Nagasuma Chandra

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7152353/publications.pdf

Version: 2024-02-01

106 papers	2,835 citations	159358 30 h-index	223531 46 g-index
109 all docs	109 docs citations	109 times ranked	4050 citing authors

#	Article	IF	Citations
1	A new blood-based RNA signature (R9), for monitoring effectiveness of tuberculosis treatment in a South Indian longitudinal cohort. IScience, 2022, 25, 103745.	1.9	1
2	SiteMotif: A graph-based algorithm for deriving structural motifs in Protein Ligand binding sites. PLoS Computational Biology, 2022, 18, e1009901.	1.5	7
3	Functional and Biochemical Characterization of the MazEF6 Toxin-Antitoxin System of Mycobacterium tuberculosis. Journal of Bacteriology, 2022, 204, e0005822.	1.0	8
4	PathExt: a general framework for path-based mining of omics-integrated biological networks. Bioinformatics, 2021, 37, 1254-1262.	1.8	11
5	VB10, a new blood biomarker for differential diagnosis and recovery monitoring of acute viral and bacterial infections. EBioMedicine, 2021, 67, 103352.	2.7	15
6	A Strategic Target Rescues Trimethoprim Sensitivity in Escherichia coli. IScience, 2020, 23, 100986.	1.9	15
7	Î©76: A designed antimicrobial peptide to combat carbapenem- and tigecycline-resistant Acinetobacter baumannii. Science Advances, 2019, 5, eaax1946.	4.7	64
8	Interrogation of genome-wide networks in biology: comparison of knowledge-based and statistical methods. International Journal of Advances in Engineering Sciences and Applied Mathematics, 2019, 11, 119-137.	0.7	5
9	An Augmented Pocketome: Detection and Analysis of Small-Molecule Binding Pockets in Proteins of Known 3D Structure. Structure, 2018, 26, 499-512.e2.	1.6	38
10	Computational antimicrobial peptide design and evaluation against multidrug-resistant clinical isolates of bacteria. Journal of Biological Chemistry, 2018, 293, 3492-3509.	1.6	93
11	Design of a heme-binding peptide motif adopting a Î²-hairpin conformation. Journal of Biological Chemistry, 2018, 293, 9412-9422.	1.6	8
12	Identification of a coâ€target for enhancing efficacy of sorafenib in HCC through a quantitative modeling approach. FEBS Journal, 2018, 285, 3977-3992.	2.2	8
13	Role of genetic heterogeneity in determining the epidemiological severity of H1N1 influenza. PLoS Computational Biology, 2018, 14, e1006069.	1.5	14
14	Unbiased Identification of Blood-based Biomarkers for Pulmonary Tuberculosis by Modeling and Mining Molecular Interaction Networks. EBioMedicine, 2017, 15, 112-126.	2.7	75
15	A Systems Perspective of Signalling Networks in Hostâ€“Pathogen Interactions. Journal of the Indian Institute of Science, 2017, 97, 41-57.	0.9	0
16	Deciphering common recognition principles of nucleoside mono/di and tri-phosphates binding in diverse proteins via structural matching of their binding sites. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1699-1712.	1.5	3
17	Resolving protein structureâ€functionâ€binding site relationships from a binding site similarity network perspective. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1319-1335.	1.5	14
18	A genome-wide structure-based survey of nucleotide binding proteins in M. tuberculosis. Scientific Reports, 2017, 7, 12489.	1.6	5

