecylphosphocholine micelles. <i>Biochemistry</i> , <b>2008</b> , 47, 5565-72	3.2	139
8	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> , <b>2008</b> , 130, 11023-9	16.4	42
7	A hierarchy of timescales in protein dynamics is linked to enzyme catalysis. <i>Nature</i> , <b>2007</b> , 450, 913-6	50.4	841
6	Intrinsic motions along an enzymatic reaction trajectory. <i>Nature</i> , <b>2007</b> , 450, 838-44	50.4	706
5	Dynamic personalities of proteins. <i>Nature</i> , <b>2007</b> , 450, 964-72	50.4	1672
4	Expression and purification of a recombinant LL-37 from Escherichia coli. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2006</b> , 1758, 1351-8	3.8	63
3	Linkage between dynamics and catalysis in a thermophilic-mesophilic enzyme pair. <i>Nature Structural and Molecular Biology</i> , <b>2004</b> , 11, 945-9	17.6	403
2	Perturbation of the hydrophobic core of lipid bilayers by the human antimicrobial peptide LL-37. <i>Biochemistry</i> , <b>2004</b> , 43, 8459-69	3.2	226
1	Unlocking the Reversal Potential of Solid Supported Membrane Electrophysiology to Determine Transport Stoichiometry		1