

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
g-index

81
all docs

81
docs citations

81
times ranked

6321
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Role of Intermolecular Forces in Defining Material Properties of Protein Nanofibrils. <i>Science</i> , 2007, 318, 1900-1903. | 12.6 | 694 |
| 2 | Structure of the HP1 chromodomain bound to histone H3 methylated at lysine 9. <i>Nature</i> , 2002, 416, 103-107. | 27.8 | 594 |
| 3 | Atomic structure and hierarchical assembly of a cross- β^2 amyloid fibril. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5468-5473. | 7.1 | 479 |
| 4 | Structural basis of HP1/PXVXL motif peptide interactions and HP1 localisation to heterochromatin. <i>EMBO Journal</i> , 2004, 23, 489-499. | 7.8 | 247 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | 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 |
| 9 | Structure of Cdc42 bound to the GTPase binding domain of PAK. <i>Nature Structural Biology</i> , 2000, 7, 384-388. | 9.7 | 168 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | Residues in Cdc42 That Specify Binding to Individual CRIB Effector Proteins. <i>Biochemistry</i> , 2000, 39, 1243-1250. | 2.5 | 67 |
| 14 | The IQGAP1-Rac1 and IQGAP1-Cdc42 Interactions. <i>Journal of Biological Chemistry</i> , 2008, 283, 1692-1704. | 3.4 | 58 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

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|----|---|-----|-----------|
| 19 | The Solution Structure of the F42A Mutant of Human Interleukin 2. <i>Journal of Molecular Biology</i> , 1995, 247, 979-994. | 4.2 | 47 |
| 20 | 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 |
| 21 | 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 |
| 22 | Structure of the Sterile $\hat{\pm}$ 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 |
| 23 | 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 |
| 24 | Secondary structure of human interleukin 2 from 3D heteronuclear NMR experiments. <i>Biochemistry</i> , 1992, 31, 7741-7744. | 2.5 | 41 |
| 25 | 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 |
| 26 | The RalB-RLIP76 Complex Reveals a Novel Mode of Ral-Effector Interaction. <i>Structure</i> , 2010, 18, 985-995. | 3.3 | 40 |
| 27 | 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 |
| 28 | 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 |
| 29 | Intrinsically disordered proteins and membranes: a marriage of convenience for cell signalling?. <i>Biochemical Society Transactions</i> , 2020, 48, 2669-2689. | 3.4 | 36 |
| 30 | Class IA PI3K regulatory subunits: p110-independent roles and structures. <i>Biochemical Society Transactions</i> , 2020, 48, 1397-1417. | 3.4 | 34 |
| 31 | Structural Analysis of the SH3 Domain of $\hat{\pm}$ -PIX and Its Interaction with $\hat{\pm}$ -p21 Activated Kinase (PAK) $\hat{\pm}$. <i>Biochemistry</i> , 2005, 44, 10977-10983. | 2.5 | 32 |
| 32 | 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 |
| 33 | Integral membrane protein structure determination using pseudocontact shifts. <i>Journal of Biomolecular NMR</i> , 2015, 61, 197-207. | 2.8 | 30 |
| 34 | 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 |
| 35 | Investigation of the Interaction between Cdc42 and Its Effector TOCA1. <i>Journal of Biological Chemistry</i> , 2016, 291, 13875-13890. | 3.4 | 27 |
| 36 | Activation of STAT transcription factors by the Rho-family GTPases. <i>Biochemical Society Transactions</i> , 2020, 48, 2213-2227. | 3.4 | 26 |

