

Lokesh Gakhar

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

2,430
citations

218381

26
h-index

205818

48
g-index

67
all docs

67
docs citations

67
times ranked

4043
citing authors

#	ARTICLE	IF	CITATIONS
1	Rieske business: Structure&function of Rieske non-heme oxygenases. Biochemical and Biophysical Research Communications, 2005, 338, 175-190.	1.0	307
2	Ectodomain shedding of angiotensin converting enzyme 2 in human airway epithelia. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2009, 297, L84-L96.	1.3	281
3	Dynamic regulation of cardiolipin by the lipid pump Atp8b1 determines the severity of lung injury in experimental pneumonia. Nature Medicine, 2010, 16, 1120-1127.	15.2	133
4	WD40 Repeat Propellers Define a Ubiquitin-Binding Domain that Regulates Turnover of F Box Proteins. Molecular Cell, 2010, 40, 433-443.	4.5	114
5	PLUNC Is a Novel Airway Surfactant Protein with Anti-Biofilm Activity. PLoS ONE, 2010, 5, e9098.	1.1	103
6	Structure of monoubiquitinated PCNA and implications for translesion synthesis and DNA polymerase exchange. Nature Structural and Molecular Biology, 2010, 17, 479-484.	3.6	98
7	The Yeast Alix Homolog Bro1 Functions as a Ubiquitin Receptor for Protein Sorting into Multivesicular Endosomes. Developmental Cell, 2013, 25, 520-533.	3.1	83
8	The NMDA Receptor NR1 C1 Region Bound to Calmodulin: Structural Insights into Functional Differences between Homologous Domains. Structure, 2007, 15, 1603-1617.	1.6	81
9	Novel, Highly Specific <i>N</i> -Demethylases Enable Bacteria To Live on Caffeine and Related Purine Alkaloids. Journal of Bacteriology, 2012, 194, 2041-2049.	1.0	81
10	Structural and Kinetic Studies of Formate Dehydrogenase from <i>Candida boidinii</i> . Biochemistry, 2016, 55, 2760-2771.	1.2	76
11	Missense mutations that cause Van der Woude syndrome and popliteal pterygium syndrome affect the DNA-binding and transcriptional activation functions of IRF6. Human Molecular Genetics, 2009, 18, 535-545.	1.4	75
12	SPLUNC1/BPIFA1 Contributes to Pulmonary Host Defense against <i>Klebsiella pneumoniae</i> Respiratory Infection. American Journal of Pathology, 2013, 182, 1519-1531.	1.9	74
13	Solution X-ray scattering combined with computational modeling reveals multiple conformations of covalently bound ubiquitin on PCNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17672-17677.	3.3	61
14	Structural basis of phosphodiesterase 6 inhibition by the C-terminal region of the β -subunit. EMBO Journal, 2009, 28, 3613-3622.	3.5	57
15	Nlrp12 mutation causes C57BL/6J strain-specific defect in neutrophil recruitment. Nature Communications, 2016, 7, 13180.	5.8	55
16	Structure and Increased Thermostability of <i>Rhodococcus</i> sp. Naphthalene 1,2-Dioxygenase. Journal of Bacteriology, 2005, 187, 7222-7231.	1.0	51
17	<i>CAPN5</i> mutation in hereditary uveitis: the R243L mutation increases calpain catalytic activity and triggers intraocular inflammation in a mouse model. Human Molecular Genetics, 2015, 24, 4584-4598.	1.4	39
18	PLUNC: a multifunctional surfactant of the airways. Biochemical Society Transactions, 2011, 39, 1012-1016.	1.6	38

