

Elsa D. Garcin

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,964
citations

279798

23
h-index

414414

32
g-index

41
all docs

41
docs citations

41
times ranked

3033
citing authors

#	ARTICLE	IF	CITATIONS
1	A fusion of the <i>Bacteroides fragilis</i> ferrous iron import proteins reveals a role for FeoA in stabilizing GTP-bound FeoB. <i>Journal of Biological Chemistry</i> , 2022, 298, 101808.	3.4	6
2	A new paradigm for gaseous ligand selectivity of hemoproteins highlighted by soluble guanylate cyclase. <i>Journal of Inorganic Biochemistry</i> , 2021, 214, 111267.	3.5	12
3	Quantitative high-throughput screening assays for the discovery and development of SIRP±-CD47 interaction inhibitors. <i>PLoS ONE</i> , 2019, 14, e0218897.	2.5	28
4	Synergistic mutations in soluble guanylyl cyclase (sGC) reveal a key role for interfacial regions in the sGC activation mechanism. <i>Journal of Biological Chemistry</i> , 2019, 294, 18451-18464.	3.4	8
5	GAPDH as a model non-canonical AU-rich RNA binding protein. <i>Seminars in Cell and Developmental Biology</i> , 2019, 86, 162-173.	5.0	40
6	Structure/function of the soluble guanylyl cyclase catalytic domain. <i>Nitric Oxide - Biology and Chemistry</i> , 2018, 77, 53-64.	2.7	24
7	Targeting Conformational Activation of CDK2 Kinase. <i>Biotechnology Journal</i> , 2017, 12, 1600531.	3.5	13
8	D-Glyceraldehyde-3-Phosphate Dehydrogenase Structure and Function. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 413-453.	2.4	44
9	The sweet side of <sc>RNA</sc> regulation: glyceraldehyde-3-phosphate dehydrogenase as a noncanonical <sc>RNA</sc>-binding protein. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 53-70.	6.4	39
10	Small-angle X-ray scattering method to characterize molecular interactions: Proof of concept. <i>Scientific Reports</i> , 2015, 5, 12085.	3.3	33
11	A Dimer Interface Mutation in Glyceraldehyde-3-Phosphate Dehydrogenase Regulates Its Binding to AU-rich RNA. <i>Journal of Biological Chemistry</i> , 2015, 290, 1770-1785.	3.4	47
12	Heat Shock Protein 90 Associates with the Per-Arnt-Sim Domain of Heme-free Soluble Guanylate Cyclase. <i>Journal of Biological Chemistry</i> , 2015, 290, 21615-21628.	3.4	22
13	Regulation of soluble guanylate cyclase by extracellular matrix thrombospondins: implications for blood flow. <i>Frontiers in Physiology</i> , 2014, 5, 134.	2.8	29
14	YC-1 Binding to the Î² Subunit of Soluble Guanylyl Cyclase Overcomes Allosteric Inhibition by the Î± Subunit. <i>Biochemistry</i> , 2014, 53, 101-114.	2.5	32
15	Interfacial Residues Promote an Optimal Alignment of the Catalytic Center in Human Soluble Guanylate Cyclase: Heterodimerization Is Required but Not Sufficient for Activity. <i>Biochemistry</i> , 2014, 53, 2153-2165.	2.5	39
16	Determining the Effect of Dithiolethione Compounds on the Activity of Human Glyceraldehyde-3-Phosphate Dehydrogenase. <i>Biophysical Journal</i> , 2013, 104, 232a.	0.5	0
17	Structural basis for the regulation of endothelin-1 mRNA stability by glyceraldehyde-3-phosphate dehydrogenase. <i>FASEB Journal</i> , 2012, 26, 951.5.	0.5	0
18	Structural studies of the regulatory domain of bovine soluble guanylate cyclase. <i>FASEB Journal</i> , 2012, 26, 573.6.	0.5	0

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19	Biochemical and structural characterization of the activation of soluble Guanylate Cyclase. <i>FASEB Journal</i> , 2011, 25, 959.4.	0.5	0
20	The expression, purification, and crystallization of the HNOX regulatory domain of bovine soluble guanylate cyclase. <i>FASEB Journal</i> , 2011, 25, 959.5.	0.5	0
21	Lys842 in Neuronal Nitric-oxide Synthase Enables the Autoinhibitory Insert to Antagonize Calmodulin Binding, Increase FMN Shielding, and Suppress Interflavin Electron Transfer. <i>Journal of Biological Chemistry</i> , 2010, 285, 3064-3075.	3.4	14
22	DNA apurinic-apyrimidinic site binding and excision by endonuclease IV. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 515-522.	8.2	93
23	Anchored plasticity opens doors for selective inhibitor design in nitric oxide synthase. <i>Nature Chemical Biology</i> , 2008, 4, 700-707.	8.0	205
24	Biphasic Coupling of Neuronal Nitric Oxide Synthase Phosphorylation to the NMDA Receptor Regulates AMPA Receptor Trafficking and Neuronal Cell Death. <i>Journal of Neuroscience</i> , 2007, 27, 3445-3455.	3.6	143
25	Surface Charge Interactions of the FMN Module Govern Catalysis by Nitric-oxide Synthase. <i>Journal of Biological Chemistry</i> , 2006, 281, 36819-36827.	3.4	53
26	Structural differences between the ready and unready oxidized states of [NiFe] hydrogenases. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 239-249.	2.6	291
27	C-terminal Tail Residue Arg1400 Enables NADPH to Regulate Electron Transfer in Neuronal Nitric-oxide Synthase. <i>Journal of Biological Chemistry</i> , 2005, 280, 39208-39219.	3.4	35
28	The Three Nitric-oxide Synthases Differ in Their Kinetics of Tetrahydrobiopterin Radical Formation, Heme-Dioxy Reduction, and Arginine Hydroxylation. <i>Journal of Biological Chemistry</i> , 2005, 280, 8929-8935.	3.4	49
29	Structural Basis for Isozyme-specific Regulation of Electron Transfer in Nitric-oxide Synthase. <i>Journal of Biological Chemistry</i> , 2004, 279, 37918-37927.	3.4	244
30	Conformational Changes in Nitric Oxide Synthases Induced by Chlorzoxazone and Nitroindazoles: Crystallographic and Computational Analyses of Inhibitor Potency. <i>Biochemistry</i> , 2002, 41, 13915-13925.	2.5	63
31	Halophilic Adaptation: Novel Solvent Protein Interactions Observed in the 2.9 and 2.6 Å Resolution Structures of the Wild Type and a Mutant of Malate Dehydrogenase from <i>Haloarcula marismortui</i> . <i>Biochemistry</i> , 2000, 39, 992-1000.	2.5	104
32	The crystal structure of a reduced [NiFeSe] hydrogenase provides an image of the activated catalytic center. <i>Structure</i> , 1999, 7, 557-566.	3.3	448
33	Structural bases for the catalytic mechanism of NiFe hydrogenase. <i>Pure and Applied Chemistry</i> , 1998, 70, 25-31.	1.9	23
34	Structural bases for the catalytic mechanism of [NiFe] hydrogenases. <i>Biochemical Society Transactions</i> , 1998, 26, 396-401.	3.4	18
35	Hydrogenase: A hydrogen-metabolizing enzyme. What do the crystal structures tell us about its mode of action?. <i>Biochimie</i> , 1997, 79, 661-666.	2.6	65
36	Structure of the [NiFe] Hydrogenase Active Site: Evidence for Biologically Uncommon Fe Ligands. <i>Journal of the American Chemical Society</i> , 1996, 118, 12989-12996.	13.7	657