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 g-index
89 all docs	89 docs citations	89 times ranked	4860 citing authors

#	Article	IF	Citations
1	Structure of human procathepsin L reveals the molecular basis of inhibition by the prosegment.. EMBO Journal, 1996, 15, 5492-5503.	7.8	345
2	Linkers in the structural biology of proteinâ€“protein interactions. Protein Science, 2013, 22, 153-167.	7.6	261
3	Inhibition of bacterial cell division protein FtsZ by cinnamaldehyde. Biochemical Pharmacology, 2007, 74, 831-840.	4.4	213
4	Berberine Targets Assembly of Escherichia coli Cell Division Protein FtsZ. Biochemistry, 2008, 47, 3225-3234.	2.5	209
5	Structural Basis for the Inhibition Mechanism of Human Cystathionine Î³-Lyase, an Enzyme Responsible for the Production of H2S. Journal of Biological Chemistry, 2009, 284, 3076-3085.	3.4	166
6	Structural basis for the neutralization and genotype specificity of hepatitis E virus. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10266-10271.	7.1	109
7	Crystal structure of human procathepsin X: a cysteine protease with the proregion covalently linked to the active site cysteine. Journal of Molecular Biology, 2000, 295, 939-951.	4.2	82
8	Structural Basis for the Active Site Inhibition Mechanism of Human Kidney-Type Glutaminase (KGA). Scientific Reports, 2014, 4, 3827.	3.3	80
9	Structural Basis of SARS-CoV-2 and SARS-CoV Antibody Interactions. Trends in Immunology, 2020, 41, 1006-1022.	6.8	79
10	Structural and Functional Characterization of a Novel Homodimeric Three-finger Neurotoxin from the Venom of Ophiophagus hannah (King Cobra). Journal of Biological Chemistry, 2010, 285, 8302-8315.	3.4	77
11	Structural basis for the neutralization of hepatitis E virus by a cross-genotype antibody. Cell Research, 2015, 25, 604-620.	12.0	69
12	Design of Noncovalent Inhibitors of Human Cathepsin L. From the 96-Residue Proregion to Optimized Tripeptides. Journal of Medicinal Chemistry, 2002, 45, 5321-5329.	6.4	68
13	Crystal Structure of Escherichia coli Glucose-1-Phosphate Thymidylyltransferase (RffH) Complexed with dTTP and Mg2+. Journal of Biological Chemistry, 2002, 277, 44214-44219.	3.4	67
14	Wnt Signaling Promotes Breast Cancer by Blocking ITCH-Mediated Degradation of YAP/TAZ Transcriptional Coactivator WBP2. Cancer Research, 2016, 76, 6278-6289.	0.9	62
15	Crystal structure of wildâ€type human procathepsin K. Protein Science, 1999, 8, 283-290.	7.6	58
16	Structural basis for a novel intrapeptidyl H-bond and reverse binding of c-Cbl-TKB domain substrates. EMBO Journal, 2008, 27, 804-816.	7.8	58
17	Structural Basis for the Interaction of Unstructured Neuron Specific Substrates Neuromodulin and Neurogranin with Calmodulin. Scientific Reports, 2013, 3, 1392.	3.3	57
18	Structure of a novel phosphotyrosine-binding domain in Hakai that targets E-cadherin. EMBO Journal, 2012, 31, 1308-1319.	7.8	56

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19	Site-Directed Mutagenesis on Human Cystathionine-Î³-Lyase Reveals Insights into the Modulation of H2S Production. Journal of Molecular Biology, 2010, 396, 708-718.	4.2	53
20	Structural Basis for the Secretion of EvpC: A Key Type VI Secretion System Protein from Edwardsiella tarda. PLoS ONE, 2010, 5, e12910.	2.5	50
21	Structural Characterization of Myotoxic Ecarpholin S From Echis carinatus Venom. Biophysical Journal, 2008, 95, 3366-3380.	0.5	45
22	Extended Loop Region of Hcp1 is Critical for the Assembly and Function of Type VI Secretion System in Burkholderia pseudomallei. Scientific Reports, 2015, 5, 8235.	3.3	43