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19	Mutations in Extracellular Matrix Genes <i>NID1</i> and <i>LAMC1</i> Cause Autosomal Dominant Dandy-Walker Malformation and Occipital Cephaloceles. <i>Human Mutation</i> , 2013, 34, 1075-1079.	1.1	38
20	Structural Modeling of a Novel <i>CAPN5</i> Mutation that Causes Uveitis and Neovascular Retinal Detachment. <i>PLoS ONE</i> , 2015, 10, e0122352.	1.1	35
21	Interaction of Aryl Hydrocarbon Receptor-interacting Protein-like 1 with the Farnesyl Moiety. <i>Journal of Biological Chemistry</i> , 2013, 288, 21320-21328.	1.6	32
22	Phosphorylation of Nox1 Regulates Association With NoxA1 Activation Domain. <i>Circulation Research</i> , 2014, 115, 911-918.	2.0	31
23	The Anti-sigma Factor RsiV Is a Bacterial Receptor for Lysozyme: Co-crystal Structure Determination and Demonstration That Binding of Lysozyme to RsiV Is Required for λ V Activation. <i>PLoS Genetics</i> , 2016, 12, e1006287.	1.5	31
24	Crystal Structure of SUMO-Modified Proliferating Cell Nuclear Antigen. <i>Journal of Molecular Biology</i> , 2011, 406, 9-17.	2.0	29
25	Oscillatory Active-Site Motions Correlate with Kinetic Isotope Effects in Formate Dehydrogenase. <i>ACS Catalysis</i> , 2019, 9, 11199-11206.	5.5	29
26	Functional Characterization of a Cancer Causing Mutation in Human Replication Protein A. <i>Molecular Cancer Research</i> , 2010, 8, 1017-1026.	1.5	28
27	Delineation of the Caffeine C-8 Oxidation Pathway in <i>Pseudomonas</i> sp. Strain CBB1 via Characterization of a New Trimethyluric Acid Monooxygenase and Genes Involved in Trimethyluric Acid Metabolism. <i>Journal of Bacteriology</i> , 2012, 194, 3872-3882.	1.0	27
28	A novel de novo <i>CAPN5</i> mutation in a patient with inflammatory vitreoretinopathy, hearing loss, and developmental delay. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002519.	0.5	23
29	Structural underpinnings of Ric8A function as a G-protein β -subunit chaperone and guanine-nucleotide exchange factor. <i>Nature Communications</i> , 2019, 10, 3084.	5.8	22
30	Role of the Nuclease of Nontypeable <i>Haemophilus influenzae</i> in Dispersal of Organisms from Biofilms. <i>Infection and Immunity</i> , 2015, 83, 950-957.	1.0	21
31	Distinct Roles for Conformational Dynamics in Protein-Ligand Interactions. <i>Structure</i> , 2016, 24, 2053-2066.	1.6	21
32	Free Energy Simulations of Active-Site Mutants of Dihydrofolate Reductase. <i>Journal of Physical Chemistry B</i> , 2015, 119, 906-916.	1.2	20
33	The structure of LsrB from <i>Yersinia pestis</i> complexed with autoinducer-2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1501-1505.	0.7	19
34	The Tiam1 guanine nucleotide exchange factor is auto-inhibited by its pleckstrin homology coiled-coil extension domain. <i>Journal of Biological Chemistry</i> , 2017, 292, 17777-17793.	1.6	19
35	Extended conformation of the proline-rich domain of human aryl hydrocarbon receptor-interacting protein-like 1: implications for retina disease. <i>Journal of Neurochemistry</i> , 2015, 135, 165-175.	2.1	18
36	Structural Insights into the Unique Activation Mechanisms of a Non-classical Calpain and Its Disease-Causing Variants. <i>Cell Reports</i> , 2020, 30, 881-892.e5.	2.9	17

