

K Sekar

List of Publications by Year in descending order

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83
papers

2,153
citations

236925

25
h-index

243625

44
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83
all docs

83
docs citations

83
times ranked

2272
citing authors

#	ARTICLE	IF	CITATIONS
1	C-halogenâ€¦pi interactions in nucleic acids: a database study. <i>Journal of Chemical Sciences</i> , 2020, 132, 1.	1.5	15
2	IMRPS: Inserted and Modified Residues in Protein Structures. A database. <i>Journal of Applied Crystallography</i> , 2020, 53, 569-573.	4.5	1
3	RepEx: A web server to extract sequence repeats from protein and DNA sequences. <i>Computational Biology and Chemistry</i> , 2019, 78, 424-430.	2.3	7
4	ACMS: a database of alternate conformations found in the atoms of main and side chains of protein structures. <i>Journal of Applied Crystallography</i> , 2019, 52, 910-913.	4.5	3
5	PlaneFinder: a methodology to find the best plane for a set of atoms involved in the metal coordination in protein structures. <i>Journal of Applied Crystallography</i> , 2018, 51, 1251-1256.	4.5	0
6	New biochemical insight of conserved water molecules at catalytic and structural Zn ²⁺ ions in human matrix metalloproteinase-I: a study by MD-simulation. <i>Journal of Molecular Modeling</i> , 2017, 23, 57.	1.8	7
7	NIMS: a database on nucleobase compounds and their interactions in macromolecular structures. <i>Journal of Applied Crystallography</i> , 2016, 49, 1093-1098.	4.5	0
8	<i>Hydrogen Bonds Computing Server</i> (<i>HBCS</i>): an online web server to compute hydrogen-bond interactions and their precision. <i>Journal of Applied Crystallography</i> , 2016, 49, 642-645.	4.5	8
9	<i>Online_DPI</i>: a web server to calculate the diffraction precision index for a protein structure. <i>Journal of Applied Crystallography</i> , 2015, 48, 939-942.	4.5	79
10	Conserved water-mediated recognition and dynamics of NAD ⁺ (carboxamide group) to hIMPDPH enzyme: water mimic approach toward the design of isoform-selective inhibitor. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1248-1262.	3.5	10
11	Role of invariant water molecules and water-mediated ionic interactions in D-xylose isomerase from <i>Streptomyces rubiginosus</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 376-384.	3.5	2
12	RepEx: Repeat extractor for biological sequences. <i>Genomics</i> , 2013, 102, 403-408.	2.9	25
13	Fragment Finder 2.0: a computing server to identify structurally similar fragments. <i>Journal of Applied Crystallography</i> , 2012, 45, 332-334.	4.5	5
14	Structural biology of <i>Mycobacterium tuberculosis</i> proteins: The Indian efforts. <i>Tuberculosis</i> , 2011, 91, 456-468.	1.9	22
15	Water-mediated ionic interactions in protein structures. <i>Journal of Biosciences</i> , 2011, 36, 253-263.	1.1	22
16	Evolution, Homology Conservation, and Identification of Unique Sequence Signatures in GH19 Family Chitinases. <i>Journal of Molecular Evolution</i> , 2010, 70, 466-478.	1.8	66
17	An algorithm to find distant repeats in a pair of protein sequences. <i>Pattern Recognition Letters</i> , 2010, 31, 2161-2169.	4.2	1
18	ProSTRIP: A method to find similar structural repeats in three-dimensional protein structures. <i>Computational Biology and Chemistry</i> , 2010, 34, 126-130.	2.3	25

