Raghuvir K Arni

List of Publications by Year in descending order

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158 papers

4,653 citations

94433 37 h-index 60 g-index

165 all docs 165
docs citations

165 times ranked 3575 citing authors

#	Article	IF	CITATIONS
1	Phospholipase A2—a structural review. Toxicon, 1996, 34, 827-841.	1.6	337
2	Enzymatic toxins from snake venom: structural characterization and mechanism of catalysis. FEBS Journal, 2011, 278, 4544-4576.	4.7	233
3	Recent advances in the understanding of brown spider venoms: From the biology of spiders to the molecular mechanisms of toxins. Toxicon, 2014, 83, 91-120.	1.6	116
4	The X-ray Crystallographic Structure of Escherichia coli Branching Enzyme. Journal of Biological Chemistry, 2002, 277, 42164-42170.	3.4	113
5	Amino acid sequence and crystal structure of BaP1, a metalloproteinase from Bothrops asper snake venom that exerts multiple tissue-damaging activities. Protein Science, 2009, 12, 2273-2281.	7.6	110
6	Structures of the noncovalent complexes of human and bovine prothrombin fragment 2 with human PPACK-thrombin. Biochemistry, 1993, 32, 4727-4737.	2.5	109
7	Inhibition of Myotoxic Activity of Bothrops asper Myotoxin II by the Anti-trypanosomal Drug Suramin. Journal of Molecular Biology, 2005, 350, 416-426.	4.2	106
8	A rapid procedure for the isolation of the Lys-49 myotoxin II from Bothrops moojeni (caissaca) venom: Biochemical characterization, crystallization, myotoxic and edematogenic activity. Toxicon, 1998, 36, 503-514.	1.6	105
9	Dissociation of Enzymatic and Pharmacological Properties of Piratoxins-I and -III, Two Myotoxic Phospholipases A2 from Bothrops pirajai Snake Venom. Archives of Biochemistry and Biophysics, 2001, 387, 188-196.	3.0	98
10	Structural and Functional Characterization of Myotoxin I, a Lys49 Phospholipase A2 Homologue from Bothrops moojeni (Caissaca) Snake Venom. Archives of Biochemistry and Biophysics, 2000, 373, 7-15.	3.0	95
11	Crystallographic and spectroscopic characterization of a molecular hinge: Conformational changes in bothropstoxin I, a dimeric Lys49-phospholipase A2 homologue. , 1998, 30, 442-454.		91
12	Structural Basis for Metal Ion Coordination and the Catalytic Mechanism of Sphingomyelinases D. Journal of Biological Chemistry, 2005, 280, 13658-13664.	3.4	90
13	Structure of a calcium-independent phospholipase-like myotoxic protein fromBothrops aspervenom. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 311-317.	2.5	81
14	Proteome analysis of snake venom toxins: pharmacological insights. Expert Review of Proteomics, 2008, 5, 787-797.	3.0	77
15	The Venomics of <i>Bothrops alternatus</i> is a Pool of Acidic Proteins with Predominant Hemorrhagic and Coagulopathic Activities. Journal of Proteome Research, 2010, 9, 2422-2437.	3.7	69
16	A Molecular Mechanism for Lys49-Phospholipase A2 Activity Based on Ligand-induced Conformational Change. Journal of Biological Chemistry, 2005, 280, 7326-7335.	3.4	66
17	Snake venomics of the Siamese Russell's viper (Daboia russelli siamensis) — Relation to pharmacological activities. Journal of Proteomics, 2009, 72, 256-269.	2.4	66
18	Thrombocytopenia and platelet hypoaggregation induced by Bothrops asper snake venom. Thrombosis and Haemostasis, 2005, 94, 123-131.	3.4	65

