N Srinivasan

List of Publications by Year
in descending order

79 papers	5,338 citations	136950 32 h-index	85541 71 g-index
80 all docs	80 docs citations	80 times ranked	6536 citing authors

#	Article	IF	Citations
1	The TRANSPARENT TESTA GLABRA1 Locus, Which Regulates Trichome Differentiation and Anthocyanin Biosynthesis in Arabidopsis, Encodes a WD40 Repeat Protein. Plant Cell, 1999, 11, 1337-1349.	6.6	905
2	PIC: Protein Interactions Calculator. Nucleic Acids Research, 2007, 35, W473-W476.	14.5	802
3	Structure of pentameric human serum amyloid P component. Nature, 1994, 367, 338-345.	27.8	471
4	Knowledge-Based Protein Modeling. Critical Reviews in Biochemistry and Molecular Biology, 1994, 29, 1-68.	5.2	206
5	Stereochemical modeling of disulfide bridges. Criteria for introduction into proteins by site-directed mutagenesis. Protein Engineering, Design and Selection, 1989, 3, 95-103.	2.1	171
6	Molecular evolution and domain structure of plasminogenâ€related growth factors (HGF/SF and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	7.6	166
7	Conformations of disulfide bridges in proteins. International Journal of Peptide and Protein Research, 1990, 36, 147-155.	0.1	164
8	A genomic perspective of protein kinases in Plasmodium falciparum. Proteins: Structure, Function and Bioinformatics, 2004, 58, 180-189.	2.6	147
9	Structural Modes of Stabilization of Permissive Phosphorylation Sites in Protein Kinases: Distinct Strategies in Ser/Thr and Tyr Kinases. Journal of Molecular Biology, 2004, 339, 1025-1039.	4.2	134
10	An evaluation of the performance of an automated procedure for comparative modelling of protein tertiary structure. Protein Engineering, Design and Selection, 1993, 6, 501-512.	2.1	111
11	On the potential significance of the enzymatic activity of mite allergens to immunogenicity. Clues to structure and function revealed by molecular characterization. Clinical and Experimental Allergy, 1997, 27, 10-21.	2.9	97
12	Comparative analyses of pentraxins: implications for protomer assembly and ligand binding. Structure, 1994, 2, 1017-1027.	3.3	96
13	Symmetry, stability, and dynamics of multidomain and multicomponent protein systems. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 14243-14248.	7.1	93
14	PALI--a database of Phylogeny and ALIgnment of homologous protein structures. Nucleic Acids Research, 2001, 29, 61-65.	14.5	88
15	Comparative modelling of major house dust mite allergen Der p I: structure validation using an extended environmental amino acid propensity table. Protein Engineering, Design and Selection, 1994, 7, 869-894.	2.1	82
16	KinG: a database of protein kinases in genomes. Nucleic Acids Research, 2004, 32, 153D-155.	14.5	75
17	CAMPASS: a database of structurally aligned protein superfamilies. Structure, 1998, 6, 1087-1094.	3.3	73
18	Diversity in domain architectures of Ser/Thr kinases and their homologues in prokaryotes. BMC Genomics, 2005, 6, 129.	2.8	65

