

# Lokesh Gakhar

## List of Publications by Citations

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56  
papers

1,981  
citations

23  
h-index

44  
g-index

67  
ext. papers

2,293  
ext. citations

6.8  
avg, IF

4.44  
L-index

#	Paper	IF	Citations
56	Rieske business: structure-function of Rieske non-heme oxygenases. <i>Biochemical and Biophysical Research Communications</i> , <b>2005</b> , 338, 175-90	3.4	261
55	Ectodomain shedding of angiotensin converting enzyme 2 in human airway epithelia. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , <b>2009</b> , 297, L84-96	5.8	222
54	Dynamic regulation of cardiolipin by the lipid pump Atp8b1 determines the severity of lung injury in experimental pneumonia. <i>Nature Medicine</i> , <b>2010</b> , 16, 1120-1127	50.5	105
53	PLUNC is a novel airway surfactant protein with anti-biofilm activity. <i>PLoS ONE</i> , <b>2010</b> , 5, e9098	3.7	93
52	WD40 repeat propellers define a ubiquitin-binding domain that regulates turnover of F box proteins. <i>Molecular Cell</i> , <b>2010</b> , 40, 433-43	17.6	89
51	Structure of monoubiquitinated PCNA and implications for translesion synthesis and DNA polymerase exchange. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 479-84	17.6	86
50	Missense mutations that cause Van der Woude syndrome and popliteal pterygium syndrome affect the DNA-binding and transcriptional activation functions of IRF6. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 1544-1544	5.6	78
49	The yeast Alix homolog Bro1 functions as a ubiquitin receptor for protein sorting into multivesicular endosomes. <i>Developmental Cell</i> , <b>2013</b> , 25, 520-33	10.2	68
48	The NMDA receptor NR1 C1 region bound to calmodulin: structural insights into functional differences between homologous domains. <i>Structure</i> , <b>2007</b> , 15, 1603-17	5.2	64
47	SPLUNC1/BPIFA1 contributes to pulmonary host defense against <i>Klebsiella pneumoniae</i> respiratory infection. <i>American Journal of Pathology</i> , <b>2013</b> , 182, 1519-31	5.8	60
46	Missense mutations that cause Van der Woude syndrome and popliteal pterygium syndrome affect the DNA-binding and transcriptional activation functions of IRF6. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 535-45	5.6	59
45	Novel, highly specific N-demethylases enable bacteria to live on caffeine and related purine alkaloids. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 2041-9	3.5	56
44	Solution X-ray scattering combined with computational modeling reveals multiple conformations of covalently bound ubiquitin on PCNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 17672-7	11.5	55
43	Structural basis of phosphodiesterase 6 inhibition by the C-terminal region of the gamma-subunit. <i>EMBO Journal</i> , <b>2009</b> , 28, 3613-22	13	49
42	Structural and Kinetic Studies of Formate Dehydrogenase From <i>Candida boidinii</i> . <i>Biochemistry</i> , <b>2016</b> , 55, 2760-71	3.2	46
41	Structure and increased thermostability of <i>Rhodococcus</i> sp. naphthalene 1,2-dioxygenase. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 7222-31	3.5	40
40	Nlrp12 mutation causes C57BL/6J strain-specific defect in neutrophil recruitment. <i>Nature Communications</i> , <b>2016</b> , 7, 13180	17.4	34

39	PLUNC: a multifunctional surfactant of the airways. <i>Biochemical Society Transactions</i> , <b>2011</b> , 39, 1012-6	5.1	34
38	CAPN5 mutation in hereditary uveitis: the R243L mutation increases calpain catalytic activity and triggers intraocular inflammation in a mouse model. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 4584-98	5.6	30
37	Structural modeling of a novel CAPN5 mutation that causes uveitis and neovascular retinal detachment. <i>PLoS ONE</i> , <b>2015</b> , 10, e0122352	3.7	29
36	Mutations in extracellular matrix genes NID1 and LAMC1 cause autosomal dominant Dandy-Walker malformation and occipital cephaloceles. <i>Human Mutation</i> , <b>2013</b> , 34, 1075-9	4.7	28
35	Interaction of aryl hydrocarbon receptor-interacting protein-like 1 with the farnesyl moiety. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 21320-21328	5.4	27
34	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 $\sigma$ Activation. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006287	6	26
33	Phosphorylation of Nox1 regulates association with NoxA1 activation domain. <i>Circulation Research</i> , <b>2014</b> , 115, 911-8	15.7	23
32	Crystal structure of SUMO-modified proliferating cell nuclear antigen. <i>Journal of Molecular Biology</i> , <b>2011</b> , 406, 9-17	6.5	23
31	Functional characterization of a cancer causing mutation in human replication protein A. <i>Molecular Cancer Research</i> , <b>2010</b> , 8, 1017-26	6.6	23
30	Distinct Roles for Conformational Dynamics in Protein-Ligand Interactions. <i>Structure</i> , <b>2016</b> , 24, 2053-2066	6.2	20
29	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> , <b>2012</b> , 194, 3872-82	3.5	20
28	Free energy simulations of active-site mutants of dihydrofolate reductase. <i>Journal of Physical Chemistry B</i> , <b>2015</b> , 119, 906-16	3.4	17
27	Role of the nuclease of nontypeable <i>Haemophilus influenzae</i> in dispersal of organisms from biofilms. <i>Infection and Immunity</i> , <b>2015</b> , 83, 950-7	3.7	16
26	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> , <b>2015</b> , 135, 165-75	6	16
25	A novel de novo mutation in a patient with inflammatory vitreoretinopathy, hearing loss, and developmental delay. <i>Journal of Physical Education and Sports Management</i> , <b>2018</b> , 4,	2.8	16
24	The structure of LsrB from <i>Yersinia pestis</i> complexed with autoinducer-2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2011</b> , 67, 1501-5		16
23	Oscillatory Active-site Motions Correlate with Kinetic Isotope Effects in Formate Dehydrogenase. <i>ACS Catalysis</i> , <b>2019</b> , 9, 11199-11206	13.1	13
22	Unique structural features of the AIPL1-FKBP domain that support prenyl lipid binding and underlie protein malfunction in blindness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6536-E6545	11.5	12

