

# Manickam Yogavel

## List of Publications by Year in descending order

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74  
papers

1,484  
citations

394286

19  
h-index

345118

36  
g-index

75  
all docs

75  
docs citations

75  
times ranked

1737  
citing authors

#	ARTICLE	IF	CITATIONS
1	Double drugging of prolyl-tRNA synthetase provides a new paradigm for anti-infective drug development. <i>PLoS Pathogens</i> , 2022, 18, e1010363.	2.1	12
2	Inhibition of <i>Plasmodium falciparum</i> phenylalanine tRNA synthetase provides opportunity for antimalarial drug development. <i>Structure</i> , 2022, 30, 962-972.e3.	1.6	4
3	A single amino acid substitution alters activity and specificity in <i>Plasmodium falciparum</i> aspartyl & asparaginyl-tRNA synthetases. <i>Molecular and Biochemical Parasitology</i> , 2022, , 111488.	0.5	1
4	Design, Synthesis, and Structural Analysis of Cladosporin-Based Inhibitors of Malaria Parasites. <i>ACS Infectious Diseases</i> , 2021, 7, 1777-1794.	1.8	5
5	Inhibition of <i>Plasmodium falciparum</i> Lysyl-tRNA Synthetase via a Piperidine Ring Scaffold Inspired Cladosporin Analogues. <i>ChemBioChem</i> , 2021, 22, 2468-2477.	1.3	7
6	Structural analyses of the malaria parasite aminoacyl-tRNA synthetases provide new avenues for antimalarial drug discovery. <i>Protein Science</i> , 2021, 30, 1793-1803.	3.1	12
7	Structural basis of malaria parasite phenylalanine tRNA-synthetase inhibition by bicyclic azetidines. <i>Nature Communications</i> , 2021, 12, 343.	5.8	19
8	Conformational changes in glutaminyl-tRNA synthetases upon binding of the substrates and analogs using molecular docking and molecular dynamics approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1-15.	2.0	6
9	Crystal structures of the two domains that constitute the <i>Plasmodium vivax</i> p43 protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 135-146.	1.1	8
10	Lysyl-tRNA synthetase as a drug target in malaria and cryptosporidiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7015-7020.	3.3	94
11	Conformational heterogeneity in apo and drug-bound structures of <i>Toxoplasma gondii</i> prolyl-tRNA synthetase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 714-724.	0.4	11
12	Drug targeting of one or more aminoacyl-tRNA synthetase in the malaria parasite <i>Plasmodium falciparum</i> . <i>Drug Discovery Today</i> , 2018, 23, 1233-1240.	3.2	47
13	Structure-Function Analysis of Liver Flavin Monooxygenase 3 that Drives Trimethylaminuria in Humans. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2018, 88, 1681-1690.	0.4	2
14	Structural and functional analysis of Glutaminyl-tRNA synthetase (TtGlnRS) from <i>Thermus thermophilus</i> HB8 and its complexes. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 1379-1386.	3.6	10
15	Engagement Rules That Underpin DBL-DARC Interactions for Ingress of <i>Plasmodium knowlesi</i> and <i>Plasmodium vivax</i> Into Human Erythrocytes. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 78.	1.6	4
16	Specific Stereoisomeric Conformations Determine the Drug Potency of Cladosporin Scaffold against Malarial Parasite. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 5664-5678.	2.9	41
17	Structure of 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase dihydropteroate synthase from <i>Plasmodium vivax</i> sheds light on drug resistance. <i>Journal of Biological Chemistry</i> , 2018, 293, 14962-14972.	1.6	18
18	Structure-Based Targeting of Orthologous Pathogen Proteins Accelerates Antiparasitic Drug Discovery. <i>ACS Infectious Diseases</i> , 2017, 3, 281-292.	1.8	13