#	Article	IF	Citations
19	Methionine synthase is localized to the nucleus in Pichia pastoris and Candida albicans and to the cytoplasm in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2017, 292, 14730-14746.	1.6	9
20	DenHunt - A Comprehensive Database of the Intricate Network of Dengue-Human Interactions. PLoS Neglected Tropical Diseases, 2016, 10, e0004965.	1.3	23
21	Structural analysis of dihydrofolate reductases enables rationalization of antifolate binding affinities and suggests repurposing possibilities. FEBS Journal, 2016, 283, 1139-1167.	2.2	19
22	Dissecting the structural and functional features of the Luteinizing hormone receptor using receptor specific single chain fragment variables. Molecular and Cellular Endocrinology, 2016, 427, 1-12.	1.6	5
23	A comparative analysis of the DNA recombination repair pathway in mycobacterial genomes. Tuberculosis, 2016, 99, 109-119.	0.8	27
24	Curcumin Reduces the Motility of Salmonella enterica Serovar Typhimurium by Binding to the Flagella, Thereby Leading to Flagellar Fragility and Shedding. Journal of Bacteriology, 2016, 198, 1798-1811.	1.0	27
25	Editorial overview: Carbohydrateâ€“protein interactions and glycosylation: integrating structural biology, informatics and systems modelling to understand glycan structure and glycan-protein interactions. Current Opinion in Structural Biology, 2016, 40, v-viii.	2.6	1
26	Identifying and Tackling Emergent Vulnerability in Drug-Resistant Mycobacteria. ACS Infectious Diseases, 2016, 2, 592-607.	1.8	34
27	EpiTracer - an algorithm for identifying epicenters in condition-specific biological networks. BMC Genomics, 2016, 17, 543.	1.2	17
28	Hypothetical protein Rv3423.1 of Mycobacterium tuberculosis is a histone acetyltransferase. FEBS Journal, 2016, 283, 265-281.	2.2	51
29	High IL-6 and low IL-15 levels mark the presence of TB infection: A preliminary study. Cytokine, 2016, 81, 57-62.	1.4	22
30	Probing the Druggability Limits for Enzymes of the NAD Biosynthetic Network in Glioma. Journal of Chemical Information and Modeling, 2016, 56, 843-853.	2.5	4
31	Complete Genome Sequences of an Escherichia coli Laboratory Strain and Trimethoprim-Resistant (TMP32XR) Mutant Strains. Genome Announcements, 2015, 3, .	0.8	4
32	Mechanism of Iron-Dependent Repressor (IdeR) Activation and DNA Binding: A Molecular Dynamics and Protein Structure Network Study. PLoS Computational Biology, 2015, 11, e1004500.	1.5	13
33	NrichD database: sequence databases enriched with computationally designed protein-like sequences aid in remote homology detection. Nucleic Acids Research, 2015, 43, D300-D305.	6.5	12
34	Enriching the annotation of Mycobacterium tuberculosis H37Rv proteome using remote homology detection approaches: Insights into structure and function. Tuberculosis, 2015, 95, 14-25.	0.8	9
35	Architectural plan of transcriptional regulation in Mycobacterium tuberculosis. Trends in Microbiology, 2015, 23, 123-125.	3.5	1
36	A molecular systems approach to modelling human skin pigmentation: identifying underlying pathways and critical components. BMC Research Notes, 2015, 8, 170.	0.6	9

