Martha M Teeter

List of Publications by Year
in descending order

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27	1,918	430442	610482
papers	citations	18 h-index	24 g-index

27	27	27	1567
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of a Zn2+-binding site on the dopamine D2 receptor. Biochemical and Biophysical Research Communications, 2006, 339, 873-879.	1.0	26
2	Structural Determinants of Pharmacological Specificity Between D1 and D2 Dopamine Receptors. Molecular Pharmacology, 2006, 69, 185-194.	1.0	31
3	Myoglobin cavities provide interior ligand pathway. Protein Science, 2004, 13, 313-318.	3.1	47
4	Modeling and Mutational Analysis of a Putative Sodium-Binding Pocket on the Dopamine D₂Receptor. Molecular Pharmacology, 2001, 60, 373-381.	1.0	78
5	CoMFA-Based Prediction of Agonist Affinities at Recombinant Wild Type versus Serine to Alanine Point Mutated D2 Dopamine Receptorsâ€. Journal of Medicinal Chemistry, 2000, 43, 3005-3019.	2.9	50
6	Experimental Observation of Bonding Electrons in Proteins. Journal of Biological Chemistry, 1999, 274, 20753-20755.	1.6	19
7	Crystal Structure of Ser-22/Ile-25 Form Crambin Confirms Solvent, Side Chain Substate Correlations. Journal of Biological Chemistry, 1997, 272, 9597-9600.	1.6	32
8	Designed additives for controlled growth of crystals of phospholipid interacting proteins: Short chain phospholipids. Journal of Crystal Growth, 1996, 160, 382-388.	0.7	7
9	Expression, purification and characterization of recombinant crambin. Protein Engineering, Design and Selection, 1996, 9, 1233-1239.	1.0	14
10	Homology Modeling of the Dopamine D2 Receptor and Its Testing by Docking of Agonists and Tricyclic Antagonists. Journal of Medicinal Chemistry, 1994, 37, 2874-2888.	2.9	92
11	Atomic Resolution (0Â·83 Ã…) Crystal Structure of the Hydrophobic Protein Crambin at 130 K. Journal of Molecular Biology, 1993, 230, 292-311.	2.0	131
12	Improvement of turn structure prediction by molecular dynamics: a case study of Î±1-purothionin. Protein Engineering, Design and Selection, 1993, 6, 837-847.	1.0	8
13	Mode of Phospholipid Binding to the Membrane Active Plant Toxin Phoratoxin-A. , 1993, , 263-274.		2
14	Calmodulin binding to Î±1-purothionin: Soloution binding and modeling of the complex. Proteins: Structure, Function and Bioinformatics, 1992, 14, 127-138.	1.5	11
15	Water-Protein Interactions: Theory and Experiment. Annual Review of Biophysics and Biophysical Chemistry, 1991, 20, 577-600.	12.2	238
16	Normal modes of crambin and molecular dynamics for structure prediction. , 1991, , 220-228.		1
17	Crystal structure of a protein-toxin Î±1-purothionin at 2.5Ã… and a comparison with predicted models. Proteins: Structure, Function and Bioinformatics, 1990, 8, 118-132.	1.5	35
18	Crystal Structure of a Protein-Toxin Solved from a Predicted Model. , 1990, , 359-366.		0

#	Article	IF	Citations
19	Mapping the Binding Site of Aflatoxin B1 in DNA: Molecular Modeling of the Binding Sites for the N(7)-Guanine Adduct of Aflatoxin B1 in Different DNA Sequences. Journal of Biomolecular Structure and Dynamics, 1988, 5, 1237-1257.	2.0	22
20	A-DNA Accomodates Adducts Derived from Diol Epoxides of Polycyclic Aromatic Hydrocarbons Bound in a â€œSide-Stackingâ€•Mode. Journal of Biomolecular Structure and Dynamics, 1987, 5, 383-404.	2.0	8
21	Nuclear magnetic resonance study of the solution structure of Î±1-purothionin. Journal of Molecular Biology, 1987, 193, 571-578.	2.0	43
22	Progress in the Water Structure of the Protein Crambin by X-Ray Diffraction at 140 K. Annals of the New York Academy of Sciences, 1986, 482, 163-165.	1.8	17
23	An empirical examination of potential-energy minimization using the well-determined structure of the protein crambin. Journal of the American Chemical Society, 1986, 108, 7163-7172.	6.6	107
24	Raman spectroscopy of homologous plant toxins: crambin and .alpha.1- and .beta.-purothionin secondary structures, disulfide conformation, and tyrosine environment. Biochemistry, 1984, 23, 6796-6802.	1.2	30
25	Primary structure of the hydrophobic plant protein crambin. Biochemistry, 1981, 20, 5437-5443.	1.2	111
26	Structure of the hydrophobic protein crambin determined directly from the anomalous scattering of sulphur. Nature, 1981, 290, 107-113.	13.7	695
27	Highly ordered crystals of the plant seed protein crambin. Journal of Molecular Biology, 1979, 127, 219-223.	2.0	63