23	Crystal Structure of the RluD Pseudouridine Synthase Catalytic Module, an Enzyme that Modifies 23S rRNA and is Essential for Normal Cell Growth of Escherichia coli. Journal of Molecular Biology, 2004, 335, 87-101.	4.2	38
24	Structure of GrlRâ€“GrlA complex that prevents GrlA activation of virulence genes. Nature Communications, 2013, 4, 2546.	12.8	38
25	Structural Basis of SARS-CoV-2â€“ and SARS-CoVâ€“Receptor Binding and Small-Molecule Blockers as Potential Therapeutics. Annual Review of Pharmacology and Toxicology, 2021, 61, 465-493.	9.4	36
26	Structural Basis for the Modulation of the Neuronal Voltage-Gated Sodium Channel NaV1.6 by Calmodulin. Scientific Reports, 2013, 3, 2435.	3.3	35
27	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. Nucleic Acids Research, 2010, 38, 4120-4132.	14.5	34
28	Structure of GrlR and the Implication of Its EDED Motif in Mediating the Regulation of Type III Secretion System in EHEC. PLoS Pathogens, 2007, 3, e69.	4.7	30
29	Structural basis for reversible and irreversible inhibition of human cathepsin L by their respective dipeptidyl glyoxal and diazomethylketone inhibitors. Journal of Structural Biology, 2011, 173, 14-19.	2.8	29
30	Exploring Inhibitor Binding at the Sâ€² Subsites of Cathepsin L. Journal of Medicinal Chemistry, 2008, 51, 1361-1368.	6.4	27
31	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. Nucleic Acids Research, 2011, 39, 1903-1918.	14.5	27
32	Structure of ScpC, a virulence protease from Streptococcus pyogenes, reveals the functional domains and maturation mechanism. Biochemical Journal, 2018, 475, 2847-2860.	3.7	23
33	Crystal Structure of Der f 7, a Dust Mite Allergen from Dermatophagoides farinae. PLoS ONE, 2012, 7, e44850.	2.5	23
34	Ringhalexin from Hemachatus haemachatus: A novel inhibitor of extrinsic tenase complex. Scientific Reports, 2016, 6, 25935.	3.3	21
35	The crystal structure of Escherichia coli spermidine synthase SpeE reveals a unique substrate-binding pocket. Journal of Structural Biology, 2010, 169, 277-285.	2.8	20
36	Structural basis for the pathogenesis of Campylobacter jejuni Hcp1, a structural and effector protein of the Type VI Secretion System. FEBS Journal, 2018, 285, 4060-4070.	4.7	20

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37	Identification and characterization of the lipid-binding property of GrlR, a locus of enterocyte effacement regulator. Biochemical Journal, 2009, 420, 191-201.	3.7	19
38	Crystal structure of a fructokinase homolog from Halothermothrix orenii. Journal of Structural Biology, 2010, 171, 397-401.	2.8	19
39	Additional Serine/Threonine Phosphorylation Reduces Binding Affinity but Preserves Interface Topography of Substrate Proteins to the c-Cbl TKB Domain. PLoS ONE, 2010, 5, e12819.	2.5	19
40	Application of isothermal titration calorimetry and column chromatography for identification of biomolecular targets. Nature Protocols, 2011, 6, 158-165.	12.0	17
41	Exploring the â€œOtherâ€•subfamily of HECT E3-ligases for therapeutic intervention. , 2021, 224, 107809.		17
42	Identification and Structural Characterization of a New Three-Finger Toxin Hemachatoxin from Hemachatus haemachatus Venom. PLoS ONE, 2012, 7, e48112.	2.5	17
43	Crystal structure of HECT domain of UBE3C E3 ligase and its ubiquitination activity. Biochemical Journal, 2020, 477, 905-923.	3.7	16
44	A Novel Serine Protease Inhibitor Acts as an Immunomodulatory Switch while Maintaining Homeostasis. Journal of Innate Immunity, 2009, 1, 465-479.	3.8	15
45	Mapping of the chaperone AcrH binding regions of translocators AopB and AopD and characterization of oligomeric and metastable AcrHâ€AopBâ€AopD complexes in the type III secretion system of Aeromonas hydrophila. Protein Science, 2009, 18, 1724-1734.	7.6	15