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19	SSMBS: a web server to locate sequentially separated motifs in biological sequences. Journal of Applied Crystallography, 2010, 43, 203-205.	4.5	1
20	MLDB: macromolecule ligand database. Journal of Applied Crystallography, 2010, 43, 200-202.	4.5	2
21	Recognition of active and inactive catalytic triads: A template based approach. International Journal of Biological Macromolecules, 2010, 46, 317-323.	7.5	7
22	An Algorithm to Find All Identical Motifs in Multiple Biological Sequences. Lecture Notes in Computer Science, 2010, , 137-148.	1.3	0
23	Large cryptic internal sequence repeats in protein structures from Homo sapiens. Journal of Biosciences, 2009, 34, 103-112.	1.1	3
24	Structure, dynamics, and interactions of jacalin. Insights from molecular dynamics simulations examined in conjunction with results of X-ray studies. Proteins: Structure, Function and Bioinformatics, 2009, 77, 760-777.	2.6	21
25	An Insight to the Dynamics of Conserved Water Molecular Triad in IMPDH II (Human): Recognition of Cofactor and Substrate to Catalytic Arg 322. Journal of Biomolecular Structure and Dynamics, 2009, 27, 149-158.	3.5	60
26	Conserved Water Mediated H-bonding Dynamics of Inhibitor, Cofactor, Asp 364 and Asn 303 in Human IMPDH II. Journal of Biomolecular Structure and Dynamics, 2009, 26, 497-507.	3.5	28
27	<i>RPMS</i>: Ramachandran plot for multiple structures. Journal of Applied Crystallography, 2008, 41, 219-221.	4.5	7
28	<i>WAP</i> (version 2.0): an updated computing and visualization server for water molecules. Journal of Applied Crystallography, 2008, 41, 952-954.	4.5	5
29	Role of water molecules and ion pairs in Dps and related ferritin-like structures. International Journal of Biological Macromolecules, 2008, 43, 333-338.	7.5	5
30	Ramachandran Plot on The Web (2.0). Protein and Peptide Letters, 2007, 14, 669-671.	0.9	124
31	Conformational Angles Database (CADB-3.0). Protein and Peptide Letters, 2007, 14, 665-668.	0.9	4
32	Structural Biology of Recombinant Bovine Pancreatic Phospholipase A2 and its Inhibitor Complexes. Current Topics in Medicinal Chemistry, 2007, 7, 779-785.	2.1	6
33	Role of N and C-terminal Tails in DNA Binding and Assembly in Dps: Structural Studies of Mycobacterium smegmatis Dps Deletion Mutants. Journal of Molecular Biology, 2007, 370, 752-767.	4.2	49
34	PSAP: protein structure analysis package. Journal of Applied Crystallography, 2007, 40, 773-777.	4.5	41
35	Ion pairs in non-redundant protein structures. Journal of Biosciences, 2007, 32, 693-704.	1.1	16
36	Third calcium ion found in an inhibitor-bound phospholipase A2. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 392-397.	2.5	0

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37	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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 717-724.	2.5	3
38	Atomic resolution structure of the double mutant (K53,56M) of bovine pancreatic phospholipase A2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1-5.	0.7	2
39	3dSS: 3D structural superposition. <i>Nucleic Acids Research</i> , 2006, 34, W128-W132.	14.5	104
40	SSEP-2.0: Secondary Structural Elements of Proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 634-636.	2.5	6
41	Structure of <i>Mycobacterium smegmatis</i> single-stranded DNA-binding protein and a comparative study involving homologous SSBs: biological implications of structural plasticity and variability in quaternary association. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1140-1148.	2.5	29
42	Atomic resolution (0.97 Å) structure of the triple mutant (K53,56,121M) of bovine pancreatic phospholipase A2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 3-7.	0.7	4
43	Unusual sugar specificity of banana lectin from <i>Musa paradisiaca</i> and its probable evolutionary origin. <i>Crystallographic and modelling studies. Glycobiology</i> , 2005, 15, 1025-1032.	2.5	61
44	Fragment Finder: a web-based software to identify similar three-dimensional structural motif. <i>Nucleic Acids Research</i> , 2005, 33, W85-W88.	14.5	14
45	Structural Basis for the Energetics of Jacalin-Sugar Interactions: Promiscuity Versus Specificity. <i>Journal of Molecular Biology</i> , 2005, 347, 181-188.	4.2	60
46	BSDD: Biomolecules Segment Display Device—a web-based interactive display tool. <i>Nucleic Acids Research</i> , 2004, 32, W645-W648.	14.5	3
47	THGS: a web-based database of Transmembrane Helices in Genome Sequences. <i>Nucleic Acids Research</i> , 2004, 32, 125D-128.	14.5	10
48	A redetermination of the structure of the triple mutant (K53,56,120M) of bovine pancreatic phospholipase A2 at 1.6 Å resolution using sulfur-SAS at 1.54 Å wavelength. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1586-1590.	2.5	8
49	Purification, crystallization and preliminary X-ray structure analysis of the banana lectin from <i>Musa paradisiaca</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2104-2106.	2.5	18
50	A FAST Pattern Matching Algorithm. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 1251-1256.	2.8	33
51	X-ray Analysis of <i>Mycobacterium smegmatis</i> Dps and a Comparative Study Involving Other Dps and Dps-like Molecules. <i>Journal of Molecular Biology</i> , 2004, 339, 1103-1103.	4.2	0
52	X-ray Analysis of <i>Mycobacterium smegmatis</i> Dps and a Comparative Study Involving Other Dps and Dps-like Molecules. <i>Journal of Molecular Biology</i> , 2004, 339, 1103-1113.	4.2	67
53	Crystal and molecular structure of 2,6-bis(4-fluorobenzylidene)cyclohexanone. <i>Crystal Research and Technology</i> , 2003, 38, 822-828.	1.3	4
54	Crystal and molecular structure of 2,6-bis(4-chlorophenyl)-3-phenylpiperidin-4-one. <i>Crystal Research and Technology</i> , 2003, 38, 918-921.	1.3	4