#	Article	IF	Citations
37	Deciphering complex patterns of classâ€‘HLAâ€“peptide crossâ€‘reactivity via hierarchical grouping. Immunology and Cell Biology, 2015, 93, 522-532.	1.0	9
38	Recognizing drug targets using evolutionary information: implications for repurposing FDA-approved drugs against Mycobacterium tuberculosis H37Rv. Molecular BioSystems, 2015, 11, 3316-3331.	2.9	20
39	De-DUFing the DUFs: Deciphering distant evolutionary relationships of Domains of Unknown Function using sensitive homology detection methods. Biology Direct, 2015, 10, 38.	1.9	34
40	Complete Genome Sequences of a Mycobacterium smegmatis Laboratory Strain (MC ² 155) and Isoniazid-Resistant (4XR1/R2) Mutant Strains. Genome Announcements, 2015, 3, .	0.8	54
41	Gene expression profiles of wild-type and isoniazid-resistant strains of Mycobacterium smegmatis. Data in Brief, 2015, 4, 186-189.	0.5	5
42	CHEXVIS: a tool for molecular channel extraction and visualization. BMC Bioinformatics, 2015, 16, 119.	1.2	74
43	Common recognition principles across diverse sequence and structural families of sialic acid binding proteins. Glycobiology, 2014, 24, 5-16.	1.3	7
44	Mapping Post-translational Modifications of Mammalian Testicular Specific Histone Variant TH2B in Tetraploid and Haploid Germ Cells and Their Implications on the Dynamics of Nucleosome Structure. Journal of Proteome Research, 2014, 13, 5603-5617.	1.8	20
45	Identifying feasible metabolic routes in Mycobacterium smegmatis and possible alterations under diverse nutrient conditions. BMC Microbiology, 2014, 14, 276.	1.3	22
46	Weighting schemes in metabolic graphs for identifying biochemical routes. Systems and Synthetic Biology, 2014, 8, 47-57.	1.0	2
47	Filling-in Void and Sparse Regions in Protein Sequence Space by Protein-Like Artificial Sequences Enables Remarkable Enhancement in Remote Homology Detection Capability. Journal of Molecular Biology, 2014, 426, 962-979.	2.0	15
48	Rationalization and prediction of drug resistant mutations in targets for clinical anti-tubercular drugs. Journal of Biomolecular Structure and Dynamics, 2013, 31, 44-58.	2.0	3
49	A multi-level multi-scale approach to study essential genes in Mycobacterium tuberculosis. BMC Systems Biology, 2013, 7, 132.	3.0	17
50	Network approaches to drug discovery. Expert Opinion on Drug Discovery, 2013, 8, 7-20.	2.5	40
51	Current trends in modeling hostâ€“pathogen interactions. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2013, 3, 109-128.	4.6	8
52	PocketAnnotate: towards site-based function annotation. Nucleic Acids Research, 2012, 40, W400-W408.	6.5	18
53	Cloning, expression, purification, and biochemical characterisation of the FIC motif containing protein of Mycobacterium tuberculosis. Protein Expression and Purification, 2012, 86, 58-67.	0.6	9
54	Crowd Sourcing a New Paradigm for Interactome Driven Drug Target Identification in Mycobacterium tuberculosis. PLoS ONE, 2012, 7, e39808.	1.1	36

#	Article	IF	Citations
55	Rule-based modelling of iron homeostasis in tuberculosis. Molecular BioSystems, 2011, 7, 2750.	2.9	13
56	Computational approaches for drug target identification in pathogenic diseases. Expert Opinion on Drug Discovery, 2011, 6, 975-979.	2.5	9
57	PocketAlign A Novel Algorithm for Aligning Binding Sites in Protein Structures. Journal of Chemical Information and Modeling, 2011, 51, 1725-1736.	2.5	36
58	Systems biology of tuberculosis. Tuberculosis, 2011, 91, 487-496.	0.8	20
59	Structural biology of Mycobacterium tuberculosis proteins: The Indian efforts. Tuberculosis, 2011, 91, 456-468.	0.8	22
60	Open source drug discoveryâ€“ A new paradigm of collaborative research in tuberculosis drug development. Tuberculosis, 2011, 91, 479-86.	0.8	42
61	Structural Annotation of Mycobacterium tuberculosis Proteome. PLoS ONE, 2011, 6, e27044.	1.1	33
62	Structural bioinformatics: Deriving biological insights from protein structures. Interdisciplinary Sciences, Computational Life Sciences, 2010, 2, 347-366.	2.2	9
63	Modeling metabolic adjustment in Mycobacterium tuberculosis upon treatment with isoniazid. Systems and Synthetic Biology, 2010, 4, 299-309.	1.0	11
64	Proteinâ€“protein interaction networks suggest different targets have different propensities for triggering drug resistance. Systems and Synthetic Biology, 2010, 4, 311-322.	1.0	21
65	The Multifunctional PE_PGRS11 Protein from Mycobacterium tuberculosis Plays a Role in Regulating Resistance to Oxidative Stress. Journal of Biological Chemistry, 2010, 285, 30389-30403.	1.6	59
66	Mycobacterium tuberculosis FtsZ requires at least one arginine residue at the C-terminal end for polymerization in vitro. Acta Biochimica Et Biophysica Sinica, 2010, 42, 58-69.	0.9	4
67	A systems perspective of hostâ€“pathogen interactions: predicting disease outcome in tuberculosis. Molecular BioSystems, 2010, 6, 516-530.	2.9	47
68	Localisation of Plasmodium falciparum uroporphyrinogen III decarboxylase of the heme-biosynthetic pathway in the apicoplast and characterisation of its catalytic properties. International Journal for Parasitology, 2009, 39, 559-568.	1.3	44
69	Structural basis for the function of anti-idiotypic antibody in immune memory. Molecular Immunology, 2009, 46, 1250-1255.	1.0	2
70	Computational systems approach for drug target discovery. Expert Opinion on Drug Discovery, 2009, 4, 1221-1236.	2.5	21
71	Flux balance analysis of biological systems: applications and challenges. Briefings in Bioinformatics, 2009, 10, 435-449.	3.2	354
72	Strategies for efficient disruption of metabolism in Mycobacterium tuberculosis from network analysis. Molecular BioSystems, 2009, 5, 1740.	2.9	35

