

Shekhar C Mande

List of Publications by Year in descending order

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59
papers

1,949
citations

236925

25
h-index

254184

43
g-index

63
all docs

63
docs citations

63
times ranked

2319
citing authors

#	ARTICLE	IF	CITATIONS
1	Structureâ€™sequence features based prediction of phosphosites of serine/threonine protein kinases of <i>Mycobacterium tuberculosis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 131-141.	2.6	3
2	Structural aspects of lesional and non-lesional skin microbiota reveal key community changes in leprosy patients from India. <i>Scientific Reports</i> , 2021, 11, 3294.	3.3	6
3	Chaperonin Abundance Enhances Bacterial Fitness. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 669996.	3.5	2
4	A novel function of <i>Mycobacterium tuberculosis</i> chaperonin paralog GroEL1 in copper homeostasis. <i>FEBS Letters</i> , 2020, 594, 3305-3323.	2.8	9
5	Role of S&T organisations in mitigation of Covid-19: CSIR as a case study. <i>Indian Chemical Engineer</i> , 2020, 62, 333-342.	1.5	2
6	CoRNeA: A Pipeline to Decrypt the Inter-Protein Interfaces from Amino Acid Sequence Information. <i>Biomolecules</i> , 2020, 10, 938.	4.0	6
7	16S rDNA based skin microbiome data of healthy individuals and leprosy patients from India. <i>Scientific Data</i> , 2019, 6, 225.	5.3	9
8	Spatially conserved motifs in complement control protein domains determine functionality in regulators of complement activation-family proteins. <i>Communications Biology</i> , 2019, 2, 290.	4.4	11
9	Structural basis of hypoxic gene regulation by the Rv0081 transcription factor of <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2019, 593, 982-995.	2.8	8
10	Rewiring of Metabolic Network in <i>Mycobacterium tuberculosis</i> During Adaptation to Different Stresses. <i>Frontiers in Microbiology</i> , 2019, 10, 2417.	3.5	30
11	A Glimpse Into the Structure and Function of Atypical Type I Chaperonins. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 31.	3.5	13
12	Functional Diversity in Mycobacterial Chaperonins: The Generalists and the Specialists. <i>Heat Shock Proteins</i> , 2017, , 67-80.	0.2	1
13	Nobel Prize in Physiology or Medicine 2016. <i>Resonance</i> , 2017, 22, 829-833.	0.3	2
14	Towards understanding the biological function of the unusual chaperonin Cpn60.1 (GroEL1) of <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2016, 97, 137-146.	1.9	23
15	GroEL2 of <i>Mycobacterium tuberculosis</i> Reveals the Importance of Structural Pliability in Chaperonin Function. <i>Journal of Bacteriology</i> , 2016, 198, 486-497.	2.2	8
16	Biology across Scales:Historical Perspective on Some Indian Contributions. <i>Current Science</i> , 2016, 110, 529.	0.8	0
17	Multiple chaperonins in bacteriaâ€™novel functions and non-canonical behaviors. <i>Cell Stress and Chaperones</i> , 2015, 20, 555-574.	2.9	49
18	From System-Wide Differential Gene Expression to Perturbed Regulatory Factors: A Combinatorial Approach. <i>PLoS ONE</i> , 2015, 10, e0142147.	2.5	2

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19	Early developments in crystallography. <i>Resonance</i> , 2014, 19, 1077-1086.	0.3	1
20	Differential enrichment of regulatory motifs in the composite network of protein-protein and gene regulatory interactions. <i>BMC Systems Biology</i> , 2014, 8, 26.	3.0	5
21	Probing Gene Regulatory Networks to Decipher Host-Pathogen Interactions. , 2013, , 37-54.		1
22	The Crystal Structure of <i>Mycobacterium tuberculosis</i> NrdH at 0.87 Å... Suggests a Possible Mode of Its Activity. <i>Biochemistry</i> , 2013, 52, 4056-4065.	2.5	12
23	Evolution of Bacterial Chaperonin 60 Paralogues and Moonlighting Activity. <i>Heat Shock Proteins</i> , 2013, , 101-121.	0.2	11
24	Understanding Communication Signals during Mycobacterial Latency through Predicted Genome-Wide Protein Interactions and Boolean Modeling. <i>PLoS ONE</i> , 2012, 7, e33893.	2.5	34
25	Structural biology of <i>Mycobacterium tuberculosis</i> proteins: The Indian efforts. <i>Tuberculosis</i> , 2011, 91, 456-468.	1.9	22
26	Delineation of key regulatory elements identifies points of vulnerability in the mitogen-activated signaling network. <i>Genome Research</i> , 2011, 21, 2067-2081.	5.5	3
27	Mapping Conformational Transitions in Cyclic AMP Receptor Protein: Crystal Structure and Normal-Mode Analysis of <i>Mycobacterium tuberculosis</i> apo-cAMP Receptor Protein. <i>Biophysical Journal</i> , 2010, 98, 305-314.	0.5	27
28	The PPE18 of <i>Mycobacterium tuberculosis</i> Interacts with TLR2 and Activates IL-10 Induction in Macrophage. <i>Journal of Immunology</i> , 2009, 183, 6269-6281.	0.8	189
29	A novel nucleoid-associated protein of <i>Mycobacterium tuberculosis</i> is a sequence homolog of GroEL. <i>Nucleic Acids Research</i> , 2009, 37, 4944-4954.	14.5	60
30	Facilitated Oligomerization of Mycobacterial GroEL: Evidence for Phosphorylation-Mediated Oligomerization. <i>Journal of Bacteriology</i> , 2009, 191, 6525-6538.	2.2	40
31	Prediction of conditional gene essentiality through graph theoretical analysis of genome-wide functional linkages. <i>Molecular BioSystems</i> , 2009, 5, 1936.	2.9	24
32	Exploiting 3D structural templates for detection of metal-binding sites in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1206-1218.	2.6	45
33	<i>Mycobacterium tuberculosis</i> heat shock protein 60 modulates immune response to PPD by manipulating the surface expression of TLR2 on macrophages. <i>Cellular Microbiology</i> , 2008, 10, 1711-1722.	2.1	28
34	Crystal Structure of <i>Mycobacterium tuberculosis</i> YefM Antitoxin Reveals that it is Not an Intrinsically Unstructured Protein. <i>Journal of Molecular Biology</i> , 2008, 383, 482-493.	4.2	51
35	Dynamic Changes in Protein Functional Linkage Networks Revealed by Integration with Gene Expression Data. <i>PLoS Computational Biology</i> , 2008, 4, e1000237.	3.2	32
36	Functional Studies of Multiple Thioredoxins from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2008, 190, 7087-7095.	2.2	54

