Sandra B Gabelli

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7758002/publications.pdf

Version: 2024-02-01

98 papers	5,840 citations	117625 34 h-index	79698 73 g-index
104 all docs	104 docs citations	104 times ranked	7843 citing authors

#	Article	IF	Citations
1	Elusive structure of mammalian DGKs. Advances in Biological Regulation, 2022, 83, 100847.	2.3	3
2	ATP synthase K+- and H+-fluxes drive ATP synthesis and enable mitochondrial K+-â€œuniporterâ€•function: II. Ion and ATP synthase flux regulation. Function, 2022, 3, zqac001.	2.3	20
3	ATP Synthase K+- and H+-Fluxes Drive ATP Synthesis and Enable Mitochondrial K+-â€œUniporterâ€• Function: I. Characterization of Ion Fluxes. Function, 2022, 3, zqab065.	2.3	25
4	A simple technique to classify diffraction data from dynamic proteins according to individual polymorphs. Acta Crystallographica Section D: Structural Biology, 2022, 78, 268-277.	2.3	5
5	Enzymatic analysis of WWP2 E3 ubiquitin ligase using protein microarrays identifies autophagy-related substrates. Journal of Biological Chemistry, 2022, 298, 101854.	3.4	6
6	Development of high-affinity nanobodies specific for NaV1.4 and NaV1.5 voltage-gated sodium channel isoforms. Journal of Biological Chemistry, 2022, 298, 101763.	3.4	7
7	Multifaceted Regulation of Akt by Diverse C-Terminal Post-translational Modifications. ACS Chemical Biology, 2022, 17, 68-76.	3.4	7
8	TCR-mimic bispecific antibodies to target the HIV-1 reservoir. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123406119.	7.1	10
9	Navigating the intricacies of cellular machinery. Journal of Biological Chemistry, 2021, 296, 100832.	3.4	1
10	Bdellovibrio bacteriovorus Hydrolyses its Prey DNA using the Dctpase Activity of Bd2220. Biophysical Journal, 2021, 120, 306a.	0.5	0
11	Bispecific antibodies targeting mutant RAS neoantigens. Science Immunology, 2021, 6, .	11.9	106
12	Targeting loss of heterozygosity for cancer-specific immunotherapy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	39
13	TCR Î² chainâ€“directed bispecific antibodies for the treatment of T cell cancers. Science Translational Medicine, 2021, 13, .	12.4	30
14	Targeting a neoantigen derived from a common TP53 mutation. Science, 2021, 371, .	12.6	194
15	Targeting public neoantigens for cancer immunotherapy. Nature Cancer, 2021, 2, 487-497.	13.2	79
16	Antibodies response induced by recombinant virus-like particles from Triatoma virus and chimeric antigens from Trypanosoma cruzi. Vaccine, 2021, 39, 4723-4732.	3.8	3
17	Structural engineering of chimeric antigen receptors targeting HLA-restricted neoantigens. Nature Communications, 2021, 12, 5271.	12.8	17
18	Structural basis of cytoplasmic NaV1.5 and NaV1.4 regulation. Journal of General Physiology, 2021, 153, .	1.9	15

