

Helen R Mott

List of Publications by Year in descending order

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77
papers

4,556
citations

159585

30
h-index

102487

66
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all docs

81
docs citations

81
times ranked

6321
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly of nuclear dimers of PI3K regulatory subunits is regulated by the Cdc42-activated tyrosine kinase ACK. <i>Journal of Biological Chemistry</i> , 2022, 298, 101916.	3.4	10
2	Membrane extraction by calmodulin underpins the disparate signalling of RalA and RalB. <i>BioEssays</i> , 2022, 44, e2200011.	2.5	1
3	Affinity maturation of the RLIP76 Ral binding domain to inform the design of stapled peptides targeting the Ral GTPases. <i>Journal of Biological Chemistry</i> , 2021, 296, 100101.	3.4	5
4	The structure and function of protein kinase C-related kinases (PRKs). <i>Biochemical Society Transactions</i> , 2021, 49, 217-235.	3.4	6
5	A Complete Survey of RhoGDI Targets Reveals Novel Interactions with Atypical Small GTPases. <i>Biochemistry</i> , 2021, 60, 1533-1551.	2.5	17
6	RLIP76: A Structural and Functional Triumvirate. <i>Cancers</i> , 2021, 13, 2206.	3.7	4
7	Molecular subversion of Cdc42 signalling in cancer. <i>Biochemical Society Transactions</i> , 2021, 49, 1425-1442.	3.4	15
8	Progress in the therapeutic inhibition of Cdc42 signalling. <i>Biochemical Society Transactions</i> , 2021, 49, 1443-1456.	3.4	25
9	Calmodulin extracts the Ras family protein RalA from lipid bilayers by engagement with two membrane-targeting motifs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	5
10	¹ H, ¹⁵ N and ¹³ C resonance assignments of the HR1c domain of PRK1, a protein kinase C-related kinase. <i>Biomolecular NMR Assignments</i> , 2020, 14, 245-250.	0.8	2
11	The discovery and maturation of peptide biologics targeting the small G-protein Cdc42: A bioblockade for Ras-driven signaling. <i>Journal of Biological Chemistry</i> , 2020, 295, 2866-2884.	3.4	14
12	NMR resonance assignments for the active and inactive conformations of the small G protein RalA. <i>Biomolecular NMR Assignments</i> , 2020, 14, 87-91.	0.8	2
13	Therapeutic peptides targeting the Ras superfamily. <i>Peptide Science</i> , 2020, 112, e24165.	1.8	10
14	Class IA PI3K regulatory subunits: p110-independent roles and structures. <i>Biochemical Society Transactions</i> , 2020, 48, 1397-1417.	3.4	34
15	Intrinsically disordered proteins and membranes: a marriage of convenience for cell signalling?. <i>Biochemical Society Transactions</i> , 2020, 48, 2669-2689.	3.4	36
16	Activation of STAT transcription factors by the Rho-family GTPases. <i>Biochemical Society Transactions</i> , 2020, 48, 2213-2227.	3.4	26
17	Bioblockades join the assault on small G protein signalling. <i>Seminars in Cancer Biology</i> , 2019, 54, 149-161.	9.6	5
18	Bond swapping from a charge cloud allows flexible coordination of upstream signals through WASP: Multiple regulatory roles for the WASP basic region. <i>Journal of Biological Chemistry</i> , 2018, 293, 15136-15151.	3.4	6

