

Sandra B Gabelli

List of Publications by Year in descending order

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98
papers

5,840
citations

117453

34
h-index

79541

73
g-index

104
all docs

104
docs citations

104
times ranked

7843
citing authors

#	ARTICLE	IF	CITATIONS
1	Elusive structure of mammalian DGKs. <i>Advances in Biological Regulation</i> , 2022, 83, 100847.	1.4	3
2	ATP synthase K ⁺ - and H ⁺ -fluxes drive ATP synthesis and enable mitochondrial K ⁺ -uniporter function: II. Ion and ATP synthase flux regulation. <i>Function</i> , 2022, 3, zqac001.	1.1	20
3	ATP Synthase K ⁺ - and H ⁺ -Fluxes Drive ATP Synthesis and Enable Mitochondrial K ⁺ -uniporter Function: I. Characterization of Ion Fluxes. <i>Function</i> , 2022, 3, zqab065.	1.1	25
4	A simple technique to classify diffraction data from dynamic proteins according to individual polymorphs. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 268-277.	1.1	5
5	Enzymatic analysis of WWP2 E3 ubiquitin ligase using protein microarrays identifies autophagy-related substrates. <i>Journal of Biological Chemistry</i> , 2022, 298, 101854.	1.6	6
6	Development of high-affinity nanobodies specific for NaV1.4 and NaV1.5 voltage-gated sodium channel isoforms. <i>Journal of Biological Chemistry</i> , 2022, 298, 101763.	1.6	7
7	Multifaceted Regulation of Akt by Diverse C-Terminal Post-translational Modifications. <i>ACS Chemical Biology</i> , 2022, 17, 68-76.	1.6	7
8	TCR-mimic bispecific antibodies to target the HIV-1 reservoir. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2123406119.	3.3	10
9	Navigating the intricacies of cellular machinery. <i>Journal of Biological Chemistry</i> , 2021, 296, 100832.	1.6	1
10	<i>Bdellovibrio bacteriovorus</i> Hydrolyses its Prey DNA using the Dctpase Activity of Bd2220. <i>Biophysical Journal</i> , 2021, 120, 306a.	0.2	0
11	Bispecific antibodies targeting mutant <i>RAS</i> neoantigens. <i>Science Immunology</i> , 2021, 6, .	5.6	106
12	Targeting loss of heterozygosity for cancer-specific immunotherapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	39
13	TCR β chain-directed bispecific antibodies for the treatment of T cell cancers. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	30
14	Targeting a neoantigen derived from a common <i>TP53</i> mutation. <i>Science</i> , 2021, 371, .	6.0	194
15	Targeting public neoantigens for cancer immunotherapy. <i>Nature Cancer</i> , 2021, 2, 487-497.	5.7	79
16	Antibodies response induced by recombinant virus-like particles from <i>Triatoma virus</i> and chimeric antigens from <i>Trypanosoma cruzi</i> . <i>Vaccine</i> , 2021, 39, 4723-4732.	1.7	3
17	Structural engineering of chimeric antigen receptors targeting HLA-restricted neoantigens. <i>Nature Communications</i> , 2021, 12, 5271.	5.8	17
18	Structural basis of cytoplasmic NaV1.5 and NaV1.4 regulation. <i>Journal of General Physiology</i> , 2021, 153, .	0.9	15

