

Sandra B Gabelli

List of Publications by Year in descending order

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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	Structure of the extracellular region of HER2 alone and in complex with the Herceptin Fab. <i>Nature</i> , 2003, 421, 756-760.	27.8	1,363
2	The Structure of a Human p110 α /p85 α Complex Elucidates the Effects of Oncogenic PI3K α Mutations. <i>Science</i> , 2007, 318, 1744-1748.	12.6	504
3	Structures and mechanisms of Nudix hydrolases. <i>Archives of Biochemistry and Biophysics</i> , 2005, 433, 129-143.	3.0	274
4	A frequent kinase domain mutation that changes the interaction between PI3K α and the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16996-17001.	7.1	255
5	Targeting a neoantigen derived from a common TP53 mutation. <i>Science</i> , 2021, 371, .	12.6	194
6	Salting out of Proteins Using Ammonium Sulfate Precipitation. <i>Methods in Enzymology</i> , 2014, 541, 85-94.	1.0	186
7	Structural Insights into Maize Viviparous14, a Key Enzyme in the Biosynthesis of the Phytohormone Abscicic Acid. <i>Plant Cell</i> , 2010, 22, 2970-2980.	6.6	152
8	Rapid PD-L1 detection in tumors with PET using a highly specific peptide. <i>Biochemical and Biophysical Research Communications</i> , 2017, 483, 258-263.	2.1	132
9	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.	2.6	123
10	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
11	Intracellular production of hydrogels and synthetic RNA granules by multivalent molecular interactions. <i>Nature Materials</i> , 2018, 17, 79-89.	27.5	106
12	Bispecific antibodies targeting mutant RAS neoantigens. <i>Science Immunology</i> , 2021, 6, .	11.9	106
13	Akt Kinase Activation Mechanisms Revealed Using Protein Semisynthesis. <i>Cell</i> , 2018, 174, 897-907.e14.	28.9	96
14	Phosphorylation-mediated PTEN conformational closure and deactivation revealed with protein semisynthesis. <i>ELife</i> , 2013, 2, e00691.	6.0	89
15	C-terminal Recognition by 14-3-3 Proteins for Surface Expression of Membrane Receptors. <i>Journal of Biological Chemistry</i> , 2005, 280, 36263-36272.	3.4	85
16	A Redox Regulatory System Critical for Mycobacterial Survival in Macrophages and Biofilm Development. <i>PLoS Pathogens</i> , 2015, 11, e1004839.	4.7	85
17	A Tunable Brake for HECT Ubiquitin Ligases. <i>Molecular Cell</i> , 2017, 66, 345-357.e6.	9.7	83
18	Structural comparisons of class I phosphoinositide 3-kinases. <i>Nature Reviews Cancer</i> , 2008, 8, 665-669.	28.4	82

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19	Targeting public neoantigens for cancer immunotherapy. <i>Nature Cancer</i> , 2021, 2, 487-497.	13.2	79
20	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.	7.1	74
21	Insights into the oncogenic effects of /PIK3CA/ mutations from the structure of p110αp85α. <i>Cell Cycle</i> , 2008, 7, 1151-1156.	2.6	73
22	Regulation of the NaV1.5 cytoplasmic domain by calmodulin. <i>Nature Communications</i> , 2014, 5, 5126.	12.8	72
23	Mechanism of the <i>Escherichia coli</i> ADP-Ribose Pyrophosphatase, a Nudix Hydrolase. <i>Biochemistry</i> , 2002, 41, 9279-9285.	2.5	66
24	Structural basis of nSH2 regulation and lipid binding in PI3K. <i>Oncotarget</i> , 2014, 5, 5198-5208.	1.8	62
25	Structure and Mechanism of MT-ADPRase, a Nudix Hydrolase from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2003, 11, 1015-1023.	3.3	58
26	Nudix hydrolases degrade protein-conjugated ADP-ribose. <i>Scientific Reports</i> , 2016, 5, 18271.	3.3	55
27	Structural Determinants of Isoform Selectivity in PI3K Inhibitors. <i>Biomolecules</i> , 2019, 9, 82.	4.0	55
28	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.	3.4	49
29	Mutation of Asn28 Disrupts the Dimerization and Enzymatic Activity of SARS 3CL ^{pro} . <i>Biochemistry</i> , 2010, 49, 4308-4317.	2.5	47
30	Development of Broad-Spectrum Halomethyl Ketone Inhibitors Against Coronavirus Main Protease 3CL ^{pro} . <i>Chemical Biology and Drug Design</i> , 2008, 72, 34-49.	3.2	43
31	PI3K Inhibitors That Inhibit Metastasis. <i>Oncotarget</i> , 2010, 1, 339-348.	1.8	42
32	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.	7.1	41
33	Structure and Biological Function of the RNA Pyrophosphohydrolase BdRppH from <i>Bdellovibrio bacteriovorus</i> . <i>Structure</i> , 2009, 17, 472-481.	3.3	40
34	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.	3.3	39
35	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, .	7.1	39
36	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.	2.2	37

