

# Peter J Steinbach

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

5,486  
citations

201674

27  
h-index

289244

40  
g-index

41  
all docs

41  
docs citations

41  
times ranked

6085  
citing authors

#	ARTICLE	IF	CITATIONS
1	OPO04: Newly identified disorder of copper metabolism caused by variants in CTR1, a high-affinity copper transporter. <i>Genetics in Medicine</i> , 2022, 24, S335-S336.	2.4	1
2	Modulation of free energy landscapes as a strategy for the design of antimicrobial peptides. <i>Journal of Biological Physics</i> , 2022, 48, 151-166.	1.5	1
3	A point mutation in the nuclease domain of MLH3 eliminates repeat expansions in a mouse stem cell model of the Fragile X-related disorders. <i>Nucleic Acids Research</i> , 2020, 48, 7856-7863.	14.5	19
4	Nanosecond-Timescale Dynamics and Conformational Heterogeneity in Human GCK Regulation and Disease. <i>Biophysical Journal</i> , 2020, 118, 1109-1118.	0.5	7
5	<i>HLA</i> and autoantibodies define scleroderma subtypes and risk in African and European Americans and suggest a role for molecular mimicry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 552-562.	7.1	52
6	Biallelic HEPHL1 variants impair ferroxidase activity and cause an abnormal hair phenotype. <i>PLoS Genetics</i> , 2019, 15, e1008143.	3.5	23
7	Enhanced spontaneous DNA twisting/bending fluctuations unveiled by fluorescence lifetime distributions promote mismatch recognition by the Rad4 nucleotide excision repair complex. <i>Nucleic Acids Research</i> , 2018, 46, 1240-1255.	14.5	23
8	Loss of function mutations in VARS encoding cytoplasmic valyl-tRNA synthetase cause microcephaly, seizures, and progressive cerebral atrophy. <i>Human Genetics</i> , 2018, 137, 293-303.	3.8	12
9	Peptide and Protein Structure Prediction with a Simplified Continuum Solvent Model. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11355-11362.	2.6	1
10	Static Kinks or Flexible Hinges: Multiple Conformations of Bent DNA Bound to Integration Host Factor Revealed by Fluorescence Lifetime Measurements. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11519-11534.	2.6	14
11	Structural Basis of Species-Dependent Differential Affinity of 6-Alkoxy-5-Aryl-3-Pyridinecarboxamide Cannabinoid-1 Receptor Antagonists. <i>Molecular Pharmacology</i> , 2015, 88, 238-244.	2.3	14
12	Drastic neofunctionalization associated with evolution of the timezyme AANAT 500 Mya. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 314-319.	7.1	64
13	Filtering artifacts from lifetime distributions when maximizing entropy using a bootstrapped model. <i>Analytical Biochemistry</i> , 2012, 427, 102-105.	2.4	31
14	Molecular and biochemical characterization of a unique mutation in CCS, the human copper chaperone to superoxide dismutase. <i>Human Mutation</i> , 2012, 33, 1207-1215.	2.5	34
15	Water-Exclusion and Liquid-Structure Forces in Implicit Solvation. <i>Journal of Physical Chemistry B</i> , 2011, 115, 14668-14682.	2.6	30
16	The Tensin-3 Protein, Including its SH2 Domain, Is Phosphorylated by Src and Contributes to Tumorigenesis and Metastasis. <i>Cancer Cell</i> , 2009, 16, 246-258.	16.8	81
17	Transglutaminase-1 gene mutations in autosomal recessive congenital ichthyosis: Summary of mutations (including 23 novel) and modeling of TGase-1. <i>Human Mutation</i> , 2009, 30, 537-547.	2.5	79
18	Prediction of side-chain conformations on protein surfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 66, 814-823.	2.6	31