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19	Berberine associated photodynamic therapy promotes autophagy and apoptosis via ROS generation in renal carcinoma cells. Biomedicine and Pharmacotherapy, 2020, 123, 109794.	5.6	64
20	Structural insights into the catalytic mechanism of sphingomyelinases D and evolutionary relationship to glycerophosphodiester phosphodiesterases. Biochemical and Biophysical Research Communications, 2006, 342, 323-329.	2.1	63
21	Crystal Structure of Myotoxin II, a Monomeric Lys49-Phospholipase A2 Homologue Isolated from the Venom of Cerrophidion (Bothrops) godmani. Archives of Biochemistry and Biophysics, 1999, 366, 177-182.	3.0	61
22	Snake Venomic of <i>Crotalus durissus terrificus</i> $\hat{a}\in$ "Correlation with Pharmacological Activities. Journal of Proteome Research, 2010, 9, 2302-2316.	3.7	60
23	Interfacial surface charge and free accessibility to the PLA2-active site-like region are essential requirements for the activity of Lys49 PLA2 homologues. Toxicon, 2007, 49, 378-387.	1.6	58
24	Crystal structure of the platelet activator convulxin, a disulfide-linked $\hat{l}\pm4\hat{l}^24$ cyclic tetramer from the venom of Crotalus durissus terrificus. Biochemical and Biophysical Research Communications, 2003, 310, 478-482.	2.1	55
25	Highly Selective Mechanism-Based Thrombin Inhibitors: Structures of Thrombin and Trypsin Inhibited with Rigid Peptidyl Aldehydesâ€. Biochemistry, 1998, 37, 12094-12103.	2.5	54
26	A SequenceSpace analysis of Lys49 phopholipases A2: clues towards identification of residues involved in a novel mechanism of membrane damage and in myotoxicity. Protein Engineering, Design and Selection, 1998, 11, 285-294.	2.1	54
27	Structural basis for branchingâ€enzyme activity of glycoside hydrolase family 57: Structure and stability studies of a novel branching enzyme from the hyperthermophilic archaeon <i>Thermococcus Kodakaraensis</i> KOD1. Proteins: Structure, Function and Bioinformatics, 2011, 79, 547-557.	2.6	54
28	Structure of a novel class II phospholipase D: Catalytic cleft is modified by a disulphide bridge. Biochemical and Biophysical Research Communications, 2011, 409, 622-627.	2.1	49
29	Structural insights for fatty acid binding in a Lys49-phospholipase A2: crystal structure of myotoxin II from Bothrops moojeni complexed with stearic acid. Biochimie, 2005, 87, 161-167.	2.6	48
30	At the interface: Crystal structures of phospholipases A2. Toxicon, 1998, 36, 1623-1633.	1.6	47
31	Correlation of temperature induced conformation change with optimum catalytic activity in the recombinant G/11 xylanase A fromBacillus subtilisstrain 168 (1A1). FEBS Letters, 2005, 579, 6505-6510.	2.8	46
32	Isolation, characterization and biological activity of acidic phospholipase A2 isoforms from Bothrops jararacussu snake venom. Biochimie, 2003, 85, 983-991.	2.6	45
33	Thrombomodulin-independent Activation of Protein C and Specificity of Hemostatically Active Snake Venom Serine Proteinases. Journal of Biological Chemistry, 2005, 280, 39309-39315.	3.4	43
34	Crystal structure of mature 2S albumin from Moringa oleifera seeds. Biochemical and Biophysical Research Communications, 2015, 468, 365-371.	2.1	43
35	Natural Products Isolated from Oriental Medicinal Herbs Inactivate Zika Virus. Viruses, 2019, 11, 49.	3. 3	41
36	Structure of a Lys49-Phospholipase A2 homologue isolated from the venom of Bothrops nummifer (jumping viper). Toxicon, 1999, 37, 371-384.	1.6	40

