Rajan Sankaranarayanan

List of Publications by Year
in descending order

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75
papers

2,841
citations

218592

26
h-index

182361

51
g-index

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. Science Advances, 2022, 8, eabj7307.	4.7	12
2	Role of the FnIII domain associated with a cell wallâ€degrading enzyme cellobiosidase of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>. Molecular Plant Pathology, 2022, 23, 1011-1021.	2.0	4
3	Chiral proofreading during protein biosynthesis and its evolutionary implications. FEBS Letters, 2022, 596, 1615-1627.	1.3	8
4	Recruitment of archaeal DTD is a key event toward the emergence of land plants. Science Advances, 2021, 7, .	4.7	10
5	A universal pocket in fatty acyl-AMP ligases ensures redirection of fatty acid pool away from coenzyme A-based activation. ELife, 2021, 10, .	2.8	7
6	Peri-natal growth retardation rate and fat mass accumulation in mice lacking Dip2A is dependent on the dietary composition. Transgenic Research, 2020, 29, 553-562.	1.3	6
7	Genomic innovation of ATD alleviates mistranslation associated with multicellularity in Animalia. ELife, 2020, 9, .	2.8	4
8	Chiral checkpoints during protein biosynthesis. Journal of Biological Chemistry, 2019, 294, 16535-16548.	1.6	29
9	Î²Î³-Crystallination Endows a Novel Bacterial Glycoside Hydrolase 64 with Ca ²⁺ -Dependent Activity Modulation. Journal of Bacteriology, 2019, 201, .	1.0	3
10	A chiral selectivity relaxed paralog of DTD for proofreading tRNA mischarging in Animalia. Nature Communications, 2018, 9, 511.	5.8	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. Molecular Plant Pathology, 2018, 19, 1364-1376.	2.0	17
12	Interface interactions between Î²Î³â€crystallin domain and Igâ€like domain render Ca²⁺â€binding site inoperative in abundant perithecial protein of <i>Neurospora crassa</i>. Molecular Microbiology, 2018, 110, 955-972.	1.2	3
13	Fatty Acyl-AMP Ligases as Mechanistic Variants of ANL Superfamily and Molecular Determinants Dictating Substrate Specificities. Journal of the Indian Institute of Science, 2018, 98, 261-272.	0.9	5
14	Enzyme action at RNAâ€"protein interface in DTD-like fold. Current Opinion in Structural Biology, 2018, 53, 107-114.	2.6	6
15	A discriminator codeâ€"based DTD surveillance ensures faithful glycine delivery for protein biosynthesis in bacteria. ELife, 2018, 7, .	2.8	12
16	A Transition Metal-Binding, Trimeric Î²Î³-Crystallin from Methane-Producing Thermophilic Archaea, <i>Methanosaeta thermophila</i>. Biochemistry, 2017, 56, 1299-1310.	1.2	7
17	Mechanistic Insights Into Catalytic RNAâ€"Protein Complexes Involved in Translation of the Genetic Code. Advances in Protein Chemistry and Structural Biology, 2017, 109, 305-353.	1.0	5
18	Editing and Proofreading in Translation â˜†. , 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. ELife, 2017, 6, .	2.8	29
20	Structural insights into the regulation of NADPH binding to reductase domains of nonribosomal peptide synthetases: A concerted loop movement model. Journal of Structural Biology, 2016, 194, 368-374.	1.3	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. PLoS Biology, 2016, 14, e1002465.	2.6	30
22	Unsaturated Lipid Assimilation by Mycobacteria Requires Auxiliary cis-trans Enoyl CoA Isomerase. Chemistry and Biology, 2015, 22, 1577-1587.	6.2	24
23	Specificity and catalysis hardwired at the RNAâ€“protein interface in a translational proofreading enzyme. Nature Communications, 2015, 6, 7552.	5.8	24
24	Delineating the reaction mechanism of reductase domains of Nonribosomal Peptide Synthetases from mycobacteria. Journal of Structural Biology, 2014, 187, 207-214.	1.3	11
25	Mechanism of chiral proofreading during translation of the genetic code. ELife, 2013, 2, e01519.	2.8	43
26	Nonprocessive [2Â+Â2]e ⁻ off-loading reductase domains from mycobacterial nonribosomal peptide synthetases. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5681-5686.	3.3	73
27	Crystallization and preliminary crystallographic studies of CbsA, a secretory exoglucanase from<i>Xanthomonas oryzae</i>pv.<i>oryzae</i>. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1191-1194.	0.7	3
