Amy H Andreotti

List of Publications by Year
in descending order

52	2,114	304743	243625
papers	citations	22 h-index	44 g-index

58	58	58	2235
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Conformational State of the BTK Substrate PLCÎ³ Contributes to Ibrutinib Resistance. Journal of Molecular Biology, 2022, 434, 167422.	4.2	4
2	Conformational switches that control the TEC kinase â€“ PLCÎ³ signaling axis. Journal of Structural Biology: X, 2022, 6, 100061.	1.3	4
3	Editorial: Targeting Bruton Tyrosine Kinase. Frontiers in Cell and Developmental Biology, 2022, 10, 909655.	3.7	1
4	Reining in BTK: Interdomain Interactions and Their Importance in the Regulatory Control of BTK. Frontiers in Cell and Developmental Biology, 2021, 9, 655489.	3.7	7
5	Differential impact of BTK active site inhibitors on the conformational state of full-length BTK. ELife, 2020, 9, .	6.0	25
6	The SH3 domains of the protein kinases ITK and LCK compete for adjacent sites on T cellâ€“specific adapter protein. Journal of Biological Chemistry, 2019, 294, 15480-15494.	3.4	9
7	Dynamic regulatory features of the protein tyrosine kinases. Biochemical Society Transactions, 2019, 47, 1101-1116.	3.4	25
8	Lipid-targeting pleckstrin homology domain turns its autoinhibitory face toward the TEC kinases. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21539-21544.	7.1	19
9	Multidomain Control Over TEC Kinase Activation State Tunes the T Cell Response. Annual Review of Immunology, 2018, 36, 549-578.	21.8	25
10	An Autoinhibitory Role for the Pleckstrin Homology Domain of Interleukin-2-Inducible Tyrosine Kinase and Its Interplay with Canonical Phospholipid Recognition. Biochemistry, 2017, 56, 2938-2949.	2.5	18
11	Achieving a Graded Immune Response: BTK Adopts a Range of Active/Inactive Conformations Dictated by Multiple Interdomain Contacts. Structure, 2017, 25, 1481-1494.e4.	3.3	44
12	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. PLoS Computational Biology, 2016, 12, e1004826.	3.2	40
13	Dynamics of the <scp>T</scp>ecâ€family tyrosine kinase <scp>SH</scp>3 domains. Protein Science, 2016, 25, 852-864.	7.6	8
14	Role of Reversible Histidine Coordination in Hydroxylamine Reduction by Plant Hemoglobins (Phytoglobins). Biochemistry, 2016, 55, 5809-5817.	2.5	9
15	A Selective NMR Probe to Monitor the Conformational Transition from Inactive to Active Kinase. ACS Chemical Biology, 2015, 10, 262-268.	3.4	8
16	Electron self-exchange in hemoglobins revealed by deutero-hemin substitution. Journal of Inorganic Biochemistry, 2015, 150, 139-147.	3.5	6
17	Defining a Two-pronged Structural Model for PB1 (Phox/Bem1p) Domain Interaction in Plant Auxin Responses. Journal of Biological Chemistry, 2015, 290, 12868-12878.	3.4	31
18	Scaffold Protein SLP-76 Primes PLCÎ³1 for Activation by ITK-Mediated Phosphorylation. Journal of Molecular Biology, 2015, 427, 2734-2747.	4.2	18

