

Rajan Sankaranarayanan

List of Publications by Year in descending order

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75
papers

2,841
citations

218677

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182427

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85
docs citations

85
times ranked

2854
citing authors

#	ARTICLE	IF	CITATIONS
1	The Structure of Threonyl-tRNA Synthetase-tRNA ^{Thr} Complex Enlightens Its Repressor Activity and Reveals an Essential Zinc Ion in the Active Site. <i>Cell</i> , 1999, 97, 371-381.	28.9	291
2	A novel mode of carbohydrate recognition in jacalin, a Moraceae plant lectin with a β^2 -prism fold. <i>Nature Structural Biology</i> , 1996, 3, 596-603.	9.7	224
3	Transfer RNA-Mediated Editing in Threonyl-tRNA Synthetase. <i>Cell</i> , 2000, 103, 877-884.	28.9	175
4	Zinc ion mediated amino acid discrimination by threonyl-tRNA synthetase. <i>Nature Structural Biology</i> , 2000, 7, 461-465.	9.7	139
5	Thermostable <i>Bacillus subtilis</i> Lipases: In Vitro Evolution and Structural Insight. <i>Journal of Molecular Biology</i> , 2008, 381, 324-340.	4.2	125
6	Structural Basis of Selection and Thermostability of Laboratory Evolved <i>Bacillus subtilis</i> Lipase. <i>Journal of Molecular Biology</i> , 2004, 341, 1271-1281.	4.2	122
7	Mechanistic and functional insights into fatty acid activation in <i>Mycobacterium tuberculosis</i> . <i>Nature Chemical Biology</i> , 2009, 5, 166-173.	8.0	119
8	A novel tunnel in mycobacterial type III polyketide synthase reveals the structural basis for generating diverse metabolites. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 894-900.	8.2	85
9	In Vitro Evolved Non-Aggregating and Thermostable Lipase: Structural and Thermodynamic Investigation. <i>Journal of Molecular Biology</i> , 2011, 413, 726-741.	4.2	77
10	Nonprocessive [2 β]e ⁻ off-loading reductase domains from mycobacterial nonribosomal peptide synthetases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5681-5686.	7.1	73
11	Crystal Structure of Low-Molecular-Weight Protein Tyrosine Phosphatase from <i>Mycobacterium tuberculosis</i> at 1.9-Å Resolution. <i>Journal of Bacteriology</i> , 2005, 187, 2175-2181.	2.2	68
12	Versatility of polyketide synthases in generating metabolic diversity. <i>Current Opinion in Structural Biology</i> , 2007, 17, 736-743.	5.7	68
13	Post-transfer editing mechanism of a D-aminoacyl-tRNA deacylase-like domain in threonyl-tRNA synthetase from archaea. <i>EMBO Journal</i> , 2006, 25, 4152-4162.	7.8	67
14	Carbohydrate specificity and quaternary association in basic winged bean lectin: X-ray analysis of the lectin at 2.5 Å... resolution. <i>Journal of Molecular Biology</i> , 1998, 276, 787-796.	4.2	65
15	A Cell Wall-Degrading Esterase of <i>Xanthomonas oryzae</i> Requires a Unique Substrate Recognition Module for Pathogenesis on Rice. <i>Plant Cell</i> , 2009, 21, 1860-1873.	6.6	64
16	The β^3 -Crystallin Superfamily Contains a Universal Motif for Binding Calcium ²⁺ . <i>Biochemistry</i> , 2009, 48, 12180-12190.	2.5	63
17	Vertebrate Homologue of <i>Drosophila</i> GAGA Factor. <i>Journal of Molecular Biology</i> , 2010, 400, 434-447.	4.2	62
18	Mechanistic insights into cognate substrate discrimination during proofreading in translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22117-22121.	7.1	60

