

Carla Mattos

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4364656/publications.pdf>

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	A Comprehensive Survey of Ras Mutations in Cancer. <i>Cancer Research</i> , 2012, 72, 2457-2467.	0.4	1,602
2	Locating and characterizing binding sites on proteins. <i>Nature Biotechnology</i> , 1996, 14, 595-599.	9.4	247
3	Allosteric modulation of Ras positions Q61 for a direct role in catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4931-4936.	3.3	211
4	Allosteric Effects of the Oncogenic RasQ61L Mutant on Raf-RBD. <i>Structure</i> , 2015, 23, 505-516.	1.6	201
5	Protein-water interactions in a dynamic world. <i>Trends in Biochemical Sciences</i> , 2002, 27, 203-208.	3.7	187
6	Analysis of Binding Site Hot Spots on the Surface of Ras GTPase. <i>Journal of Molecular Biology</i> , 2011, 413, 773-789.	2.0	139
7	Multiple Solvent Crystal Structures: Probing Binding Sites, Plasticity and Hydration. <i>Journal of Molecular Biology</i> , 2006, 357, 1471-1482.	2.0	138
8	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
9	Transformation Efficiency of RasQ61 Mutants Linked to Structural Features of the Switch Regions in the Presence of Raf. <i>Structure</i> , 2007, 15, 1618-1629.	1.6	97
10	Analogous inhibitors of elastase do not always bind analogously. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 55-58.	3.6	88
11	Allosteric Modulation of Ras-GTP Is Linked to Signal Transduction through RAF Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 3323-3331.	1.6	74
12	Direct Attack on RAS: Intramolecular Communication and Mutation-Specific Effects. <i>Clinical Cancer Research</i> , 2015, 21, 1810-1818.	3.2	73
13	Analysis of Two-residue Turns in Proteins. <i>Journal of Molecular Biology</i> , 1994, 238, 733-747.	2.0	67
14	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
15	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
16	An engineered protein antagonist of K-Ras/B-Raf interaction. <i>Scientific Reports</i> , 2017, 7, 5831.	1.6	55
17	The Ras-Membrane Interface: Isoform-Specific Differences in the Catalytic Domain. <i>Molecular Cancer Research</i> , 2015, 13, 595-603.	1.5	49
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

#	ARTICLE	IF	CITATIONS
19	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
20	Tyrosine phosphorylation of RAS by ABL allosterically enhances effector binding. <i>FASEB Journal</i> , 2015, 29, 3750-3761.	0.2	40
21	Organic Solvents Order the Dynamic Switch II in Ras Crystals. <i>Structure</i> , 2003, 11, 747-751.	1.6	39
22	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
23	DRoP: A Water Analysis Program Identifies Ras-GTP-Specific Pathway of Communication between Membrane-Interacting Regions and the Active Site. <i>Journal of Molecular Biology</i> , 2014, 426, 611-629.	2.0	38
24	Multiple solvent crystal structures of ribonuclease A: An assessment of the method. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 861-881.	1.5	36
25	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
26	Analysis of the binding surfaces of proteins. , 1999, 19, 321-331.		35
27	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
28	Crystal Structure Reveals the Full Ras-Raf Interface and Advances Mechanistic Understanding of Raf Activation. <i>Biomolecules</i> , 2021, 11, 996.	1.8	35
29	Shift in the Equilibrium between On and Off States of the Allosteric Switch in Ras-GppNHp Affected by Small Molecules and Bulk Solvent Composition. <i>Biochemistry</i> , 2012, 51, 6114-6126.	1.2	33
30	The Allosteric Switch and Conformational States in Ras GTPase Affected by Small Molecules. <i>The Enzymes</i> , 2013, 33 Pt A, 41-67.	0.7	31
31	The Structural Basis of the Farnesylated and Methylated KRas4B Interaction with Calmodulin. <i>Structure</i> , 2019, 27, 1647-1659.e4.	1.6	30
32	Allosteric modulation of caspase 3 through mutagenesis. <i>Bioscience Reports</i> , 2012, 32, 401-411.	1.1	24
33	Minimizing frustration by folding in an aqueous environment. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 118-131.	1.4	18
34	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
35	Thermodynamic, enzymatic and structural effects of removing a salt bridge at the base of loop 4 in (pro)caspase-3. <i>Archives of Biochemistry and Biophysics</i> , 2011, 508, 31-38.	1.4	13
36	Rapid Folding and Unfolding of Apaf-1 CARD. <i>Journal of Molecular Biology</i> , 2007, 369, 290-304.	2.0	11

