

# Nagendra Singh

## List of Publications by Year in descending order

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61  
papers

1,299  
citations

304602

22  
h-index

377752

34  
g-index

62  
all docs

62  
docs citations

62  
times ranked

1731  
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring potential inhibitor of SARS-CoV2 replicase from FDA approved drugs using insilico drug discovery methods. Journal of Biomolecular Structure and Dynamics, 2022, 40, 5507-5514.	2.0	16
2	<i>In silico</i> identification and validation of natural antiviral compounds as potential inhibitors of SARS-CoV-2 methyltransferase. Journal of Biomolecular Structure and Dynamics, 2022, 40, 6534-6544.	2.0	21
3	Expression of Regucalcin, a calcium-binding protein is regulated by hypoxia-inducible factor-1 $\pm$ . Life Sciences, 2022, 292, 120278.	2.0	5
4	Identification of potential inhibitors of SARS-COV-2 endoribonuclease (EndoU) from FDA approved drugs: a drug repurposing approach to find therapeutics for COVID-19. Journal of Biomolecular Structure and Dynamics, 2021, 39, 4201-4211.	2.0	52
5	Identification of hot spot residues on serine-arginine protein kinase-1 by molecular dynamics simulation studies. Journal of Biomolecular Structure and Dynamics, 2021, 39, 1579-1587.	2.0	4
6	Identification of a novel and potent small molecule inhibitor of SRPK1: mechanism of dual inhibition of SRPK1 for the inhibition of cancer progression. Aging, 2021, 13, 163-180.	1.4	12
7	Traditional Nutritional and Health Practices Targeting Lifestyle Behavioral Changes in Humans. Journal of Lifestyle Medicine, 2020, 10, 67-73.	0.3	9
8	Identification and evaluation of quercetin as a potential inhibitor of naphthoate synthase from <i>Enterococcus faecalis</i> . Journal of Molecular Recognition, 2019, 32, e2802.	1.1	5
9	Structural studies on dihydrouridine synthase A (DusA) from <i>Pseudomonas aeruginosa</i> . International Journal of Biological Macromolecules, 2019, 132, 254-264.	3.6	3
10	Search of multiple hot spots on the surface of peptidyl-tRNA hydrolase: structural, binding and antibacterial studies. Biochemical Journal, 2018, 475, 547-560.	1.7	5
11	Bioengineering of crop plants for improved tetrahydrofolate production. Bioengineered, 2018, 9, 152-158.	1.4	5
12	Aptamer-Based TB Antigen Tests for the Rapid Diagnosis of Pulmonary Tuberculosis: Potential Utility in Screening for Tuberculosis. ACS Infectious Diseases, 2018, 4, 1718-1726.	1.8	51
13	Recombinant overexpression of dihydroneopterin aldolase catalyst potentially regulates folate $\pm$ biofortification. Journal of Basic Microbiology, 2017, 57, 517-524.	1.8	3
14	Direct detection of <i>Mycobacterium tuberculosis</i> rifampin resistance in bio-safe stained sputum smears. PLoS ONE, 2017, 12, e0189149.	1.1	3
15	Molecular basis for nonspecificity of nonsteroidal anti-inflammatory drugs (NSAIDs). Drug Discovery Today, 2015, 20, 863-873.	3.2	53
16	The Mode of Inhibitor Binding to Peptidyl-tRNA Hydrolase: Binding Studies and Structure Determination of Unbound and Bound Peptidyl-tRNA Hydrolase from <i>Acinetobacter baumannii</i> . PLoS ONE, 2013, 8, e67547.	1.1	21
17	Synthesis, Structure $\pm$ Activity Relationship and Docking Studies of Substituted Aryl Thiazolyl Phenylsulfonamides as Potential Protein Tyrosine Phosphatase $\pm$ 1B Inhibitors. ChemMedChem, 2012, 7, 1185-1190.	1.6	16
18	Crystal structure of peptidyl-tRNA hydrolase from <i>mycobacterium smegmatis</i> reveals novel features related to enzyme dynamics. International Journal of Biochemistry and Molecular Biology, 2012, 3, 58-69.	0.1	9