46	Structural Basis for a Unique ATP Synthase Core Complex from Nanoarcheaum equitans. Journal of Biological Chemistry, 2015, 290, 27280-27296.	3.4	14
47	Structural insights into a HECT-type E3 ligase AREL1 and its ubiquitination activities in vitro. Journal of Biological Chemistry, 2019, 294, 19934-19949.	3.4	14
48	A Novel Trans Conformation of Ligand-Free Calmodulin. PLoS ONE, 2013, 8, e54834.	2.5	14
49	A universal method for fishing target proteins from mixtures of biomolecules using isothermal titration calorimetry. Protein Science, 2008, 17, 1798-1804.	7.6	13
50	Crystal Structure of the Heteromolecular Chaperone, AscE-AscG, from the Type III Secretion System in Aeromonas hydrophila. PLoS ONE, 2011, 6, e19208.	2.5	13
51	Structure of LNX1:Ubc13 ~ Ubiquitin Complex Reveals the Role of Additional Motifs for the E3 Ligase Activity of LNX1. Journal of Molecular Biology, 2018, 430, 1173-1188.	4.2	13
52	Dimeric Switch of Hakai-truncated Monomers during Substrate Recognition. Journal of Biological Chemistry, 2014, 289, 25611-25623.	3.4	12
53	Fulditoxin, representing a new class of dimeric snake toxins, defines novel pharmacology at nicotinic ACh receptors. British Journal of Pharmacology, 2020, 177, 1822-1840.	5.4	12
54	Domain Organization and Crystal Structure of the Catalytic Domain of E.coli RluF, a Pseudouridine Synthase that Acts on 23S rRNA. Journal of Molecular Biology, 2006, 359, 998-1009.	4.2	11

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55	Structure of AscE and induced burial regions in AscE and AscG upon formation of the chaperone needleâ€subunit complex of type III secretion system in Aeromonas hydrophila. Protein Science, 2008, 17, 1748-1760.	7.6	11
56	A Combined Crystallographic and Molecular Dynamics Study of Cathepsin L Retrobinding Inhibitors. Journal of Medicinal Chemistry, 2009, 52, 6335-6346.	6.4	11
57	Dimerization of VirD2 Binding Protein Is Essential for Agrobacterium Induced Tumor Formation in Plants. PLoS Pathogens, 2014, 10, e1003948.	4.7	11
58	An adjacent arginine, and the phosphorylated tyrosine in the c-Met receptor target sequence, dictates the orientation of c-Cbl binding. FEBS Letters, 2011, 585, 281-285.	2.8	10
59	Structural Basis for Dual-Inhibition Mechanism of a Non-Classical Kazal-Type Serine Protease Inhibitor from Horseshoe Crab in Complex with Subtilisin. PLoS ONE, 2011, 6, e18838.	2.5	10
60	A Disordered Region in the EvpP Protein from the Type VI Secretion System of Edwardsiella tarda is Essential for EvpC Binding. PLoS ONE, 2014, 9, e110810.	2.5	10
61	Structural basis for the indispensable role of a unique zinc finger motif in LNX2 ubiquitination. Oncotarget, 2015, 6, 34342-34357.	1.8	10
62	A method to trap transient and weak interacting protein complexes for structural studies. Intrinsically Disordered Proteins, 2013, 1, e25464.	1.9	9
63	Computer aided design of FtsZ targeting oligopeptides. RSC Advances, 2013, 3, 1739-1743.	3.6	8
64	Structure of the pseudouridine synthase RsuA fromHaemophilus influenzae. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 350-354.	0.7	7
65	Structural characterization of BVU_3255, a methyltransferase from human intestine antibiotic resistant pathogen Bacteroides vulgatus. Journal of Structural Biology, 2011, 176, 409-413.	2.8	7
66	Structural basis of mapping the spontaneous mutations with 5-flurouracil in uracil phosphoribosyltransferase from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2015, 467, 577-582.	2.1	7
67	Structural basis for p50RhoGAP BCH domainâ€“mediated regulation of Rho inactivation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2014242118.	7.1	7