28	Decoding the Molecular Design Principles Underlying Ca2+ Binding to Î²Î³-Crystallin Motifs. Journal of Molecular Biology, 2012, 415, 75-91.	2.0	21
29	Molecular Basis of the Functional Divergence of Fatty Acyl-AMP Ligase Biosynthetic Enzymes of Mycobacterium tuberculosis. Journal of Molecular Biology, 2012, 416, 221-238.	2.0	40
30	Aggregation-Prone Near-Native Intermediate Formation during Unfolding of a Structurally Similar Nonlenticular Î²Î³-Crystallin Domain. Biochemistry, 2012, 51, 8502-8513.	1.2	12
31	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analyses of threonyl-tRNA synthetase editing domain fromAeropyrum pernix. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1390-1393.	0.7	1
32	Signals and Pathways Regulating Nucleolar Retention of Novel Putative Nucleolar GTPase NGP-1(GNL-2). Biochemistry, 2011, 50, 4521-4536.	1.2	7
33	In Vitro Evolved Non-Aggregating and Thermostable Lipase: Structural and Thermodynamic Investigation. Journal of Molecular Biology, 2011, 413, 726-741.	2.0	77
34	Structural biology of Mycobacterium tuberculosis proteins: The Indian efforts. Tuberculosis, 2011, 91, 456-468.	0.8	22
35	Fatty acyl-AMP ligases and polyketide synthases are unique enzymes of lipid biosynthetic machinery in Mycobacterium tuberculosis. Tuberculosis, 2011, 91, 448-455.	0.8	18
36	Evolutionary and functional insights into Leishmania META1: evidence for lateral gene transfer and a role for META1 in secretion. BMC Evolutionary Biology, 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. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 509-512.	0.7	1
38	Mechanistic insights into cognate substrate discrimination during proofreading in translation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22117-22121.	3.3	60
39	Vertebrate Homologue of Drosophila GAGA Factor. Journal of Molecular Biology, 2010, 400, 434-447.	2.0	62
40	A Cell Wallâ€“Degrading Esterase of <i>Xanthomonas oryzae</i> Requires a Unique Substrate Recognition Module for Pathogenesis on Rice. Plant Cell, 2009, 21, 1860-1873.	3.1	64
41	Mechanistic and functional insights into fatty acid activation in Mycobacterium tuberculosis. Nature Chemical Biology, 2009, 5, 166-173.	3.9	119
42	Crystal structure of a fungal protease inhibitor from Antheraea mylitta. Journal of Structural Biology, 2009, 166, 79-87.	1.3	12
43	Three-Dimensional Domain Swapping in Nitrollin, a Single-Domain Î²Î³-Crystallin from Nitrosospira multiformis, Controls Protein Conformation and Stability but Not Dimerization. Journal of Molecular Biology, 2009, 385, 163-177.	2.0	18
44	The Î²Î³-Crystallin Superfamily Contains a Universal Motif for Binding Calcium[,]. Biochemistry, 2009, 48, 12180-12190.	1.2	63
45	ATPase activity of RecD is essential for growth of the Antarctic <i>Pseudomonas syringae</i> Lz4W at low temperature. FEBS Journal, 2008, 275, 1835-1851.	2.2	9
46	Structural insights into biosynthesis of resorcinolic lipids by a type III polyketide synthase in Neurospora crassa. Journal of Structural Biology, 2008, 162, 411-421.	1.3	37
47	Thermostable Bacillus subtilis Lipases: In Vitro Evolution and Structural Insight. Journal of Molecular Biology, 2008, 381, 324-340.	2.0	125
48	Exploring the Limits of Sequence and Structure in a Variant Î²Î³-Crystallin Domain of the Protein Absent in Melanoma-1 (AIM1). Journal of Molecular Biology, 2008, 381, 509-518.	2.0	26
49	Crystallization and preliminary crystallographic studies of LipA, a secretory lipase/esterase from<i>Xanthomonas oryzae</i>pv.<i>oryzae</i>. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 708-710.	0.7	10
50	Versatility of polyketide synthases in generating metabolic diversity. Current Opinion in Structural Biology, 2007, 17, 736-743.	2.6	68
51	Crystallization and preliminary X-ray crystallographic investigations on a Î²Î³-crystallin domain of absent in melanoma 1 (AIM1), a protein fromHomo sapiens. Acta Crystallographica Section F: Structural Biology Communications, 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 fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 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 silkwormAntheraea mylitta. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 669-671.	0.7	4
54	A type III PKS makes the DIFference. Nature Chemical Biology, 2006, 2, 451-452.	3.9	4