#	Article	IF	Citations
73	Functionally important movements in RecA molecules and filaments: studies involving mutation and environmental changes. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1146-1157.	2.5	11
74	HLA-A*0201-restricted Cytotoxic T-cell Epitopes in Three PE/PPE Family Proteins of Mycobacterium tuberculosis. Scandinavian Journal of Immunology, 2008, 67, 411-417.	1.3	16
75	Scanning the Genome of Mycobacterium tuberculosis to Identify Potential Lectins. Protein and Peptide Letters, 2007, 14, 683-691.	0.4	9
76	Perpetuation of immunological memory through common MHC-I binding modes of peptidomimic and antigenic peptides. Biochemical and Biophysical Research Communications, 2007, 364, 308-312.	1.0	2
77	Snapshots of RecA Protein Involving Movement of the C-domain and Different Conformations of the DNA-binding Loops: Crystallographic and Comparative Analysis of 11 Structures of Mycobacterium smegmatis RecA. Journal of Molecular Biology, 2007, 367, 1130-1144.	2.0	40
78	Diagnosis and therapy of oral squamous cell carcinoma. Expert Review of Anticancer Therapy, 2007, 7, 317-329.	1.1	19
79	Conformationally locked thiosugars as potent Î±-mannosidase inhibitors: Synthesis, biochemical and docking studies. Bioorganic and Medicinal Chemistry, 2007, 15, 5659-5665.	1.4	17
80	Parallel implementation ofAutoDock. Journal of Applied Crystallography, 2007, 40, 598-599.	1.9	31
81	Hallmarks of mycolic acid biosynthesis: A comparative genomics study. Proteins: Structure, Function and Bioinformatics, 2007, 69, 358-368.	1.5	11
82	Functional interaction of diphenols with polyphenol oxidase. FEBS Journal, 2007, 274, 4177-4187.	2.2	25
83	Metabolome Based Reaction Graphs of M. tuberculosis and M. leprae: A Comparative Network Analysis. PLoS ONE, 2007, 2, e881.	1.1	38
84	In-Silico Pharmacodynamics. Applied Bioinformatics, 2006, 5, 141-150.	1.7	4
85	A K52Q substitution in the globular domain of histone H1t modulates its nucleosome binding properties. FEBS Letters, 2006, 580, 5999-6006.	1.3	9
86	A combined immuno-informatics and structure-based modeling approach for prediction of T cell epitopes of secretory proteins of Mycobacterium tuberculosis. Microbes and Infection, 2006, 8, 738-746.	1.0	33
87	Common Scaffolds, Diverse Recognition Profiles. Structure, 2006, 14, 1093-1094.	1.6	3
88	Crystallographic identification of an ordered C-terminal domain and a second nucleotide-binding site in RecA: new insights into allostery. Nucleic Acids Research, 2006, 34, 2186-2195.	6.5	38
89	Lectindb: a plant lectin database. Glycobiology, 2006, 16, 938-946.	1.3	53
90	Molecular Mechanism of Dimerization of Bowman-Birk Inhibitors. Journal of Biological Chemistry, 2004, 279, 30425-30432.	1.6	46