#	Article	IF	Citations
19	The structural basis of PTEN regulation by multi-site phosphorylation. Nature Structural and Molecular Biology, 2021, 28, 858-868.	8.2	20
20	Bisphosphonate-Based Molecules as Potential New Antiparasitic Drugs. Molecules, 2020, 25, 2602.	3.8	18
21	Structure of the RECK CC domain, an evolutionary anomaly. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15104-15111.	7.1	10
22	Identifying Structural Determinants of Product Specificity in Leishmania major Farnesyl Diphosphate Synthase. Biochemistry, 2020, 59, 2751-2759.	2.5	5
23	Allosteric Activation of PI3KÎ± Results in Dynamic Access to Catalytically Competent Conformations. Structure, 2020, 28, 465-474.e5.	3.3	13
24	An engineered antibody fragment targeting mutant Î²-catenin via major histocompatibility complex I neoantigen presentation. Journal of Biological Chemistry, 2019, 294, 19322-19334.	3.4	15
25	Structural analyses of NudT16â€“ADP-ribose complexes direct rational design of mutants with improved processing of poly(ADP-ribosyl)ated proteins. Scientific Reports, 2019, 9, 5940.	3.3	15
26	Structural Determinants of Isoform Selectivity in PI3K Inhibitors. Biomolecules, 2019, 9, 82.	4.0	55
27	Getting the Most Out of Your Crystals: Data Collection at the New High-Flux, Microfocus MX Beamlines at NSLS-II. Molecules, 2019, 24, 496.	3.8	13
28	Ca2+-dependent regulation of sodium channels NaV1.4 and NaV1.5 is controlled by the post-IQ motif. Nature Communications, 2019, 10, 1514.	12.8	30
29	Diacylglycerol kinases: Relationship to other lipid kinases. Advances in Biological Regulation, 2019, 71, 104-110.	2.3	18
30	Bilobal architecture is a requirement for calmodulin signaling to Ca _V 1.3 channels. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3026-E3035.	7.1	20
31	Nudt19 is a renal CoA diphosphohydrolase with biochemical and regulatory properties that are distinct from the hepatic Nudt7 isoform. Journal of Biological Chemistry, 2018, 293, 4134-4148.	3.4	49
32	Intracellular production of hydrogels and syntheticÂRNA granules by multivalent molecularÂinteractions. Nature Materials, 2018, 17, 79-89.	27.5	106
33	Akt Kinase Activation Mechanisms Revealed Using Protein Semisynthesis. Cell, 2018, 174, 897-907.e14.	28.9	96
34	Effects of copper occupancy on the conformational landscape of peptidylglycine Î±-hydroxylating monooxygenase. Communications Biology, 2018, 1, 74.	4.4	17
35	Identification of allosteric binding sites for PI3KÎ± oncogenic mutant specific inhibitor design. Bioorganic and Medicinal Chemistry, 2017, 25, 1481-1486.	3.0	24
36	A Tunable Brake for HECT Ubiquitin Ligases. Molecular Cell, 2017, 66, 345-357.e6.	9.7	83

#	Article	IF	Citations
37	Investigating Ca 2+ -Dependent Regulation of Sodium Channels via Thermodynamic and Structural Analysis of Nav1.4 and Nav1.5 Carboxy Tail Interactions with Calmodulin. Biophysical Journal, 2017, 112, 19a.	0.5	0
38	Rapid PD-L1 detection in tumors with PET using a highly specific peptide. Biochemical and Biophysical Research Communications, 2017, 483, 258-263.	2.1	132
39	Kinetic and structural analyses reveal residues in phosphoinositide 3-kinase Î± that are critical for catalysis and substrate recognition. Journal of Biological Chemistry, 2017, 292, 13541-13550.	3.4	36
40	Nudix hydrolases degrade protein-conjugated ADP-ribose. Scientific Reports, 2016, 5, 18271.	3.3	55
41	Kinetic and mutational studies of the adenosine diphosphate ribose hydrolase from Mycobacterium tuberculosis. Journal of Bioenergetics and Biomembranes, 2016, 48, 557-567.	2.3	3
42	Calmodulin and Ca²⁺control of voltage gated Na⁺channels. Channels, 2016, 10, 45-54.	2.8	29
43	A Nudix Hydrolase Necessary for Mycobacterium Tuberculosis Survival under Oxidative Stress. Biophysical Journal, 2015, 108, 533a.	0.5	0
44	Cardiac Sodium Channel: Activation by CaM Involves a NaV1.5-NaV1.5 Interaction. Biophysical Journal, 2015, 108, 127a-128a.	0.5	0
45	Oncogenic mutations weaken the interactions that stabilize the p110Î±â€p85Î± heterodimer in phosphatidylinositol 3â€kinase Î±. FEBS Journal, 2015, 282, 3528-3542.	4.7	33
46	Generation of MANAbodies specific to HLA-restricted epitopes encoded by somatically mutated genes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9967-9972.	7.1	41
47	A Redox Regulatory System Critical for Mycobacterial Survival in Macrophages and Biofilm Development. PLoS Pathogens, 2015, 11, e1004839.	4.7	85
48	Affinity Purification of a Recombinant Protein Expressed as a Fusion with the Maltose-Binding Protein (MBP) Tag. Methods in Enzymology, 2015, 559, 17-26.	1.0	22
49	Structural and Enzymatic Characterization of a Nucleoside Diphosphate Sugar Hydrolase from Bdellovibrio bacteriovorus. PLoS ONE, 2015, 10, e0141716.	2.5	6
50	Abstract PR02: Targeting PI3K: The PIP2 binding site. , 2015, , .		0
51	Structural basis of nSH2 regulation and lipid binding in PI3KÎ±. Oncotarget, 2014, 5, 5198-5208.	1.8	62
52	Structural and thermodynamic basis of the inhibition of Leishmania major farnesyl diphosphate synthase by nitrogen-containing bisphosphonates. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 802-810.	2.5	20
53	Activation of PI3KÎ± by physiological effectors and by oncogenic mutations: structural and dynamic effects. Biophysical Reviews, 2014, 6, 89-95.	3.2	29
54	Regulation of the NaV1.5 cytoplasmic domain by calmodulin. Nature Communications, 2014, 5, 5126.	12.8	72