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19	Structural basis of translational control by Escherichia coli threonyl tRNA synthetase. Nature Structural Biology, 2002, 9, 343-7.	9.7	56
20	Conformational Movements and Cooperativity upon Amino Acid, ATP and tRNA Binding in Threonyl-tRNA Synthetase. Journal of Molecular Biology, 2003, 331, 201-211.	4.2	53
21	A D-amino acid editing module coupled to the translational apparatus in archaea. Nature Structural and Molecular Biology, 2005, 12, 556-557.	8.2	52
22	Mechanism of chiral proofreading during translation of the genetic code. ELife, 2013, 2, e01519.	6.0	43
23	Molecular Basis of the Functional Divergence of Fatty Acyl-AMP Ligase Biosynthetic Enzymes of Mycobacterium tuberculosis. Journal of Molecular Biology, 2012, 416, 221-238.	4.2	40
24	PhyA, a Secreted Protein of Xanthomonas oryzae pv. oryzae, Is Required for Optimum Virulence and Growth on Phytic Acid as a Sole Phosphate Source. Molecular Plant-Microbe Interactions, 2003, 16, 973-982.	2.6	38
25	Structural insights into biosynthesis of resorcinolic lipids by a type III polyketide synthase in Neurospora crassa. Journal of Structural Biology, 2008, 162, 411-421.	2.8	37
26	A chiral selectivity relaxed paralog of DTD for proofreading tRNA mischarging in Animalia. Nature Communications, 2018, 9, 511.	12.8	31
27	The modular structure of Escherichia coli threonyl-tRNA synthetase as both an enzyme and a regulator of gene expression. Molecular Microbiology, 2003, 47, 961-974.	2.5	30
28	Elongation Factor Tu Prevents Misediting of Gly-tRNA(Gly) Caused by the Design Behind the Chiral Proofreading Site of D-Aminoacyl-tRNA Deacylase. PLoS Biology, 2016, 14, e1002465.	5.6	30
29	Chiral checkpoints during protein biosynthesis. Journal of Biological Chemistry, 2019, 294, 16535-16548.	3.4	29
30	Role of D-aminoacyl-tRNA deacylase beyond chiral proofreading as a cellular defense against glycine mischarging by AlaRS. ELife, 2017, 6, .	6.0	29
31	Exploring the Limits of Sequence and Structure in a Variant Î²-Crystallin Domain of the Protein Absent in Melanoma-1 (AIM1). Journal of Molecular Biology, 2008, 381, 509-518.	4.2	26
32	Unsaturated Lipid Assimilation by Mycobacteria Requires Auxiliary cis-trans Enoyl CoA Isomerase. Chemistry and Biology, 2015, 22, 1577-1587.	6.0	24
33	Specificity and catalysis hardwired at the RNA-protein interface in a translational proofreading enzyme. Nature Communications, 2015, 6, 7552.	12.8	24
34	Crystallization and Preliminary X-ray Studies of the Basic Lectin from Winged Bean (Psophocarpus Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	4.2	22
35	Structural biology of Mycobacterium tuberculosis proteins: The Indian efforts. Tuberculosis, 2011, 91, 456-468.	1.9	22
36	Decoding the Molecular Design Principles Underlying Ca ²⁺ Binding to Î²-Crystallin Motifs. Journal of Molecular Biology, 2012, 415, 75-91.	4.2	21

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37	Three-Dimensional Domain Swapping in Nitrollin, a Single-Domain β -Crystallin from <i>Nitrosospira multiformis</i> , Controls Protein Conformation and Stability but Not Dimerization. <i>Journal of Molecular Biology</i> , 2009, 385, 163-177.	4.2	18
38	Fatty acyl-AMP ligases and polyketide synthases are unique enzymes of lipid biosynthetic machinery in <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2011, 91, 448-455.	1.9	18
39	A mutation in an exoglucanase of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> , which confers an endo mode of activity, affects bacterial virulence, but not the induction of immune responses, in rice. <i>Molecular Plant Pathology</i> , 2018, 19, 1364-1376.	4.2	17
40	The fidelity of the translation of the genetic code. <i>Acta Biochimica Polonica</i> , 2001, 48, 323-35.	0.5	15
41	Crystal structure of a fungal protease inhibitor from <i>Antheraea mylitta</i> . <i>Journal of Structural Biology</i> , 2009, 166, 79-87.	2.8	12
42	Aggregation-Prone Near-Native Intermediate Formation during Unfolding of a Structurally Similar Nonlenticular β -Crystallin Domain. <i>Biochemistry</i> , 2012, 51, 8502-8513.	2.5	12
43	A discriminator codeâ€‘based DTD surveillance ensures faithful glycine delivery for protein biosynthesis in bacteria. <i>ELife</i> , 2018, 7, .	6.0	12
44	Switching a conflicted bacterial DTD-tRNA code is essential for the emergence of mitochondria. <i>Science Advances</i> , 2022, 8, eabj7307.	10.3	12
45	Crystallization and preliminary X-ray crystallographic studies of the N-terminal domain of FadD28, a fatty-acyl AMP ligase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 350-352.	0.7	11
46	Delineating the reaction mechanism of reductase domains of Nonribosomal Peptide Synthetases from mycobacteria. <i>Journal of Structural Biology</i> , 2014, 187, 207-214.	2.8	11
47	Crystallization and preliminary crystallographic studies of LipA, a secretory lipase/esterase from <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 708-710.	0.7	10
48	Recruitment of archaeal DTD is a key event toward the emergence of land plants. <i>Science Advances</i> , 2021, 7, .	10.3	10
49	ATPase activity of RecD is essential for growth of the Antarctic <i>Pseudomonas syringae</i> Lz4W at low temperature. <i>FEBS Journal</i> , 2008, 275, 1835-1851.	4.7	9
50	Evolutionary and functional insights into <i>Leishmania</i> META1: evidence for lateral gene transfer and a role for META1 in secretion. <i>BMC Evolutionary Biology</i> , 2011, 11, 334.	3.2	9
51	Structural insights into the regulation of NADPH binding to reductase domains of nonribosomal peptide synthetases: A concerted loop movement model. <i>Journal of Structural Biology</i> , 2016, 194, 368-374.	2.8	9
52	Chiral proofreading during protein biosynthesis and its evolutionary implications. <i>FEBS Letters</i> , 2022, 596, 1615-1627.	2.8	8
53	Signals and Pathways Regulating Nucleolar Retention of Novel Putative Nucleolar GTPase NCP-1 (GNL-2). <i>Biochemistry</i> , 2011, 50, 4521-4536.	2.5	7
54	A Transition Metal-Binding, Trimeric β -Crystallin from Methane-Producing Thermophilic Archaea, <i>Methanosaeta thermophila</i> . <i>Biochemistry</i> , 2017, 56, 1299-1310.	2.5	7