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19	The structural basis of PTEN regulation by multi-site phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 858-868.	3.6	20
20	Bisphosphonate-Based Molecules as Potential New Antiparasitic Drugs. <i>Molecules</i> , 2020, 25, 2602.	1.7	18
21	Structure of the RECK CC domain, an evolutionary anomaly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15104-15111.	3.3	10
22	Identifying Structural Determinants of Product Specificity in <i>Leishmania major</i> Farnesyl Diphosphate Synthase. <i>Biochemistry</i> , 2020, 59, 2751-2759.	1.2	5
23	Allosteric Activation of PI3K Results in Dynamic Access to Catalytically Competent Conformations. <i>Structure</i> , 2020, 28, 465-474.e5.	1.6	13
24	An engineered antibody fragment targeting mutant β -catenin via major histocompatibility complex I neoantigen presentation. <i>Journal of Biological Chemistry</i> , 2019, 294, 19322-19334.	1.6	15
25	Structural analyses of NudT16-ADP-ribose complexes direct rational design of mutants with improved processing of poly(ADP-ribosyl)ated proteins. <i>Scientific Reports</i> , 2019, 9, 5940.	1.6	15
26	Structural Determinants of Isoform Selectivity in PI3K Inhibitors. <i>Biomolecules</i> , 2019, 9, 82.	1.8	55
27	Getting the Most Out of Your Crystals: Data Collection at the New High-Flux, Microfocus MX Beamlines at NSLS-II. <i>Molecules</i> , 2019, 24, 496.	1.7	13
28	Ca ²⁺ -dependent regulation of sodium channels NaV1.4 and NaV1.5 is controlled by the post-IQ motif. <i>Nature Communications</i> , 2019, 10, 1514.	5.8	30
29	Diacylglycerol kinases: Relationship to other lipid kinases. <i>Advances in Biological Regulation</i> , 2019, 71, 104-110.	1.4	18
30	Bilobal architecture is a requirement for calmodulin signaling to Ca _v 1.3 channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3026-E3035.	3.3	20
31	Nudt19 is a renal CoA diphosphohydrolase with biochemical and regulatory properties that are distinct from the hepatic Nudt7 isoform. <i>Journal of Biological Chemistry</i> , 2018, 293, 4134-4148.	1.6	49
32	Intracellular production of hydrogels and synthetic RNA granules by multivalent molecular interactions. <i>Nature Materials</i> , 2018, 17, 79-89.	13.3	106
33	Akt Kinase Activation Mechanisms Revealed Using Protein Semisynthesis. <i>Cell</i> , 2018, 174, 897-907.e14.	13.5	96
34	Effects of copper occupancy on the conformational landscape of peptidylglycine β -hydroxylating monooxygenase. <i>Communications Biology</i> , 2018, 1, 74.	2.0	17
35	Identification of allosteric binding sites for PI3K oncogenic mutant specific inhibitor design. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 1481-1486.	1.4	24
36	A Tunable Brake for HECT Ubiquitin Ligases. <i>Molecular Cell</i> , 2017, 66, 345-357.e6.	4.5	83

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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. <i>Biophysical Journal</i> , 2017, 112, 19a.	0.2	0
38	Rapid PD-L1 detection in tumors with PET using a highly specific peptide. <i>Biochemical and Biophysical Research Communications</i> , 2017, 483, 258-263.	1.0	132
39	Kinetic and structural analyses reveal residues in phosphoinositide 3-kinase β that are critical for catalysis and substrate recognition. <i>Journal of Biological Chemistry</i> , 2017, 292, 13541-13550.	1.6	36
40	Nudix hydrolases degrade protein-conjugated ADP-ribose. <i>Scientific Reports</i> , 2016, 5, 18271.	1.6	55
41	Kinetic and mutational studies of the adenosine diphosphate ribose hydrolase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bioenergetics and Biomembranes</i> , 2016, 48, 557-567.	1.0	3
42	Calmodulin and Ca ²⁺ control of voltage gated Na ⁺ channels. <i>Channels</i> , 2016, 10, 45-54.	1.5	29
43	A Nudix Hydrolase Necessary for <i>Mycobacterium Tuberculosis</i> Survival under Oxidative Stress. <i>Biophysical Journal</i> , 2015, 108, 533a.	0.2	0
44	Cardiac Sodium Channel: Activation by CaM Involves a Nav1.5-Nav1.5 Interaction. <i>Biophysical Journal</i> , 2015, 108, 127a-128a.	0.2	0
45	Oncogenic mutations weaken the interactions that stabilize the p110 β -p85 β heterodimer in phosphatidylinositol 3-kinase β . <i>FEBS Journal</i> , 2015, 282, 3528-3542.	2.2	33
46	Generation of MANAbodies specific to HLA-restricted epitopes encoded by somatically mutated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9967-9972.	3.3	41
47	A Redox Regulatory System Critical for <i>Mycobacterial</i> Survival in Macrophages and Biofilm Development. <i>PLoS Pathogens</i> , 2015, 11, e1004839.	2.1	85
48	Affinity Purification of a Recombinant Protein Expressed as a Fusion with the Maltose-Binding Protein (MBP) Tag. <i>Methods in Enzymology</i> , 2015, 559, 17-26.	0.4	22
49	Structural and Enzymatic Characterization of a Nucleoside Diphosphate Sugar Hydrolase from <i>Bdellovibrio bacteriovorus</i> . <i>PLoS ONE</i> , 2015, 10, e0141716.	1.1	6
50	Abstract PR02: Targeting PI3K: The PIP2 binding site. , 2015, , .		0
51	Structural basis of nSH2 regulation and lipid binding in PI3K β . <i>Oncotarget</i> , 2014, 5, 5198-5208.	0.8	62
52	Structural and thermodynamic basis of the inhibition of <i>Leishmania major</i> farnesyl diphosphate synthase by nitrogen-containing bisphosphonates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 802-810.	2.5	20
53	Activation of PI3K β by physiological effectors and by oncogenic mutations: structural and dynamic effects. <i>Biophysical Reviews</i> , 2014, 6, 89-95.	1.5	29
54	Regulation of the Nav1.5 cytoplasmic domain by calmodulin. <i>Nature Communications</i> , 2014, 5, 5126.	5.8	72