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37	Restrained least-squares refinement of the crystal structure of the ribonuclease T1*2'-guanylic acid complex at 1·9 à resolution. Acta Crystallographica Section B: Structural Science, 1987, 43, 548-554.	1.8	39
38	A structure based model for liposome disruption and the role of catalytic activity in myotoxic phospholipase A2s. Toxicon, 2003, 42, 903-913.	1.6	38
39	SMase II, a new sphingomyelinase D from Loxosceles laeta venom gland: Molecular cloning, expression, function and structural analysis. Toxicon, 2009, 53, 743-753.	1.6	38
40	Crystal structure of piratoxin-l: A calcium-independent, myotoxic phospholipase A2-homologue from Bothrops pirajai venom. Toxicon, 1998, 36, 1395-1406.	1.6	37
41	Structural studies of BmooMPα-I, a non-hemorrhagic metalloproteinase from Bothrops moojeni venom. Toxicon, 2010, 55, 361-368.	1.6	37
42	Structure of the polypeptide crotamine from the Brazilian rattlesnake <i>Crotalus durissus terrificus</i> . Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1958-1964.	2.5	37
43	Purification, characterization and crystallization of Jararacussin-I, a fibrinogen-clotting enzyme isolated from the venom of Bothrops jararacussu. Toxicon, 2002, 40, 1307-1312.	1.6	36
44	Intermolecular Interactions and Characterization of the Novel Factor Xa Exosite Involved in Macromolecular Recognition and Inhibition: Crystal Structure of Human Gla-domainless Factor Xa Complexed with the Anticoagulant Protein NAPc2 from the Hematophagous Nematode Ancylostoma caninum. Journal of Molecular Biology, 2007, 366, 602-610.	4.2	36
45	Molecular adaptability of nucleoside diphosphate kinase b from trypanosomatid parasites: stability, oligomerization and structural determinants of nucleotide binding. Molecular BioSystems, 2011, 7, 2189.	2.9	36
46	The X-ray Crystallographic Structure of the Angiogenesis Inhibitor Angiostatin. Journal of Molecular Biology, 2002, 318, 1009-1017.	4.2	35
47	Proteomic analysis of the rare Uracoan rattlesnake Crotalus vegrandis venom: Evidence of a broad arsenal of toxins. Toxicon, 2015, 107, 234-251.	1.6	35
48	<i>Pseudechis australis</i> Venomics: Adaptation for a Defense against Microbial Pathogens and Recruitment of Body Transferrin. Journal of Proteome Research, 2011, 10, 2440-2464.	3.7	34
49	Forty Years of the Description of Brown Spider Venom Phospholipases-D. Toxins, 2020, 12, 164.	3.4	33
50	Crystal structure of an acidic platelet aggregation inhibitor and hypotensive phospholipase A2 in the monomeric and dimeric states: insights into its oligomeric state. Biochemical and Biophysical Research Communications, 2004, 323, 24-31.	2.1	30
51	Active site mapping of Loxosceles phospholipases D: Biochemical and biological features. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2016, 1861, 970-979.	2.4	29
52	Venomics of the Australian eastern brown snake (Pseudonaja textilis): Detection of new venom proteins and splicing variants. Toxicon, 2015, 107, 252-265.	1.6	28
53	The Repurposed Drugs Suramin and Quinacrine Cooperatively Inhibit SARS-CoV-2 3CLpro In Vitro. Viruses, 2021, 13, 873.	3.3	28
54	The structure of a native <scp>l</scp> -amino acid oxidase, the major component of the Vipera ammodytes ammodytes venomic, reveals dynamic active site and quaternary structure stabilization by divalent ions. Molecular BioSystems, 2011, 7, 379-384.	2.9	27