68	Mapping of molecular interactions between human E3 ligase TRIM69 and Dengue virus NS3 protease using hydrogenâ€“deuterium exchange mass spectrometry. Cellular and Molecular Life Sciences, 2022, 79, 233.	5.4	7
69	Crystallization of rat procathepsin B. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 874-875.	2.5	6
70	Modifying the Substrate Specificity of Carcinoscorpius rotundicauda Serine Protease Inhibitor Domain 1 to Target Thrombin. PLoS ONE, 2010, 5, e15258.	2.5	6
71	Insights into the biology of Escherichia coli through structural proteomics. Journal of Structural and Functional Genomics, 2007, 8, 45-55.	1.2	5
72	Structure and mapping of spontaneous mutational sites of PyrR from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2016, 471, 409-415.	2.1	5

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73	Ligand-mediated changes in conformational dynamics of NpmA: implications for ribosomal interactions. Scientific Reports, 2016, 6, 37061.	3.3	5
74	Binding specificity of type three secretion system effector <scp>NleH2</scp> to multiâ€cargo chaperone <scp>CesT</scp> and their phosphorylation. Protein Science, 2021, 30, 2433-2444.	7.6	5
75	Structure of Aedes aegypti carboxypeptidase B1 â€inhibitor complex uncover the disparity between mosquito and nonâ€mosquito insect carboxypeptidase inhibition mechanism. Protein Science, 2021, 30, 2445-2456.	7.6	4
76	Structural basis for the hydrolysis of ATP by a nucleotide binding subunit of an amino acid ABC transporter from Thermus thermophilus. Journal of Structural Biology, 2015, 190, 367-372.	2.8	3
77	Bacterial antagonism of Chromobacterium haemolyticum and characterization of its putative type VI secretion system. Research in Microbiology, 2022, 173, 103918.	2.1	3
78	Identification of putative binding interface of PI(3,5)P2 lipid on rice black-streaked dwarf virus (RBSDV) P10 protein. Virology, 2022, 570, 81-95.	2.4	3
79	Biophysical studies and modelling indicate the binding preference of TAZ WW domain for LATS1 PPxY motif. Biochemical and Biophysical Research Communications, 2018, 502, 307-312.	2.1	2
80	Structural Basis for the Inhibition Mechanism of Ecotin against Neutrophil Elastase by Targeting the Active Site and Secondary Binding Site. Biochemistry, 2020, 59, 2788-2795.	2.5	2
81	A Conformational Switch in the Active Site of BT_2972, a Methyltransferase from an Antibiotic Resistant Pathogen B. thetaiotaomicron. PLoS ONE, 2011, 6, e27543.	2.5	2
82	Structure of Aedes aegypti procarboxypeptidase B1 and its binding with Dengue virus for controlling infection. Life Science Alliance, 2022, 5, e202101211.	2.8	2
83	Crystal structure of Aedes aegypti trypsin inhibitor in complex with Î¼â€plasmin reveals role for scaffold stability in Kazalâ€type serine protease inhibitor. Protein Science, 2021, , .	7.6	2
84	Sequence preference and scaffolding requirement for the inhibition of human neutrophil elastase by ecotin peptide. Protein Science, 2022, 31, 933-941.	7.6	1
85	The Autocatalytic Cleavage Domain Is Not Required for the Activity of ScpC, a Virulence Protease from Streptococcus pyogenes: A Structural Insight. Biochemistry, 2021, 60, 1564-1568.	2.5	0
86	Application of linker technique to trap transiently interacting protein complexes for structural studies. Journal of Biological Methods, 2016, 3, e34.	0.6	0
87	Unusual quaternary structure of a homodimeric synergistic-type toxin from mamba snake venom defines its molecular evolution. Biochemical Journal, 2020, 477, 3951-3962.	3.7	0
88	Scaffold stability and P14â€™ residue steric hindrance in the differential inhibition of FXIIa by Aedes aegypti trypsin inhibitor versus Infestin-4. Bioscience Reports, 2022, , .	2.4	0