

# James H Geiger

## List of Publications by Year in descending order

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81  
papers

3,843  
citations

147801

31  
h-index

128289

60  
g-index

84  
all docs

84  
docs citations

84  
times ranked

3684  
citing authors

#	ARTICLE	IF	CITATIONS
1	A structural explanation for the mechanism and specificity of plant branching enzymes I and IIb. <i>Journal of Biological Chemistry</i> , 2022, 298, 101395.	3.4	9
2	A hydrophobic residue stabilizes dimers of regulatory ACT-like domains in plant basic helix-loop-helix transcription factors. <i>Journal of Biological Chemistry</i> , 2021, 296, 100708.	3.4	9
3	Design of Large Stokes Shift Fluorescent Proteins Based on Excited State Proton Transfer of an Engineered Photobase. <i>Journal of the American Chemical Society</i> , 2021, 143, 15091-15102.	13.7	33
4	Control of Protonated Schiff Base Excited State Decay within Visual Protein Mimics: A Unified Model for Retinal Chromophores. <i>Chemistry - A European Journal</i> , 2021, 27, 16389-16400.	3.3	9
5	Cg10062 Catalysis Forges a Link between Acetylenecarboxylic Acid and Bacterial Metabolism. <i>Biochemistry</i> , 2021, 60, 3879-3886.	2.5	0
6	Engineering of a Red Fluorogenic Protein/Merocyanine Complex for Live-Cell Imaging. <i>ChemBioChem</i> , 2020, 21, 723-729.	2.6	10
7	Computational and Spectroscopic Characterization of the Photocycle of an Artificial Rhodopsin. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 4245-4252.	4.6	7
8	No-wash live cell imaging with a photoswitchable near-infrared hCRBP-II protein-fluorophore tag. <i>Methods in Enzymology</i> , 2020, 639, 389-411.	1.0	0
9	Human Cellular Retinol Binding Protein II Forms a Domain-Swapped Trimer Representing a Novel Fold and a New Template for Protein Engineering. <i>ChemBioChem</i> , 2020, 21, 3192-3196.	2.6	1
10	Engineering the hCRBP-II Domain-Swapped Dimer into a New Class of Protein Switches. <i>Journal of the American Chemical Society</i> , 2019, 141, 17125-17132.	13.7	9
11	Mimicking Microbial Rhodopsin Isomerization in a Single Crystal. <i>Journal of the American Chemical Society</i> , 2019, 141, 1735-1741.	13.7	10
12	Free-Energy-Based Protein Design: Re-Engineering Cellular Retinoic Acid Binding Protein II Assisted by the Moveable-Type Approach. <i>Journal of the American Chemical Society</i> , 2018, 140, 3483-3486.	13.7	5
13	A Genetically Encoded Ratiometric pH Probe: Wavelength Regulation-Inspired Design of pH Indicators. <i>ChemBioChem</i> , 2018, 19, 1288-1295.	2.6	9
14	A Near-Infrared Photoswitchable Protein-Fluorophore Tag for No-Wash Live Cell Imaging. <i>Angewandte Chemie</i> , 2018, 130, 16315-16319.	2.0	1
15	A Near-Infrared Photoswitchable Protein-Fluorophore Tag for No-Wash Live Cell Imaging. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 16083-16087.	13.8	23
16	Titelbild: Ultrafast Dynamics of a $\beta$ -Super-Photobase ( <i>Angew. Chem.</i> 45/2018). <i>Angewandte Chemie</i> , 2018, 130, 14869-14869.	2.0	0
17	Ultrafast Dynamics of a $\beta$ -Super-Photobase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 14742-14746.	13.8	36
18	Light-Activated Reversible Imine Isomerization: Towards a Photochromic Protein Switch. <i>ChemBioChem</i> , 2016, 17, 407-414.	2.6	13