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19	Biological Effect of a Novel Mutation in the Third Leucine-Rich Repeat of Human Luteinizing Hormone Receptor. <i>Molecular Endocrinology</i> , 2006, 20, 2493-2503.	3.7	20
20	Polyproline and the "spectroscopic ruler" revisited with single-molecule fluorescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2754-2759.	7.1	422
21	Eukaryotic RNases H1 act processively by interactions through the duplex RNA-binding domain. <i>Nucleic Acids Research</i> , 2005, 33, 2166-2175.	14.5	46
22	Mutation in the leucine-rich repeat C-flanking region of platelet glycoprotein Ib $\beta$ impairs assembly of von Willebrand factor receptor. <i>Thrombosis and Haemostasis</i> , 2004, 92, 75-88.	3.4	20
23	Exploring peptide energy landscapes: A test of force fields and implicit solvent models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 665-677.	2.6	49
24	Inferring Lifetime Distributions from Kinetics by Maximizing Entropy Using a Bootstrapped Model. <i>Journal of Chemical Information and Computer Sciences</i> , 2002, 42, 1476-1478.	2.8	86
25	Effects of Chain Stiffness on the Dynamics of Loop Formation in Polypeptides. Appendix: Testing a 1-Dimensional Diffusion Model for Peptide Dynamics. <i>Journal of Physical Chemistry B</i> , 2002, 106, 11628-11640.	2.6	197
26	Redesign of a Four-helix Bundle Protein by Phage Display Coupled with Proteolysis and Structural Characterization by NMR and X-ray Crystallography. <i>Journal of Molecular Biology</i> , 2002, 323, 253-262.	4.2	84
27	Analysis of Kinetics Using a Hybrid Maximum-Entropy/Nonlinear-Least-Squares Method: Application to Protein Folding. <i>Biophysical Journal</i> , 2002, 82, 2244-2255.	0.5	174
28	Human Ca <sup>2+</sup> Receptor Extracellular Domain. <i>Journal of Biological Chemistry</i> , 2001, 276, 32145-32151.	3.4	39
29	Characterization of the <i>Saccharomyces cerevisiae</i> Homolog of the Melatonin Rhythm Enzyme Arylalkylamine N-Acetyltransferase (EC 2.3.1.87). <i>Journal of Biological Chemistry</i> , 2001, 276, 47239-47247.	3.4	54
30	Probing hydrogen bonds in the antibody-bound HIV-1 gp120 V3 loop by solid state NMR REDOR measurements. <i>Journal of Biomolecular NMR</i> , 2000, 16, 313-327.	2.8	26
31	Crystallin of the Scallop Lens. <i>Journal of Biological Chemistry</i> , 2000, 275, 41064-41073.	3.4	63
32	Identification of Substrate Binding Site of Cyclin-dependent Kinase 5. <i>Journal of Biological Chemistry</i> , 1999, 274, 9600-9606.	3.4	36
33	Identification of the Cysteine Residues in the Amino-terminal Extracellular Domain of the Human Ca <sup>2+</sup> Receptor Critical for Dimerization. <i>Journal of Biological Chemistry</i> , 1999, 274, 27642-27650.	3.4	169
34	Solid-state NMR evidence for an antibody-dependent conformation of the V3 loop of HIV-1 gp120. <i>Nature Structural Biology</i> , 1999, 6, 141-145.	9.7	78
35	The ubiquitin pathway in Parkinson's disease. <i>Nature</i> , 1998, 395, 451-452.	27.8	1,518
36	Protein simulation below the glass-transition temperature. Dependence on cooling protocol. <i>Chemical Physics Letters</i> , 1994, 226, 447-452.	2.6	38

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37	New spherical-cutoff methods for long-range forces in macromolecular simulation. <i>Journal of Computational Chemistry</i> , 1994, 15, 667-683.	3.3	1,002
38	Ligand binding to heme proteins: connection between dynamics and function. <i>Biochemistry</i> , 1991, 30, 3988-4001.	2.5	392
39	The effects of environment and hydration on protein dynamics: A simulation study of myoglobin. <i>Chemical Physics</i> , 1991, 158, 383-394.	1.9	84
40	Rebinding and relaxation in the myoglobin pocket. <i>Biophysical Chemistry</i> , 1987, 26, 337-355.	2.8	372