

# Andrew M Hemmings

## List of Publications by Year in descending order

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64  
papers

3,490  
citations

136950

32  
h-index

138484

58  
g-index

64  
all docs

64  
docs citations

64  
times ranked

3666  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of a cereal purple acid phytase provides new insights to phytate degradation in plants. <i>Plant Communications</i> , 2022, 3, 100305.	7.7	5
2	Insights to the Structural Basis for the Stereospecificity of the Escherichia coli Phytase, AppA. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6346.	4.1	4
3	Allosteric Site on SHIP2 Identified Through Fluorescent Ligand Screening and Crystallography: A Potential New Target for Intervention. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 3813-3826.	6.4	5
4	Frontiers in PROTACs. <i>Drug Discovery Today</i> , 2021, 26, 2377-2383.	6.4	15
5	Key carboxylate residues for iron transit through the prokaryotic ferritin SynFtn. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	2
6	Snapshots during the catalytic cycle of a histidine acid phytase reveal an induced-fit structural mechanism. <i>Journal of Biological Chemistry</i> , 2020, 295, 17724-17737.	3.4	6
7	Bacterial iron detoxification at the molecular level. <i>Journal of Biological Chemistry</i> , 2020, 295, 17602-17623.	3.4	63
8	Routes of iron entry into, and exit from, the catalytic ferroxidase sites of the prokaryotic ferritin SynFtn. <i>Dalton Transactions</i> , 2020, 49, 1545-1554.	3.3	10
9	An ATP-responsive metabolic cassette comprised of inositol tris/tetrakisphosphate kinase 1 (ITPK1) and inositol pentakisphosphate 2-kinase (IPK1) buffers diphosphoinositol phosphate levels. <i>Biochemical Journal</i> , 2020, 477, 2621-2638.	3.7	40
10	Reaction of O <sub>2</sub> with a diiron protein generates a mixed-valent Fe <sup>2+</sup> /Fe <sup>3+</sup> center and peroxide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2058-2067.	7.1	22
11	Analysis of Two New Arabinosyltransferases Belonging to the Carbohydrate-Active Enzyme (CAZY) Glycosyl Transferase Family1 Provides Insights into Disease Resistance and Sugar Donor Specificity. <i>Plant Cell</i> , 2018, 30, 3038-3057.	6.6	43
12	Discovery of Small Molecule WWP2 Ubiquitin Ligase Inhibitors. <i>Chemistry - A European Journal</i> , 2018, 24, 17677-17680.	3.3	25
13	A Fluorescent Probe Identifies Active Site Ligands of Inositol Pentakisphosphate 2-Kinase. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 8838-8846.	6.4	6
14	A conserved amino acid residue critical for product and substrate specificity in plant triterpene synthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4407-14.	7.1	53
15	Three Aromatic Residues are Required for Electron Transfer during Iron Mineralization in Bacterioferritin. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 14763-14767.	13.8	24
16	Three Aromatic Residues are Required for Electron Transfer during Iron Mineralization in Bacterioferritin. <i>Angewandte Chemie</i> , 2015, 127, 14976-14980.	2.0	14
17	Structural basis for adaptation of lactobacilli to gastrointestinal mucus. <i>Environmental Microbiology</i> , 2014, 16, 888-903.	3.8	102
18	Structural and molecular insights into novel surface-exposed mucus adhesins from <i>Lactobacillus reuteri</i> human strains. <i>Molecular Microbiology</i> , 2014, 92, 543-556.	2.5	29