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|----|---|-----|-----------|
| 37 | Human Interleukin-1 receptor antagonist High yield expression in E. coli and examination of cysteine residues. FEBS Letters, 1992, 310, 63-65. | 2.8 | 25 |
| 38 | Progress in the therapeutic inhibition of Cdc42 signalling. Biochemical Society Transactions, 2021, 49, 1443-1456. | 3.4 | 25 |
| 39 | Inhibition of Ral GTPases Using a Stapled Peptide Approach. Journal of Biological Chemistry, 2016, 291, 18310-18325. | 3.4 | 20 |
| 40 | Allostery and dynamics in small G proteins. Biochemical Society Transactions, 2018, 46, 1333-1343. | 3.4 | 19 |
| 41 | Specificity Determinants on Cdc42 for Binding Its Effector Protein ACK. Biochemistry, 2005, 44, 12373-12383. | 2.5 | 18 |
| 42 | A Complete Survey of RhoGDI Targets Reveals Novel Interactions with Atypical Small GTPases. Biochemistry, 2021, 60, 1533-1551. | 2.5 | 17 |
| 43 | Structure and function of RLIP76 (RalBP1): an intersection point between Ras and Rho signalling. Biochemical Society Transactions, 2014, 42, 52-58. | 3.4 | 15 |
| 44 | Molecular subversion of Cdc42 signalling in cancer. Biochemical Society Transactions, 2021, 49, 1425-1442. | 3.4 | 15 |
| 45 | Mutational Analysis Reveals a Single Binding Interface between RhoA and Its Effector, PRK1. Biochemistry, 2011, 50, 2860-2869. | 2.5 | 14 |
| 46 | The discovery and maturation of peptide biologics targeting the small G-protein Cdc42: A bioblockade for Ras-driven signaling. Journal of Biological Chemistry, 2020, 295, 2866-2884. | 3.4 | 14 |
| 47 | A dock and coalesce mechanism driven by hydrophobic interactions governs Cdc42 binding with its effector protein ACK. Journal of Biological Chemistry, 2017, 292, 11361-11373. | 3.4 | 13 |
| 48 | Structure Determination of Protein Complexes by NMR. , 2004, 278, 255-288. | | 11 |
| 49 | Thermodynamic Mapping of Effector Protein Interfaces with RalA and RalB. Biochemistry, 2015, 54, 1380-1389. | 2.5 | 11 |
| 50 | Application of Maximum Entropy Methods to Three-Dimensional NMR Spectroscopy. Journal of Magnetic Resonance Series B, 1993, 101, 218-222. | 1.6 | 10 |
| 51 | 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. Structure, 2013, 21, 2131-2142. | 3.3 | 10 |
| 52 | Therapeutic peptides targeting the Ras superfamily. Peptide Science, 2020, 112, e24165. | 1.8 | 10 |
| 53 | Assembly of nuclear dimers of PI3K regulatory subunits is regulated by the Cdc42-activated tyrosine kinase ACK. Journal of Biological Chemistry, 2022, 298, 101916. | 3.4 | 10 |
| 54 | Double Mutant Cycle Thermodynamic Analysis of the Hydrophobic Cdc42-ACK Protein-Protein Interaction. Biochemistry, 2007, 46, 14087-14099. | 2.5 | 9 |

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|----|--|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | RLIP76 (RalBP1). <i>Small GTPases</i> , 2010, 1, 157-160. | 1.6 | 7 |
| 58 | In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860. | 8.2 | 6 |
| 59 | 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 |
| 60 | CRIB effector disorder: exquisite function from chaos. <i>Biochemical Society Transactions</i> , 2018, 46, 1289-1302. | 3.4 | 6 |
| 61 | The structure and function of protein kinase C-related kinases (PRKs). <i>Biochemical Society Transactions</i> , 2021, 49, 217-235. | 3.4 | 6 |
| 62 | Bioblockades join the assault on small G protein signalling. <i>Seminars in Cancer Biology</i> , 2019, 54, 149-161. | 9.6 | 5 |
| 63 | 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 |
| 64 | 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 |
| 65 | 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 |
| 66 | RLIP76: A Structural and Functional Triumvirate. <i>Cancers</i> , 2021, 13, 2206. | 3.7 | 4 |
| 67 | 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 |
| 68 | 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 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |

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|----|--|-----|-----------|
| 73 | 1H, 13C and 15N resonance assignments of the Cdc42-binding domain of TOCA1. Biomolecular NMR Assignments, 2016, 10, 407-411. | 0.8 | 1 |
| 74 | Structural Analysis of Rho Protein Complexes. , 2005, , 31-72. | | 1 |
| 75 | Membrane extraction by calmodulin underpins the disparate signalling of RalA and RalB. BioEssays, 2022, 44, e2200011. | 2.5 | 1 |
| 76 | Structure of Rho Family Targets. , 2010, , 1827-1842. | | 0 |
| 77 | Structure of Rho Family Targets. , 2003, , 745-750. | | 0 |