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37	Kinetic and structural analyses reveal residues in phosphoinositide 3-kinase $\hat{\pm}$ that are critical for catalysis and substrate recognition. <i>Journal of Biological Chemistry</i> , 2017, 292, 13541-13550.	3.4	36
38	Binding of nitrogen-containing bisphosphonates (NBPs) to the <i>Trypanosoma cruzi</i> farnesyl diphosphate synthase homodimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 888-899.	2.6	33
39	Oncogenic mutations weaken the interactions that stabilize the p110 $\hat{\pm}$ p85 $\hat{\pm}$ heterodimer in phosphatidylinositol 3-kinase $\hat{\pm}$. <i>FEBS Journal</i> , 2015, 282, 3528-3542.	4.7	33
40	Gel Filtration Chromatography (Size Exclusion Chromatography) of Proteins. <i>Methods in Enzymology</i> , 2014, 541, 105-114.	1.0	31
41	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.	6.4	30
42	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.	12.8	30
43	TCR $\hat{2}$ chain-directed bispecific antibodies for the treatment of T cell cancers. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	30
44	Activation of PI3K $\hat{\pm}$ by physiological effectors and by oncogenic mutations: structural and dynamic effects. <i>Biophysical Reviews</i> , 2014, 6, 89-95.	3.2	29
45	Calmodulin and Ca ²⁺ control of voltage gated Na ⁺ channels. <i>Channels</i> , 2016, 10, 45-54.	2.8	29
46	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.	3.3	28
47	ATP Synthase K ⁺ and H ⁺ -Fluxes Drive ATP Synthesis and Enable Mitochondrial K ⁺ -Uniporter $\hat{\bullet}$ Function: I. Characterization of Ion Fluxes. <i>Function</i> , 2022, 3, zqab065.	2.3	25
48	Identification of allosteric binding sites for PI3K $\hat{\pm}$ oncogenic mutant specific inhibitor design. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 1481-1486.	3.0	24
49	Structural Effects of Oncogenic PI3K $\hat{\pm}$ Mutations. <i>Current Topics in Microbiology and Immunology</i> , 2010, 347, 43-53.	1.1	22
50	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.	1.0	22
51	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
52	Using Ion Exchange Chromatography to Purify a Recombinantly Expressed Protein. <i>Methods in Enzymology</i> , 2014, 541, 95-103.	1.0	20
53	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.	7.1	20
54	The structural basis of PTEN regulation by multi-site phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 858-868.	8.2	20

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55	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.	2.3	20
56	Diacylglycerol kinases: Relationship to other lipid kinases. <i>Advances in Biological Regulation</i> , 2019, 71, 104-110.	2.3	18
57	Bisphosphonate-Based Molecules as Potential New Antiparasitic Drugs. <i>Molecules</i> , 2020, 25, 2602.	3.8	18
58	Somatic mutations in PI3KÎ±: Structural basis for enzyme activation and drug design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 533-540.	2.3	17
59	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.	3.4	17
60	Effects of copper occupancy on the conformational landscape of peptidylglycine Î±-hydroxylating monooxygenase. <i>Communications Biology</i> , 2018, 1, 74.	4.4	17
61	Structural engineering of chimeric antigen receptors targeting HLA-restricted neoantigens. <i>Nature Communications</i> , 2021, 12, 5271.	12.8	17
62	Pyridinylquinazolines Selectively Inhibit Human Methionine Aminopeptidase-1 in Cells. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 3996-4016.	6.4	16
63	An engineered antibody fragment targeting mutant Î²-catenin via major histocompatibility complex I neoantigen presentation. <i>Journal of Biological Chemistry</i> , 2019, 294, 19322-19334.	3.4	15
64	Structural analyses of NudT16â€‘ADP-ribose complexes direct rational design of mutants with improved processing of poly(ADP-ribosyl)ated proteins. <i>Scientific Reports</i> , 2019, 9, 5940.	3.3	15
65	Structural basis of cytoplasmic NaV1.5 and NaV1.4 regulation. <i>Journal of General Physiology</i> , 2021, 153, .	1.9	15
66	Structural studies of the Nudix GDPâ€‘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.	2.6	14
67	Identification of <i>Bdellovibrio bacteriovorus</i> HD100 Bd0714 as a Nudix dGTPase. <i>Journal of Bacteriology</i> , 2008, 190, 8215-8219.	2.2	13
68	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.	3.8	13
69	Allosteric Activation of PI3KÎ± Results in Dynamic Access to Catalytically Competent Conformations. <i>Structure</i> , 2020, 28, 465-474.e5.	3.3	13
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.	2.2	10
71	Pyridinylpyrimidines selectively inhibit human methionine aminopeptidase-1. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 2600-2617.	3.0	10
72	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.	7.1	10