21	Crystal structure of a complex of NOD1 CARD and ubiquitin. <i>PLoS ONE</i> , <b>2014</b> , 9, e104017	3.7	12
20	Structural underpinnings of Ric8A function as a G-protein $\beta$ subunit chaperone and guanine-nucleotide exchange factor. <i>Nature Communications</i> , <b>2019</b> , 10, 3084	17.4	11
19	Structure and functional analysis of the BRCT domain of translesion synthesis DNA polymerase Rev1. <i>Biochemistry</i> , <b>2013</b> , 52, 254-63	3.2	10
18	The Tiam1 guanine nucleotide exchange factor is auto-inhibited by its pleckstrin homology coiled-coil extension domain. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 17777-17793	5.4	10
17	A charged residue at the subunit interface of PCNA promotes trimer formation by destabilizing alternate subunit interactions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 560-6		10
16	Small-angle X-ray scattering of calpain-5 reveals a highly open conformation among calpains. <i>Journal of Structural Biology</i> , <b>2016</b> , 196, 309-318	3.4	10
15	Molecular basis for metabolite channeling in a ring opening enzyme of the phenylacetate degradation pathway. <i>Nature Communications</i> , <b>2019</b> , 10, 4127	17.4	9
14	Opposing orientations of the anti-psychotic drug trifluoperazine selected by alternate conformations of M144 in calmodulin. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 989-96	4.2	9
13	Quantitation of SPLUNC1 in saliva with an xMAP particle-based antibody capture and detection immunoassay. <i>Archives of Oral Biology</i> , <b>2012</b> , 57, 197-204	2.8	9
12	Structural Insights into the Unique Activation Mechanisms of a Non-classical Calpain and Its Disease-Causing Variants. <i>Cell Reports</i> , <b>2020</b> , 30, 881-892.e5	10.6	8
11	Allosteric Tuning of Caspase-7: A Fragment-Based Drug Discovery Approach. <i>Angewandte Chemie - International Edition</i> , <b>2017</b> , 56, 14443-14447	16.4	7
10	Crystallization and preliminary X-ray diffraction analysis of naphthalene dioxygenase from <i>Rhodococcus</i> sp. strain NCIMB 12038. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 2173-4		6
9	High-resolution structure of the Tiam1 PHn-CC-Ex domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 744-52		4
8	A possible additional role of mineral oil in successful flash cooling. <i>Journal of Applied Crystallography</i> , <b>2005</b> , 38, 945-950	3.8	4
7	Benzothiourea Derivatives Target the Secretory Pathway of the Human Fungal Pathogen. <i>ACS Infectious Diseases</i> , <b>2020</b> , 6, 529-539	5.5	3
6	The solution structure of the transducin- $\beta$ uncoordinated 119 protein complex suggests occlusion of the G $\beta$ binding sites. <i>FEBS Journal</i> , <b>2015</b> , 282, 550-61	5.7	3
5	Characterization of a nontypeable <i>Haemophilus influenzae</i> thermonuclease. <i>PLoS ONE</i> , <b>2018</b> , 13, e0197019	3.7	1
4	An extended motif in the SARS-CoV-2 spike modulates binding and release of host coatmer in retrograde trafficking.. <i>Communications Biology</i> , <b>2022</b> , 5, 115	6.7	0

- 3 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 3.5 ○
- 2 Determinants of human glucokinase activation and implications for small molecule allosteric control. *Biochimica Et Biophysica Acta - General Subjects*, **2018**, 1862, 1902-1912 4
- 1 Allosteric Tuning of Caspase-7: A Fragment-Based Drug Discovery Approach. *Angewandte Chemie*, **2017**, 129, 14635-14639 3.6