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19	A Bacterial Homolog of a Eukaryotic Inositol Phosphate Signaling Enzyme Mediates Cross-kingdom Dialog in the Mammalian Gut. <i>Cell Reports</i> , 2014, 6, 646-656.	6.4	88
20	Novel WWP2 ubiquitin ligase isoforms as potential prognostic markers and molecular targets in cancer. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2013, 1832, 2127-2135.	3.8	21
21	Biochemical analysis of a multifunctional cytochrome P450 (CYP51) enzyme required for synthesis of antimicrobial triterpenes in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3360-7.	7.1	137
22	Coiled-coil protein Scy is a key component of a multiprotein assembly controlling polarized growth in <i>Streptomyces</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E397-406.	7.1	90
23	Redox and Chemical Activities of the Hemes in the Sulfur Oxidation Pathway Enzyme SoxAX. <i>Journal of Biological Chemistry</i> , 2012, 287, 40350-40359.	3.4	13
24	Characterization of the active site and calcium binding in cytochrome <i>c</i> nitrite reductases. <i>Biochemical Society Transactions</i> , 2011, 39, 1871-1875.	3.4	8
25	Kinetic and thermodynamic resolution of the interactions between sulfite and the pentahaem cytochrome NrfA from <i>Escherichia coli</i> . <i>Biochemical Journal</i> , 2010, 431, 73-80.	3.7	33
26	Crystal Structure of a Mucus-binding Protein Repeat Reveals an Unexpected Functional Immunoglobulin Binding Activity. <i>Journal of Biological Chemistry</i> , 2009, 284, 32444-32453.	3.4	70
27	A Tetranuclear Cu(I) Cluster in the Metallochaperone Protein CopZ. <i>Biochemistry</i> , 2009, 48, 9324-9326.	2.5	31
28	Mechanistic insights into Cu(I) cluster transfer between the chaperone CopZ and its cognate Cu(I)-transporting P-type ATPase, CopA. <i>Biochemical Journal</i> , 2009, 424, 347-356.	3.7	30
29	A <i>Solanum tuberosum</i> inositol phosphate kinase (StITPK1) displaying inositol phosphateâ€“inositol phosphate and inositol phosphateâ€“ADP phosphotransferase activities. <i>FEBS Letters</i> , 2008, 582, 1731-1737.	2.8	19
30	Role of a Conserved Glutamine Residue in Tuning the Catalytic Activity of <i>Escherichia coli</i> Cytochrome <i>c</i> Nitrite Reductase. <i>Biochemistry</i> , 2008, 47, 3789-3799.	2.5	36
31	<i>Escherichia coli</i> Cytochrome <i>c</i> Nitrite Reductase NrfA. <i>Methods in Enzymology</i> , 2008, 437, 63-77.	1.0	36
32	Spectropotentiometric and Structural Analysis of the Periplasmic Nitrate Reductase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 6425-6437.	3.4	94
33	The SoxYZ Complex Carries Sulfur Cycle Intermediates on a Peptide Swinging Arm*. <i>Journal of Biological Chemistry</i> , 2007, 282, 23194-23204.	3.4	90
34	The crystal structure of the pentahaem <i>c</i> -type cytochrome NrfB and characterization of its solution-state interaction with the pentahaem nitrite reductase NrfA. <i>Biochemical Journal</i> , 2007, 406, 19-30.	3.7	69
35	In Vitro Characterization of a Bacterial Manganese Uptake Regulator of the Fur Superfamily. <i>Biochemistry</i> , 2006, 45, 2686-2698.	2.5	30
36	MLEM Deconvolution of Protein X-Ray Diffraction Images Based on a Multiple-PSF Model. <i>IEEE Transactions on Nanobioscience</i> , 2006, 5, 95-102.	3.3	0