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37	Unique structural features of the AIPL1â€™FKBP domain that support prenyl lipid binding and underlie protein malfunction in blindness. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6536-E6545.	3.3	16
38	Crystal Structure of a Complex of NOD1 CARD and Ubiquitin. PLoS ONE, 2014, 9, e104017.	1.1	14
39	Molecular basis for metabolite channeling in a ring opening enzyme of the phenylacetate degradation pathway. Nature Communications, 2019, 10, 4127.	5.8	14
40	A charged residue at the subunit interface of PCNA promotes trimer formation by destabilizing alternate subunit interactions. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 560-566.	2.5	12
41	Small-angle X-ray scattering of calpain-5 reveals a highly open conformation among calpains. Journal of Structural Biology, 2016, 196, 309-318.	1.3	12
42	Quantitation of SPLUNC1 in saliva with an xMAP particle-based antibody capture and detection immunoassay. Archives of Oral Biology, 2012, 57, 197-204.	0.8	11
43	Structure and Functional Analysis of the BRCT Domain of Translesion Synthesis DNA Polymerase Rev1. Biochemistry, 2013, 52, 254-263.	1.2	11
44	Opposing orientations of the anti-psychotic drug trifluoperazine selected by alternate conformations of M144 in calmodulin. Proteins: Structure, Function and Bioinformatics, 2015, 83, 989-996.	1.5	11
45	Allosteric Tuning of Caspaseâ€™7: A Fragmentâ€™Based Drug Discovery Approach. Angewandte Chemie - International Edition, 2017, 56, 14443-14447.	7.2	11
46	A possible additional role of mineral oil in successful flash cooling. Journal of Applied Crystallography, 2005, 38, 945-950.	1.9	9
47	An extended motif in the SARS-CoV-2 spike modulates binding and release of host coatmer in retrograde trafficking. Communications Biology, 2022, 5, 115.	2.0	9
48	Crystallization and preliminary X-ray diffraction analysis of naphthalene dioxygenase from Rhodococcus sp. strain NCIMB 12038. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2173-2174.	2.5	8
49	Interactions of ubiquitin and CHMP5 with the V domain of HD-PTP reveals role for regulation of Vps4 ATPase. Molecular Biology of the Cell, 2021, 32, ar42.	0.9	8
50	High-resolution structure of the Tiam1 PH_n-CC-Ex domain. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 744-752.	0.7	5
51	The solution structure of the transducinâ€™1â€™uncoordinated 119 protein complex suggests occlusion of the GÎ²₁Î³₁â€™binding sites. FEBS Journal, 2015, 282, 550-561.	2.2	4
52	Benzothiourea Derivatives Target the Secretory Pathway of the Human Fungal Pathogen Cryptococcus neoformans. ACS Infectious Diseases, 2020, 6, 529-539.	1.8	4
53	ANTH domains within CALM, HIP1R, and Sla2 recognize ubiquitin internalization signals. ELife, 2021, 10, .	2.8	2
54	PLUNC: a multifunctional surfactant of the airways. Biochemical Society Transactions, 2011, 39, 1549-1549.	1.6	1

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55	Characterization of a nontypeable Haemophilus influenzae thermonuclease. PLoS ONE, 2018, 13, e0197010.	1.1	1
56	Missense mutations that cause Van der Woude syndrome and popliteal pterygium syndrome affect the DNA-binding and transcriptional activation functions of IRF6. Human Molecular Genetics, 2009, 18, 1544-1544.	1.4	0
57	Conformational Dynamics and Structure Underlie the Novel Ligand Binding Specificity of a Tiam1 PDZ Domain Mutant. Biophysical Journal, 2016, 110, 514a.	0.2	0
58	Insights into the Autoinhibition Mechanism of the Tiam1 Guanine Nucleotide Exchange Factor. Biophysical Journal, 2016, 110, 206a.	0.2	0
59	Structural Differences in Calmodulin Bound to Voltage-Gated Sodium Channel IQ Motifs. Biophysical Journal, 2016, 110, 109a.	0.2	0
60	Structural and Biochemical Characterization of CASK PDZ Interaction with Protein and Lipid Binding Partners. Biophysical Journal, 2016, 110, 42a.	0.2	0
61	Allosteric Tuning of Caspase-7: A Fragment-Based Drug Discovery Approach. Angewandte Chemie, 2017, 129, 14635-14639.	1.6	0
62	Rational Design of PDZ Domain Specificity. Biophysical Journal, 2018, 114, 410a.	0.2	0
63	Determinants of human glucokinase activation and implications for small molecule allosteric control. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 1902-1912.	1.1	0
64	Crystal structure of the human calpain-5 catalytic core. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a31-a32.	0.0	0
65	Accurately characterizing protein assembly states in solution with a combination of size-exclusion chromatography (SEC), multi-angle light scattering (MALS) and small-angle X-ray scattering (SAXS). Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a234-a234.	0.0	0