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55	Sequence of a cDNA encoding bothropstoxin I, a myotoxin from the venom of Bothrops jararacussu. Gene, 1995, 156, 305-306.	2.2	26
56	Potential Implications for Designing Drugs Against the Brown Spider Venom Phospholipaseâ€D. Journal of Cellular Biochemistry, 2017, 118, 726-738.	2.6	26
57	Structure of the non-covalent complex of prothrombin kringle 2 with PPACK-thrombin. Chemistry and Physics of Lipids, 1994, 67-68, 59-66.	3.2	25
58	Amino acid sequence of a myotoxic Lys49-phospholipase A2 homologue from the venom of Cerrophidion (Bothrops) godmani. BBA - Proteins and Proteomics, 1998, 1384, 204-208.	2.1	25
59	The crystal chemistry of Mn3+ in the clino- and orthozoisite structure types, Ca2M3 3+[OH O SiO4 Si2O7]: A structural and spectroscopic study of some natural piemontites and "thulites―and their synthetic equivalents. Zeitschrift Fur Kristallographie - Crystalline Materials, 2002. 217. 563-580.	0.8	25
60	Active and Exo-site Inhibition of Human Factor Xa: Structure of des-Gla Factor Xa Inhibited by NAP5, a Potent Nematode Anticoagulant Protein from Ancylostoma caninum. Journal of Molecular Biology, 2007, 371, 774-786.	4.2	25
61	Structural insights into selectivity and cofactor binding in snake venom l-amino acid oxidases. Biochemical and Biophysical Research Communications, 2012, 421, 124-128.	2.1	25
62	Zika virus NS2B/NS3 proteinase: A new target for an old drug - Suramin a lead compound for NS2B/NS3 proteinase inhibition Antiviral Research, 2018, 160, 118-125.	4.1	25
63	Venom peptide analysis of Vipera ammodytes meridionalis (Viperinae) and Bothrops jararacussu (Crotalinae) demonstrates subfamily-specificity of the peptidome in the family Viperidae. Molecular BioSystems, 2011, 7, 3298.	2.9	24
64	Brown Spider (Loxosceles) Venom Toxins as Potential Biotools for the Development of Novel Therapeutics. Toxins, 2019, 11, 355.	3.4	24
65	Tertiary Structural Changes of the $\hat{l}\pm$ -Hemolysin from Staphylococcus aureuson Association with Liposome Membranes. Archives of Biochemistry and Biophysics, 1998, 351, 47-52.	3.0	23
66	Mistletoe lectin I in complex with galactose and lactose reveals distinct sugar-binding properties. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 17-25.	0.7	22
67	Insights into metal ion binding inÂphospholipases A2: ultra high-resolution crystal structures ofÂanÂacidic phospholipase A2 inÂtheÂCa2+ free andÂbound states. Biochimie, 2006, 88, 543-549.	2.6	22
68	Putative virulence factors of Corynebacterium pseudotuberculosis FRC41: vaccine potential and protein expression. Microbial Cell Factories, 2016, 15, 83.	4.0	22
69	Purification and Characterization of Jararassin-I, A Thrombin-like Enzyme from Bothrops jararaca Snake Venom. Acta Biochimica Et Biophysica Sinica, 2004, 36, 798-802.	2.0	21
70	Functional and structural analysis of two fibrinogen-activating enzymes isolated from the venoms of & amp;lt;italic> and & amp;lt;italic> Crotalus durissus terrificus. Acta Biochimica Et Biophysica Sinica, 2009, 41, 21-29.	2.0	21
71	Elapid Snake Venom Analyses Show the Specificity of the Peptide Composition at the Level of Genera Naja and Notechis. Toxins, 2014, 6, 850-868.	3.4	20
72	Pseudechis guttatus venom proteome: Insights into evolution and toxin clustering. Journal of Proteomics, 2014, 110, 32-44.	2.4	20

