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	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
2	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
3	Investigations of Ramachandran disallowed conformations in protein domain families. International Journal of Biological Macromolecules, 2014, 63, 119-125.	7.5	14
4	DoSA: Database of Structural Alignments. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat048-bat048.	3.0	2
5	Repertoire of Protein Kinases Encoded in the Genome of<i>Takifugu rubripes</i>. Comparative and Functional Genomics, 2012, 2012, 1-12.	2.0	3
6	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
7	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
8	Improvement of protein structure comparison using a structural alphabet. Biochimie, 2011, 93, 1434-1445.	2.6	37
9	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
10	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
11	Identification and Characterization of a Novel Deoxyhypusine Synthase in Leishmania donovani. Journal of Biological Chemistry, 2010, 285, 453-463.	3.4	47
12	Recognition of Interaction Interface Residues in Low-Resolution Structures of Protein Assemblies Solely from the Positions of CÎ± Atoms. PLoS ONE, 2009, 4, e4476.	2.5	8
13	Classification of Nonenzymatic Homologues of Protein Kinases. Comparative and Functional Genomics, 2009, 2009, 1-17.	2.0	8
14	Conformation of glycyl residues in globular proteins. International Journal of Peptide and Protein Research, 2009, 29, 629-637.	0.1	12
15	A glutathione-specific aldose reductase of Leishmania donovani and its potential implications for methylglyoxal detoxification pathway. Gene, 2009, 429, 1-9.	2.2	13
16	Analysis on conservation of disulphide bonds and their structural features in homologous protein domain families. BMC Structural Biology, 2008, 8, 55.	2.3	37
17	Protein structure mining using a structural alphabet. Proteins: Structure, Function and Bioinformatics, 2008, 71, 920-937.	2.6	52
18	Analysis of the protein kinome of <i>Entamoeba histolytica</i>. Proteins: Structure, Function and Bioinformatics, 2008, 71, 995-1006.	2.6	47

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19	Comparative Kinomics of Plasmodium Organisms: Unity in Diversity. Protein and Peptide Letters, 2007, 14, 509-517.	0.9	21
20	PIC: Protein Interactions Calculator. Nucleic Acids Research, 2007, 35, W473-W476.	14.5	802
21	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
22	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
23	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
24	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
25	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
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	MulPSSM: a database of multiple position-specific scoring matrices of protein domain families. Nucleic Acids Research, 2006, 34, D243-D246.	14.5	29
28	Cascade PSI-BLAST web server: a remote homology search tool for relating protein domains. Nucleic Acids Research, 2006, 34, W143-W146.	14.5	17
29	HARMONY: a server for the assessment of protein structures. Nucleic Acids Research, 2006, 34, W231-W234.	14.5	37
30	Computational Biology and Bioinformatics: A tinge of Indian spice. Bioinformation, 2006, 1, 105-109.	0.5	2
31	Diversity in domain architectures of Ser/Thr kinases and their homologues in prokaryotes. BMC Genomics, 2005, 6, 129.	2.8	65
32	Use of multiple profiles corresponding to a sequence alignment enables effective detection of remote homologues. Bioinformatics, 2005, 21, 2821-2826.	4.1	27
33	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
34	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
35	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
36	KinG: a database of protein kinases in genomes. Nucleic Acids Research, 2004, 32, 153D-155.	14.5	75

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37	SUPFAM: a database of sequence superfamilies of protein domains. BMC Bioinformatics, 2004, 5, 28.	2.6	36
38	A genomic perspective of protein kinases in Plasmodium falciparum. Proteins: Structure, Function and Bioinformatics, 2004, 58, 180-189.	2.6	147
39	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
40	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
41	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
42	Structural basis of regulation and substrate specificity of protein kinase CK2 deduced from the modeling of protein-protein interactions. , 2003, 3, 4.		20
43	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
44	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
45	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
46	Effective detection of remote homologues by searching in sequence dataset of a protein domain fold. FEBS Letters, 2003, 552, 225-230.	2.8	9
47	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
48	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
49	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
50	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
51	The ascent of nucleotide cyclases: conservation and evolution of a theme. Journal of Biosciences, 2002, 27, 85-91.	1.1	8
52	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
53	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
54	PALI--a database of Phylogeny and ALIgnment of homologous protein structures. Nucleic Acids Research, 2001, 29, 61-65.	14.5	88

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55	PALI: a database of alignments and phylogeny of homologous protein structures. Bioinformatics, 2001, 17, 375-376.	4.1	27
56	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
57	The carboxy terminal WD domain of the pre-mRNA splicing factor Prp17p is critical for function. Rna, 2000, 6, 1289-1305.	3.5	9
58	Biochemical Characterization of the Intracellular Domain of the Human Guanylyl Cyclase C Receptor Provides Evidence for a Catalytically Active Homotrimerâ€. Biochemistry, 2000, 39, 16075-16083.	2.5	31
59	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
60	Interactions of protein kinase CK2 subunits. Molecular and Cellular Biochemistry, 1999, 191, 75-83.	3.1	12
61	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
62	CAMPASS: a database of structurally aligned protein superfamilies. Structure, 1998, 6, 1087-1094.	3.3	73
63	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
64	Domain Structure of Hepatocyte Growth Factor/Scatter Factor (HGF/SF). Novartis Foundation Symposium, 1997, 212, 84-104.	1.1	0
65	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
66	Structural aspects of the functional modules in human protein kinase-CÎ± deduced from comparative analyses. , 1996, 26, 217-235.		29
67	Protein three-dimensional structure and molecular recognition: a story of soft locks and keys. Pharmaceutica Acta Helvetiae, 1995, 69, 185-192.	1.2	8
68	Knowledge-Based Protein Modeling. Critical Reviews in Biochemistry and Molecular Biology, 1994, 29, 1-68.	5.2	206
69	Threeâ€dimensional model and quaternary structure of the human eye lens protein Î³Sâ€crystallin based on Î²â€and Î³â€crystallin Xâ€ray coordinates and ultracentrifugation. Protein Science, 1994, 3, 1840-1846.	7.6	29
70	Molecular evolution and domain structure of plasminogenâ€related growth factors (HGF/SF and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	7.6	166
71	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
72	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

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73	Structure of pentameric human serum amyloid P component. Nature, 1994, 367, 338-345.	27.8	471
74	Comparative analyses of pentraxins: implications for protomer assembly and ligand binding. Structure, 1994, 2, 1017-1027.	3.3	96
75	Conformational characteristics of asparaginyl residues in proteins. International Journal of Peptide and Protein Research, 1994, 44, 112-122.	0.1	34
76	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
77	Orthogonal ββ motifs in proteins. Journal of Molecular Biology, 1992, 223, 845-851.	4.2	20
78	Conformations of disulfide bridges in proteins. International Journal of Peptide and Protein Research, 1990, 36, 147-155.	0.1	164
79	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