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19	Domain-Swapped Dimers of Intracellular Lipid-Binding Proteins: Evidence for Ordered Folding Intermediates. <i>Structure</i> , 2016, 24, 1590-1598.	3.3	6
20	Crystal structures of <i>Escherichia coli</i> branching enzyme in complex with cyclodextrins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 641-647.	2.3	32
21	A Photoisomerizing Rhodopsin Mimic Observed at Atomic Resolution. <i>Journal of the American Chemical Society</i> , 2016, 138, 8802-8808.	13.7	25
22	A model for genesis of transcription systems. <i>Transcription</i> , 2016, 7, 1-13.	3.1	18
23	Kinetically and Crystallographically Guided Mutations of a Benzoate CoA Ligase (BadA) Elucidate Mechanism and Expand Substrate Permissivity. <i>Biochemistry</i> , 2015, 54, 6230-6242.	2.5	25
24	Crystal Structures of <i>Escherichia coli</i> Branching Enzyme in Complex with Linear Oligosaccharides. <i>Biochemistry</i> , 2015, 54, 6207-6218.	2.5	52
25	Turn-On Protein Fluorescence: In Situ Formation of Cyanine Dyes. <i>Journal of the American Chemical Society</i> , 2015, 137, 1073-1080.	13.7	58
26	The photochemical determinants of color vision. <i>BioEssays</i> , 2014, 36, 65-74.	2.5	37
27	Structures of holo wild-type human cellular retinol-binding protein II (hCRBP II) bound to retinol and retinal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3226-3232.	2.5	14
28	Toward an Understanding of the Retinal Chromophore in Rhodopsin Mimics. <i>Journal of Physical Chemistry B</i> , 2013, 117, 10053-10070.	2.6	41
29	Rational Design of a Colorimetric pH Sensor from a Soluble Retinoic Acid Chaperone. <i>Journal of the American Chemical Society</i> , 2013, 135, 16111-16119.	13.7	51
30	Tuning the Electronic Absorption of Protein-Embedded All- <i>trans</i> -Retinal. <i>Science</i> , 2012, 338, 1340-1343.	12.6	111
31	Formation of High-Capacity Protein-Adsorbing Membranes through Simple Adsorption of Poly(acrylic) Tj ETQq1 1 0,784314 rgBT /Ove	3.5	47
32	Insights into the Mechanistic Pathway of the <i>Pantoea agglomerans</i> Phenylalanine Aminomutase. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 2898-2902.	13.8	37
33	Probing Wavelength Regulation with an Engineered Rhodopsin Mimic and a C15 Retinal Analogue. <i>ChemPlusChem</i> , 2012, 77, 273-276.	2.8	17
34	An all-aqueous route to polymer brush-modified membranes with remarkable permeabilities and protein capture rates. <i>Journal of Membrane Science</i> , 2012, 389, 117-125.	8.2	33
35	Polymer Brush-Modified Magnetic Nanoparticles for His-Tagged Protein Purification. <i>Langmuir</i> , 2011, 27, 3106-3112.	3.5	113
36	Mechanistic, Mutational, and Structural Evaluation of a <i>Taxus</i> Phenylalanine Aminomutase. <i>Biochemistry</i> , 2011, 50, 2919-2930.	2.5	55