#	Article	IF	Citations
91	A database analysis of jacalin-like lectins: sequence-structure-function relationships. Glycobiology, 2004, 14, 1247-1263.	1.3	70
92	Î´-Aminolevulinic Acid Dehydratase from Plasmodium falciparum. Journal of Biological Chemistry, 2004, 279, 6934-6942.	1.6	62
93	Extracting Hydrogen-Bond Signature Patterns from Protein Structure Data. Applied Bioinformatics, 2004, 3, 125-135.	1.7	2
94	Structural studies on MtRecA-nucleotide complexes: Insights into DNA and nucleotide binding and the structural signature of NTP recognition. Proteins: Structure, Function and Bioinformatics, 2003, 50, 474-485.	1.5	58
95	Determinants of histamine recognition: implications for the design of antihistamines. Biochemical and Biophysical Research Communications, 2003, 309, 425-431.	1.0	6
96	Conformation of gramicidin-A in CTAB micellar media. Journal of Photochemistry and Photobiology B: Biology, 2003, 70, 117-124.	1.7	5
97	Computational analysis of multivalency in lectins: structures of garlic lectin-oligosaccharide complexes and their aggregates. Glycobiology, 2003, 13, 765-775.	1.3	25
98	Molecular modeling of the chromatosome particle. Nucleic Acids Research, 2003, 31, 4264-4274.	6.5	68
99	Crystal Structures of Mycobacterium smegmatis RecA and Its Nucleotide Complexes. Journal of Bacteriology, 2003, 185, 4280-4284.	1.0	61
100	Re-refinement using reprocessed data to improve the quality of the structure: a case study involving garlic lectin. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 414-420.	2.5	18
101	Prediction of an HMG-box fold in the C-terminal domain of histone H1: Insights into its role in DNA condensation. Proteins: Structure, Function and Bioinformatics, 2002, 49, 71-81.	1.5	39
102	Crystal Structure of a Dimeric Mannose-specific Agglutinin from Garlic: Quaternary Association and Carbohydrate Specificity. Journal of Molecular Biology, 1999, 285, 1157-1168.	2.0	95
103	X-ray Studies on Crystalline Complexes Involving Amino Acids and Peptides. XXXIII. Crystal Structures of L- and DL-Arginine Complexed with Oxalic Acid and a Comparative Study of Amino Acidâ€“Oxalic Acid Complexes. Acta Crystallographica Section B: Structural Science, 1998, 54, 257-263.	1.8	19
104	Xray Studies on Crystalline Complexes Involving Amino Acids and Peptides XXXIV. Novel Mode of Aggregation, Interaction Patterns and Chiral Effects in the Maleic Acid Complexes of DL- and L-Arginine. Journal of Biomolecular Structure and Dynamics, 1998, 15, 1093-1100.	2.0	22
105	Crystallization and preliminary crystallographic studies on the mannose-specific lectin from garlic. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 787-788.	2.5	6
106	Water-dependent domain motion and flexibility in ribonuclease A and the invariant features in its hydration shell. An X-ray study of two low-humidity crystal forms of the enzyme. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 703-710.	2.5	28