

# Saurav Misra

## List of Publications by Year in descending order

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62  
papers

3,438  
citations

159585  
30  
h-index

138484  
58  
g-index

63  
all docs

63  
docs citations

63  
times ranked

4477  
citing authors

#	ARTICLE	IF	CITATIONS
1	Maturation, inactivation, and recovery mechanisms of soluble guanylyl cyclase. Journal of Biological Chemistry, 2021, 296, 100336.	3.4	32
2	A swine arterivirus deubiquitinase stabilizes two major envelope proteins and promotes production of viral progeny. PLoS Pathogens, 2021, 17, e1009403.	4.7	14
3	Optimal RNA binding by Egalitarian, a Dynein cargo adaptor, is critical for maintaining oocyte fate in <i>Drosophila</i> . RNA Biology, 2021, 18, 2376-2389.	3.1	9
4	Hyper-phosphorylation of nsp2-related proteins of porcine reproductive and respiratory syndrome virus. Virology, 2020, 543, 63-75.	2.4	3
5	Heat shock protein 90 regulates soluble guanylyl cyclase maturation by a dual mechanism. Journal of Biological Chemistry, 2019, 294, 12880-12891.	3.4	17
6	Development and characterization of monoclonal antibodies against p30 protein of African swine fever virus. Virus Research, 2019, 269, 197632.	2.2	41
7	S27 of IFN $\beta$ 1 Contributes to Its Low Affinity for IFNAR2 and Weak Antiviral Activity. Journal of Interferon and Cytokine Research, 2019, 39, 283-292.	1.2	2
8	Molecular mechanisms of missense mutations that generate ectopic N-glycosylation sites in coagulation factor VIII. Biochemical Journal, 2018, 475, 873-886.	3.7	11
9	A Naturally Occurring Recombinant Enterovirus Expresses a Torovirus Deubiquitinase. Journal of Virology, 2017, 91, .	3.4	41
10	Missense mutations near the N-glycosylation site of the A2 domain lead to various intracellular trafficking defects in coagulation factor VIII. Scientific Reports, 2017, 7, 45033.	3.3	9
11	Symmetry breaking during homodimeric assembly activates an E3 ubiquitin ligase. Scientific Reports, 2017, 7, 1789.	3.3	17
12	A Bipartite Interaction between Hsp70 and CHIP Regulates Ubiquitination of Chaperoned Client Proteins. Structure, 2015, 23, 472-482.	3.3	78
13	Heat Shock Protein 90 Associates with the Per-Arnt-Sim Domain of Heme-free Soluble Guanylate Cyclase. Journal of Biological Chemistry, 2015, 290, 21615-21628.	3.4	22
14	Dissecting structural and electronic effects in inducible nitric oxide synthase. Biochemical Journal, 2015, 467, 153-165.	3.7	4
15	Cyclin E/Cdk2-dependent phosphorylation of Mcl-1 determines its stability and cellular sensitivity to BH3 mimetics. Oncotarget, 2015, 6, 16912-16925.	1.8	53
16	Crystal structure of the nucleotide-binding domain of mortalin, the mitochondrial Hsp70 chaperone. Protein Science, 2014, 23, 833-842.	7.6	40
17	The Differential Regulation of Human ACT1 Isoforms by Hsp90 in IL-17 Signaling. Journal of Immunology, 2014, 193, 1590-1599.	0.8	22
18	Structural Characterization of Carbohydrate Binding by LMAN1 Protein Provides New Insight into the Endoplasmic Reticulum Export of Factors V (FV) and VIII (FVIII). Journal of Biological Chemistry, 2013, 288, 20499-20509.	3.4	46

