

Sivaraman J

List of Publications by Year in descending order

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88
papers

3,160
citations

186265

28
h-index

168389

53
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89
all docs

89
docs citations

89
times ranked

4860
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of <i>Aedes aegypti</i> procarboxypeptidase B1 and its binding with Dengue virus for controlling infection. <i>Life Science Alliance</i> , 2022, 5, e202101211.	2.8	2
2	Sequence preference and scaffolding requirement for the inhibition of human neutrophil elastase by ecotin peptide. <i>Protein Science</i> , 2022, 31, 933-941.	7.6	1
3	Bacterial antagonism of <i>Chromobacterium haemolyticum</i> and characterization of its putative type VI secretion system. <i>Research in Microbiology</i> , 2022, 173, 103918.	2.1	3
4	Identification of putative binding interface of PI(3,5)P2 lipid on rice black-streaked dwarf virus (RBSDV) P10 protein. <i>Virology</i> , 2022, 570, 81-95.	2.4	3
5	Mapping of molecular interactions between human E3 ligase TRIM69 and Dengue virus NS3 protease using hydrogen-deuterium exchange mass spectrometry. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 233.	5.4	7
6	Scaffold stability and P14 residue steric hindrance in the differential inhibition of FXIIa by <i>Aedes aegypti</i> trypsin inhibitor versus Infestin-4. <i>Bioscience Reports</i> , 2022, , .	2.4	0
7	Structural Basis of SARS-CoV-2 and SARS-CoV Receptor Binding and Small-Molecule Blockers as Potential Therapeutics. <i>Annual Review of Pharmacology and Toxicology</i> , 2021, 61, 465-493.	9.4	36
8	The Autocatalytic Cleavage Domain Is Not Required for the Activity of ScpC, a Virulence Protease from <i>Streptococcus pyogenes</i> : A Structural Insight. <i>Biochemistry</i> , 2021, 60, 1564-1568.	2.5	0
9	Structural basis for p50RhoGAP BCH domain-mediated regulation of Rho inactivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2014242118.	7.1	7
10	Exploring the "Other" subfamily of HECT E3-ligases for therapeutic intervention. , 2021, 224, 107809.		17
11	Binding specificity of type three secretion system effector <i>ScpNleH2</i> to multi-cargo chaperone <i>CesT</i> and their phosphorylation. <i>Protein Science</i> , 2021, 30, 2433-2444.	7.6	5
12	Structure of <i>Aedes aegypti</i> carboxypeptidase B1 inhibitor complex uncover the disparity between mosquito and non-mosquito insect carboxypeptidase inhibition mechanism. <i>Protein Science</i> , 2021, 30, 2445-2456.	7.6	4
13	Crystal structure of <i>Aedes aegypti</i> trypsin inhibitor in complex with α -plasmin reveals role for scaffold stability in Kazal-type serine protease inhibitor. <i>Protein Science</i> , 2021, , .	7.6	2
14	Fulditoxin, representing a new class of dimeric snake toxins, defines novel pharmacology at nicotinic ACh receptors. <i>British Journal of Pharmacology</i> , 2020, 177, 1822-1840.	5.4	12
15	Structural Basis of SARS-CoV-2 and SARS-CoV Antibody Interactions. <i>Trends in Immunology</i> , 2020, 41, 1006-1022.	6.8	79
16	Structural Basis for the Inhibition Mechanism of Ecotin against Neutrophil Elastase by Targeting the Active Site and Secondary Binding Site. <i>Biochemistry</i> , 2020, 59, 2788-2795.	2.5	2
17	Crystal structure of HECT domain of UBE3C E3 ligase and its ubiquitination activity. <i>Biochemical Journal</i> , 2020, 477, 905-923.	3.7	16
18	Unusual quaternary structure of a homodimeric synergistic-type toxin from mamba snake venom defines its molecular evolution. <i>Biochemical Journal</i> , 2020, 477, 3951-3962.	3.7	0

