Petety V Balaji

List of Publications by Year
in descending order

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55 papers	1,377 citations	361413 20 h-index	345221 36 g-index
58 all docs	58 docs citations	58 times ranked	1667 citing authors

#	Article	IF	Citations
1	Understanding the relationship between the primary structure of proteins and its propensity to be soluble on overexpression inEscherichia coli. Protein Science, 2005, 14, 582-592.	7.6	147
2	Crystal Structure of Î²1,4-Galactosyltransferase Complex with UDP-Gal Reveals an Oligosaccharide Acceptor Binding Site. Journal of Molecular Biology, 2002, 318, 491-502.	4.2	116
3	A support vector machine-based method for predicting the propensity of a protein to be soluble or to form inclusion body on overexpression in Escherichia coli. Bioinformatics, 2006, 22, 278-284.	4.1	101
4	Griseofulvin stabilizes microtubule dynamics, activates p53 and inhibits the proliferation of MCF-7 cells synergistically with vinblastine. BMC Cancer, 2010, 10, 213.	2.6	86
5	Energetics of galactose- and glucose-aromatic amino acid interactions: Implications for binding in galactose-specific proteins. Protein Science, 2004, 13, 2502-2514.	7.6	74
6	Identification of common structural features of binding sites in galactose-specific proteins. Proteins: Structure, Function and Bioinformatics, 2004, 55, 44-65.	2.6	74
7	Insights into the Role of the Aromatic Residue in Galactose-Binding Sites:â€‰ MP2/6-311G++** Study on Galactoseâˆ’ and Glucoseâˆ’Aromatic Residue Analogue Complexes. Biochemistry, 2005, 44, 8554-8562.	2.5	73
8	Identification of linkage-specific sequence motifs in sialyltransferases. Glycobiology, 2006, 16, 108-116.	2.5	58
9	Expression of deletion constructs of bovine Î²-1, 4-galactosyltransferase in Escherichia coli: importance of Cysl34 for its activity. Protein Engineering, Design and Selection, 1993, 6, 779-785.	2.1	48
10	Monomerization alters the dynamics of the lid region inCampylobacter jejuniCstII: an MD simulation study. Journal of Biomolecular Structure and Dynamics, 2016, 34, 778-791.	3.5	41
11	C-Hâ€¦pi interactions in proteins: prevalence, pattern of occurrence, residue propensities, location, and contribution to protein stability. Journal of Molecular Modeling, 2014, 20, 2136.	1.8	40
12	Characterization of Symmetric and Asymmetric Lipid Bilayers Composed of Varying Concentrations of Ganglioside GM1 and DPPC. Journal of Physical Chemistry B, 2008, 112, 3346-3356.	2.6	31
13	Molecular dynamics simulations of high-mannose oligosaccharides. Glycobiology, 1994, 4, 497-515.	2.5	30
14	E93R Substitution of Escherichia coli FtsZ Induces Bundling of Protofilaments, Reduces GTPase Activity, and Impairs Bacterial Cytokinesis. Journal of Biological Chemistry, 2010, 285, 31796-31805.	3.4	29
15	Quantification of binding affinities of essential sugars with a tryptophan analogue and the ubiquitous role of Câ€“Hâ‹Ï€ interactions. Physical Chemistry Chemical Physics, 2011, 13, 6517.	2.8	25
16	Understanding the relationship between the primary structure of proteins and their amyloidogenic propensity: clues from inclusion body formation. Protein Engineering, Design and Selection, 2005, 18, 175-180.	2.1	24
17	MP2/6-311++G(d,p) study on galactoseâ€“aromatic residue analog complexes in different position-orientations of the saccharide relative to aromatic residue. Computational and Theoretical Chemistry, 2007, 814, 11-24.	1.5	24
18	Dynamics of Ganglioside Headgroup in Lipid Environment:â€‰ Molecular Dynamics Simulations of GM1 Embedded in Dodecylphosphocholine Micelle. Journal of Physical Chemistry B, 2001, 105, 7033-7041.	2.6	23