#	ARTICLE	IF	CITATIONS
37	Structurally Conserved Nop56/58 N-terminal Domain Facilitates Archaeal Box C/D Ribonucleoprotein-guided Methyltransferase Activity. <i>Journal of Biological Chemistry</i> , 2012, 287, 19418-19428.	1.6	11
38	Introduction: Promoting concept driven teaching strategies in biochemistry and molecular biology. <i>Biochemistry and Molecular Biology Education</i> , 2013, 41, 287-288.	0.5	11
39	Regulation of GTPase function by autophosphorylation. <i>Molecular Cell</i> , 2022, 82, 950-968.e14.	4.5	9
40	Computational studies of the principle of dynamic-change-driven protein interactions. <i>Structure</i> , 2022, , .	1.6	8
41	DRoP: Automated detection of conserved solvent-binding sites on proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 152-165.	1.5	7
42	Mechanisms of isoform-specific residue influence on GTP-bound HRas, KRas, and NRas. <i>Biophysical Journal</i> , 2022, 121, 3616-3629.	0.2	5
43	Ras: structural details to guide direct targeting. <i>Aging</i> , 2015, 7, 344-345.	1.4	4
44	Predicting X-ray solution scattering from flexible macromolecules. <i>Protein Science</i> , 2018, 27, 2023-2036.	3.1	3
45	Water in Ras Superfamily Evolution. <i>Journal of Computational Chemistry</i> , 2020, 41, 402-414.	1.5	3
46	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
47	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
48	Commentary: Biochemistry and molecular biology educators launch national network. <i>Biochemistry and Molecular Biology Education</i> , 2010, 38, 266-267.	0.5	1
49	Study of Ras catalytic mechanism of intrinsic hydrolysis of GTP. <i>FASEB Journal</i> , 2013, 27, 831.10.	0.2	1
50	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
51	Ras Residue Y71 Promotes Flexibility of Switch I and Switch II. <i>FASEB Journal</i> , 2017, 31, 913.15.	0.2	1
52	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
53	Molecular dynamics simulations of the Rap1A reveal unique features in the active site. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
54	Regulation of RAS function by active site autophosphorylation. <i>FASEB Journal</i> , 2021, 35, .	0.2	0

#	ARTICLE	IF	CITATIONS
55	Raf promotes dimerization of the Ras Gâ€domain with increased allosteric connections. FASEB Journal, 2021, 35, .	0.2	0
56	Dataâ€driven model of the KRas4B/Calmodulin complex. FASEB Journal, 2021, 35, .	0.2	0
57	Comparison between experimental Multiple Solvent Crystal Structures and Computational Solvent Mapping of Hen Eggwhite Lysozyme. FASEB Journal, 2006, 20, A476.	0.2	0
58	Multiple solvent crystal structures of RNase A. FASEB Journal, 2007, 21, A1010.	0.2	0
59	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
60	Barrierâ€toâ€autointegration Factor (BAF): purification, crystallization and multiple solvent crystal structure. FASEB Journal, 2007, 21, A638.	0.2	0
61	Multiple Solvent Crystal Structures of Chymotrypsin: Comparison with Elastase. FASEB Journal, 2007, 21, A639.	0.2	0
62	Removing the barrier between teaching in the classroom and research in the laboratory. FASEB Journal, 2007, 21, A39.	0.2	0
63	The crystal structures of Rap1a bound to GTP and GppNHp. FASEB Journal, 2007, 21, A640.	0.2	0
64	Mechanism of intrinsic hydrolysis in Ras and the effect of Raf on oncogenic Ras mutants. FASEB Journal, 2009, 23, 204.3.	0.2	0
65	Allosteric modulation of Ras: a novel role for Glutamine 61 in catalysis. FASEB Journal, 2010, 24, 867.4.	0.2	0
66	Collaboration within the Laboratory Group. FASEB Journal, 2011, 25, 207.1.	0.2	0
67	Multiple Solvent Crystal Structures of Rap1a GTPase. FASEB Journal, 2013, 27, .	0.2	0
68	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
69	A Superfamily Reunion: Conserved Water Analysis of Small GTPases Using the Crystallography Tool DRoP. FASEB Journal, 2015, 29, 893.13.	0.2	0
70	Probing the Structure and Function of the Helixâ€5 Waterâ€Mediated Network in Hâ€Ras. FASEB Journal, 2015, 29, 893.12.	0.2	0
71	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
72	Expression, Purification, and Crystallization of the Kâ€Ras Q61L and D92Y mutations. FASEB Journal, 2015, 29, 893.10.	0.2	0

#	ARTICLE	IF	CITATIONS
73	Ras Isoforms Conformational Clustering and Community Networks Studies: Simulating Ras with Accelerated Molecular Dynamics. FASEB Journal, 2015, 29, LB203.	0.2	0
74	Probing the Ras-membrane Interaction from a Structural Biology Perspective. FASEB Journal, 2015, 29, 893.23.	0.2	0
75	Crystallization and Structural Determination of NRas. FASEB Journal, 2015, 29, LB202.	0.2	0
76	Neutron Crystal Structure of Ras GTPase sets New Paradigm for GTP Hydrolysis. FASEB Journal, 2015, 29, 893.7.	0.2	0
77	The Effect of Y71 Mutants on The Allosteric Switch of Ras. FASEB Journal, 2016, 30, 1116.5.	0.2	0
78	Allosteric role of R97 on the NRas active site. FASEB Journal, 2016, 30, 1116.6.	0.2	0
79	Crystallographic Study of Wild-type and Mg ²⁺ -free Ras GTPase. FASEB Journal, 2016, 30, 1116.3.	0.2	0
80	Characterizing Conformational Ensemble of H-, K-, and N-Ras Using Accelerated Molecular Dynamics and Wide-Angle X-ray Solution Scattering (WAXS). FASEB Journal, 2016, 30, 1116.4.	0.2	0
81	Balance of Conformational States Affect the Intrinsic Hydrolysis of NRas When Compared to Other Ras Isoforms. FASEB Journal, 2017, 31, 764.14.	0.2	0
82	Targeting Cancer from a Structural Biology Perspective. , 2019, , 295-320.		0
83	Isoform-Specific Destabilization of the Active Site Reveals Molecular Mechanism of Intrinsic Activation of KRas G13D. SSRN Electronic Journal, 0, , .	0.4	0