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19	The psoriasis-associated D10N variant of the adaptor Act1 with impaired regulation by the molecular chaperone hsp90. <i>Nature Immunology</i> , 2013, 14, 72-81.	14.5	98
20	RACK1 interacts with filamin-A to regulate plasma membrane levels of the cystic fibrosis transmembrane conductance regulator. <i>American Journal of Physiology - Cell Physiology</i> , 2013, 305, C111-C120.	4.6	4
21	Molecular Basis of Antiangiogenic Thrombospondin-1 Type 1 Repeat Domain Interactions With CD36. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1655-1662.	2.4	41
22	Structural Insights into the Conformation and Oligomerization of E2 <sup>ub</sup> Ubiquitin Conjugates. <i>Biochemistry</i> , 2012, 51, 4175-4187.	2.5	78
23	Do <sc>GGA</sc> Adaptors Bind Internal <sc>DXXLL</sc> Motifs?. <i>Traffic</i> , 2012, 13, 1315-1325.	2.7	16
24	Three-dimensional structure of a schistosome serpin revealing an unusual configuration of the helical subdomain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 686-694.	2.5	6
25	Crystallization and preliminary X-ray crystallographic analysis of the Bag2 amino-terminal domain from <i>Mus musculus</i>. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 647-651.	0.7	6
26	Expression, purification and structural characterization of functionally replete thrombospondin-1 type 1 repeats in a bacterial expression system. <i>Protein Expression and Purification</i> , 2011, 80, 253-259.	1.3	16
27	Structure of filamin A immunoglobulin-like repeat 10 from <i>Homo sapiens</i>. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 871-876.	0.7	14
28	A CC <sup>2</sup> Loop Decoy Peptide Blocks the Interaction Between Act1 and IL-17RA to Attenuate IL-17 <sup>α</sup> and IL-25 <sup>α</sup> -Induced Inflammation. <i>Science Signaling</i> , 2011, 4, ra72.	3.6	44
29	The inducible kinase IKKi is required for IL-17-dependent signaling associated with neutrophilia and pulmonary inflammation. <i>Nature Immunology</i> , 2011, 12, 844-852.	14.5	174
30	Biochemical Basis of the Interaction between Cystic Fibrosis Transmembrane Conductance Regulator and Immunoglobulin-like Repeats of Filamin. <i>Journal of Biological Chemistry</i> , 2010, 285, 17166-17176.	3.4	20
31	Structure of an integrin $\alpha$ IIb $\beta$ 3 transmembrane-cytoplasmic heterocomplex provides insight into integrin activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17729-17734.	7.1	145
32	Act1, a U-box E3 Ubiquitin Ligase for IL-17 Signaling. <i>Science Signaling</i> , 2009, 2, ra63.	3.6	179
33	Regulation of Hsp70 <sup>α</sup> -linked ubiquitination by CHIP and Bag2. <i>FASEB Journal</i> , 2009, 23, 317.2.	0.5	0
34	Stabilization of Reaction Intermediates in the Catalytic Cycle of Nitric Oxide Synthases. <i>FASEB Journal</i> , 2009, 23, 890.1.	0.5	0
35	Filamin <sup>α</sup> modulates CFTR surface expression via Filamin <sup>α</sup> Ig repeat 21 and interacts with the scaffold protein RACK1. <i>FASEB Journal</i> , 2009, 23, 796.28.	0.5	0
36	Interactions between the quality control ubiquitin ligase CHIP and ubiquitin conjugating enzymes. <i>BMC Structural Biology</i> , 2008, 8, 26.	2.3	113

