

Carla Mattos

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

4,140
citations

201385

27
h-index

182168

51
g-index

87
all docs

87
docs citations

87
times ranked

5577
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Regulation of GTPase function by autophosphorylation. <i>Molecular Cell</i> , 2022, 82, 950-968.e14. | 4.5 | 9 |
| 2 | Computational studies of the principle of dynamic-change-driven protein interactions. <i>Structure</i> , 2022, , . | 1.6 | 8 |
| 3 | Mechanisms of isoform-specific residue influence on GTP-bound HRas, KRas, and NRas. <i>Biophysical Journal</i> , 2022, 121, 3616-3629. | 0.2 | 5 |
| 4 | Raf promotes dimerization of the Ras G-domain with increased allosteric connections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 39 |
| 5 | Molecular dynamics simulations of the Rap1A reveal unique features in the active site. <i>FASEB Journal</i> , 2021, 35, . | 0.2 | 0 |
| 6 | Regulation of RAS function by active site autophosphorylation. <i>FASEB Journal</i> , 2021, 35, . | 0.2 | 0 |
| 7 | Raf promotes dimerization of the Ras G-domain with increased allosteric connections. <i>FASEB Journal</i> , 2021, 35, . | 0.2 | 0 |
| 8 | Data-driven model of the KRas4B/Calmodulin complex. <i>FASEB Journal</i> , 2021, 35, . | 0.2 | 0 |
| 9 | Crystal Structure Reveals the Full Ras-Raf Interface and Advances Mechanistic Understanding of Raf Activation. <i>Biomolecules</i> , 2021, 11, 996. | 1.8 | 35 |
| 10 | DRoP: Automated detection of conserved solvent-binding sites on proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 152-165. | 1.5 | 7 |
| 11 | Water in Ras Superfamily Evolution. <i>Journal of Computational Chemistry</i> , 2020, 41, 402-414. | 1.5 | 3 |
| 12 | Development of a structure-analysis pipeline using multiple-solvent crystal structures of barrier-to-autointegration factor. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1001-1014. | 1.1 | 1 |
| 13 | Isoform-Specific Destabilization of the Active Site Reveals a Molecular Mechanism of Intrinsic Activation of KRas G13D. <i>Cell Reports</i> , 2019, 28, 1538-1550.e7. | 2.9 | 63 |
| 14 | The Structural Basis of the Farnesylated and Methylated KRas4B Interaction with Calmodulin. <i>Structure</i> , 2019, 27, 1647-1659.e4. | 1.6 | 30 |
| 15 | Titration of ionizable groups in proteins using multiple neutron data sets from a single crystal: application to the small GTPase Ras. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 111-115. | 0.4 | 3 |
| 16 | Targeting Cancer from a Structural Biology Perspective. , 2019, , 295-320. | | 0 |
| 17 | The K-Ras, N-Ras, and H-Ras Isoforms: Unique Conformational Preferences and Implications for Targeting Oncogenic Mutants. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2018, 8, a031427. | 2.9 | 36 |
| 18 | Neutron scattering in the biological sciences: progress and prospects. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1129-1168. | 1.1 | 47 |

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|----|--|-----|-----------|
| 19 | Predicting X-ray solution scattering from flexible macromolecules. <i>Protein Science</i> , 2018, 27, 2023-2036. | 3.1 | 3 |
| 20 | K-Ras Populates Conformational States Differently from Its Isoform H-Ras and Oncogenic Mutant K-RasG12D. <i>Structure</i> , 2018, 26, 810-820.e4. | 1.6 | 66 |
| 21 | The small GTPases K-Ras, N-Ras, and H-Ras have distinct biochemical properties determined by allosteric effects. <i>Journal of Biological Chemistry</i> , 2017, 292, 12981-12993. | 1.6 | 105 |
| 22 | An engineered protein antagonist of K-Ras/B-Raf interaction. <i>Scientific Reports</i> , 2017, 7, 5831. | 1.6 | 55 |
| 23 | Balance of Conformational States Affect the Intrinsic Hydrolysis of NRas When Compared to Other Ras Isoforms. <i>FASEB Journal</i> , 2017, 31, 764.14. | 0.2 | 0 |
| 24 | Ras Residue Y71 Promotes Flexibility of Switch I and Switch II. <i>FASEB Journal</i> , 2017, 31, 913.15. | 0.2 | 1 |
| 25 | Expression, purification, crystallization and X-ray data collection for RAS and its mutants. <i>Data in Brief</i> , 2016, 6, 423-427. | 0.5 | 15 |
| 26 | Crystal structures of acetylated HRas K104 mimic K104Q and mutant K104A suggest unique role of K104 in interlobe communication across HRas. <i>FASEB Journal</i> , 2016, 30, 1116.2. | 0.2 | 1 |
| 27 | The Effect of Y71 Mutants on The Allosteric Switch of Ras. <i>FASEB Journal</i> , 2016, 30, 1116.5. | 0.2 | 0 |
| 28 | Allosteric role of R97 on the NRas active site. <i>FASEB Journal</i> , 2016, 30, 1116.6. | 0.2 | 0 |
| 29 | Crystallographic Study of Wild-type and Mg ²⁺ -free Ras GTPase. <i>FASEB Journal</i> , 2016, 30, 1116.3. | 0.2 | 0 |
| 30 | Characterizing Conformational Ensemble of H-Ras, K-Ras, and N-Ras Using Accelerated Molecular Dynamics and Wide-Angle X-ray Solution Scattering (WAXS). <i>FASEB Journal</i> , 2016, 30, 1116.4. | 0.2 | 0 |
| 31 | Tyrosine phosphorylation of RAS by ABL allosterically enhances effector binding. <i>FASEB Journal</i> , 2015, 29, 3750-3761. | 0.2 | 40 |
| 32 | The Ras-Membrane Interface: Isoform-Specific Differences in the Catalytic Domain. <i>Molecular Cancer Research</i> , 2015, 13, 595-603. | 1.5 | 49 |
| 33 | Neutron Crystal Structure of RAS GTPase Puts in Question the Protonation State of the GTP γ -Phosphate. <i>Journal of Biological Chemistry</i> , 2015, 290, 31025-31036. | 1.6 | 44 |
| 34 | Direct Attack on RAS: Intramolecular Communication and Mutation-Specific Effects. <i>Clinical Cancer Research</i> , 2015, 21, 1810-1818. | 3.2 | 73 |
| 35 | Allosteric Effects of the Oncogenic RasQ61L Mutant on Raf-RBD. <i>Structure</i> , 2015, 23, 505-516. | 1.6 | 201 |
| 36 | Ras: structural details to guide direct targeting. <i>Aging</i> , 2015, 7, 344-345. | 1.4 | 4 |