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19	Structural insights into a HECT-type E3 ligase AREL1 and its ubiquitination activities in vitro. <i>Journal of Biological Chemistry</i> , 2019, 294, 19934-19949.	3.4	14
20	Structure of LNX1:Ubc13 ~ Ubiquitin Complex Reveals the Role of Additional Motifs for the E3 Ligase Activity of LNX1. <i>Journal of Molecular Biology</i> , 2018, 430, 1173-1188.	4.2	13
21	Structural basis for the pathogenesis of <i>Campylobacter jejuni</i> Hcp1, a structural and effector protein of the Type VI Secretion System. <i>FEBS Journal</i> , 2018, 285, 4060-4070.	4.7	20
22	Structure of ScpC, a virulence protease from <i>Streptococcus pyogenes</i> , reveals the functional domains and maturation mechanism. <i>Biochemical Journal</i> , 2018, 475, 2847-2860.	3.7	23
23	Biophysical studies and modelling indicate the binding preference of TAZ WW domain for LATS1 PPxY motif. <i>Biochemical and Biophysical Research Communications</i> , 2018, 502, 307-312.	2.1	2
24	Structure and mapping of spontaneous mutational sites of PyrR from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 409-415.	2.1	5
25	Wnt Signaling Promotes Breast Cancer by Blocking ITCH-Mediated Degradation of YAP/TAZ Transcriptional Coactivator WBP2. <i>Cancer Research</i> , 2016, 76, 6278-6289.	0.9	62
26	Ringhalexin from <i>Hemachatus haemachatus</i> : A novel inhibitor of extrinsic tenase complex. <i>Scientific Reports</i> , 2016, 6, 25935.	3.3	21
27	Ligand-mediated changes in conformational dynamics of NpmA: implications for ribosomal interactions. <i>Scientific Reports</i> , 2016, 6, 37061.	3.3	5
28	Application of linker technique to trap transiently interacting protein complexes for structural studies. <i>Journal of Biological Methods</i> , 2016, 3, e34.	0.6	0
29	Structural Basis for a Unique ATP Synthase Core Complex from <i>Nanoarchaeum equitans</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 27280-27296.	3.4	14
30	Extended Loop Region of Hcp1 is Critical for the Assembly and Function of Type VI Secretion System in <i>Burkholderia pseudomallei</i> . <i>Scientific Reports</i> , 2015, 5, 8235.	3.3	43
31	Structural basis for the hydrolysis of ATP by a nucleotide binding subunit of an amino acid ABC transporter from <i>Thermus thermophilus</i> . <i>Journal of Structural Biology</i> , 2015, 190, 367-372.	2.8	3
32	Structural basis for the neutralization of hepatitis E virus by a cross-genotype antibody. <i>Cell Research</i> , 2015, 25, 604-620.	12.0	69
33	Structural basis of mapping the spontaneous mutations with 5-fluorouracil in uracil phosphoribosyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 577-582.	2.1	7
34	Structural basis for the indispensable role of a unique zinc finger motif in LNX2 ubiquitination. <i>Oncotarget</i> , 2015, 6, 34342-34357.	1.8	10
35	Dimerization of VirD2 Binding Protein Is Essential for <i>Agrobacterium</i> Induced Tumor Formation in Plants. <i>PLoS Pathogens</i> , 2014, 10, e1003948.	4.7	11
36	Dimeric Switch of Hakai-truncated Monomers during Substrate Recognition. <i>Journal of Biological Chemistry</i> , 2014, 289, 25611-25623.	3.4	12