#	Article	IF	Citations
55	Salting out of Proteins Using Ammonium Sulfate Precipitation. Methods in Enzymology, 2014, 541, 85-94.	1.0	186
56	Gel Filtration Chromatography (Size Exclusion Chromatography) of Proteins. Methods in Enzymology, 2014, 541, 105-114.	1.0	31
57	Explanatory Chapter: Troubleshooting Protein Expression. Methods in Enzymology, 2014, 541, 231-247.	1.0	2
58	Using Ion Exchange Chromatography to Purify a Recombinantly Expressed Protein. Methods in Enzymology, 2014, 541, 95-103.	1.0	20
59	Explanatory Chapter: Troubleshooting Recombinant Protein Expression. Methods in Enzymology, 2014, 541, 209-229.	1.0	7
60	Abstract LB-326: Structural basis of lipid-binding and regulation in PI3KÎ±. , 2014, , .		0
61	Pyridinylpyrimidines selectively inhibit human methionine aminopeptidase-1. Bioorganic and Medicinal Chemistry, 2013, 21, 2600-2617.	3.0	10
62	Pyridinylquinazolines Selectively Inhibit Human Methionine Aminopeptidase-1 in Cells. Journal of Medicinal Chemistry, 2013, 56, 3996-4016.	6.4	16
63	A UDP-X Diphosphatase from Streptococcus pneumoniae Hydrolyzes Precursors of Peptidoglycan Biosynthesis. PLoS ONE, 2013, 8, e64241.	2.5	2
64	Phosphorylation-mediated PTEN conformational closure and deactivation revealed with protein semisynthesis. ELife, 2013, 2, e00691.	6.0	89
65	Abstract 2225: The molecular architecture of p85Î± as determined by SAXS and chemical cross-linking.. , 2013, , .		1
66	Design, Synthesis, Calorimetry, and Crystallographic Analysis of 2-Alkylaminoethyl-1,1-bisphosphonates as Inhibitors of Trypanosoma cruzi Farnesyl Diphosphate Synthase. Journal of Medicinal Chemistry, 2012, 55, 6445-6454.	6.4	30
67	CDP-Chase, a CDP-Choline Pyrophosphatase, is a Member of a Novel Nudix Family in Gram-Positive Bacteria. Biophysical Journal, 2011, 100, 218a.	0.5	0
68	Capitalizing on tumor genotyping: Towards the design of mutation specific inhibitors of phosphoinsitide-3-kinase. Advances in Enzyme Regulation, 2011, 51, 273-279.	2.6	4
69	Structural studies of the Nudix GDPâ€mannose hydrolase from E. coli reveals a new motif for mannose recognition. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2455-2466.	2.6	14
70	The Nudix Hydrolase CDP-Chase, a CDP-Choline Pyrophosphatase, Is an Asymmetric Dimer with Two Distinct Enzymatic Activities. Journal of Bacteriology, 2011, 193, 3175-3185.	2.2	10
71	Somatic mutations in PI3KÎ±: Structural basis for enzyme activation and drug design. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 533-540.	2.3	17
72	Binding of nitrogenâ€containing bisphosphonates (Nâ€BPs) to the Trypanosoma cruzi farnesyl diphosphate synthase homodimer. Proteins: Structure, Function and Bioinformatics, 2010, 78, 888-899.	2.6	33