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37	Stereochemistry and Mechanism of a Microbial Phenylalanine Aminomutase. <i>Journal of the American Chemical Society</i> , 2011, 133, 8531-8533.	13.7	53
38	The crystal structure of the calcium-bound con-G[Q6A] peptide reveals a novel metal-dependent helical trimer. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 257-266.	2.6	4
39	Metal ion determinants of conantokin dimerization as revealed in the X-ray crystallographic structure of the Cd <sup>2+</sup> /Mg <sup>2+</sup> -con-T[K71 <sup>3</sup> ] complex. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 667-675.	2.6	4
40	Solution structure of the complex of VEK-30 and plasminogen kringle 2. <i>Journal of Structural Biology</i> , 2010, 169, 349-359.	2.8	21
41	Protein Purification with Polymeric Affinity Membranes Containing Functionalized Poly(acid) Brushes. <i>Biomacromolecules</i> , 2010, 11, 1019-1026.	5.4	56
42	The Crystal Structures of the Open and Catalytically Competent Closed Conformation of <i>Escherichia coli</i> Glycogen Synthase. <i>Journal of Biological Chemistry</i> , 2009, 284, 17796-17807.	3.4	81
43	Dissection of the critical binding determinants of cellular retinoic acid binding protein II by mutagenesis and fluorescence binding assay. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 281-290.	2.6	13
44	Elucidating the exact role of engineered CRABPII residues for the formation of a retinal protonated Schiff base. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 812-822.	2.6	12
45	Oligosaccharide Binding in <i>Escherichia coli</i> Glycogen Synthase. <i>Biochemistry</i> , 2009, 48, 10089-10097.	2.5	32
46	The selectivity of conantokin-G for ion channel inhibition of NR2B subunit-containing NMDA receptors is regulated by amino acid residues in the S2 region of NR2B. <i>Neuropharmacology</i> , 2009, 57, 127-136.	4.1	15
47	Structural analysis of site-directed mutants of cellular retinoic acid-binding protein II addresses the relationship between structural integrity and ligand binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1228-1239.	2.5	12
48	The Lack of Binding of VEK-30, an Internal Peptide from the Group A Streptococcal M-like Protein, PAM, to Murine Plasminogen Is due to Two Amino Acid Replacements in the Plasminogen Kringle-2 Domain. <i>Journal of Biological Chemistry</i> , 2008, 283, 1580-1587.	3.4	19
49	Helix-Helix Interactions between Homo- and Heterodimeric $\hat{I}^3$ -Carboxylglutamate-containing Conantokin Peptides and Their Derivatives. <i>Journal of Biological Chemistry</i> , 2007, 282, 12641-12649.	3.4	19
50	Intermolecular Interactions and Characterization of the Novel Factor Xa Exosite Involved in Macromolecular Recognition and Inhibition: Crystal Structure of Human Gla-domainless Factor Xa Complexed with the Anticoagulant Protein NAPc2 from the Hematophagous Nematode <i>Ancylostoma caninum</i> . <i>Journal of Molecular Biology</i> , 2007, 366, 602-610.	4.2	36
51	The Crystal Structures of the Calcium-Bound con-G and con-T[K71 <sup>3</sup> ] Dimeric Peptides Demonstrate a Metal-Dependent Helix-Forming Motif. <i>Journal of the American Chemical Society</i> , 2007, 129, 1586-1593.	13.7	27
52	Protein Design: Reengineering Cellular Retinoic Acid Binding Protein II into a Rhodopsin Protein Mimic. <i>Journal of the American Chemical Society</i> , 2007, 129, 6140-6148.	13.7	46
53	Engineering a Rhodopsin Protein Mimic. <i>Journal of the American Chemical Society</i> , 2006, 128, 4522-4523.	13.7	33
54	X-ray Crystallographic Structure of the Angiogenesis Inhibitor, Angiostatin, Bound to a Peptide from the Group A Streptococcal Surface Protein PAM. <i>Biochemistry</i> , 2006, 45, 11052-11060.	2.5	23