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19	Targeting Prolyl-tRNA Synthetase to Accelerate Drug Discovery against Malaria, Leishmaniasis, Toxoplasmosis, Cryptosporidiosis, and Coccidiosis. <i>Structure</i> , 2017, 25, 1495-1505.e6.	1.6	68
20	Structural and Biochemical Characterization of Apicomplexan Inorganic Pyrophosphatases. <i>Scientific Reports</i> , 2017, 7, 5255.	1.6	2
21	Dimerization of Arginyl-tRNA Synthetase by Free Heme Drives Its Inactivation in <i>Plasmodium falciparum</i> . <i>Structure</i> , 2016, 24, 1476-1487.	1.6	17
22	Structural and functional attributes of malaria parasite diadenosine tetraphosphate hydrolase. <i>Scientific Reports</i> , 2016, 6, 19981.	1.6	12
23	Protein Translation Enzyme lysyl-tRNA Synthetase Presents a New Target for Drug Development against Causative Agents of Leishmaniasis and Schistosomiasis. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005084.	1.3	25
24	Inhibition of Protein Synthesis and Malaria Parasite Development by Drug Targeting of Methionyl-tRNA Synthetases. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1856-1867.	1.4	53
25	Structure of Prolyl-tRNA Synthetase-Halofuginone Complex Provides Basis for Development of Drugs against Malaria and Toxoplasmosis. <i>Structure</i> , 2015, 23, 819-829.	1.6	92
26	Structural and Functional Highlights of Vacuolar Soluble Protein 1 from Pathogen <i>Trypanosoma brucei brucei</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 30498-30513.	1.6	10
27	Atomic resolution crystal structure of glutaredoxin 1 from <i>Plasmodium falciparum</i> and comparison with other glutaredoxins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 91-100.	2.5	12
28	Structural and functional analysis of the anti-malarial drug target prolyl-tRNA synthetase. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 181-190.	1.2	40
29	Structural basis of malaria parasite lysyl-tRNA synthetase inhibition by cladosporin. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 63-71.	1.2	62
30	A <i>Toxoplasma</i> dense granule protein, GRA24, modulates the early immune response to infection by promoting a direct and sustained host p38 MAPK activation. <i>Journal of Experimental Medicine</i> , 2013, 210, 2071-2086.	4.2	252
31	Characterization of <i>Plasmodium falciparum</i> Calcium-dependent Protein Kinase 1 (PfCDPK1) and Its Role in Microneme Secretion during Erythrocyte Invasion. <i>Journal of Biological Chemistry</i> , 2013, 288, 1590-1602.	1.6	86
32	An Appended Domain Results in an Unusual Architecture for Malaria Parasite Tryptophanyl-tRNA Synthetase. <i>PLoS ONE</i> , 2013, 8, e66224.	1.1	25
33	Systematic Analysis of Proteomes with Emphasis on Insertions in Malaria Parasite <i>Plasmodium falciparum</i> . <i>Protein and Peptide Letters</i> , 2013, 20, 1088-1097.	0.4	1
34	Utility of anion and cation combinations for phasing of protein structures. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 135-143.	1.2	7
35	Structural delineation of histone post-translation modifications in histone-nucleosome assembly protein complex. <i>Journal of Structural Biology</i> , 2012, 180, 1-9.	1.3	13
36	Malaria parasite tyrosyl-tRNA synthetase secretion triggers pro-inflammatory responses. <i>Nature Communications</i> , 2011, 2, 530.	5.8	58

