

Rajan Sankaranarayanan

List of Publications by Year in descending order

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75
papers

2,841
citations

218677

26
h-index

182427

51
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85
all docs

85
docs citations

85
times ranked

2854
citing authors

#	ARTICLE	IF	CITATIONS
1	Switching a conflicted bacterial DTD-tRNA code is essential for the emergence of mitochondria. <i>Science Advances</i> , 2022, 8, eabj7307.	10.3	12
2	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
3	Chiral proofreading during protein biosynthesis and its evolutionary implications. <i>FEBS Letters</i> , 2022, 596, 1615-1627.	2.8	8
4	Recruitment of archaeal DTD is a key event toward the emergence of land plants. <i>Science Advances</i> , 2021, 7, .	10.3	10
5	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
6	Peri-natal growth retardation rate and fat mass accumulation in mice lacking Dip2A is dependent on the dietary composition. <i>Transgenic Research</i> , 2020, 29, 553-562.	2.4	6
7	Genomic innovation of ATD alleviates mistranslation associated with multicellularity in Animalia. <i>ELife</i> , 2020, 9, .	6.0	4
8	Chiral checkpoints during protein biosynthesis. <i>Journal of Biological Chemistry</i> , 2019, 294, 16535-16548.	3.4	29
9	$\hat{\Gamma}^3$ -Crystallination Endows a Novel Bacterial Glycoside Hydrolase 64 with Ca ²⁺ -Dependent Activity Modulation. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	3
10	A chiral selectivity relaxed paralog of DTD for proofreading tRNA mischarging in Animalia. <i>Nature Communications</i> , 2018, 9, 511.	12.8	31
11	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
12	Interface interactions between $\hat{\Gamma}^3$ -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
13	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
14	Enzyme action at RNA-protein interface in DTD-like fold. <i>Current Opinion in Structural Biology</i> , 2018, 53, 107-114.	5.7	6
15	A discriminator code-based DTD surveillance ensures faithful glycine delivery for protein biosynthesis in bacteria. <i>ELife</i> , 2018, 7, .	6.0	12
16	A Transition Metal-Binding, Trimeric $\hat{\Gamma}^3$ -Crystallin from Methane-Producing Thermophilic Archaea, <i>Methanoseta thermophila</i> . <i>Biochemistry</i> , 2017, 56, 1299-1310.	2.5	7
17	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
18	Editing and Proofreading in Translation . . . , 2017, . . .		1

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19	Role of D-aminoacyl-tRNA deacylase beyond chiral proofreading as a cellular defense against glycine mischarging by AlaRS. <i>ELife</i> , 2017, 6, .	6.0	29
20	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
21	Elongation Factor Tu Prevents Misediting of Gly-tRNA(Gly) Caused by the Design Behind the Chiral Proofreading Site of D-Aminoacyl-tRNA Deacylase. <i>PLoS Biology</i> , 2016, 14, e1002465.	5.6	30
22	Unsaturated Lipid Assimilation by Mycobacteria Requires Auxiliary cis-trans Enoyl CoA Isomerase. <i>Chemistry and Biology</i> , 2015, 22, 1577-1587.	6.0	24
23	Specificity and catalysis hardwired at the RNA-protein interface in a translational proofreading enzyme. <i>Nature Communications</i> , 2015, 6, 7552.	12.8	24
24	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
25	Mechanism of chiral proofreading during translation of the genetic code. <i>ELife</i> , 2013, 2, e01519.	6.0	43
26	Nonprocessive [2 \hat{A} + \hat{A} 2]e ^{<sup>-</sup>} 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
27	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
28	Decoding the Molecular Design Principles Underlying Ca ²⁺ Binding to $\hat{I}^2\hat{I}^3$ -Crystallin Motifs. <i>Journal of Molecular Biology</i> , 2012, 415, 75-91.	4.2	21
29	Molecular Basis of the Functional Divergence of Fatty Acyl-AMP Ligase Biosynthetic Enzymes of <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2012, 416, 221-238.	4.2	40
30	Aggregation-Prone Near-Native Intermediate Formation during Unfolding of a Structurally Similar Nonlenticular $\hat{I}^2\hat{I}^3$ -Crystallin Domain. <i>Biochemistry</i> , 2012, 51, 8502-8513.	2.5	12
31	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analyses of threonyl-tRNA synthetase editing domain from <i>Aeropyrum pernix</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1390-1393.	0.7	1
32	Signals and Pathways Regulating Nucleolar Retention of Novel Putative Nucleolar GTPase NGP-1(GNL-2). <i>Biochemistry</i> , 2011, 50, 4521-4536.	2.5	7
33	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
34	Structural biology of <i>Mycobacterium tuberculosis</i> proteins: The Indian efforts. <i>Tuberculosis</i> , 2011, 91, 456-468.	1.9	22
35	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
36	Evolutionary and functional insights into <i>Leishmania META1</i> : evidence for lateral gene transfer and a role for META1 in secretion. <i>BMC Evolutionary Biology</i> , 2011, 11, 334.	3.2	9