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19	Biochemical studies and crystal structure determination of dihydrodipicolinate synthase from <i>Pseudomonas aeruginosa</i> . <i>International Journal of Biological Macromolecules</i> , 2011, 48, 779-787.	3.6	29
20	Identification of a novel and potent inhibitor of phospholipase A2 in a medicinal plant: Crystal structure at 1.93Å... and Surface Plasmon Resonance analysis of phospholipase A2 complexed with berberine. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 657-663.	1.1	39
21	Structural Basis of Recognition of Pathogen-associated Molecular Patterns and Inhibition of Proinflammatory Cytokines by Camel Peptidoglycan Recognition Protein. <i>Journal of Biological Chemistry</i> , 2011, 286, 16208-16217.	1.6	36
22	First structural evidence for the mode of diffusion of aromatic ligands and ligand-induced closure of the hydrophobic channel in heme peroxidases. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 1099-1107.	1.1	24
23	Substituted hydrazinecarbothioamide as potent antitubercular agents: Synthesis and quantitative structure-activity relationship (QSAR). <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 2597-2600.	1.0	18
24	Modulation of inhibitory activity of xylanase - Î±-amylase inhibitor protein (XAIP): binding studies and crystal structure determination of XAIP- II from <i>Scadoxus multiflorus</i> at 1.2 Å... resolution. <i>BMC Structural Biology</i> , 2010, 10, 41.	2.3	4
25	Crystal structure determination and inhibition studies of a novel xylanase and Î±-amylase inhibitor protein (XAIP) from <i>Scadoxus multiflorus</i> . <i>FEBS Journal</i> , 2010, 277, 2868-2882.	2.2	12
26	Mode of Binding of the Tuberculosis Prodrug Isoniazid to Heme Peroxidases. <i>Journal of Biological Chemistry</i> , 2010, 285, 1569-1576.	1.6	45
27	Specific interactions of C-terminal half (C-lobe) of lactoferrin protein with edible sugars: Binding and structural studies with implications on diabetes. <i>International Journal of Biological Macromolecules</i> , 2010, 47, 50-59.	3.6	11
28	Structural and binding studies of C-terminal half (C-lobe) of lactoferrin protein with COX-2-specific non-steroidal anti-inflammatory drugs (NSAIDs). <i>Archives of Biochemistry and Biophysics</i> , 2010, 500, 196-202.	1.4	5
29	Binding Modes of Aromatic Ligands to Mammalian Heme Peroxidases with Associated Functional Implications. <i>Journal of Biological Chemistry</i> , 2009, 284, 20311-20318.	1.6	39
30	Structural Evidence of Substrate Specificity in Mammalian Peroxidases. <i>Journal of Biological Chemistry</i> , 2009, 284, 14849-14856.	1.6	50
31	Simultaneous inhibition of anti-coagulation and inflammation: crystal structure of phospholipase A <sub>2</sub> complexed with indomethacin at 1.4Å... resolution reveals the presence of the new common ligand-binding site. <i>Journal of Molecular Recognition</i> , 2009, 22, 437-445.	1.1	27
32	Tryptophan as a three-way switch in regulating the function of the secretory signalling glycoprotein (SPS-40) from mammary glands: structure of SPS-40 complexed with 2-methylpentane-2,4-diol at 1.6Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 375-378.	2.5	1
33	Purification and preliminary X-ray crystallographic studies of Î² <sub>2</sub> -microseminoprotein from human seminal plasma. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 518-521.	0.7	3
34	Isolation, purification, crystallization and preliminary crystallographic studies of amaryllin, a plant pathogenesis-related protein from <i>Amaryllis belladonna</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 635-637.	0.7	6
35	Polysaccharide binding sites in hyaluronate lyase - crystal structures of native phage-encoded hyaluronate lyase and its complexes with ascorbic acid and lactose. <i>FEBS Journal</i> , 2009, 276, 3392-3402.	2.2	27
36	Inhibition of Lactoperoxidase by Its Own Catalytic Product: Crystal Structure of the Hypothiocyanate-Inhibited Bovine Lactoperoxidase at 2.3-Å... Resolution. <i>Biophysical Journal</i> , 2009, 96, 646-654.	0.2	54