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37	Structure of D-tyrosyl-tRNA <sup>Tyr</sup> deacylase using home-source Cu <sup>K<math>\alpha</math></sup> and moderate-quality iodide-SAD data: structural polymorphism and HEPES-bound enzyme states. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 584-592.	2.5	12
38	Structural analysis of actinidin and a comparison of cadmium and sulfur anomalous signals from actinidin crystals measured using in-house copper- and chromium-anode X-ray sources. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1323-1333.	2.5	13
39	Ligand-bound Structures Provide Atomic Snapshots for the Catalytic Mechanism of d-Amino Acid Deacylase. Journal of Biological Chemistry, 2010, 285, 5917-5930.	1.6	29
40	Structure, localization and histone binding properties of nuclear-associated nucleosome assembly protein from Plasmodium falciparum. Malaria Journal, 2010, 9, 90.	0.8	15
41	Crystal Structure of Malaria Parasite Nucleosome Assembly Protein. Journal of Biological Chemistry, 2009, 284, 10076-10087.	1.6	32
42	Iodide-SAD, SIR and SIRAS phasing for structure solution of a nucleosome assembly protein. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 618-622.	2.5	12
43	Structure of a superoxide dismutase and implications for copper-ion chelation. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 892-901.	2.5	26
44	Crystal Structure of Soluble Domain of Malaria Sporozoite Protein UIS3 in Complex with Lipid. Journal of Biological Chemistry, 2008, 283, 24077-24088.	1.6	35
45	Structural Analysis of ABC-family Periplasmic Zinc Binding Protein Provides New Insights Into Mechanism of Ligand Uptake and Release. Journal of Molecular Biology, 2007, 367, 970-982.	2.0	70
46	SAD phasing of a structure based on cocrystallized iodides using an in-house Cu <sup>K<math>\alpha</math></sup> X-ray source: effects of data redundancy and completeness on structure solution. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 931-934.	2.5	19
47	Suggestive evidence for the involvement of the second calcium and surface loop in interfacial binding: monoclinic and trigonal crystal structures of a quadruple mutant of phospholipase A2. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 717-724.	2.5	3
48	10-Benzyl-3,3,6,6,9-pentamethyl-3,4,6,7,9,10-hexahydroacridine-1,8(2H,5H)-dione. Acta Crystallographica Section E: Structure Reports Online, 2005, 61, o2761-o2763.	0.2	2
49	{N,N-Bis[3-(phenylsulfanyl)-1-(phenylsulfonyl)indol-2-ylmethyl]amino}acetaldehyde dimethyl acetal. Acta Crystallographica Section E: Structure Reports Online, 2005, 61, o3205-o3207.	0.2	0
50	1,4-Bis{2-hydroxy-3-[N-(2-hydroxyethyl)imino]-5-methylbenzyl}piperazine. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o83-o85.	0.2	2
51	8-Chloro-4-[1-(phenylsulfonyl)indol-3-yl]-3a,4,5,9b-tetrahydro-3H-cyclopenta[c]quinoline. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o49-o51.	0.2	0
52	1,2-Bis[1-phenylsulfonyl-3-(phenylthio)indol-2-yl]ethene. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o99-o101.	0.2	0
53	5-Amino-4-(4-dimethylaminophenyl)-2-(4-methoxyphenyl)-7-(pyrrolidin-1-yl)-1,6-naphthyridine-8-carbonitrile. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o200-o202.	0.2	0
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55	3-Benzoyl-2-hydroxy-2-methylchromene. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o266-o268.	0.2	0
56	2-Cyano-3-dimethylamino-N-(2,5-dimethylphenyl)acrylamide. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o353-o355.	0.2	0
57	3-Acetyl-2-hydroxy-2-methylchromene. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o591-o593.	0.2	0
58	3-Phenyl-4a,5-dihydro-1,2,4-triazolo[3,4-b][1,3]benzothiazine. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o622-o624.	0.2	1
59	10-[2-(4-Acetylpiperzin-1-yl)ethyl]-9-(4-chlorophenyl)-3,3,6,6-tetramethyl-3,4,6,7,9,10-hexahydro-2H,5H-acridine-1,8-dione. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o696-o698.	0.2	0
60	4-Acetamido-2-methoxy-5-[3-(phenylsulfanyl)indole-2-carbonyl]benzoic acid. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o718-o720.	0.2	0
61	N,N-Dimethyl-N'-phenylformamidinium perchlorate. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o662-o664.	0.2	2
62	3,3,6,6-Tetramethyl-9-(4-pyridyl)-3,4,6,7,9,10-hexahydro-1,8(2H,5H)-acridinedione monohydrate. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o659-o661.	0.2	2
63	2-[2-(5-Ethoxy-4-methoxy-2-nitrophenyl)vinyl]-1H-indole. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o672-o674.	0.2	0
64	3-[2-(2,4-Dichlorophenyl)vinyl]-2-methyl-1-phenylsulfonyl-1H-indole. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o703-o705.	0.2	1
65	[6a,16b]-cis-7,7-Dimethyl-6,6a,7,16b-tetrahydrochromeno[4 $\alpha$ :3 $\beta$ ]pyrano[3,2-c]-1 $\pm$ -naphthocoumarin. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o667-o669.	0.2	0
66	3,4:9,10-Dibenzo-1,12-diformyl-5,8-dioxododecane. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o806-o807.	0.2	5
67	1,2,3,4,4a,12a-Hexahydro-2,5,5-trimethyl-1H-[2]benzopyrano[3,2-c]coumarin. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o808-o809.	0.2	0
68	3-(1-Phenylsulfonyl-2-methylindol-3-ylcarbonyl)propanoic acid. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o875-o877.	0.2	0
69	6a,14a-cis-6,6a,7,14a-Tetrahydrochromeno[4 $\alpha$ :3 $\beta$ ]pyrano[3,2-c]coumarin. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o1395-o1397.	0.2	0
70	3-Chloro-3-(9-ethyl-6-methyl-9H-carbazol-3-yl)propenal. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o1432-o1434.	0.2	0
71	2-Benzoyl-3-cyclohexyl-4-(p-methoxyphenyl)-5-phenylpyrrolidine-3-spiro-3 $\alpha$ -chroman-4 $\alpha$ -one. Acta Crystallographica Section E: Structure Reports Online, 2003, 59, o1572-o1574.	0.2	0
72	Crystal Structures of the Free and Anisic Acid Bound Triple Mutant of Phospholipase A2. Journal of Molecular Biology, 2003, 333, 367-376.	2.0	28

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73	Observation of Additional Calcium Ion in the Crystal Structure of the Triple Mutant K56,120,121M of Bovine Pancreatic Phospholipase A2. <i>Journal of Molecular Biology</i> , 2002, 324, 755-762.	2.0	19
74	2-Methoxybenzaldehyde thiosemicarbazone. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2002, 58, o1336-o1338.	0.2	5