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19	Molecular dynamics simulations of oligosaccharides and their conformation in the crystal structure of lectin-carbohydrate complex: importance of the torsion angle Ï^ for the orientation of Î±1,6-arm. Glycobiology, 1994, 4, 805-815.	2.5	22
20	Functional domains of bovine ?-1,4 galactosyltransferase. Glycoconjugate Journal, 1995, 12, 865-878.	2.7	21
21	Characterization of the conformational and orientational dynamics of ganglioside GM1 in a dipalmitoylphosphatidylcholine bilayer by molecular dynamics simulations. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 1628-1640.	2.6	20
22	Exploration of CHâ‹¯Ï€ mediated stacking interactions in saccharide: aromatic residue complexes through conformational sampling. Carbohydrate Research, 2012, 361, 133-140.	2.3	20
23	Molecular dynamics simulations of ?2 ? 8-linked disialoside: Conformational analysis and implications for binding to proteins. Biopolymers, 2002, 63, 168-180.	2.4	18
24	Effect of the Choice of the Pressure Coupling Method on the Spontaneous Aggregation of DPPC Molecules. Journal of Physical Chemistry B, 2005, 109, 14667-14674.	2.6	17
25	Comparative analysis of ganglioside conformations by MD simulations: implications for specific recognition by proteins. Computational and Theoretical Chemistry, 2002, 583, 215-232.	1.5	14
26	Conformational mapping and energetics of saccharideâ€“aromatic residue interactions: implications for the discrimination of anomers and epimers and in protein engineering. Organic and Biomolecular Chemistry, 2012, 10, 4186.	2.8	14
27	Computer simulation of proteinâ€”carbohydrate complexes: application to arabinose-binding protein and pea lectin. Journal of Molecular Structure, 1989, 194, 203-214.	3.6	13
28	Contribution of C-H â€¦ π Interactions to the Affinity and Specificity of Carbohydrate Binding Sites. Mini-Reviews in Organic Chemistry, 2011, 8, 222-228.	1.3	13
29	Size, orientation and organization of oligomers that nucleate amyloid fibrils: Clues from MD simulations of pre-formed aggregates. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 963-973.	2.3	12
30	In vitro characterization of N-terminal truncated EpsC from Bacillus subtilis 168, a UDP-N-acetylglucosamine 4,6-dehydratase. Archives of Biochemistry and Biophysics, 2018, 657, 78-88.	3.0	11
31	Computer Modelling Studies of Ribonuclease A - Pyrimidine Nucleotide Complexes. Journal of Biomolecular Structure and Dynamics, 1993, 11, 395-415.	3.5	10
32	Î²-Hairpins with native-like and non-native hydrogen bonding patterns could form during the refolding of staphylococcal nuclease. Journal of Molecular Graphics and Modelling, 2006, 25, 103-115.	2.4	10
33	Molecular dynamics simulations of hybrid and complex type oligosaccharides. International Journal of Biological Macromolecules, 1996, 18, 101-114.	7.5	9
34	Comparative genomics analysis of completely sequenced microbial genomes reveals the ubiquity of N-linked glycosylation in prokaryotes. Molecular BioSystems, 2011, 7, 1629.	2.9	9
35	Molecular events during the early stages of aggregation of GNNQQNY: An all atom MD simulation study of randomly dispersed peptides. Journal of Structural Biology, 2015, 192, 376-391.	2.8	9
36	EpsN from Bacillus subtilis 168 has UDP-2,6-dideoxy 2-acetamido 4-keto glucose aminotransferase activity in vitro. Glycobiology, 2018, 28, 802-812.	2.5	9

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37	Letter to the Glyco-Forum Controversial iduronate ring conformation in dermatan sulphate. Glycobiology, 1995, 5, 273-276.	2.5	8
38	Conformational analysis of Asn-linked oligosaccharides: implications in biological processes. Computational and Theoretical Chemistry, 1997, 395-396, 333-360.	1.5	8
39	Fold-recognition and comparative modeling of human alpha2,3-sialyltransferases reveal their sequence and structural similarities to CstII from Campylobacter jejuni. , 2006, 6, 9.		8
40	The sequence TGAAKAVALVL from glyceraldehyde-3-phosphate dehydrogenase displays structural ambivalence and interconverts between Î±-helical and Î²-hairpin conformations mediated by collapsed conformational states. Journal of Peptide Science, 2007, 13, 314-326.	1.4	8
41	Computer Modelling Studies on the Mechanism of Action of Ribonuclease T₁. Journal of Biomolecular Structure and Dynamics, 1991, 9, 215-231.	3.5	6
42	Rv3634c from Mycobacterium tuberculosis H37Rv encodes an enzyme with UDP-Gal/Glc and UDP-GalNAc 4-epimerase activities. PLoS ONE, 2017, 12, e0175193.	2.5	6
43	The glycan alphabet is not universal: a hypothesis. Microbial Genomics, 2020, 6, .	2.0	6
44	Length and Composition Analysis of the Cytoplasmic, Transmembrane and Stem Regions of Human Golgi Glycosyltransferases. Protein and Peptide Letters, 2007, 14, 601-609.	0.9	4
45	Structure and Dynamics of Glycosphingolipids in Lipid Bilayers: Insights from Molecular Dynamics Simulations. International Journal of Carbohydrate Chemistry, 2011, 2011, 1-9.	1.5	4
46	Interplay of Sequence, Topology and Termini Charge in Determining the Stability of the Aggregates of GNNQQNY Mutants: A Molecular Dynamics Study. PLoS ONE, 2014, 9, e96660.	2.5	4
47	EpsM from Bacillus subtilis 168 has UDP-2,4,6-trideoxy-2-acetamido-4-amino glucose acetyltransferase activity inÂvitro. Biochemical and Biophysical Research Communications, 2018, 505, 1057-1062.	2.1	4
48	Computer Modeling Studies on the Binding of 2â€²,5â€²-linked Dinucleoside Phosphates to Ribonuclease T₁-Influence of Subsite Interactions on the Substrate Specificity. Journal of Biomolecular Structure and Dynamics, 1993, 10, 891-903.	3.5	3
49	The Cys78â€“Asn88 loop region of the Campylobacter jejuni CstII is essential for Î±2,3-sialyltransferase activity: analysis of the His85 mutants. Journal of Biochemistry, 2014, 156, 229-238.	1.7	3
50	Modes of Binding of 2â€²-AMP to RNase T1A Computer Modeling Study. Journal of Biomolecular Structure and Dynamics, 1992, 9, 959-969.	3.5	2
51	Fold-recognition and comparative modeling of human Î²3GalT I, II, IV, V and VI and Î²3GalNAcT I: Prediction of residues conferring acceptor substrate specificity. Journal of Molecular Graphics and Modelling, 2007, 26, 255-268.	2.4	2
52	Monosaccharide biosynthesis pathways database. Glycobiology, 2021, 31, 1636-1644.	2.5	2
53	Computer Modeling Studies on the Subsite Interactions of Ribonuclease T1. Journal of Biomolecular Structure and Dynamics, 1992, 9, 971-989.	3.5	1
54	Characterization of leftâ€handed beta helixâ€domains, and identification and functional annotation of proteins containing such domains. Proteins: Structure, Function and Bioinformatics, 2021, 89, 6-20.	2.6	1

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55	Clues to reaction specificity in <scp>PLP</scp>â€dependent fold type I aminotransferases of monosaccharide biosynthesis. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1247-1258.	2.6	0