

# Wayne A Hendrickson

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

11,205  
citations

126907

33  
h-index

123424

61  
g-index

68  
all docs

68  
docs citations

68  
times ranked

10798  
citing authors

#	ARTICLE	IF	CITATIONS
1	The protein-folding problem: Not yet solved. <i>Science</i> , 2022, 375, 507-507.	12.6	43
2	Structures and gating mechanisms of human bestrophin anion channels. <i>Nature Communications</i> , 2022, 13, .	12.8	8
3	Intermediates in allosteric equilibria of DnaK-ATP interactions with substrate peptides. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 606-617.	2.3	2
4	Structure and activity of SLAC1 channels for stomatal signaling in leaves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35
5	Gating movements and ion permeation in HCN4 pacemaker channels. <i>Molecular Cell</i> , 2021, 81, 2929-2943.e6.	9.7	41
6	Conformational equilibria in allosteric control of Hsp70 chaperones. <i>Molecular Cell</i> , 2021, 81, 3919-3933.e7.	9.7	16
7	Identification of gp120 Residue His105 as a Novel Target for HIV-1 Neutralization by Small-Molecule CD4-Mimics. <i>ACS Medicinal Chemistry Letters</i> , 2021, 12, 1824-1831.	2.8	8
8	Symmetric activation and modulation of the human calcium-sensing receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	23
9	Theory of Allosteric Regulation in Hsp70 Molecular Chaperones. <i>QRB Discovery</i> , 2020, 1, .	1.6	7
10	Structure of the Regulatory Cytosolic Domain of a Eukaryotic Potassium-Chloride Cotransporter. <i>Structure</i> , 2020, 28, 1051-1060.e4.	3.3	11
11	Structure of human GABAB receptor in an inactive state. <i>Nature</i> , 2020, 584, 304-309.	27.8	59
12	Structural and functional characterization of the bestrophin-2 anion channel. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 382-391.	8.2	25
13	PyMDA: microcrystal data assembly using Python. <i>Journal of Applied Crystallography</i> , 2020, 53, 277-281.	4.5	6
14	Structural basis for activity of TRIC counter-ion channels in calcium release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4238-4243.	7.1	26
15	Synchrotron microcrystal native-SAD phasing at a low energy. <i>IUCr</i> , 2019, 6, 532-542.	2.2	14
16	Single-channel recordings of RyR1 at microsecond resolution in CMOS-suspended membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1789-E1798.	7.1	21
17	Structure and activity of lipid bilayer within a membrane-protein transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12985-12990.	7.1	119
18	Sample manipulation and data assembly for robust microcrystal synchrotron crystallography. <i>IUCr</i> , 2018, 5, 238-246.	2.2	30

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19	Structure-based analysis of CysZ-mediated cellular uptake of sulfate. <i>ELife</i> , 2018, 7, .	6.0	10
20	Structural basis for conductance through TRIC cation channels. <i>Nature Communications</i> , 2017, 8, 15103.	12.8	12
21	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 710-728.	2.3	205
22	Contemporary Use of Anomalous Diffraction in Biomolecular Structure Analysis. <i>Methods in Molecular Biology</i> , 2017, 1607, 377-399.	0.9	15
23	Structures of the colossal RyR1 calcium release channel. <i>Current Opinion in Structural Biology</i> , 2016, 39, 144-152.	5.7	25
24	Structure of the STRA6 receptor for retinol uptake. <i>Science</i> , 2016, 353, .	12.6	103
25	Structural Basis for Gating and Activation of RyR1. <i>Cell</i> , 2016, 167, 145-157.e17.	28.9	301
26	Atomic-level analysis of membrane-protein structure. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 464-467.	8.2	50
27	Small-Molecule CD4-Mimics: Structure-Based Optimization of HIV-1 Entry Inhibition. <i>ACS Medicinal Chemistry Letters</i> , 2016, 7, 330-334.	2.8	86
28	Structural basis for phosphatidylinositol-phosphate biosynthesis. <i>Nature Communications</i> , 2015, 6, 8505.	12.8	43
29	Structure and activity of tryptophan-rich TSPO proteins. <i>Science</i> , 2015, 347, 551-555.	12.6	149
30	Structural insights into mis-regulation of protein kinase A in human tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1374-1379.	7.1	78
31	Structural and Mechanistic Insights into the Latrophilin3-FLRT3 Complex that Mediates Glutamatergic Synapse Development. <i>Structure</i> , 2015, 23, 1665-1677.	3.3	42
32	Crystallographic phasing from weak anomalous signals. <i>Current Opinion in Structural Biology</i> , 2015, 34, 99-107.	5.7	39
33	Structure of a mammalian ryanodine receptor. <i>Nature</i> , 2015, 517, 44-49.	27.8	350
34	Preassociated apocalmodulin mediates Ca <sup>2+</sup> -dependent sensitization of activation and inactivation of TMEM16A/16B Ca <sup>2+</sup> -gated Cl <sup>-</sup> channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18213-18218.	7.1	36
35	Anomalous diffraction in crystallographic phase evaluation. <i>Quarterly Reviews of Biophysics</i> , 2014, 47, 49-93.	5.7	92
36	Structure-Based Design, Synthesis and Validation of CD4-Mimetic Small Molecule Inhibitors of HIV-1 Entry: Conversion of a Viral Entry Agonist to an Antagonist. <i>Accounts of Chemical Research</i> , 2014, 47, 1228-1237.	15.6	88