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19	Protein Block Expert (PBE): a web-based protein structure analysis server using a structural alphabet. Nucleic Acids Research, 2006, 34, W119-W123.	14.5	52
20	Protein structure mining using a structural alphabet. Proteins: Structure, Function and Bioinformatics, 2008, 71, 920-937.	2.6	52
21	Prediction of protein–protein interactions between human host and a pathogen and its application to three pathogenic bacteria. International Journal of Biological Macromolecules, 2011, 48, 613-619.	7.5	49
22	A Survey of Nucleotide Cyclases in Actinobacteria: Unique Domain Organization and Expansion of the Class III Cyclase Family inMycobacterium tuberculosis. Comparative and Functional Genomics, 2004, 5, 17-38.	2.0	48
23	Analysis of the protein kinome of <i>Entamoeba histolytica</i>. Proteins: Structure, Function and Bioinformatics, 2008, 71, 995-1006.	2.6	47
24	Identification and Characterization of a Novel Deoxyhypusine Synthase in Leishmania donovani. Journal of Biological Chemistry, 2010, 285, 453-463.	3.4	47
25	The repertoire of protein kinases encoded in the draft version of the human genome: atypical variations and uncommon domain combinations. Genome Biology, 2002, 3, research0066.1.	9.6	42
26	Genome-wide comparative analyses of domain organisation of repertoires of protein kinases of Arabidopsis thaliana and Oryza sativa. Gene, 2006, 380, 1-13.	2.2	42
27	SUPFAM--a database of potential protein superfamily relationships derived by comparing sequence-based and structure-based families: implications for structural genomics and function annotation in genomes. Nucleic Acids Research, 2002, 30, 289-293.	14.5	40
28	Integration of related sequences with protein three-dimensional structural families in an updated version of PALI database. Nucleic Acids Research, 2003, 31, 486-488.	14.5	38
29	HARMONY: a server for the assessment of protein structures. Nucleic Acids Research, 2006, 34, W231-W234.	14.5	37
30	Analysis on conservation of disulphide bonds and their structural features in homologous protein domain families. BMC Structural Biology, 2008, 8, 55.	2.3	37
31	Improvement of protein structure comparison using a structural alphabet. Biochimie, 2011, 93, 1434-1445.	2.6	37
32	SUPFAM: a database of sequence superfamilies of protein domains. BMC Bioinformatics, 2004, 5, 28.	2.6	36
33	Conformational characteristics of asparaginyl residues in proteins. International Journal of Peptide and Protein Research, 1994, 44, 112-122.	0.1	34
34	Functional Inactivation of the Human Guanylyl Cyclase C Receptor:â€‰ Modeling and Mutation of the Protein Kinase-like Domain. Biochemistry, 2001, 40, 9196-9206.	2.5	32
35	Mutational analysis of the Mycobacterium tuberculosis Rv1625c adenylyl cyclase: residues that confer nucleotide specificity contribute to dimerization. FEBS Letters, 2003, 545, 253-259.	2.8	32
36	Comparison of sequence-based and structure-based phylogenetic trees of homologous proteins: Inferences on protein evolution. Journal of Biosciences, 2007, 32, 83-96.	1.1	32

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37	Structure–function studies of <i><scp>HNF1A</scp></i> (<scp>MODY3</scp>) gene mutations in South Indian patients with monogenic diabetes. Clinical Genetics, 2016, 90, 486-495.	2.0	32
38	Biochemical Characterization of the Intracellular Domain of the Human Guanylyl Cyclase C Receptor Provides Evidence for a Catalytically Active Homotrimer†. Biochemistry, 2000, 39, 16075-16083.	2.5	31
39	A Unique Modification of the Eukaryotic Initiation Factor 5A Shows the Presence of the Complete Hypusine Pathway in Leishmania donovani. PLoS ONE, 2012, 7, e33138.	2.5	30
40	Three‐dimensional model and quaternary structure of the human eye lens protein γS‐crystallin based on β‐and γ‐crystallin X‐ray coordinates and ultracentrifugation. Protein Science, 1994, 3, 1840-1846.	7.6	29
41	Structural aspects of the functional modules in human protein kinase-Cα deduced from comparative analyses. , 1996, 26, 217-235.		29
42	MulPSSM: a database of multiple position-specific scoring matrices of protein domain families. Nucleic Acids Research, 2006, 34, D243-D246.	14.5	29
43	PALI: a database of alignments and phylogeny of homologous protein structures. Bioinformatics, 2001, 17, 375-376.	4.1	27
44	Use of a database of structural alignments and phylogenetic trees in investigating the relationship between sequence and structural variability among homologous proteins. Protein Engineering, Design and Selection, 2001, 14, 219-226.	2.1	27
45	Interaction interfaces of protein domains are not topologically equivalent across families within superfamilies: Implications for metabolic and signaling pathways. Proteins: Structure, Function and Bioinformatics, 2004, 58, 339-353.	2.6	27
46	Use of multiple profiles corresponding to a sequence alignment enables effective detection of remote homologues. Bioinformatics, 2005, 21, 2821-2826.	4.1	27
47	Survey for g-proteins in the prokaryotic genomes: Prediction of functional roles based on classification. Proteins: Structure, Function and Bioinformatics, 2003, 52, 585-597.	2.6	25
48	Lipopolysaccharide phosphorylating enzymes encoded in the genomes of Gram-negative bacteria are related to the eukaryotic protein kinases. Protein Science, 2002, 11, 1580-1584.	7.6	24
49	Assessment of a Rigorous Transitive Profile Based Search Method to Detect Remotely Similar Proteins. Journal of Biomolecular Structure and Dynamics, 2005, 23, 283-298.	3.5	22
50	Comparative Kinomics of Plasmodium Organisms: Unity in Diversity. Protein and Peptide Letters, 2007, 14, 509-517.	0.9	21
51	Orthogonal ββ motifs in proteins. Journal of Molecular Biology, 1992, 223, 845-851.	4.2	20
52	Structural basis of regulation and substrate specificity of protein kinase CK2 deduced from the modeling of protein-protein interactions. , 2003, 3, 4.		20
53	Structural interpretation of site-directed mutagenesis and specificity of the catalytic subunit of protein kinase CK2 using comparative modelling. Protein Engineering, Design and Selection, 1999, 12, 119-127.	2.1	18
54	Cascade PSI-BLAST web server: a remote homology search tool for relating protein domains. Nucleic Acids Research, 2006, 34, W143-W146.	14.5	17