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|----|---|-----|-----------|
| 37 | A Superfamily Reunion: Conserved Water Analysis of Small GTPases Using the Crystallography Tool DRoP. FASEB Journal, 2015, 29, 893.13. | 0.2 | 0 |
| 38 | Probing the Structure and Function of the Helixâ€5 Waterâ€Mediated Network in Hâ€Ras. FASEB Journal, 2015, 29, 893.12. | 0.2 | 0 |
| 39 | Multiple Solvent Crystal Structures of phage P22 tailspike protein: An analysis of binding site hot spots and surface hydration. FASEB Journal, 2015, 29, . | 0.2 | 0 |
| 40 | Expression, Purification, and Crystallization of the Kâ€Ras Q61L and D92Y mutations. FASEB Journal, 2015, 29, 893.10. | 0.2 | 0 |
| 41 | Ras Isoforms Conformational Clustering and Community Networks Studies: Simulating Ras with Accelerated Molecular Dynamics. FASEB Journal, 2015, 29, LB203. | 0.2 | 0 |
| 42 | Probing the Rasâ€membrane Interaction from a Structural Biology Perspective. FASEB Journal, 2015, 29, 893.23. | 0.2 | 0 |
| 43 | Crystallization and Structural Determination of NRas. FASEB Journal, 2015, 29, LB202. | 0.2 | 0 |
| 44 | Neutron Crystal Structure of Ras GTPase sets New Paradigm for GTP Hydrolysis. FASEB Journal, 2015, 29, 893.7. | 0.2 | 0 |
| 45 | DRoP: A Water Analysis Program Identifies Ras-GTP-Specific Pathway of Communication between Membrane-Interacting Regions and the Active Site. Journal of Molecular Biology, 2014, 426, 611-629. | 2.0 | 38 |
| 46 | The Allosteric Switch and Conformational States in Ras GTPase Affected by Small Molecules. The Enzymes, 2013, 33 Pt A, 41-67. | 0.7 | 31 |
| 47 | Introduction: Promoting concept driven teaching strategies in biochemistry and molecular biology. Biochemistry and Molecular Biology Education, 2013, 41, 287-288. | 0.5 | 11 |
| 48 | Multiple Solvent Crystal Structures of Rap1a GTPase. FASEB Journal, 2013, 27, . | 0.2 | 0 |
| 49 | Study of the effect of Ca(OAc)2 concentration on the state of the Allosteric Switch in Ras GTPase. FASEB Journal, 2013, 27, 831.17. | 0.2 | 0 |
| 50 | Study of Ras catalytic mechanism of intrinsic hydrolysis of GTP. FASEB Journal, 2013, 27, 831.10. | 0.2 | 1 |
| 51 | Allosteric modulation of caspase 3 through mutagenesis. Bioscience Reports, 2012, 32, 401-411. | 1.1 | 24 |
| 52 | Shift in the Equilibrium between On and Off States of the Allosteric Switch in Ras-GppNHp Affected by Small Molecules and Bulk Solvent Composition. Biochemistry, 2012, 51, 6114-6126. | 1.2 | 33 |
| 53 | Structurally Conserved Nop56/58 N-terminal Domain Facilitates Archaeal Box C/D Ribonucleoprotein-guided Methyltransferase Activity. Journal of Biological Chemistry, 2012, 287, 19418-19428. | 1.6 | 11 |
| 54 | A Comprehensive Survey of Ras Mutations in Cancer. Cancer Research, 2012, 72, 2457-2467. | 0.4 | 1,602 |