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55	The Structure and Mechanism of myo-Inositol-1-Phosphate Synthase. , 2006, 39, 157-180.		21
56	The Structure of Apo-wild-type Cellular Retinoic Acid Binding Protein II at 1.4Å... and its Relationship to Ligand Binding and Nuclear Translocation. Journal of Molecular Biology, 2006, 363, 687-701.	4.2	35
57	Co-expression of multiple subunits enables recombinant SNAPC assembly and function for transcription by human RNA polymerases II and III. Protein Expression and Purification, 2006, 48, 215-223.	1.3	6
58	The Unorthodox SNAP50 Zinc Finger Domain Contributes to Cooperative Promoter Recognition by Human SNAPC. Journal of Biological Chemistry, 2006, 281, 31050-31060.	3.4	16
59	Crystal structure of potato tuber ADP-glucose pyrophosphorylase. EMBO Journal, 2005, 24, 694-704.	7.8	143
60	Genetic Perturbation of Glycolysis Results in Inhibition of de Novo Inositol Biosynthesis. Journal of Biological Chemistry, 2005, 280, 41805-41810.	3.4	31
61	The Structure of the 1l-myo-inositol-1-phosphate Synthase-NAD <sup>+</sup> -2-deoxy-d-glucitol 6-(E)-Vinylhomophosphonate Complex Demands a Revision of the Enzyme Mechanism. Journal of Biological Chemistry, 2004, 279, 13889-13895.	3.4	26
62	What the structure of angiostatin may tell us about its mechanism of action. Journal of Thrombosis and Haemostasis, 2004, 2, 23-34.	3.8	36
63	Sugar Tongs Get a Grip on the Starch Granule in Barley ±-Amylase 1. Structure, 2003, 11, 903-904.	3.3	3
64	Structures of NAD <sup>+</sup> - and NADH-bound 1-L-myo-inositol 1-phosphate synthase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1154-1164.	2.5	26
65	NTP-driven Translocation by Human RNA Polymerase II. Journal of Biological Chemistry, 2003, 278, 18303-18312.	3.4	80
66	The Crystal Structure and Mechanism of 1-l-myo-Inositol- 1-phosphate Synthase. Journal of Biological Chemistry, 2002, 277, 9484-9491.	3.4	63
67	Activator recruitment by the general transcription machinery: X-ray structural analysis of the Oct-1 POU domain/human U1 octamer/SNAP190 peptide ternary complex. Genes and Development, 2002, 16, 2772-2777.	5.9	17
68	The X-ray Crystallographic Structure of Escherichia coli Branching Enzyme. Journal of Biological Chemistry, 2002, 277, 42164-42170.	3.4	113
69	The X-ray Crystallographic Structure of the Angiogenesis Inhibitor Angiostatin. Journal of Molecular Biology, 2002, 318, 1009-1017.	4.2	35
70	Crystallization and preliminary X-ray diffraction studies of Escherichia coli branching enzyme. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 359-361.	2.5	4
71	Crystallization of the Oct-1/SNAP190 peptide/DNA complex. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 511-512.	2.5	1
72	Crystallization and preliminary X-ray diffraction studies of human angiostatin. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 513-514.	2.5	0

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73	Crystal Structure of the Msx-1 Homeodomain/DNA Complex. <i>Biochemistry</i> , 2001, 40, 12013-12021.	2.5	58
74	Structural studies of MIP synthase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 348-350.	2.5	10
75	Structural studies of the Msx-1 homeodomain-DNA complex I. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2039-2040.	2.5	3
76	The Crystal Structure of a Hyperthermophilic Archaeal TATA-box Binding Protein. <i>Journal of Molecular Biology</i> , 1996, 264, 1072-1084.	4.2	159
77	Crystal Structure of the Yeast TFIIA/TBP/DNA Complex. <i>Science</i> , 1996, 272, 830-836.	12.6	265
78	Crystal structure of a yeast TBP/TATA-box complex. <i>Nature</i> , 1993, 365, 512-520.	27.8	1,140
79	Stereochemical consequences of a parity restriction on dynamic gearing in tris(9-triptycyl)germanium chloride and tris(9-triptycyl)cyclopropenium perchlorate. <i>Journal of the American Chemical Society</i> , 1990, 112, 3540-3547.	13.7	37
80	A parity restriction on dynamic gearing immobilizes the rotors in tris(9-triptycyl)germanium chloride and tris(9-triptycyl)cyclopropenium perchlorate. <i>Journal of the American Chemical Society</i> , 1989, 111, 2326-2327.	13.7	43
81	Proton NMR spectra of (Z)- and (E)-1,2-di-9-anthrylethene. <i>Journal of Organic Chemistry</i> , 1986, 51, 5471-5472.	3.2	4