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73	Ac2-26 Mimetic Peptide of Annexin A1 Inhibits Local and Systemic Inflammatory Processes Induced by Bothrops moojeni Venom and the Lys-49 Phospholipase A2 in a Rat Model. PLoS ONE, 2015, 10, e0130803.	2.5	20
74	Serine proteinases from Bothrops snake venom activates PI3K/Akt mediated angiogenesis. Toxicon, 2016, 124, 63-72.	1.6	20
7 5	Exfoliative toxin E, a new Staphylococcus aureus virulence factor with host-specific activity. Scientific Reports, 2019, 9, 16336.	3.3	20
76	Kinetic and mechanistic characterization of the Sphingomyelinases D from Loxosceles intermedia spider venom. Toxicon, 2006, 47, 380-386.	1.6	19
77	Crystal structure of Jararacussinâ€i: The highly negatively charged catalytic interface contributes to macromolecular selectivity in snake venom thrombinâ€ike enzymes. Protein Science, 2013, 22, 128-132.	7.6	19
78	Heterologous expression, purification and biochemical characterization of a new xylanase from Myceliophthora heterothallica F.2.1.4. International Journal of Biological Macromolecules, 2019, 131, 798-805.	7.5	19
79	Three-Dimensional Structure of Ribonuclease T1Complexed with an Isosteric Phosphonate Substrate Analogue of GpU: Alternate Substrate Binding Modes and Catalysisâ€,‡. Biochemistry, 1999, 38, 2452-2461.	2.5	17
80	Crystallographic portrayal of different conformational states of a Lys49 phospholipase A2 homologue: Insights into structural determinants for myotoxicity and dimeric configuration. International Journal of Biological Macromolecules, 2012, 51, 209-214.	7.5	17
81	Rapid purification of serine proteinases from Bothrops alternatus and Bothrops moojeni venoms. Toxicon, 2013, 76, 282-290.	1.6	17
82	P-I class metalloproteinase from Bothrops moojeni venom is a post-proline cleaving peptidase with kininogenase activity: Insights into substrate selectivity and kinetic behavior. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 545-552.	2.3	17
83	In vitro study of Hesperetin and Hesperidin as inhibitors of zika and chikungunya virus proteases. PLoS ONE, 2021, 16, e0246319.	2.5	17
84	Crystallization and preliminary diffraction data of two myotoxins isolated from the venoms of Bothrops Asper (terciopelo) and Bothrops Nummifer (jumping viper). Toxicon, 1993, 31, 1061-1064.	1.6	16
85	Crystal structure of a novel myotoxic Arg49 phospholipase A2 homolog (zhaoermiatoxin) from Zhaoermia mangshanensis snake venom: Insights into Arg49 coordination and the role of Lys122 in the polarization of the C-terminus. Toxicon, 2008, 51, 723-735.	1.6	16
86	A panel of recombinant proteins for the serodiagnosis of caseous lymphadenitis in goats and sheep. Microbial Biotechnology, 2019, 12, 1313-1323.	4.2	16
87	Structural Insights into Substrate Binding of Brown Spider Venom Class II Phospholipases D. Current Protein and Peptide Science, 2015, 16, 768-774.	1.4	16
88	Cold Shock Protein A from Corynebacterium pseudotuberculosis: Role of Electrostatic Forces in the Stability of the Secondary Structure. Protein and Peptide Letters, 2017, 24, 358-367.	0.9	15
89	Purification, Biochemical and Functional Characterization of Miliin, a New Thiol-Dependent Serine Protease Isolated from the Latex of Euphorbia milii. Protein and Peptide Letters, 2008, 15, 724-730.	0.9	14
90	Purification, crystallization and preliminary X-ray diffraction analysis of crotamine, a myotoxic polypeptide from the Brazilian snakeCrotalus durissus terrificus. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1052-1054.	0.7	14