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37	Structural basis of nucleotide exchange and client binding by the Hsp70 cochaperone Bag2. Nature Structural and Molecular Biology, 2008, 15, 1309-1317.	8.2	85
38	Nuclear Co-translocation of Myotrophin and p65 Stimulates Myocyte Growth. Journal of Biological Chemistry, 2008, 283, 27947-27956.	3.4	6
39	Stabilization and Characterization of a Heme-Oxy Reaction Intermediate in Inducible Nitric-oxide Synthase. Journal of Biological Chemistry, 2008, 283, 33498-33507.	3.4	46
40	Apical targeting of syntaxin 3 is essential for epithelial cell polarity. Journal of Cell Biology, 2006, 173, 937-948.	5.2	82
41	Structure and Interactions of the Helical and U-Box Domains of CHIP, the C Terminus of HSP70 Interacting Protein,. Biochemistry, 2006, 45, 4749-4759.	2.5	55
42	Structural Basis for the Phosphorylation-regulated Focal Adhesion Targeting of Type II <sup>3</sup> Phosphatidylinositol Phosphate Kinase (PIPKII <sup>3</sup> ) by Talin. Journal of Molecular Biology, 2006, 359, 47-54.	4.2	24
43	Mechanism of Ubiquitin Recognition by the CUE Domain of Vps9p. Cell, 2003, 113, 609-620.	28.9	215
44	Structure of the GAT domain of human GGA1: A syntaxin amino-terminal domain fold in an endosomal trafficking adaptor. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4451-4456.	7.1	42
45	Structural genomics and signaling domains. Trends in Biochemical Sciences, 2002, 27, 48-53.	7.5	20
46	Structural basis for acidic-cluster-dileucine sorting-signal recognition by VHS domains. Nature, 2002, 415, 933-937.	27.8	161
47	Phosphoregulation of sorting signal-VHS domain interactions by a direct electrostatic mechanism. Nature Structural Biology, 2002, 9, 532-6.	9.7	44
48	Recognizing Phosphatidylinositol 3-Phosphate. Cell, 2001, 107, 559-562.	28.9	91
49	Kinetics and pH dependence of light-induced deprotonation of the Schiff base of rhodopsin: possible coupling to proton uptake and formation of the active form of Meta II. Biochemistry (Moscow), 2001, 66, 1283-1299.	1.5	17
50	Signaling and Subcellular Targeting by Membrane-Binding Domains. Annual Review of Biophysics and Biomolecular Structure, 2000, 29, 49-79.	18.3	255
51	Structure of the VHS Domain of Human Tom1 (Target of Myb 1): Insights into Interactions with Proteins and Membranes. Biochemistry, 2000, 39, 11282-11290.	2.5	73
52	Crystal Structure of a Phosphatidylinositol 3-Phosphate-Specific Membrane-Targeting Motif, the FYVE Domain of Vps27p. Cell, 1999, 97, 657-666.	28.9	250
53	Chloride Binding Regulates the Schiff Base pKin Gecko P521 Cone-Type Visual Pigment. Biochemistry, 1999, 38, 4649-4654.	2.5	15
54	Structure of Type II <sup>2</sup> Phosphatidylinositol Phosphate Kinase. Cell, 1998, 94, 829-839.	28.9	235

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55	Contribution of Proton Release to the B2 Photocurrent of Bacteriorhodopsin. Biophysical Journal, 1998, 75, 382-388.	0.5	13
56	Proton Uptake and Release Are Rate-Limiting Steps in the Photocycle of the Bacteriorhodopsin Mutant E204Q. Biochemistry, 1997, 36, 4875-4883.	2.5	41
57	Mutation of a Surface Residue, Lysine-129, Reverses the Order of Proton Release and Uptake in Bacteriorhodopsin; Guanidine Hydrochloride Restores It. Biophysical Journal, 1997, 72, 886-898.	0.5	27
58	Mutation of Arginine 134 to Lysine Alters the pKas of Key Groups Involved in Proton Pumping by Bacteriorhodopsin. Photochemistry and Photobiology, 1997, 66, 774-783.	2.5	15
59	Charge Movements in the 13-c/s Photocycles of the Bacteriorhodopsin Mutants R82K and R82Q*. Photochemistry and Photobiology, 1997, 65, 1039-1044.	2.5	3
60	The two pKa's of aspartate-85 and control of thermal isomerization and proton release in the arginine-82 to lysine mutant of bacteriorhodopsin. Biochemistry, 1995, 34, 8820-8834.	2.5	142
61	Probing of the Retinal Binding Site of Bacteriorhodopsin by Affinity Labeling. Biochemistry, 1994, 33, 11624-11630.	2.5	8
62	pH dependence of light-induced proton release by bacteriorhodopsin. FEBS Letters, 1993, 331, 31-34.	2.8	58