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37	Structural Basis for the Active Site Inhibition Mechanism of Human Kidney-Type Glutaminase (KGA). <i>Scientific Reports</i> , 2014, 4, 3827.	3.3	80
38	A Disordered Region in the EvpP Protein from the Type VI Secretion System of <i>Edwardsiella tarda</i> is Essential for EvpC Binding. <i>PLoS ONE</i> , 2014, 9, e110810.	2.5	10
39	Computer aided design of FtsZ targeting oligopeptides. <i>RSC Advances</i> , 2013, 3, 1739-1743.	3.6	8
40	Structural Basis for the Modulation of the Neuronal Voltage-Gated Sodium Channel NaV1.6 by Calmodulin. <i>Scientific Reports</i> , 2013, 3, 2435.	3.3	35
41	Structure of GrlRâ€“GrlA complex that prevents GrlA activation of virulence genes. <i>Nature Communications</i> , 2013, 4, 2546.	12.8	38
42	Linkers in the structural biology of proteinâ€“protein interactions. <i>Protein Science</i> , 2013, 22, 153-167.	7.6	261
43	Structural Basis for the Interaction of Unstructured Neuron Specific Substrates Neuromodulin and Neurogranin with Calmodulin. <i>Scientific Reports</i> , 2013, 3, 1392.	3.3	57
44	A method to trap transient and weak interacting protein complexes for structural studies. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e25464.	1.9	9
45	A Novel Trans Conformation of Ligand-Free Calmodulin. <i>PLoS ONE</i> , 2013, 8, e54834.	2.5	14
46	Structure of a novel phosphotyrosine-binding domain in Hakai that targets E-cadherin. <i>EMBO Journal</i> , 2012, 31, 1308-1319.	7.8	56
47	Crystal Structure of Der f 7, a Dust Mite Allergen from <i>Dermatophagoides farinae</i> . <i>PLoS ONE</i> , 2012, 7, e44850.	2.5	23
48	Identification and Structural Characterization of a New Three-Finger Toxin Hemachatoxin from <i>Hemachatus haemachatus</i> Venom. <i>PLoS ONE</i> , 2012, 7, e48112.	2.5	17
49	Structural basis for the neutralization and genotype specificity of hepatitis E virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10266-10271.	7.1	109
50	Structural basis for reversible and irreversible inhibition of human cathepsin L by their respective dipeptidyl glyoxal and diazomethylketone inhibitors. <i>Journal of Structural Biology</i> , 2011, 173, 14-19.	2.8	29
51	Structural characterization of BVU_3255, a methyltransferase from human intestine antibiotic resistant pathogen <i>Bacteroides vulgatus</i> . <i>Journal of Structural Biology</i> , 2011, 176, 409-413.	2.8	7
52	Crystal Structure of the Heteromolecular Chaperone, AscE-AscG, from the Type III Secretion System in <i>Aeromonas hydrophila</i> . <i>PLoS ONE</i> , 2011, 6, e19208.	2.5	13
53	Application of isothermal titration calorimetry and column chromatography for identification of biomolecular targets. <i>Nature Protocols</i> , 2011, 6, 158-165.	12.0	17
54	An adjacent arginine, and the phosphorylated tyrosine in the c-Met receptor target sequence, dictates the orientation of c-Cbl binding. <i>FEBS Letters</i> , 2011, 585, 281-285.	2.8	10

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55	Structural basis for the methylation of A1408 in 16S rRNA by a panaminoglycoside resistance methyltransferase NpmA from a clinical isolate and analysis of the NpmA interactions with the 30S ribosomal subunit. <i>Nucleic Acids Research</i> , 2011, 39, 1903-1918.	14.5	27
56	Structural Basis for Dual-Inhibition Mechanism of a Non-Classical Kazal-Type Serine Protease Inhibitor from Horseshoe Crab in Complex with Subtilisin. <i>PLoS ONE</i> , 2011, 6, e18838.	2.5	10
57	A Conformational Switch in the Active Site of BT_2972, a Methyltransferase from an Antibiotic Resistant Pathogen <i>B. thetaiotaomicron</i> . <i>PLoS ONE</i> , 2011, 6, e27543.	2.5	2
58	Structural basis for the methylation of G1405 in 16S rRNA by aminoglycoside resistance methyltransferase Sgm from an antibiotic producer: a diversity of active sites in m ⁷ G methyltransferases. <i>Nucleic Acids Research</i> , 2010, 38, 4120-4132.	14.5	34
59	Structural and Functional Characterization of a Novel Homodimeric Three-finger Neurotoxin from the Venom of <i>Ophiophagus hannah</i> (King Cobra). <i>Journal of Biological Chemistry</i> , 2010, 285, 8302-8315.	3.4	77
60	The crystal structure of <i>Escherichia coli</i> spermidine synthase SpeE reveals a unique substrate-binding pocket. <i>Journal of Structural Biology</i> , 2010, 169, 277-285.	2.8	20
61	Crystal structure of a fructokinase homolog from <i>Halothermothrix orenii</i> . <i>Journal of Structural Biology</i> , 2010, 171, 397-401.	2.8	19
62	Site-Directed Mutagenesis on Human Cystathionine- β -Lyase Reveals Insights into the Modulation of H ₂ S Production. <i>Journal of Molecular Biology</i> , 2010, 396, 708-718.	4.2	53
63	Additional Serine/Threonine Phosphorylation Reduces Binding Affinity but Preserves Interface Topography of Substrate Proteins to the c-Cbl TKB Domain. <i>PLoS ONE</i> , 2010, 5, e12819.	2.5	19
64	Structural Basis for the Secretion of EvpC: A Key Type VI Secretion System Protein from <i>Edwardsiella tarda</i> . <i>PLoS ONE</i> , 2010, 5, e12910.	2.5	50
65	Modifying the Substrate Specificity of <i>Carcinoscorpius rotundicauda</i> Serine Protease Inhibitor Domain 1 to Target Thrombin. <i>PLoS ONE</i> , 2010, 5, e15258.	2.5	6
66	A Novel Serine Protease Inhibitor Acts as an Immunomodulatory Switch while Maintaining Homeostasis. <i>Journal of Innate Immunity</i> , 2009, 1, 465-479.	3.8	15
67	Structural Basis for the Inhibition Mechanism of Human Cystathionine β -Lyase, an Enzyme Responsible for the Production of H ₂ S. <i>Journal of Biological Chemistry</i> , 2009, 284, 3076-3085.	3.4	166
68	Mapping of the chaperone AcrH binding regions of translocators AopB and AopD and characterization of oligomeric and metastable AcrH-AopB-AopD complexes in the type III secretion system of <i>Aeromonas hydrophila</i> . <i>Protein Science</i> , 2009, 18, 1724-1734.	7.6	15
69	A Combined Crystallographic and Molecular Dynamics Study of Cathepsin L Retrobinding Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 6335-6346.	6.4	11
70	Identification and characterization of the lipid-binding property of GrLR, a locus of enterocyte effacement regulator. <i>Biochemical Journal</i> , 2009, 420, 191-201.	3.7	19
71	A universal method for fishing target proteins from mixtures of biomolecules using isothermal titration calorimetry. <i>Protein Science</i> , 2008, 17, 1798-1804.	7.6	13
72	Structural basis for a novel intrapeptidyl H-bond and reverse binding of c-Cbl-TKB domain substrates. <i>EMBO Journal</i> , 2008, 27, 804-816.	7.8	58