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55	Post-transfer editing mechanism of a D-aminoacyl-tRNA deacylase-like domain in threonyl-tRNA synthetase from archaea. EMBO Journal, 2006, 25, 4152-4162.	3.5	67
56	A D-amino acid editing module coupled to the translational apparatus in archaea. Nature Structural and Molecular Biology, 2005, 12, 556-557.	3.6	52
57	Crystal Structure of Low-Molecular-Weight Protein Tyrosine Phosphatase from Mycobacterium tuberculosis at 1.9-AÌŠ Resolution. Journal of Bacteriology, 2005, 187, 2175-2181.	1.0	68
58	A novel tunnel in mycobacterial type III polyketide synthase reveals the structural basis for generating diverse metabolites. Nature Structural and Molecular Biology, 2004, 11, 894-900.	3.6	85
59	Crystallization and preliminary X-ray crystallographic investigations on several thermostable forms of aBacillus subtilislipase. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 160-162.	2.5	5
60	Crystallization and preliminary X-ray crystallographic investigations of an unusual type III polyketide synthase PKS18 fromMycobacterium tuberculosis. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 749-751.	2.5	4
61	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic investigations of a unique editing domain from archaebacteria. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1662-1664.	2.5	2
62	Structural Basis of Selection and Thermostability of Laboratory Evolved Bacillus subtilis Lipase. Journal of Molecular Biology, 2004, 341, 1271-1281.	2.0	122
63	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.	1.2	30
64	Conformational Movements and Cooperativity upon Amino Acid, ATP and tRNA Binding in Threonyl-tRNA Synthetase. Journal of Molecular Biology, 2003, 331, 201-211.	2.0	53
65	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.	1.4	38
66	Structural basis of translational control by Escherichia coli threonyl tRNA synthetase. Nature Structural Biology, 2002, 9, 343-7.	9.7	56
67	The fidelity of the translation of the genetic code. Acta Biochimica Polonica, 2001, 48, 323-35.	0.3	15
68	Aminoacylation at the Atomic Level in Class IIa Aminoacyl-tRNA Synthetases. Journal of Biomolecular Structure and Dynamics, 2000, 17, 23-27.	2.0	3
69	Transfer RNAâ€“Mediated Editing in Threonyl-tRNA Synthetase. Cell, 2000, 103, 877-884.	13.5	175
70	Zinc ion mediated amino acid discrimination by threonyl-tRNA synthetase. Nature Structural Biology, 2000, 7, 461-465.	9.7	139
71	The Structure of Threonyl-tRNA Synthetase-tRNAThr Complex Enlightens Its Repressor Activity and Reveals an Essential Zinc Ion in the Active Site. Cell, 1999, 97, 371-381.	13.5	291
72	Carbohydrate specificity and quaternary association in basic winged bean lectin: X-ray analysis of the lectin at 2.5 Ã… resolution. Journal of Molecular Biology, 1998, 276, 787-796.	2.0	65

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73	A novel mode of carbohydrate recognition in jacalin, a Moraceae plant lectin with a Î²-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 (Psophocarpus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.0	22
75	DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. ELife, 0, 11, .	2.8	5