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37	In vitro characterization of the cysteine-rich capping domains in a plant leucine rich repeat protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1043-1053.	2.3	19
38	A different function for a member of an ancient and highly conserved cytochrome P450 family: From essential sterols to plant defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18848-18853.	7.1	169
39	Analysis of ligation and DNA binding by <i>Escherichia coli</i> DNA ligase (LigA). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1749, 113-122.	2.3	37
40	Purification and Spectropotentiometric Characterization of <i>Escherichia coli</i> NrfB, a Decaheme Homodimer That Transfers Electrons to the Decaheme Periplasmic Nitrite Reductase Complex. <i>Journal of Biological Chemistry</i> , 2004, 279, 41333-41339.	3.4	33
41	Purification, crystallization and preliminary X-ray diffraction analysis of a fungal saponin-detoxifying enzyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1331-1333.	2.5	1
42	Multistep Binding of Transition Metals to the H <sup>+</sup> -N <sup>+</sup> -H Endonuclease Toxin Colicin E9. <i>Biochemistry</i> , 2002, 41, 10234-10244.	2.5	22
43	Structural dynamics of the membrane translocation domain of colicin E9 and its interaction with TolB. <i>Journal of Molecular Biology</i> , 2002, 318, 787-804.	4.2	38
44	Structural aspects of the inhibition of DNase and rRNase colicins by their immunity proteins. <i>Biochimie</i> , 2002, 84, 439-446.	2.6	23
45	Structure and Spectroscopy of the Periplasmic Cytochrome <i>c</i> Nitrite Reductase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2002, 41, 2921-2931.	2.5	151
46	Structural basis for the oxidation of thiosulfate by a sulfur cycle enzyme. <i>EMBO Journal</i> , 2002, 21, 5599-5610.	7.8	143
47	Mechanism and cleavage specificity of the H-N-H endonuclease colicin E9 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 2001, 314, 735-749.	4.2	96
48	A 76-residue polypeptide of colicin E9 confers receptor specificity and inhibits the growth of vitamin B12-dependent <i>Escherichia coli</i> 113/3 cells. <i>Molecular Microbiology</i> , 2000, 38, 639-649.	2.5	35
49	NMR studies of metal ion binding to the Zn-finger-like HNH motif of colicin E9. <i>Journal of Inorganic Biochemistry</i> , 2000, 79, 365-370.	3.5	20
50	The structure of TolB, an essential component of the tol-dependent translocation system, and its protein-protein interaction with the translocation domain of colicin E9. <i>Structure</i> , 2000, 8, 57-66.	3.3	83
51	Inhibition of a ribosome-inactivating ribonuclease: the crystal structure of the cytotoxic domain of colicin E3 in complex with its immunity protein. <i>Structure</i> , 2000, 8, 949-960.	3.3	41
52	NMR investigation of the interaction of the inhibitor protein Im9 with its partner DNase. <i>Protein Science</i> , 2000, 9, 1709-1718.	7.6	11
53	Slow conformational dynamics of an endonuclease persist in its complex with its natural protein inhibitor. <i>Protein Science</i> , 2000, 9, 713-720.	7.6	18
54	Homing in on the Role of Transition Metals in the HNH Motif of Colicin Endonucleases. <i>Journal of Biological Chemistry</i> , 1999, 274, 27153-27160.	3.4	70

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55	Preliminary X-ray crystallographic analysis of the complex between the DNAase domain of colicin E9 and its cognate immunity protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 256-259.	2.5	4
56	Structural and mechanistic basis of immunity toward endonuclease colicins. <i>Nature Structural Biology</i> , 1999, 6, 243-252.	9.7	156
57	Open conformation of a flavocytochrome c3 fumarate reductase. <i>Nature Structural Biology</i> , 1999, 6, 1104-1107.	9.7	77
58	NMR study of Ni <sup>2+</sup> binding to the H <sub>4</sub> N <sub>4</sub> C <sub>4</sub> H endonuclease domain of colicin E9. <i>Protein Science</i> , 1999, 8, 1711-1713.	7.6	11
59	Structural parsimony in endonuclease active sites: should the number of homing endonuclease families be redefined?. <i>FEBS Letters</i> , 1999, 463, 1-2.	2.8	102
60	Immunity proteins and their specificity for endonuclease colicins: telling right from wrong in protein-protein recognition. <i>Molecular Microbiology</i> , 1998, 28, 227-233.	2.5	88
61	Dual Recognition and the Role of Specificity-Determining Residues in Colicin E9 DNase~Immunity Protein Interactions. <i>Biochemistry</i> , 1998, 37, 11771-11779.	2.5	54
62	A Peptide that Stimulates Phosphorylation of the Plant Insulin-Binding Protein. Isolation, Primary Structure and cDNA Cloning. <i>FEBS Journal</i> , 1994, 224, 167-172.	0.2	70
63	The 3-D structure of HIV-1 proteinase and the design of antiviral agents for the treatment of AIDS. <i>Trends in Biochemical Sciences</i> , 1990, 15, 425-430.	7.5	78
64	X-ray analysis of HIV-1 proteinase at 2.7 Å... resolution confirms structural homology among retroviral enzymes. <i>Nature</i> , 1989, 342, 299-302.	27.8	477