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73	Structural Characterization of Myotoxic Ecarpholin S From <i>Echis carinatus</i> Venom. <i>Biophysical Journal</i> , 2008, 95, 3366-3380.	0.5	45
74	Structure of AscE and induced burial regions in AscE and AscG upon formation of the chaperone needle subunit complex of type III secretion system in <i>Aeromonas hydrophila</i> . <i>Protein Science</i> , 2008, 17, 1748-1760.	7.6	11
75	Berberine Targets Assembly of <i>Escherichia coli</i> Cell Division Protein FtsZ. <i>Biochemistry</i> , 2008, 47, 3225-3234.	2.5	209
76	Exploring Inhibitor Binding at the S2 Subsites of Cathepsin L. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 1361-1368.	6.4	27
77	Structure of GrlR and the Implication of Its EDED Motif in Mediating the Regulation of Type III Secretion System in EHEC. <i>PLoS Pathogens</i> , 2007, 3, e69.	4.7	30
78	Inhibition of bacterial cell division protein FtsZ by cinnamaldehyde. <i>Biochemical Pharmacology</i> , 2007, 74, 831-840.	4.4	213
79	Insights into the biology of <i>Escherichia coli</i> through structural proteomics. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 45-55.	1.2	5
80	Domain Organization and Crystal Structure of the Catalytic Domain of <i>E. coli</i> RluF, a Pseudouridine Synthase that Acts on 23S rRNA. <i>Journal of Molecular Biology</i> , 2006, 359, 998-1009.	4.2	11
81	Structure of the pseudouridine synthase RsuA from <i>Haemophilus influenzae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 350-354.	0.7	7
82	Crystal Structure of the RluD Pseudouridine Synthase Catalytic Module, an Enzyme that Modifies 23S rRNA and is Essential for Normal Cell Growth of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2004, 335, 87-101.	4.2	38
83	Crystal Structure of <i>Escherichia coli</i> Glucose-1-Phosphate Thymidyltransferase (RffH) Complexed with dTTP and Mg ²⁺ . <i>Journal of Biological Chemistry</i> , 2002, 277, 44214-44219.	3.4	67
84	Design of Noncovalent Inhibitors of Human Cathepsin L. From the 96-Residue Proregion to Optimized Tripeptides. <i>Journal of Medicinal Chemistry</i> , 2002, 45, 5321-5329.	6.4	68
85	Crystal structure of human procathepsin X: a cysteine protease with the proregion covalently linked to the active site cysteine. <i>Journal of Molecular Biology</i> , 2000, 295, 939-951.	4.2	82
86	Crystal structure of wild-type human procathepsin K. <i>Protein Science</i> , 1999, 8, 283-290.	7.6	58
87	Structure of human procathepsin L reveals the molecular basis of inhibition by the prosegment. <i>EMBO Journal</i> , 1996, 15, 5492-5503.	7.8	345
88	Crystallization of rat procathepsin B. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 874-875.	2.5	6