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19	Allostery and dynamics in small G proteins. <i>Biochemical Society Transactions</i> , 2018, 46, 1333-1343.	3.4	19
20	CRIB effector disorder: exquisite function from chaos. <i>Biochemical Society Transactions</i> , 2018, 46, 1289-1302.	3.4	6
21	A dock and coalesce mechanism driven by hydrophobic interactions governs Cdc42 binding with its effector protein ACK. <i>Journal of Biological Chemistry</i> , 2017, 292, 11361-11373.	3.4	13
22	Structural basis for the shielding function of the dynamic trypanosome variant surface glycoprotein coat. <i>Nature Microbiology</i> , 2017, 2, 1523-1532.	13.3	48
23	Genomic Subtypes of Non-invasive Bladder Cancer with Distinct Metabolic Profile and Female Gender Bias in KDM6A Mutation Frequency. <i>Cancer Cell</i> , 2017, 32, 701-715.e7.	16.8	224
24	Cdc42 in actin dynamics: An ordered pathway governed by complex equilibria and directional effector handover. <i>Small GTPases</i> , 2017, 8, 237-244.	1.6	39
25	¹ H, ¹³ C and ¹⁵ N resonance assignments of the Cdc42-binding domain of TOCA1. <i>Biomolecular NMR Assignments</i> , 2016, 10, 407-411.	0.8	1
26	Inhibition of Ral GTPases Using a Stapled Peptide Approach. <i>Journal of Biological Chemistry</i> , 2016, 291, 18310-18325.	3.4	20
27	Investigation of the Interaction between Cdc42 and Its Effector TOCA1. <i>Journal of Biological Chemistry</i> , 2016, 291, 13875-13890.	3.4	27
28	Thermodynamic Mapping of Effector Protein Interfaces with RalA and RalB. <i>Biochemistry</i> , 2015, 54, 1380-1389.	2.5	11
29	Integral membrane protein structure determination using pseudocontact shifts. <i>Journal of Biomolecular NMR</i> , 2015, 61, 197-207.	2.8	30
30	Structures of Ras superfamily effector complexes: What have we learnt in two decades?. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015, 50, 85-133.	5.2	71
31	Structure and function of RLIP76 (RalBP1): an intersection point between Ras and Rho signalling. <i>Biochemical Society Transactions</i> , 2014, 42, 52-58.	3.4	15
32	Atomic structure and hierarchical assembly of a cross- β amyloid fibril. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5468-5473.	7.1	479
33	Differential Binding of RhoA, RhoB, and RhoC to Protein Kinase C-Related Kinase (PRK) Isoforms PRK1, PRK2, and PRK3: PRKs Have the Highest Affinity for RhoB. <i>Biochemistry</i> , 2013, 52, 7999-8011.	2.5	37
34	The Structure of the RLIP76 RhoGAP-Ral Binding Domain Dyad: Fixed Position of the Domains Leads to Dual Engagement of Small G Proteins at the Membrane. <i>Structure</i> , 2013, 21, 2131-2142.	3.3	10
35	¹ H, ¹³ C and ¹⁵ N resonance assignments of the GTPase-activating (GAP) and Ral binding domains (GBD) of RLIP76 (RalBP1). <i>Biomolecular NMR Assignments</i> , 2012, 6, 119-122.	0.8	3
36	In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860.	8.2	6

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37	Mutational Analysis Reveals a Single Binding Interface between RhoA and Its Effector, PRK1. <i>Biochemistry</i> , 2011, 50, 2860-2869.	2.5	14
38	The RalB-RLIP76 Complex Reveals a Novel Mode of Ral-Effector Interaction. <i>Structure</i> , 2010, 18, 985-995.	3.3	40
39	Structure determination of the seven-helix transmembrane receptor sensory rhodopsin II by solution NMR spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 768-774.	8.2	198
40	Structure of Rho Family Targets. , 2010, , 1827-1842.		0
41	RLIP76 (RalBP1). <i>Small GTPases</i> , 2010, 1, 157-160.	1.6	7
42	The Structure of Binder of Arl2 (BART) Reveals a Novel G Protein Binding Domain. <i>Journal of Biological Chemistry</i> , 2009, 284, 992-999.	3.4	9
43	Hydrodynamic gene delivery of baboon trypanosome lytic factor eliminates both animal and human-infective African trypanosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19509-19514.	7.1	58
44	¹ H, ¹³ C and ¹⁵ N resonance assignments for Binder of Arl2, BART. <i>Biomolecular NMR Assignments</i> , 2009, 3, 33-36.	0.8	1
45	Solution Structure and Dynamics of the Small GTPase RalB in Its Active Conformation: Significance for Effector Protein Binding. <i>Biochemistry</i> , 2009, 48, 2192-2206.	2.5	41
46	¹ H, ¹³ C and ¹⁵ N resonance assignments for the active conformation of the small G protein RalB in complex with its effector RLIP76. <i>Biomolecular NMR Assignments</i> , 2008, 2, 179-182.	0.8	3
47	Resonance assignments for the RLIP76 Ral binding domain in its free form and in complex with the small G protein RalB. <i>Biomolecular NMR Assignments</i> , 2008, 2, 191-194.	0.8	3
48	The Rac1 Polybasic Region Is Required for Interaction with Its Effector PRK1. <i>Journal of Biological Chemistry</i> , 2008, 283, 1492-1500.	3.4	46
49	The IQGAP1-Rac1 and IQGAP1-Cdc42 Interactions. <i>Journal of Biological Chemistry</i> , 2008, 283, 1692-1704.	3.4	58
50	Structure of a Glycosylphosphatidylinositol-anchored Domain from a Trypanosome Variant Surface Glycoprotein. <i>Journal of Biological Chemistry</i> , 2008, 283, 3584-3593.	3.4	29
51	Double Mutant Cycle Thermodynamic Analysis of the Hydrophobic Cdc42 ^{ACK} Protein-Protein Interaction. <i>Biochemistry</i> , 2007, 46, 14087-14099.	2.5	9
52	Role of Intermolecular Forces in Defining Material Properties of Protein Nanofibrils. <i>Science</i> , 2007, 318, 1900-1903.	12.6	694
53	Variant Surface Glycoprotein gene repertoires in <i>Trypanosoma brucei</i> have diverged to become strain-specific. <i>BMC Genomics</i> , 2007, 8, 234.	2.8	44
54	¹ H, ¹³ C, and ¹⁵ N resonance assignments for the small G protein RalB in its active conformation. <i>Biomolecular NMR Assignments</i> , 2007, 1, 147-149.	0.8	7

