

# Jeffrey B Bonanno

## List of Publications by Year in descending order

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Version: 2024-02-01

23  
papers

989  
citations

516710

16  
h-index

677142

22  
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24  
all docs

24  
docs citations

24  
times ranked

1998  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of the SARS-CoV-2 S Protein: Biophysical, Biochemical, Structural, and Antigenic Analysis. <i>ACS Omega</i> , 2021, 6, 85-102.	3.5	54
2	HVEM structures and mutants reveal distinct functions of binding to LIGHT and BTLA/CD160. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	15
3	Mechanistic dissection of the PD-L1:B7-1 co-inhibitory immune complex. <i>PLoS ONE</i> , 2020, 15, e0233578.	2.5	23
4	Structures of FOX-4 Cephamycinase in Complex with Transition-State Analog Inhibitors. <i>Biomolecules</i> , 2020, 10, 671.	4.0	4
5	A Binary Arginine Methylation Switch on Histone H3 Arginine 2 Regulates Its Interaction with WDR5. <i>Biochemistry</i> , 2020, 59, 3696-3708.	2.5	21
6	Structure of a single-chain H2A/H2B dimer. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 194-198.	0.8	1
7	An essential bifunctional enzyme in <i>Mycobacterium tuberculosis</i> for itaconate dissimilation and leucine catabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15907-15913.	7.1	42
8	Structural Basis of CD160:HVEM Recognition. <i>Structure</i> , 2019, 27, 1286-1295.e4.	3.3	33
9	Mechanism and Structure of $\hat{1}^3$ -Resorcylyate Decarboxylase. <i>Biochemistry</i> , 2018, 57, 3167-3175.	2.5	30
10	Structures of the L27 Domain of Disc Large Homologue 1 Protein Illustrate a Self-Assembly Module. <i>Biochemistry</i> , 2018, 57, 1293-1305.	2.5	6
11	Anti-CTLA-4 therapy requires an Fc domain for efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3912-3917.	7.1	121
12	Substrate Profile of the Phosphotriesterase Homology Protein from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2018, 57, 6219-6227.	2.5	5
13	Functional assignment of multiple catabolic pathways for d-apiose. <i>Nature Chemical Biology</i> , 2018, 14, 696-705.	8.0	26
14	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. <i>Structure</i> , 2017, 25, 434-445.	3.3	61
15	Structural basis for cancer immunotherapy by the first-in-class checkpoint inhibitor ipilimumab. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4223-E4232.	7.1	121
16	Stilbene epoxidation and detoxification in a <i>Photobacterium luminescens</i> -nematode symbiosis. <i>Journal of Biological Chemistry</i> , 2017, 292, 6680-6694.	3.4	20
17	Structural insights into substrate and inhibitor binding sites in human indoleamine 2,3-dioxygenase 1. <i>Nature Communications</i> , 2017, 8, 1693.	12.8	129
18	Structural Insights into Thioether Bond Formation in the Biosynthesis of Sactipeptides. <i>Journal of the American Chemical Society</i> , 2017, 139, 11734-11744.	13.7	119

#	ARTICLE	IF	CITATIONS
19	Crystal Structure of the Complex of Human FasL and Its Decoy Receptor DcR3. <i>Structure</i> , 2016, 24, 2016-2023.	3.3	39
20	Substrate Distortion and the Catalytic Reaction Mechanism of 5-Carboxyvanillate Decarboxylase. <i>Journal of the American Chemical Society</i> , 2016, 138, 826-836.	13.7	41
21	Determinants of the CmoB carboxymethyl transferase utilized for selective tRNA wobble modification. <i>Nucleic Acids Research</i> , 2015, 43, 4602-4613.	14.5	23
22	Increased Heterologous Protein Expression in <i>Drosophila</i> S2 Cells for Massive Production of Immune Ligands/Receptors and Structural Analysis of Human HVEM. <i>Molecular Biotechnology</i> , 2015, 57, 914-922.	2.4	10
23	Mechanistic Basis for Functional Promiscuity in the TNF and TNF Receptor Superfamilies: Structure of the LIGHT:DcR3 Assembly. <i>Structure</i> , 2014, 22, 1252-1262.	3.3	27