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37	Inferring genome-wide functional linkages in <i>E. coli</i> by combining improved genome context methods: Comparison with high-throughput experimental data. <i>Genome Research</i> , 2007, 17, 527-535.	5.5	57
38	Cation-Mediated Interplay of Loops in Chaperonin-10. <i>Journal of Biomolecular Structure and Dynamics</i> , 2006, 23, 365-375.	3.5	2
39	Multiple Gene Duplication and Rapid Evolution in the groEL Gene: Functional Implications. <i>Journal of Molecular Evolution</i> , 2006, 63, 781-787.	1.8	60
40	The unusual chaperonins of <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2005, 85, 385-394.	1.9	61
41	Effect of alcohols on protein hydration: crystallographic analysis of hen egg-white lysozyme in the presence of alcohols. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1005-1008.	2.5	34
42	Conformational flexibility of <i>Mycobacterium tuberculosis</i> thioredoxin reductase: crystal structure and normal-mode analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1603-1611.	2.5	32
43	Crystal Structure of the 65-Kilodalton Heat Shock Protein, Chaperonin 60.2, of <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 8105-8113.	2.2	66
44	Expression, purification, crystallization and preliminary X-ray crystallographic studies of <i>Mycobacterium tuberculosis</i> thioredoxin reductase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 777-779.	2.5	7
45	<i>Mycobacterium tuberculosis</i> GroEL Homologues Unusually Exist as Lower Oligomers and Retain the Ability to Suppress Aggregation of Substrate Proteins. <i>Journal of Molecular Biology</i> , 2004, 342, 605-617.	4.2	88
46	Chimeric <i>Vitreoscilla</i> Hemoglobin (VHb) Carrying a Flavoreductase Domain Relieves Nitrosative Stress in <i>Escherichia coli</i> : New Insight into the Functional Role of VHb. <i>Applied and Environmental Microbiology</i> , 2002, 68, 152-160.	3.1	68
47	Involvement of a Nine-residue Loop of Streptokinase in the Generation of Macromolecular Substrate Specificity by the Activator Complex through Interaction with Substrate Kringle Domains. <i>Journal of Biological Chemistry</i> , 2002, 277, 13257-13267.	3.4	26
48	Structure of <i>Mycobacterium tuberculosis</i> chaperonin-10 at 3.5 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 260-266.	2.5	20
49	Homology Model of a Novel Xylanase: Molecular Basis for High-Thermostability and Alkaline Stability. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 18, 137-144.	3.5	3
50	Contributory presentations/posters. <i>Journal of Biosciences</i> , 1999, 24, 33-198.	1.1	0
51	Identification of the INO1 gene of <i>Mycobacterium tuberculosis</i> H37Rv reveals a novel class of inositol-1-phosphate synthase enzyme 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1999, 291, 531-536.	4.2	63
52	Function of the central domain of streptokinase in substrate plasminogen docking and processing revealed by site-directed mutagenesis. <i>Protein Science</i> , 1999, 8, 2791-2805.	7.6	37
53	Identification of an ABC transporter gene that exhibits mRNA level overexpression in fluoroquinolone-resistant <i>Mycobacterium smegmatis</i> . <i>FEBS Letters</i> , 1998, 425, 151-156.	2.8	18
54	Hemoglobin Biosynthesis in <i>Vitreoscilla stercoraria</i> DW: Cloning, Expression, and Characterization of a New Homolog of a Bacterial Globin Gene. <i>Applied and Environmental Microbiology</i> , 1998, 64, 2220-2228.	3.1	17

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55	Three hTIM Mutants that Provide New Insights on why TIM is a Dimer. Journal of Molecular Biology, 1996, 257, 441-456.	4.2	101
56	Crystal structure of recombinant triosephosphate isomerase from <i>Bacillus stearothermophilus</i> . An analysis of potential thermostability factors in six isomerases with known three-dimensional structures points to the importance of hydrophobic interactions. Protein Science, 1995, 4, 2594-2604.	7.6	117
57	Crystal structure of recombinant human triosephosphate isomerase at 2.8 Å resolution. Triosephosphate isomerase-related human genetic disorders and comparison with the trypanosomal enzyme. Protein Science, 1994, 3, 810-821.	7.6	110
58	Protein crystallography and infectious diseases. Protein Science, 1994, 3, 1670-1686.	7.6	48
59	Cloning and Overexpression of the Triosephosphate Isomerase Genes from Psychrophilic and Thermophilic Bacteria. Journal of Molecular Biology, 1993, 229, 85-93.	4.2	89