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55	Structure of the C-terminal Domain from <i>Trypanosoma brucei</i> Variant Surface Glycoprotein MITat1.2. <i>Journal of Biological Chemistry</i> , 2005, 280, 7228-7235.	3.4	42
56	Specificity Determinants on Cdc42 for Binding Its Effector Protein ACK. <i>Biochemistry</i> , 2005, 44, 12373-12383.	2.5	18
57	Structural Analysis of the SH3 Domain of β -PIX and Its Interaction with β -p21 Activated Kinase (PAK). <i>Biochemistry</i> , 2005, 44, 10977-10983.	2.5	32
58	Structural Analysis of Rho Protein Complexes. , 2005, , 31-72.		1
59	Fluorescence Properties of Green Fluorescent Protein FRET Pairs Concatenated with the Small G Protein, Rac, and Its Interacting Domain of the Kinase, p21-Activated Kinase. <i>Assay and Drug Development Technologies</i> , 2004, 2, 659-673.	1.2	4
60	Structure of the Sterile β Motif (SAM) Domain of the <i>Saccharomyces cerevisiae</i> Mitogen-activated Protein Kinase Pathway-modulating Protein STE50 and Analysis of Its Interaction with the STE11 SAM. <i>Journal of Biological Chemistry</i> , 2004, 279, 2192-2201.	3.4	42
61	Structural basis of HP1/PXVXL motif peptide interactions and HP1 localisation to heterochromatin. <i>EMBO Journal</i> , 2004, 23, 489-499.	7.8	247
62	Structure Determination of Protein Complexes by NMR. , 2004, 278, 255-288.		11
63	Structure of the GTPase-binding Domain of Sec5 and Elucidation of its Ral Binding Site. <i>Journal of Biological Chemistry</i> , 2003, 278, 17053-17059.	3.4	31
64	Molecular Dissection of the Interaction between the Small G Proteins Rac1 and RhoA and Protein Kinase C-related Kinase 1 (PRK1). <i>Journal of Biological Chemistry</i> , 2003, 278, 50578-50587.	3.4	49
65	Structure of Rho Family Targets. , 2003, , 745-750.		0
66	Structure of the HP1 chromodomain bound to histone H3 methylated at lysine 9. <i>Nature</i> , 2002, 416, 103-107.	27.8	594
67	Structure of Cdc42 bound to the GTPase binding domain of PAK. <i>Nature Structural Biology</i> , 2000, 7, 384-388.	9.7	168
68	Residues in Cdc42 That Specify Binding to Individual CRIB Effector Proteins. <i>Biochemistry</i> , 2000, 39, 1243-1250.	2.5	67
69	Structure of the small G protein Cdc42 bound to the GTPase-binding domain of ACK. <i>Nature</i> , 1999, 399, 384-388.	27.8	172
70	Structural and Functional Analysis of a Mutant Ras Protein That Is Insensitive to Nitric Oxide Activation. <i>Biochemistry</i> , 1997, 36, 3640-3644.	2.5	70
71	NMR Analysis of Interacting Soluble Forms of the Cell-Cell Recognition Molecules CD2 and CD48. <i>Biochemistry</i> , 1996, 35, 5982-5991.	2.5	53
72	The solution structure of the Raf-1 cysteine-rich domain: a novel ras and phospholipid binding site.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 8312-8317.	7.1	201

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73	Four-helix bundle growth factors and their receptors: protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 1995, 5, 114-121.	5.7	82
74	The Solution Structure of the F42A Mutant of Human Interleukin 2. <i>Journal of Molecular Biology</i> , 1995, 247, 979-994.	4.2	47
75	Application of Maximum Entropy Methods to Three-Dimensional NMR Spectroscopy. <i>Journal of Magnetic Resonance Series B</i> , 1993, 101, 218-222.	1.6	10
76	Secondary structure of human interleukin 2 from 3D heteronuclear NMR experiments. <i>Biochemistry</i> , 1992, 31, 7741-7744.	2.5	41
77	Human Interleukin-1 receptor antagonist High yield expression in <i>E. coli</i> and examination of cysteine residues. <i>FEBS Letters</i> , 1992, 310, 63-65.	2.8	25