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37	The Structural Basis for the Prevention of Nonsteroidal Antiinflammatory Drug-Induced Gastrointestinal Tract Damage by the C-Lobe of Bovine Colostrum Lactoferrin. <i>Biophysical Journal</i> , 2009, 97, 3178-3186.	0.2	32
38	Isolation, purification, crystallization and preliminary crystallographic studies of sagitoxin, an oligomeric cardiotoxin from the venom of <i>Naja naja saggitifera</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 545-547.	0.7	1
39	Crystal Structure of Lactoperoxidase at 2.4 Å Resolution. <i>Journal of Molecular Biology</i> , 2008, 376, 1060-1075.	2.0	102
40	Crystal Structure of the Peptidoglycan Recognition Protein at 1.8 Å Resolution Reveals Dual Strategy to Combat Infection Through Two Independent Functional Homodimers. <i>Journal of Molecular Biology</i> , 2008, 378, 923-932.	2.0	14
41	Structural Elements of Ligand Recognition Site in Secretory Phospholipase A2 and Structure-Based Design of Specific Inhibitors. <i>Current Topics in Medicinal Chemistry</i> , 2007, 7, 757-764.	1.0	20
42	Structural Plasticity and Enzyme Action: Crystal Structures of <i>Mycobacterium tuberculosis</i> Peptidyl-tRNA Hydrolase. <i>Journal of Molecular Biology</i> , 2007, 372, 186-193.	2.0	58
43	Carbohydrate-binding properties of goat secretory glycoprotein (SPG-40) and its functional implications: structures of the native glycoprotein and its four complexes with chitin-like oligosaccharides. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 437-446.	2.5	11
44	Crystal structures of complexes of phospholipase A 2 with natural and synthetic inhibitors. <i>FASEB Journal</i> , 2007, 21, A638.	0.2	0
45	Crystal structure of a highly acidic neurotoxin from scorpion <i>Buthus tamulus</i> at 2.2 Å resolution reveals novel structural features. <i>Journal of Structural Biology</i> , 2006, 155, 52-62.	1.3	9
46	Crystal structure of a secretory signalling glycoprotein from sheep at 2.0 Å resolution. <i>Journal of Structural Biology</i> , 2006, 156, 505-516.	1.3	22
47	Specific binding of non-steroidal anti-inflammatory drugs (NSAIDs) to phospholipase A2: structure of the complex formed between phospholipase A2 and diclofenac at 2.7 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 410-416.	2.5	32
48	Cloning, expression, purification, crystallization and preliminary X-ray analysis of peptidyl-tRNA hydrolase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 913-915.	0.7	7
49	Crystal structures of the complexes of a group IIA phospholipase A 2 with two natural anti-inflammatory agents, anisic acid, and atropine reveal a similar mode of binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 89-100.	1.5	25
50	Detection of native peptides as potent inhibitors of enzymes. <i>FEBS Journal</i> , 2005, 272, 562-572.	2.2	23
51	Structure of the zinc-induced heterodimer of two calcium-free isoforms of phospholipase A2 from <i>Naja naja saggitifera</i> at 2.7 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 302-308.	2.5	5
52	Structure of the zinc-saturated C-terminal lobe of bovine lactoferrin at 2.0 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1107-1115.	2.5	19
53	Non-steroidal anti-inflammatory drugs as potent inhibitors of phospholipase A2: structure of the complex of phospholipase A2 with niflumic acid at 2.5 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1579-1586.	2.5	19
54	Crystal structure of a calcium-induced dimer of two isoforms of cobra phospholipase A2 at 1.6 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 856-863.	1.5	7

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55	Crystal structure of a heterodimer of phospholipase A2 from <i>Naja naja sagittifera</i> at 2.3 Å... resolution reveals the presence of a new PLA2-like protein with a novel cys 32-Cys 49 disulphide bridge with a bound sugar at the substrate-binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 329-337.	1.5	13
56	Evidence for a role of initiation factor 3 in recycling of ribosomal complexes stalled on mRNAs in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2005, 33, 5591-5601.	6.5	27
57	Crystal structure of the complex of group I PLA2 with a group II-specific peptide Leu-Ala-Ile-Tyr-Ser (LAIYS) at 2.6 Å... resolution. <i>Journal of Drug Targeting</i> , 2005, 13, 367-374.	2.1	9
58	Crystal structure of a novel phospholipase A2 from <i>Naja naja sagittifera</i> with a strong anticoagulant activity. <i>Toxicon</i> , 2005, 46, 865-875.	0.8	20
59	A physiological connection between tmRNA and peptidyl-tRNA hydrolase functions in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2004, 32, 6028-6037.	6.5	68
60	Phospholipase A2 as a Target Protein for Nonsteroidal Anti-Inflammatory Drugs (NSAIDs): Crystal Structure of the Complex Formed between Phospholipase A2 and Oxyphenbutazone at 1.6 Å... Resolution. <i>Biochemistry</i> , 2004, 43, 14577-14583.	1.2	26
61	Lactoferrin-melanin interaction and its possible implications in melanin polymerization: Crystal structure of the complex formed between mare lactoferrin and melanin monomers at 2.7-Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 229-236.	1.5	7