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55	Salting out of Proteins Using Ammonium Sulfate Precipitation. <i>Methods in Enzymology</i> , 2014, 541, 85-94.	0.4	186
56	Gel Filtration Chromatography (Size Exclusion Chromatography) of Proteins. <i>Methods in Enzymology</i> , 2014, 541, 105-114.	0.4	31
57	Explanatory Chapter: Troubleshooting Protein Expression. <i>Methods in Enzymology</i> , 2014, 541, 231-247.	0.4	2
58	Using Ion Exchange Chromatography to Purify a Recombinantly Expressed Protein. <i>Methods in Enzymology</i> , 2014, 541, 95-103.	0.4	20
59	Explanatory Chapter: Troubleshooting Recombinant Protein Expression. <i>Methods in Enzymology</i> , 2014, 541, 209-229.	0.4	7
60	Abstract LB-326: Structural basis of lipid-binding and regulation in PI3K β . , 2014, , .		0
61	Pyridinylpyrimidines selectively inhibit human methionine aminopeptidase-1. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 2600-2617.	1.4	10
62	Pyridinylquinazolines Selectively Inhibit Human Methionine Aminopeptidase-1 in Cells. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 3996-4016.	2.9	16
63	A UDP-X Diphosphatase from <i>Streptococcus pneumoniae</i> Hydrolyzes Precursors of Peptidoglycan Biosynthesis. <i>PLoS ONE</i> , 2013, 8, e64241.	1.1	2
64	Phosphorylation-mediated PTEN conformational closure and deactivation revealed with protein semisynthesis. <i>ELife</i> , 2013, 2, e00691.	2.8	89
65	Abstract 2225: The molecular architecture of p85 β 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 <i>Trypanosoma cruzi</i> Farnesyl Diphosphate Synthase. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 6445-6454.	2.9	30
67	CDP-Chase, a CDP-Choline Pyrophosphatase, is a Member of a Novel Nudix Family in Gram-Positive Bacteria. <i>Biophysical Journal</i> , 2011, 100, 218a.	0.2	0
68	Capitalizing on tumor genotyping: Towards the design of mutation specific inhibitors of phosphoinositide-3-kinase. <i>Advances in Enzyme Regulation</i> , 2011, 51, 273-279.	2.9	4
69	Structural studies of the Nudix GDP β -mannose hydrolase from <i>E. coli</i> reveals a new motif for mannose recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2455-2466.	1.5	14
70	The Nudix Hydrolase CDP-Chase, a CDP-Choline Pyrophosphatase, Is an Asymmetric Dimer with Two Distinct Enzymatic Activities. <i>Journal of Bacteriology</i> , 2011, 193, 3175-3185.	1.0	10
71	Somatic mutations in PI3K β : Structural basis for enzyme activation and drug design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 533-540.	1.1	17
72	Binding of nitrogen β -containing bisphosphonates (NBPs) to the <i>Trypanosoma cruzi</i> farnesyl diphosphate synthase homodimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 888-899.	1.5	33