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|----|---|-----|-----------|
| 55 | Thermodynamic, enzymatic and structural effects of removing a salt bridge at the base of loop 4 in (pro)caspase-3. Archives of Biochemistry and Biophysics, 2011, 508, 31-38. | 1.4 | 13 |
| 56 | Analysis of Binding Site Hot Spots on the Surface of Ras GTPase. Journal of Molecular Biology, 2011, 413, 773-789. | 2.0 | 139 |
| 57 | Allosteric Modulation of Ras-GTP Is Linked to Signal Transduction through RAF Kinase. Journal of Biological Chemistry, 2011, 286, 3323-3331. | 1.6 | 74 |
| 58 | Collaboration within the Laboratory Group. FASEB Journal, 2011, 25, 207.1. | 0.2 | 0 |
| 59 | Commentary: Biochemistry and molecular biology educators launch national network. Biochemistry and Molecular Biology Education, 2010, 38, 266-267. | 0.5 | 1 |
| 60 | Allosteric modulation of Ras positions Q61 for a direct role in catalysis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4931-4936. | 3.3 | 211 |
| 61 | Allosteric modulation of Ras: a novel role for Glutamine 61 in catalysis. FASEB Journal, 2010, 24, 867.4. | 0.2 | 0 |
| 62 | Multiple solvent crystal structures of ribonuclease A: An assessment of the method. Proteins: Structure, Function and Bioinformatics, 2009, 76, 861-881. | 1.5 | 36 |
| 63 | Mechanism of intrinsic hydrolysis in Ras and the effect of Raf on oncogenic Ras mutants. FASEB Journal, 2009, 23, 204.3. | 0.2 | 0 |
| 64 | Minimizing frustration by folding in an aqueous environment. Archives of Biochemistry and Biophysics, 2008, 469, 118-131. | 1.4 | 18 |
| 65 | Rapid Folding and Unfolding of Apaf-1 CARD. Journal of Molecular Biology, 2007, 369, 290-304. | 2.0 | 11 |
| 66 | Transformation Efficiency of RasQ61 Mutants Linked to Structural Features of the Switch Regions in the Presence of Raf. Structure, 2007, 15, 1618-1629. | 1.6 | 97 |
| 67 | Multiple solvent crystal structures of RNase A. FASEB Journal, 2007, 21, A1010. | 0.2 | 0 |
| 68 | The structures of Q61 Ras mutants solved in a new space group reveals insights into the mechanism of intrinsic GTPase activity. FASEB Journal, 2007, 21, A640. | 0.2 | 0 |
| 69 | Barrier to Autointegration Factor (BAF): purification, crystallization and multiple solvent crystal structure. FASEB Journal, 2007, 21, A638. | 0.2 | 0 |
| 70 | Multiple Solvent Crystal Structures of Chymotrypsin: Comparison with Elastase. FASEB Journal, 2007, 21, A639. | 0.2 | 0 |
| 71 | Removing the barrier between teaching in the classroom and research in the laboratory. FASEB Journal, 2007, 21, A39. | 0.2 | 0 |
| 72 | The crystal structures of Rap1a bound to GTP and GppNHp. FASEB Journal, 2007, 21, A640. | 0.2 | 0 |

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|----|--|-----|-----------|
| 73 | Multiple Solvent Crystal Structures: Probing Binding Sites, Plasticity and Hydration. <i>Journal of Molecular Biology</i> , 2006, 357, 1471-1482. | 2.0 | 138 |
| 74 | Comparison between experimental Multiple Solvent Crystal Structures and Computational Solvent Mapping of Hen Eggwhite Lysozyme. <i>FASEB Journal</i> , 2006, 20, A476. | 0.2 | 0 |
| 75 | Crystal Structures of Ral-GppNHp and Ral-GDP Reveal Two Binding Sites that Are Also Present in Ras and Rap. <i>Structure</i> , 2004, 12, 2025-2036. | 1.6 | 35 |
| 76 | X-ray structural and simulation analysis of a protein mutant: The value of a combined approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 733-742. | 1.5 | 2 |
| 77 | Organic Solvents Order the Dynamic Switch II in Ras Crystals. <i>Structure</i> , 2003, 11, 747-751. | 1.6 | 39 |
| 78 | Protein-water interactions in a dynamic world. <i>Trends in Biochemical Sciences</i> , 2002, 27, 203-208. | 3.7 | 187 |
| 79 | Analysis of the binding surfaces of proteins. , 1999, 19, 321-331. | | 35 |
| 80 | Locating and characterizing binding sites on proteins. <i>Nature Biotechnology</i> , 1996, 14, 595-599. | 9.4 | 247 |
| 81 | Analogous inhibitors of elastase do not always bind analogously. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 55-58. | 3.6 | 88 |
| 82 | Analysis of Two-residue Turns in Proteins. <i>Journal of Molecular Biology</i> , 1994, 238, 733-747. | 2.0 | 67 |
| 83 | Isoform-Specific Destabilization of the Active Site Reveals Molecular Mechanism of Intrinsic Activation of KRas G13D. <i>SSRN Electronic Journal</i> , 0, , . | 0.4 | 0 |