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55	The Conserved and Non-conserved Regions of Rpb4 Are Involved in Multiple Phenotypes in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2003, 278, 51566-51576.	3.4	16
56	The recognition of protein structure and function from sequence: adding value to genome data. Philosophical Transactions of the Royal Society B: Biological Sciences, 1994, 344, 373-381.	4.0	15
57	Domainal organization of the lower eukaryotic homologs of the yeast RNA polymerase II core subunit Rpb7 reflects functional conservation. Nucleic Acids Research, 2004, 32, 201-210.	14.5	14
58	Investigations of Ramachandran disallowed conformations in protein domain families. International Journal of Biological Macromolecules, 2014, 63, 119-125.	7.5	14
59	A glutathione-specific aldose reductase of Leishmania donovani and its potential implications for methylglyoxal detoxification pathway. Gene, 2009, 429, 1-9.	2.2	13
60	Interactions of protein kinase CK2 subunits. Molecular and Cellular Biochemistry, 1999, 191, 75-83.	3.1	12
61	Strategies for the effective identification of remotely related sequences in multiple PSSM search approach. Proteins: Structure, Function and Bioinformatics, 2007, 67, 789-794.	2.6	12
62	Conformation of glycyl residues in globular proteins. International Journal of Peptide and Protein Research, 2009, 29, 629-637.	0.1	12
63	The carboxy terminal WD domain of the pre-mRNA splicing factor Prp17p is critical for function. Rna, 2000, 6, 1289-1305.	3.5	9
64	Effective detection of remote homologues by searching in sequence dataset of a protein domain fold. FEBS Letters, 2003, 552, 225-230.	2.8	9
65	PRODOC: a resource for the comparison of tethered protein domain architectures with in-built information on remotely related domain families. Nucleic Acids Research, 2005, 33, W126-W129.	14.5	9
66	Analycys: A database for conservation and conformation of disulphide bonds in homologous protein domains. Proteins: Structure, Function and Bioinformatics, 2007, 67, 255-261.	2.6	9
67	Cascaded walks in protein sequence space: use of artificial sequences in remote homology detection between natural proteins. Molecular BioSystems, 2012, 8, 2076.	2.9	9
68	Protein three-dimensional structure and molecular recognition: a story of soft locks and keys. Pharmaceutica Acta Helvetiae, 1995, 69, 185-192.	1.2	8
69	The ascent of nucleotide cyclases: conservation and evolution of a theme. Journal of Biosciences, 2002, 27, 85-91.	1.1	8
70	Recognition of Interaction Interface Residues in Low-Resolution Structures of Protein Assemblies Solely from the Positions of Cα Atoms. PLoS ONE, 2009, 4, e4476.	2.5	8
71	Classification of Nonenzymatic Homologues of Protein Kinases. Comparative and Functional Genomics, 2009, 2009, 1-17.	2.0	8
72	Tolerance to the substitution of buried apolar residues by charged residues in the homologous protein structures. Proteins: Structure, Function and Bioinformatics, 2003, 53, 783-791.	2.6	6

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73	Repertoire of Protein Kinases Encoded in the Genome of<i>Takifugu rubripes</i>. Comparative and Functional Genomics, 2012, 2012, 1-12.	2.0	3
74	REPERTOIRE OF PROTEIN KINASES ENCODED IN THE GENOME OF ZEBRAFISH SHOWS REMARKABLY LARGE POPULATION OF PIM KINASES. Journal of Bioinformatics and Computational Biology, 2014, 12, 1350014.	0.8	3
75	DoSA: Database of Structural Alignments. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat048-bat048.	3.0	2
76	Computational Biology and Bioinformatics: A tinge of Indian spice. Bioinformation, 2006, 1, 105-109.	0.5	2
77	Analysis on sliding helices and strands in protein structural comparisons: A case study with protein kinases. Journal of Biosciences, 2007, 32, 921-928.	1.1	0
78	Domain Structure of Hepatocyte Growth Factor/Scatter Factor (HGF/SF). Novartis Foundation Symposium, 1997, 212, 84-104.	1.1	0
79	Influence of Genomic and Other Biological Data Sets in the Understanding of Protein Structures, Functions and Interactions. International Journal of Knowledge Discovery in Bioinformatics, 2011, 2, 24-44.	0.8	0