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19	Calmodulin and PI(3,4,5)P ₃ cooperatively bind to the Itk pleckstrin homology domain to promote efficient calcium signaling and IL-17A production. Science Signaling, 2014, 7, ra74.	3.6	22
20	A Conserved Isoleucine Maintains the Inactive State of Bruton's Tyrosine Kinase. Journal of Molecular Biology, 2014, 426, 3656-3669.	4.2	10
21	Substrate Recognition of PLCÎ³1 via a Specific Docking Surface on Itk. Journal of Molecular Biology, 2013, 425, 683-696.	4.2	16
22	Activation Loop Dynamics Determine the Different Catalytic Efficiencies of B Cellâ€“ and T Cellâ€“Specific Tec Kinases. Science Signaling, 2013, 6, ra76.	3.6	27
23	In Vivo Consequences of Disrupting SH3-Mediated Interactions of the Inducible T-Cell Kinase. Journal of Signal Transduction, 2012, 2012, 1-10.	2.0	8
24	Structure of the interleukin-2 tyrosine kinase Src homology 2 domain; comparison between X-ray and NMR-derived structures. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 145-153.	0.7	7
25	Rescue of the aggregation prone Itk Pleckstrin Homology domain by two mutations derived from the related kinases, Btk and Tec. Protein Science, 2012, 21, 1288-1297.	7.6	12
26	Controlling the Activity of the Tec Kinase Itk by Mutation of the Phenylalanine Gatekeeper Residue. Biochemistry, 2011, 50, 221-229.	2.5	14
27	Purification, crystallization and preliminary crystallographic analysis of the SH2 domain of IL-2-inducible T-cell kinase. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 269-273.	0.7	1
28	Disrupting the Intermolecular Self-Association of Itk Enhances T Cell Signaling. Journal of Immunology, 2010, 184, 4228-4235.	0.8	13
29	T-Cell Signaling Regulated by the Tec Family Kinase, Itk. Cold Spring Harbor Perspectives in Biology, 2010, 2, a002287-a002287.	5.5	200
30	Identification of an Allosteric Signaling Network within Tec Family Kinases. Journal of Molecular Biology, 2010, 403, 231-242.	4.2	39
31	Itk tyrosine kinase substrate docking is mediated by a nonclassical SH2 domain surface of PLCÎ³1. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21143-21148.	7.1	35
32	Conformational snapshots of Tec kinases during signaling. Immunological Reviews, 2009, 228, 74-92.	6.0	17
33	Proline Isomerization Preorganizes the Itk SH2 Domain for Binding to the Itk SH3 Domain. Journal of Molecular Biology, 2009, 387, 726-743.	4.2	37
34	SH2-Dependent Autophosphorylation within the Tec Family Kinase Itk. Journal of Molecular Biology, 2009, 391, 164-177.	4.2	17
35	Murine Itk SH3 domain. Journal of Biomolecular NMR, 2008, 40, 285-290.	2.8	9
36	Bacterial expression and purification of Interleukin-2 Tyrosine kinase: Single step separation of the chaperonin impurity. Protein Expression and Purification, 2008, 60, 194-197.	1.3	46

#	Article	IF	Citations
37	Positive regulation of Itk PH domain function by soluble IP4 is required for thymocyte positive selection but dispensable for negative selection. FASEB Journal, 2008, 22, 843.8.	0.5	0
38	Positive Regulation of Itk PH Domain Function by Soluble IP4. Science, 2007, 316, 886-889.	12.6	100
39	Mechanism and Functional Significance of Itk Autophosphorylation. Journal of Molecular Biology, 2007, 373, 1281-1292.	4.2	31
40	A Remote Substrate Docking Mechanism for the Tec Family Tyrosine Kinases. Biochemistry, 2007, 46, 5595-5603.	2.5	41
41	The Linker between SH2 and Kinase Domains Positively Regulates Catalysis of the Tec Family Kinases. Biochemistry, 2007, 46, 5455-5462.	2.5	48
42	Molecular Details of Itk Activation by Prolyl Isomerization and Phospholigand Binding: The NMR Structure of the Itk SH2 Domain Bound to a Phosphopeptide. Journal of Molecular Biology, 2006, 357, 550-561.	4.2	41
43	Opening the pore hinges on proline. Nature Chemical Biology, 2006, 2, 13-14.	8.0	15
44	A case study of proline isomerization in cell signaling. Frontiers in Bioscience - Landmark, 2005, 10, 385.	3.0	27
45	Cyclophilin A Regulates TCR Signal Strength in CD4+ T Cells via a Proline-Directed Conformational Switch in Itk. Immunity, 2004, 21, 189-201.	14.3	194
46	Native State Proline Isomerization:Â An Intrinsic Molecular Switchâ€. Biochemistry, 2003, 42, 9515-9524.	2.5	239
47	Determinants of Intra versus Intermolecular Self-association Within the Regulatory Domains of Rlk and Itk. Journal of Molecular Biology, 2003, 329, 1011-1020.	4.2	31
48	Ligand Specificity Modulated by Prolyl Imide Bond Cis/Trans Isomerization in the Itk SH2 Domain:Â A Quantitative NMR Study. Journal of the American Chemical Society, 2003, 125, 15706-15707.	13.7	40
49	Regulation of the tyrosine kinase Itk by the peptidyl-prolyl isomerase cyclophilin A. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1899-1904.	7.1	262
50	Structural characterization of a proline-driven conformational switch within the Itk SH2 domain. Nature Structural Biology, 2002, 9, 900-905.	9.7	111
51	Competing modes of selfâ€association in the regulatory domains of Bruton's tyrosine kinase: Intramolecular contact versus asymmetric homodimerization. Protein Science, 2002, 11, 36-57.	7.6	24
52	A specific intermolecular association between the regulatory domains of a tec family kinase. Journal of Molecular Biology, 2000, 302, 607-623.	4.2	78