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55	Câ€“halogenâ€“ interactions in proteins: a database study. <i>Crystal Engineering</i> , 2003, 6, 69-77.	0.7	86
56	WAP: water analysis package â€“ a Web-based package to calculate geometrical parameters between water oxygen and protein atoms. <i>Journal of Applied Crystallography</i> , 2003, 36, 167-168.	4.5	8
57	Crystallization and preliminary X-ray diffraction analysis of <i>Mycobacterium smegmatis</i> Dps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2254-2256.	2.5	8
58	CAP: conformation angles package--displaying the conformation angles of side chains in proteins. <i>Bioinformatics</i> , 2003, 19, 1043-1044.	4.1	4
59	Side-chain conformation angles of amino acids: effect of temperature factor cut-off. <i>Journal of Structural Biology</i> , 2003, 143, 181-184.	2.8	7
60	Crystal Structures of the Free and Anisic Acid Bound Triple Mutant of Phospholipase A2. <i>Journal of Molecular Biology</i> , 2003, 333, 367-376.	4.2	28
61	Structure of <i>Mycobacterium tuberculosis</i> Single-stranded DNA-binding Protein. Variability in Quaternary Structure and Its Implications. <i>Journal of Molecular Biology</i> , 2003, 331, 385-393.	4.2	62
62	Structural Basis of the Carbohydrate Specificities of Jacalin: An X-ray and Modeling Study. <i>Journal of Molecular Biology</i> , 2003, 332, 217-228.	4.2	58
63	CADB: Conformation Angles DataBase of proteins. <i>Nucleic Acids Research</i> , 2003, 31, 448-451.	14.5	12
64	SEM (Symmetry Equivalent Molecules): a web-based GUI to generate and visualize the macromolecules. <i>Nucleic Acids Research</i> , 2003, 31, 3356-3358.	14.5	4
65	SSEP: secondary structural elements of proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3404-3405.	14.5	6
66	Ramachandran plot on the web. <i>Bioinformatics</i> , 2002, 18, 1548-1549.	4.1	69
67	Crystal structures of artocarpin, a Moraceae lectin with mannose specificity, and its complex with methyl- β -d-mannose: implications to the generation of carbohydrate specificity. <i>Journal of Molecular Biology</i> , 2002, 317, 237-247.	4.2	97
68	Crystal Structure of the Jacalinâ€“T-antigen Complex and a Comparative Study of Lectinâ€“T-antigen Complexes. <i>Journal of Molecular Biology</i> , 2002, 321, 637-645.	4.2	77
69	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.	4.2	19
70	Crystal and Molecular Structure of an Acridinedione. <i>Crystal Research and Technology</i> , 2002, 37, 1029-1037.	1.3	6
71	PDB Goodies â€“ a web-based GUI to manipulate the Protein Data Bank file. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1385-1386.	2.5	24
72	Structural Basis of the Anionic Interface Preference and Activation of Pancreatic Phospholipase A2. <i>Biochemistry</i> , 2000, 39, 12312-12323.	2.5	52

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73	High-resolution refinement of orthorhombic bovine pancreatic phospholipase A2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 46-50.	2.5	14
74	Structures of the catalytic site mutants D99A and H48Q and the calcium-loop mutant D49E of phospholipase A2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 443-447.	2.5	11
75	Structure of the Complex of Bovine Pancreatic Phospholipase A2 with a Transition-State Analogue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 334-341.	2.5	16
76	1.72 Å... Resolution Refinement of the Trigonal Form of Bovine Pancreatic Phospholipase A2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 342-346.	2.5	5
77	Phospholipase A2 Engineering. Structural and Functional Roles of the Highly Conserved Active Site Residue Aspartate-99. <i>Biochemistry</i> , 1997, 36, 3104-3114.	2.5	53
78	Crystal Structure of the Complex of Bovine Pancreatic Phospholipase A2 with the Inhibitor 1-Hexadecyl-3-(trifluoroethyl)-sn-glycero-2-phosphomethanol. <i>Biochemistry</i> , 1997, 36, 14186-14191.	2.5	49
79	Phospholipase A2 Engineering. Deletion of the C-Terminus Segment Changes Substrate Specificity and Uncouples Calcium and Substrate Binding at the Zwitterionic Interface. <i>Biochemistry</i> , 1996, 35, 12164-12174.	2.5	37
80	A novel mode of carbohydrate recognition in jacalin, a Moraceae plant lectin with a \hat{I}^2 -prism fold. <i>Nature Structural Biology</i> , 1996, 3, 596-603.	9.7	224
81	Crystal and molecular structure of 1-methyl-3-ethyl-2,6-diphenyl-4-piperidone and a study of the geometry of the 4-piperidone ring. <i>Journal of Crystallographic and Spectroscopic Research</i> , 1993, 23, 101-105.	0.2	4
82	Structure of 4-piperidone derivatives. I. 3-Methyl-2,6-diphenyl-4-piperidone. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1990, 46, 1153-1155.	0.4	3
83	Structure of 4-piperidone derivatives. II. 2,6-Bis(p-methoxyphenyl)-3,5-dimethyl-4-piperidone. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1990, 46, 1338-1340.	0.4	3