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73	Structural Insights into Maize Viviparous14, a Key Enzyme in the Biosynthesis of the Phytohormone Abscisic Acid. <i>Plant Cell</i> , 2010, 22, 2970-2980.	3.1	152
74	NHE3 Activity Is Dependent on Direct Phosphoinositide Binding at the N Terminus of Its Intracellular Cytosolic Region. <i>Journal of Biological Chemistry</i> , 2010, 285, 34566-34578.	1.6	17
75	Mutation of Asn28 Disrupts the Dimerization and Enzymatic Activity of SARS 3CL ^{pro} . <i>Biochemistry</i> , 2010, 49, 4308-4317.	1.2	47
76	Structural Effects of Oncogenic PI3K ^{K17E} Mutations. <i>Current Topics in Microbiology and Immunology</i> , 2010, 347, 43-53.	0.7	22
77	PI3K ^{K17E} Inhibitors That Inhibit Metastasis. <i>Oncotarget</i> , 2010, 1, 339-348.	0.8	42
78	A frequent kinase domain mutation that changes the interaction between PI3K ^{K17E} and the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16996-17001.	3.3	255
79	Structure and Biological Function of the RNA Pyrophosphohydrolase BdRppH from <i>Bdellovibrio bacteriovorus</i> . <i>Structure</i> , 2009, 17, 472-481.	1.6	40
80	Development of Broad-spectrum Halomethyl Ketone Inhibitors Against Coronavirus Main Protease 3CL ^{pro} . <i>Chemical Biology and Drug Design</i> , 2008, 72, 34-49.	1.5	43
81	Structural comparisons of class I phosphoinositide 3-kinases. <i>Nature Reviews Cancer</i> , 2008, 8, 665-669.	12.8	82
82	Insights into the oncogenic effects of PIK3CA mutations from the structure of p110 ^α /p85 ^α . <i>Cell Cycle</i> , 2008, 7, 1151-1156.	1.3	73
83	Identification of <i>Bdellovibrio bacteriovorus</i> HD100 Bd0714 as a Nudix dGTPase. <i>Journal of Bacteriology</i> , 2008, 190, 8215-8219.	1.0	13
84	The Structure of a Human p110 ^α /p85 ^α Complex Elucidates the Effects of Oncogenic PI3K ^{K17E} Mutations. <i>Science</i> , 2007, 318, 1744-1748.	6.0	504
85	Structure and Function of the <i>E. coli</i> Dihydroneopterin Triphosphate Pyrophosphatase: A Nudix Enzyme Involved in Folate Biosynthesis. <i>Structure</i> , 2007, 15, 1014-1022.	1.6	39
86	X-ray, NMR, and Mutational Studies of the Catalytic Cycle of the GDP-Mannose Mannosyl Hydrolase Reaction. <i>Biochemistry</i> , 2006, 45, 11290-11303.	1.2	3
87	Hydrogen bonding in the mechanism of GDP-mannose mannosyl hydrolase. <i>Journal of Molecular Structure</i> , 2006, 790, 160-167.	1.8	1
88	Structure and mechanism of the farnesyl diphosphate synthase from <i>Trypanosoma cruzi</i> : Implications for drug design. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 80-88.	1.5	123
89	C-terminal Recognition by 14-3-3 Proteins for Surface Expression of Membrane Receptors. <i>Journal of Biological Chemistry</i> , 2005, 280, 36263-36272.	1.6	85
90	Structure and activity of the axon guidance protein MICAL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16830-16835.	3.3	74

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91	Mutational, Structural, and Kinetic Evidence for a Dissociative Mechanism in the GDP-Mannose Mannosyl Hydrolase Reaction. <i>Biochemistry</i> , 2005, 44, 8989-8997.	1.2	7
92	Structures and mechanisms of Nudix hydrolases. <i>Archives of Biochemistry and Biophysics</i> , 2005, 433, 129-143.	1.4	274
93	Structure and Mechanism of GDP-Mannose Glycosyl Hydrolase, a Nudix Enzyme that Cleaves at Carbon Instead of Phosphorus. <i>Structure</i> , 2004, 12, 927-935.	1.6	28
94	Structure and Mechanism of MT-ADPRase, a Nudix Hydrolase from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2003, 11, 1015-1023.	1.6	58
95	Structure of the extracellular region of HER2 alone and in complex with the Herceptin Fab. <i>Nature</i> , 2003, 421, 756-760.	13.7	1,363
96	Structure of a Coenzyme A Pyrophosphatase from <i>Deinococcus radiodurans</i> : a Member of the Nudix Family. <i>Journal of Bacteriology</i> , 2003, 185, 4110-4118.	1.0	37
97	Mechanism of the <i>Escherichia coli</i> ADP-Ribose Pyrophosphatase, a Nudix Hydrolase. <i>Biochemistry</i> , 2002, 41, 9279-9285.	1.2	66
98	The structure of ADP-ribose pyrophosphatase reveals the structural basis for the versatility of the Nudix family. <i>Nature Structural Biology</i> , 2001, 8, 467-472.	9.7	109