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37	Structure and selectivity in bestrophin ion channels. <i>Science</i> , 2014, 346, 355-359.	12.6	133
38	Structural basis for a pH-sensitive calcium leak across membranes. <i>Science</i> , 2014, 344, 1131-1135.	12.6	86
39	Evolution of diffraction methods for solving crystal structures. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, 51-59.	0.3	23
40	Allosteric opening of the polypeptide-binding site when an Hsp70 binds ATP. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 900-907.	8.2	221
41	Cys-loop ion channels and G-protein coupled receptors as targets for structure-inspired drug discovery. <i>FASEB Journal</i> , 2009, 23, 92.3.	0.5	0
42	Exchange We Can Believe in. <i>Structure</i> , 2008, 16, 1153-1155.	3.3	15
43	Insights into Hsp70 Chaperone Activity from a Crystal Structure of the Yeast Hsp110 Sse1. <i>Cell</i> , 2007, 131, 106-120.	28.9	234
44	Transduction of biochemical signals across cell membranes. <i>Quarterly Reviews of Biophysics</i> , 2005, 38, 321-330.	5.7	14
45	Structure of an HIV gp120 envelope glycoprotein in complex with the CD4 receptor and a neutralizing human antibody. <i>Nature</i> , 1998, 393, 648-659.	27.8	2,788
46	The antigenic structure of the HIV gp120 envelope glycoprotein. <i>Nature</i> , 1998, 393, 705-711.	27.8	1,152
47	Structure of a heparin-linked biologically active dimer of fibroblast growth factor. <i>Nature</i> , 1998, 393, 812-817.	27.8	354
48	Dimeric association and segmental variability in the structure of human CD4. <i>Nature</i> , 1997, 387, 527-530.	27.8	259
49	Crystallographic analysis of the pH-dependent binding of iminobiotin by streptavidin. <i>Protein Science</i> , 1997, 6, 1338-1342.	7.6	14
50	Production of crystallizable fragments of membrane proteins. <i>Journal of Bioenergetics and Biomembranes</i> , 1996, 28, 35-40.	2.3	6
51	Production and crystallization of a selenomethionyl variant of UmuD <sup>2</sup> , an <i>E. coli</i> SOS response protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 506-509.	2.6	1
52	Structure of the UmuD <sup>2</sup> protein and its regulation in response to DNA damage. <i>Nature</i> , 1996, 380, 727-730.	27.8	166
53	Characterization of crystals of the thermostable DNA polymerase I from <i>thermus aquaticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 111-114.	2.6	4
54	Quantification of tertiary structural conservation despite primary sequence drift in the globin fold. <i>Protein Science</i> , 1994, 3, 1706-1711.	7.6	52

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55	Crystallization of a fragment of human fibronectin: Introduction of methionine by site-directed mutagenesis to allow phasing via selenomethionine. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 48-54.	2.6	86
56	Crystal structure of the tyrosine kinase domain of the human insulin receptor. <i>Nature</i> , 1994, 372, 746-754.	27.8	1,105
57	Structure of a C-type mannose-binding protein complexed with an oligosaccharide. <i>Nature</i> , 1992, 360, 127-134.	27.8	953
58	Exploration of disorder in protein structures by X-ray restrained molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 340-358.	2.6	105
59	Crystal structure of an HIV-binding recombinant fragment of human CD4. <i>Nature</i> , 1990, 348, 419-426.	27.8	599
60	Crystallographic structure analysis of lamprey hemoglobin from anomalous dispersion of synchrotron radiation. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 77-88.	2.6	111
61	The reactivity of anti-peptide antibodies is a function of the atomic mobility of sites in a protein. <i>Nature</i> , 1984, 312, 127-134.	27.8	505