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73	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
74	Mutational, Structural, and Kinetic Evidence for a Dissociative Mechanism in the GDP-Mannose Mannosyl Hydrolase Reaction. Biochemistry, 2005, 44, 8989-8997.	2.5	7
75	Explanatory Chapter: Troubleshooting Recombinant Protein Expression. Methods in Enzymology, 2014, 541, 209-229.	1.0	7
76	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
77	Multifaceted Regulation of Akt by Diverse C-Terminal Post-translational Modifications. ACS Chemical Biology, 2022, 17, 68-76.	3.4	7
78	Structural and Enzymatic Characterization of a Nucleoside Diphosphate Sugar Hydrolase from Bdellovibrio bacteriovorus. PLoS ONE, 2015, 10, e0141716.	2.5	6
79	Enzymatic analysis of WWP2 E3 ubiquitin ligase using protein microarrays identifies autophagy-related substrates. Journal of Biological Chemistry, 2022, 298, 101854.	3.4	6
80	Identifying Structural Determinants of Product Specificity in <i>Leishmania major</i> Farnesyl Diphosphate Synthase. Biochemistry, 2020, 59, 2751-2759.	2.5	5
81	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
82	Capitalizing on tumor genotyping: Towards the design of mutation specific inhibitors of phosphoinositide-3-kinase. Advances in Enzyme Regulation, 2011, 51, 273-279.	2.6	4
83	X-ray, NMR, and Mutational Studies of the Catalytic Cycle of the GDP-Mannose Mannosyl Hydrolase Reaction. Biochemistry, 2006, 45, 11290-11303.	2.5	3
84	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
85	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
86	Elusive structure of mammalian DGKs. Advances in Biological Regulation, 2022, 83, 100847.	2.3	3
87	A UDP-X Diphosphatase from Streptococcus pneumoniae Hydrolyzes Precursors of Peptidoglycan Biosynthesis. PLoS ONE, 2013, 8, e64241.	2.5	2
88	Explanatory Chapter: Troubleshooting Protein Expression. Methods in Enzymology, 2014, 541, 231-247.	1.0	2
89	Hydrogen bonding in the mechanism of GDP-mannose mannosyl hydrolase. Journal of Molecular Structure, 2006, 790, 160-167.	3.6	1
90	Navigating the intricacies of cellular machinery. Journal of Biological Chemistry, 2021, 296, 100832.	3.4	1

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91	Abstract 2225: The molecular architecture of p85 ^{1±} as determined by SAXS and chemical cross-linking.. , 2013, , .		1
92	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
93	A Nudix Hydrolase Necessary for Mycobacterium Tuberculosis Survival under Oxidative Stress. Biophysical Journal, 2015, 108, 533a.	0.5	0
94	Cardiac Sodium Channel: Activation by CaM Involves a Nav1.5-Nav1.5 Interaction. Biophysical Journal, 2015, 108, 127a-128a.	0.5	0
95	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
96	Bdellovibrio bacteriovorus Hydrolyses its Prey DNA using the Dctpase Activity of Bd2220. Biophysical Journal, 2021, 120, 306a.	0.5	0
97	Abstract LB-326: Structural basis of lipid-binding and regulation in PI3K ^{1±} . , 2014, , .		0
98	Abstract PR02: Targeting PI3K: The PIP2 binding site. , 2015, , .		0