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91	Structure of thrombin complexed with selective non-electrophilic inhibitors having cyclohexyl moieties at P1. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 294-303.	2.5	13
92	Biochemical and Structural Investigations of Bothropstoxin-II, a Myotoxic Asp49 Phospholipase A2 from Bothrops jararacussu Venom. Protein and Peptide Letters, 2008, 15, 1002-1008.	0.9	13
93	Crystallization and preliminary X-ray diffraction analysis of a class II phospholipase D from <i>Loxosceles intermedia</i> venom. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 234-236.	0.7	13
94	Expression, purification and characterization of cold shock protein A of Corynebacterium pseudotuberculosis. Protein Expression and Purification, 2015, 112, 15-20.	1.3	13
95	Crystal structure of Staphylococcus aureus exfoliative toxin D-like protein: Structural basis for the high specificity of exfoliative toxins. Biochemical and Biophysical Research Communications, 2015, 467, 171-177.	2.1	13
96	Crystallization and preliminary diffraction data of bothropstoxin I isolated from the venom of Bothrops jararacussu. Toxicon, 1995, 33, 383-386.	1.6	12
97	Three-dimensional structure of Gln25-ribonuclease T1 at 1.84ANG. resolution: structural variations at the base recognition and catalytic sites. Biochemistry, 1992, 31, 3126-3135.	2.5	10
98	Structure of myotoxin II, a catalytically inactive Lys49 phospholipase A2homologue fromAtropoides nummifervenom. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 423-426.	0.7	10
99	Exfoliative Toxins of Staphylococcus aureus. , 0, , .		10
100	Crystallization and preliminary X-ray crystallographic analysis of the heterodimeric crotoxin complex and the isolated subunits crotapotin and phospholipase A2. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 287-290.	0.7	9
101	Promising Natural Compounds against Flavivirus Proteases: Citrus Flavonoids Hesperetin and Hesperidin. Plants, 2021, 10, 2183.	3.5	9
102	Design of D-Amino Acids SARS-CoV-2 Main Protease Inhibitors Using the Cationic Peptide from Rattlesnake Venom as a Scaffold. Pharmaceuticals, 2022, 15, 540.	3.8	9
103	Crystallization and preliminary X-ray diffraction analysis of anL-amino-acid oxidase fromBothrops jararacussuvenom. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 211-213.	0.7	8
104	Crystallization and preliminary X-ray diffraction studies of an <scp>L</scp> -amino-acid oxidase from <i>Lachesis muta</i> venom. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1556-1559.	0.8	8
105	Crystallization and preliminary X-ray diffraction analysis of a novel sphingomyelinase D fromLoxosceles gauchovenom. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1418-1420.	0.8	8
106	A protective vaccine against the toxic activities following Brown spider accidents based on recombinant mutated phospholipases D as antigens. International Journal of Biological Macromolecules, 2021, 192, 757-770.	7.5	8
107	Crystallization of piratoxin I, a myotoxic Lys49-phospholipase A2 homologue isolated from the venom of Bothrops pirajai. Toxicon, 1998, 36, 547-551.	1.6	7
108	Structure of 2-keto-3-deoxy-6-phosphogluconate (KDPG) aldolase fromPseudomonas putida. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1454-1458.	2.5	7

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109	Crystal Structure of Bucain, a Three-Fingered Toxin from the Venom of the Malayan Krait (Bungarus) Tj ETQq1 1	0.784314	rgBT /Overlo
110	Exploring the Binding Mechanism of Flavonoid Quercetin to Phospholipase A2: Fluorescence Spectroscopy and Computational Approach. European Journal of Experimental Biology, 2017, 07, .	0.3	7
111	Brown Spiders' Phospholipases-D with Potential Therapeutic Applications: Functional Assessment of Mutant Isoforms. Biomedicines, 2021, 9, 320.	3.2	7
112	Initiating Structural Studies Of Lys49-Pla2 Homologues Complexed With An Anionic Detergent, A Fatty Acid And A Natural Lipid. Protein and Peptide Letters, 2003, 10, 525-530.	0.9	7
113	Purification and partial characterization of cathepsin D from porcine (Sus scrofa) liver using affinity chromatography. IUBMB Life, 1998, 45, 797-803.	3.4	6
114	Crystallization of bothrombin, a fibrinogen-converting serine protease isolated from the venom ofBothrops jararaca. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1036-1038.	2.5	6
115	Crystallization and preliminary X-ray diffraction analysis of suramin, a highly charged polysulfonated napthylurea, complexed with a myotoxic PLA2 from Bothrops asper venom. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1703, 83-85.	2.3	6
116	Purification, crystallization and preliminary X-ray diffraction analysis of a class P-III metalloproteinase (BmMP-III) from the venom of <i>Bothrops moojeni < i>Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1222-1225.</i>	0.7	6
117	Crystal structure of a dimeric Ser49 PLA2-like myotoxic component of the Vipera ammodytes meridionalis venomics reveals determinants of myotoxicity and membrane damaging activity. Molecular BioSystems, 2012, 8, 1405.	2.9	6
118	Chemical and thermal influence of the [4Fe–4S]2+ cluster of A/G-specific adenine glycosylase from Corynebacterium pseudotuberculosis. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 393-400.	2.4	6
119	Bacterial and Arachnid Sphingomyelinases D: Comparison of Biophysical and Pathological Activities. Journal of Cellular Biochemistry, 2017, 118, 2053-2063.	2.6	6
120	Biochemical and biophysical characterization of a mycoredoxin protein glutaredoxin A1 from Corynebacterium pseudotuberculosis. International Journal of Biological Macromolecules, 2018, 107, 1999-2007.	7.5	6
121	Structure and interaction ofCorynebacterium pseudotuberculosiscold shock protein A with Yâ€box singleâ€strandedDNAfragment. FEBS Journal, 2018, 285, 372-390.	4.7	6
122	Modeling and molecular dynamics indicate that snake venom phospholipase B-like enzymes are Ntn-hydrolases. Toxicon, 2018, 153, 106-113.	1.6	6
123	Binding studies of a putative C. pseudotuberculosis target protein from Vitamin B12 Metabolism. Scientific Reports, 2019, 9, 6350.	3.3	6
124	P-I metalloproteinases and L-amino acid oxidases from Bothrops species inhibit angiogenesis. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2021, 27, e20200180.	1.4	6
125	Crystallization and initial crystallographic results for pepstatin A inhibited bovine cathepsin D. Journal of Molecular Biology, 1992, 227, 1265-1268.	4.2	5
126	Crystallization and preliminary X-ray diffraction analysis of the catalytic subunit of ADP–glucose pyrophosphorylase from potato tuber. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 192-194.	2.5	5