#	Article	IF	Citations
73	Structural Insights into Maize Viviparous14, a Key Enzyme in the Biosynthesis of the Phytohormone Abscisic Acid. Plant Cell, 2010, 22, 2970-2980.	6.6	152
74	NHE3 Activity Is Dependent on Direct Phosphoinositide Binding at the N Terminus of Its Intracellular Cytosolic Region. Journal of Biological Chemistry, 2010, 285, 34566-34578.	3.4	17
75	Mutation of Asn28 Disrupts the Dimerization and Enzymatic Activity of SARS 3CL^{pro},. Biochemistry, 2010, 49, 4308-4317.	2.5	47
76	Structural Effects of Oncogenic PI3KÎ± Mutations. Current Topics in Microbiology and Immunology, 2010, 347, 43-53.	1.1	22
77	PI3KÎ± Inhibitors That Inhibit Metastasis. Oncotarget, 2010, 1, 339-348.	1.8	42
78	A frequent kinase domain mutation that changes the interaction between PI3KÎ± and the membrane. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16996-17001.	7.1	255
79	Structure and Biological Function of the RNA Pyrophosphohydrolase BdRppH from Bdellovibrio bacteriovorus. Structure, 2009, 17, 472-481.	3.3	40
80	Development of Broadâ€Spectrum Halomethyl Ketone Inhibitors Against Coronavirus Main Protease 3CL^{pro}. Chemical Biology and Drug Design, 2008, 72, 34-49.	3.2	43
81	Structural comparisons of class I phosphoinositide 3-kinases. Nature Reviews Cancer, 2008, 8, 665-669.	28.4	82
82	Insights into the oncogenic effects of /PIK3CA/ mutations from the structure of p110α/p85α. Cell Cycle, 2008, 7, 1151-1156.	2.6	73
83	Identification of Bdellovibrio bacteriovorus HD100 Bd0714 as a Nudix dGTPase. Journal of Bacteriology, 2008, 190, 8215-8219.	2.2	13
84	The Structure of a Human p110Î±/p85Î± Complex Elucidates the Effects of Oncogenic PI3KÎ± Mutations. Science, 2007, 318, 1744-1748.	12.6	504
85	Structure and Function of the E. coli Dihydroneopterin Triphosphate Pyrophosphatase: A Nudix Enzyme Involved in Folate Biosynthesis. Structure, 2007, 15, 1014-1022.	3.3	39
86	X-ray, NMR, and Mutational Studies of the Catalytic Cycle of the GDP-Mannose Mannosyl Hydrolase Reactionâ€,â€¡. Biochemistry, 2006, 45, 11290-11303.	2.5	3
87	Hydrogen bonding in the mechanism of GDP-mannose mannosyl hydrolase. Journal of Molecular Structure, 2006, 790, 160-167.	3.6	1
88	Structure and mechanism of the farnesyl diphosphate synthase from Trypanosoma cruzi: Implications for drug design. Proteins: Structure, Function and Bioinformatics, 2005, 62, 80-88.	2.6	123
89	C-terminal Recognition by 14-3-3 Proteins for Surface Expression of Membrane Receptors. Journal of Biological Chemistry, 2005, 280, 36263-36272.	3.4	85
90	Structure and activity of the axon guidance protein MICAL. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16830-16835.	7.1	74

#	Article	IF	Citations
91	Mutational, Structural, and Kinetic Evidence for a Dissociative Mechanism in the GDP-Mannose Mannosyl Hydrolase Reaction. Biochemistry, 2005, 44, 8989-8997.	2.5	7
92	Structures and mechanisms of Nudix hydrolases. Archives of Biochemistry and Biophysics, 2005, 433, 129-143.	3.0	274
93	Structure and Mechanism of GDP-Mannose Glycosyl Hydrolase, a Nudix Enzyme that Cleaves at Carbon Instead of Phosphorus. Structure, 2004, 12, 927-935.	3.3	28
94	Structure and Mechanism of MT-ADPRase, a Nudix Hydrolase from Mycobacterium tuberculosis. Structure, 2003, 11, 1015-1023.	3.3	58
95	Structure of the extracellular region of HER2 alone and in complex with the Herceptin Fab. Nature, 2003, 421, 756-760.	27.8	1,363
96	Structure of a Coenzyme A Pyrophosphatase from Deinococcus radiodurans : a Member of the Nudix Family. Journal of Bacteriology, 2003, 185, 4110-4118.	2.2	37
97	Mechanism of theEscherichia coliADP-Ribose Pyrophosphatase, a Nudix Hydrolaseâ€,â€¡. Biochemistry, 2002, 41, 9279-9285.	2.5	66
98	The structure of ADP-ribose pyrophosphatase reveals the structural basis for the versatility of the Nudix family. Nature Structural Biology, 2001, 8, 467-472.	9.7	109