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55	A universal pocket in fatty acyl-AMP ligases ensures redirection of fatty acid pool away from coenzyme A-based activation. <i>ELife</i> , 2021, 10, .	6.0	7
56	Enzyme action at RNA-protein interface in DTD-like fold. <i>Current Opinion in Structural Biology</i> , 2018, 53, 107-114.	5.7	6
57	Peri-natal growth retardation rate and fat mass accumulation in mice lacking <i>Dip2A</i> is dependent on the dietary composition. <i>Transgenic Research</i> , 2020, 29, 553-562.	2.4	6
58	Crystallization and preliminary X-ray crystallographic investigations on several thermostable forms of a <i>Bacillus subtilis</i> lipase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 160-162.	2.5	5
59	Mechanistic Insights Into Catalytic RNA-Protein Complexes Involved in Translation of the Genetic Code. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017, 109, 305-353.	2.3	5
60	Fatty Acyl-AMP Ligases as Mechanistic Variants of ANL Superfamily and Molecular Determinants Dictating Substrate Specificities. <i>Journal of the Indian Institute of Science</i> , 2018, 98, 261-272.	1.9	5
61	DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. <i>ELife</i> , 0, 11, .	6.0	5
62	Crystallization and preliminary X-ray crystallographic investigations of an unusual type III polyketide synthase PKS18 from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 749-751.	2.5	4
63	Crystallization and preliminary X-ray diffraction analysis of a protease inhibitor from the haemolymph of the Indian tasar silkworm <i>Antheraea mylitta</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 669-671.	0.7	4
64	A type III PKS makes the Difference. <i>Nature Chemical Biology</i> , 2006, 2, 451-452.	8.0	4
65	Genomic innovation of ATD alleviates mistranslation associated with multicellularity in Animalia. <i>ELife</i> , 2020, 9, .	6.0	4
66	Role of the FnIII domain associated with a cell wall-degrading enzyme cellobiosidase of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Molecular Plant Pathology</i> , 2022, 23, 1011-1021.	4.2	4
67	Aminoacylation at the Atomic Level in Class IIa Aminoacyl-tRNA Synthetases. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 17, 23-27.	3.5	3
68	Crystallization and preliminary X-ray crystallographic investigations on a β -crystallin domain of absent in melanoma 1 (AIM1), a protein from <i>Homo sapiens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 282-284.	0.7	3
69	Crystallization and preliminary crystallographic studies of CbsA, a secretory exoglucanase from <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1191-1194.	0.7	3
70	Interface interactions between β -crystallin domain and Ig-like domain render Ca ²⁺ binding site inoperative in abundant perithecial protein of <i>Neurospora crassa</i> . <i>Molecular Microbiology</i> , 2018, 110, 955-972.	2.5	3
71	β -Crystallination Endows a Novel Bacterial Glycoside Hydrolase 64 with Ca ²⁺ -Dependent Activity Modulation. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	3
72	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic investigations of a unique editing domain from archaeobacteria. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1662-1664.	2.5	2

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73	Cloning, overexpression, purification, crystallization and preliminary X-ray analysis of a female-specific lipocalin (FLP) expressed in the lacrimal glands of Syrian hamsters. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 509-512.	0.7	1
74	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analyses of threonyl-tRNA synthetase editing domain from <i>Aeropyrum pernix</i> . Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1390-1393.	0.7	1
75	Editing and Proofreading in Translation \hat{a} †. , 2017, , .		1