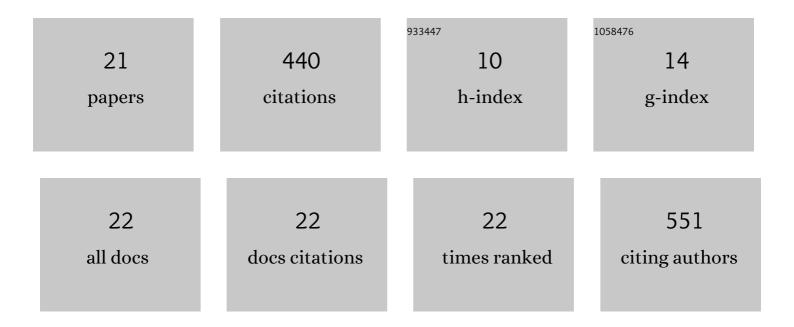
Todd M Weaver

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Crystallographic Studies of the Catalytic and a Second Site in Fumarase C fromEscherichia coliâ€,‡. Biochemistry, 1996, 35, 13955-13965.	2.5	97
2	The Ï€â€helix translates structure into function. Protein Science, 2000, 9, 201-206.	7.6	93
3	Missense Mutations in Fumarate Hydratase in Multiple Cutaneous and Uterine Leiomyomatosis and Renal Cell Cancer. Journal of Molecular Diagnostics, 2005, 7, 437-443.	2.8	56
4	Mutations of fumarase that distinguish between the active site and a nearby dicarboxylic acid binding site. Protein Science, 1997, 6, 834-842.	7.6	37
5	X-ray crystallographic and kinetic correlation of a clinically observed human fumarase mutation. Protein Science, 2002, 11, 1552-1557.	7.6	36
6	Structural and Functional Studies of Truncated Hemolysin A from Proteus mirabilis. Journal of Biological Chemistry, 2009, 284, 22297-22309.	3.4	33
7	The role of the allosteric B site in the fumarase reaction. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3393-3397.	7.1	28
8	Structure of free fumarase C fromEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1395-1401.	2.5	17
9	Purification and Crystallization of Fumarase C from Escherichia coli. Journal of Molecular Biology, 1993, 231, 141-144.	4.2	15
10	Biochemical Characterization of Two Clinically-Relevant Human Fumarase Variants Defective for Oligomerization. The Open Biochemistry Journal, 2018, 12, 1-15.	0.5	15
11	Exploring protein function and evolution using free online bioinformatics tools. Biochemistry and Molecular Biology Education, 2005, 33, 319-322.	1.2	6
12	Sequential unfolding of the hemolysin twoâ€partner secretion domain from <scp><i>P</i></scp> <i>roteus mirabilis</i> . Protein Science, 2015, 24, 1841-1855.	7.6	4
13	Closed fumarase C activeâ€site structures reveal SS Loop residue contribution in catalysis. FEBS Letters, 2020, 594, 337-357.	2.8	2
14	Proteolysis of truncated hemolysin A yields a stable dimerization interface. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 138-145.	0.8	1
15	Negative design at the carboxyâ€ŧerminal betaâ€edge of truncated hemolysin A. FASEB Journal, 2010, 24, 490.6.	O.5	0
16	Betaâ€arc 2 hydrogen bond network within hemolysin A facilitates hemolytic activation. FASEB Journal, 2013, 27, 996.12.	0.5	0
17	The Tale of Two Domains. FASEB Journal, 2015, 29, 882.3.	0.5	0
18	Piâ€system Stabilization of a 220 à 3 Buried Solvent Network. FASEB Journal, 2015, 29, 882.2.	0.5	0

#	Article	IF	CITATIONS
19	Carboxyâ€ŧerminal Disruption of HpmA265 Caused by Trypsin and its Effect on Stability and Activity. FASEB Journal, 2015, 29, 882.6.	0.5	0
20	Systematic Disruption of the Nonpolar βâ€Helix Core of Hemolysin A and its Siteâ€Specific Effect on Protein Structure, Function, and Secretion. FASEB Journal, 2019, 33, 779.36.	0.5	0
21	Determining the Mechanism of Hemolytic Function and Type Vb Secretion by a Gramâ€Negative Pathogen. FASEB Journal, 2019, 33, 780.13.	0.5	0