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37	Cloning, overexpression, purification, crystallization and preliminary X-ray analysis of a female-specific lipocalin (FLP) expressed in the lacrimal glands of Syrian hamsters. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 509-512.	0.7	1
38	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
39	Vertebrate Homologue of Drosophila GAGA Factor. <i>Journal of Molecular Biology</i> , 2010, 400, 434-447.	4.2	62
40	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
41	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
42	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
43	Three-Dimensional Domain Swapping in Nitrollin, a Single-Domain $\beta^2\beta^3$ -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
44	The $\beta^2\beta^3$ -Crystallin Superfamily Contains a Universal Motif for Binding Calcium ^{<sup></sup>. <i>Biochemistry</i>, 2009, 48, 12180-12190.}	2.5	63
45	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
46	Structural insights into biosynthesis of resorcinolic lipids by a type III polyketide synthase in <i>Neurospora crassa</i> . <i>Journal of Structural Biology</i> , 2008, 162, 411-421.	2.8	37
47	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
48	Exploring the Limits of Sequence and Structure in a Variant $\beta^2\beta^3$ -Crystallin Domain of the Protein Absent in Melanoma-1 (AIM1). <i>Journal of Molecular Biology</i> , 2008, 381, 509-518.	4.2	26
49	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
50	Versatility of polyketide synthases in generating metabolic diversity. <i>Current Opinion in Structural Biology</i> , 2007, 17, 736-743.	5.7	68
51	Crystallization and preliminary X-ray crystallographic investigations on a $\beta^2\beta^3$ -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
52	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
53	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
54	A type III PKS makes the Difference. <i>Nature Chemical Biology</i> , 2006, 2, 451-452.	8.0	4

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55	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
56	A D-amino acid editing module coupled to the translational apparatus in archaea. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 556-557.	8.2	52
57	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
58	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
59	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
60	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
61	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
62	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
63	The modular structure of <i>Escherichia coli</i> threonyl-tRNA synthetase as both an enzyme and a regulator of gene expression. <i>Molecular Microbiology</i> , 2003, 47, 961-974.	2.5	30
64	Conformational Movements and Cooperativity upon Amino Acid, ATP and tRNA Binding in Threonyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2003, 331, 201-211.	4.2	53
65	PhyA, a Secreted Protein of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> , Is Required for Optimum Virulence and Growth on Phytic Acid as a Sole Phosphate Source. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 973-982.	2.6	38
66	Structural basis of translational control by <i>Escherichia coli</i> threonyl tRNA synthetase. <i>Nature Structural Biology</i> , 2002, 9, 343-7.	9.7	56
67	The fidelity of the translation of the genetic code. <i>Acta Biochimica Polonica</i> , 2001, 48, 323-35.	0.5	15
68	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
69	Transfer RNA-Mediated Editing in Threonyl-tRNA Synthetase. <i>Cell</i> , 2000, 103, 877-884.	28.9	175
70	Zinc ion mediated amino acid discrimination by threonyl-tRNA synthetase. <i>Nature Structural Biology</i> , 2000, 7, 461-465.	9.7	139
71	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
72	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

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73	A novel mode of carbohydrate recognition in jacalin, a Moraceae plant lectin with a β -prism fold. Nature Structural Biology, 1996, 3, 596-603.	9.7	224
74	Crystallization and Preliminary X-ray Studies of the Basic Lectin from Winged Bean (<i>Psophocarpus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	4.2	22
75	DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. ELife, 0, 11, .	6.0	5