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127	Crystallization and preliminary crystallographic analysis of SMase I, a sphingomyelinase fromLoxosceles laetaspider venom. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1112-1114.	2.5	5
128	Crystallization and high-resolution X-ray diffraction data collection of an Asp49 PLA2 from Bothrops jararacussu venom both in the presence and absence of Ca2+ ions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1703, 79-81.	2.3	5
129	Three-Dimensional Modelling of Honeybee Venom Allergenic Proteases: Relation to Allergenicity. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2011, 66, 305-312.	1.4	5
130	The polyanions heparin and suramin impede binding of free adenine to a DNA glycosylase from C. pseudotuberculosis. International Journal of Biological Macromolecules, 2019, 125, 459-468.	7. 5	5
131	Review of -omics studies on mosquito-borne viruses of the Flavivirus genus. Virus Research, 2022, 307, 198610.	2.2	5
132	Crystallization and preliminary X-ray analysis of bucain, a novel toxin from the Malayan kraitBungarus candidus. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1879-1881.	2.5	4
133	Crystallization and preliminary X-ray crystallographic studies of the mesophilic xylanase A fromBacillus subtilis1A1. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 219-220.	0.7	4
134	Tyrosine binding and promiscuity in the arginine repressor from the pathogenic bacterium Corynebacterium pseudotuberculosis. Biochemical and Biophysical Research Communications, 2016, 475, 350-355.	2.1	4
135	Crystallization of bothropstoxin II isolated from the venom of Bothrops jararacussu. Toxicon, 1996, 34, 614-617.	1.6	3
136	Crystallization of the Lys49 PLA2 homologue, myotoxin II, from the venom of Atropoides nummifer. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1703, 87-89.	2.3	3
137	Production, purification, crystallization and preliminary X-ray diffraction studies of the nucleoside diphosphate kinase b fromLeishmania major. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1116-1119.	0.7	3
138	Three-Dimensional Modelling of Honeybee Venom Allergenic Proteases: Relation to Allergenicity. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2011, 66, 0305.	1.4	3
139	Riboflavin, a Potent Neuroprotective Vitamin: Focus on Flavivirus and Alphavirus Proteases. Microorganisms, 2022, 10, 1331.	3.6	3
140	Crystallization and preliminary diffraction data of a platelet-aggregation inhibitor from the venom of Agkistrodon piscivorus piscivorus (North American water moccasin). Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1468-1470.	2.5	2
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