

# Kyle A Barlow

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7078957/publications.pdf>

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10  
papers

3,033  
citations

932766

10  
h-index

1372195

10  
g-index

15  
all docs

15  
docs citations

15  
times ranked

4673  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947.	5.8	16
2	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	9.0	513
3	Computational design of a modular protein sense-response system. <i>Science</i> , 2019, 366, 1024-1028.	6.0	91
4	Deamidation and isomerization liability analysis of 131 clinical-stage antibodies. <i>MAbs</i> , 2019, 11, 45-57.	2.6	96
5	Flex ddG: Rosetta Ensemble-Based Estimation of Changes in Protein-Protein Binding Affinity upon Mutation. <i>Journal of Physical Chemistry B</i> , 2018, 122, 5389-5399.	1.2	192
6	Extending chemical perturbations of the ubiquitin fitness landscape in a classroom setting reveals new constraints on sequence tolerance. <i>Biology Open</i> , 2018, 7, .	0.6	17
7	Determination of ubiquitin fitness landscapes under different chemical stresses in a classroom setting. <i>ELife</i> , 2016, 5, .	2.8	71
8	A Web Resource for Standardized Benchmark Datasets, Metrics, and Rosetta Protocols for Macromolecular Modeling and Design. <i>PLoS ONE</i> , 2015, 10, e0130433.	1.1	85
9	Improved specificity of TALE-based genome editing using an expanded RVD repertoire. <i>Nature Methods</i> , 2015, 12, 465-471.	9.0	91
10	A TALE nuclease architecture for efficient genome editing. <i>Nature Biotechnology</i> , 2011, 29, 143-148.	9.4	1,855