List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Differential Targeting of Prosurvival Bcl-2 Proteins by Their BH3-Only Ligands Allows Complementary Apoptotic Function. Molecular Cell, 2005, 17, 393-403.	4.5	1,639
2	The B30.2 domain of pyrin, the familial Mediterranean fever protein, interacts directly with caspase-1 to modulate IL-1beta production. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9982-9987.	3.3	502
3	Bax Crystal Structures Reveal How BH3 Domains Activate Bax and Nucleate Its Oligomerization to Induce Apoptosis. Cell, 2013, 152, 519-531.	13.5	491
4	A newly discovered protein export machine in malaria parasites. Nature, 2009, 459, 945-949.	13.7	437
5	Structural insights into the degradation of Mcl-1 induced by BH3 domains. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6217-6222.	3.3	397
6	How insulin engages its primary binding site on the insulin receptor. Nature, 2013, 493, 241-245.	13.7	364
7	Structure-guided design of a selective BCL-XL inhibitor. Nature Chemical Biology, 2013, 9, 390-397.	3.9	324
8	Assigning absolute values to proton affinities: a differentiation between competing scales. Journal of the American Chemical Society, 1993, 115, 4885-4888.	6.6	244
9	Discovery of a Potent and Selective BCL-X _L Inhibitor with <i>in Vivo</i> Activity. ACS Medicinal Chemistry Letters, 2014, 5, 1088-1093.	1.3	242
10	Crystal structure of ABT-737 complexed with Bcl-xL: implications for selectivity of antagonists of the Bcl-2 family. Cell Death and Differentiation, 2007, 14, 1711-1713.	5.0	235
11	Transition structures for the interchange of hydrogen atoms within the water dimer. Journal of Chemical Physics, 1990, 92, 1240-1247.	1.2	230
12	Gaussianâ€2 (G2) theory: Reduced basis set requirements. Journal of Chemical Physics, 1996, 104, 5148-5152.	1.2	216
13	The Structure of the Fusion Glycoprotein of Newcastle Disease Virus Suggests a Novel Paradigm for the Molecular Mechanism of Membrane Fusion. Structure, 2001, 9, 255-266.	1.6	201
14	Calculation of Proton Affinities Using the G2(MP2,SVP) Procedure. The Journal of Physical Chemistry, 1995, 99, 6468-6471.	2.9	179
15	Transferrin receptor 1 is a reticulocyte-specific receptor for <i>Plasmodium vivax</i> . Science, 2018, 359, 48-55.	6.0	158
16	Conformational switching of the pseudokinase domain promotes human MLKL tetramerization and cell death by necroptosis. Nature Communications, 2018, 9, 2422.	5.8	154
17	Evaluation of Diverse α/β-Backbone Patterns for Functional α-Helix Mimicry: Analogues of the Bim BH3 Domain. Journal of the American Chemical Society, 2012, 134, 315-323.	6.6	144
18	Highâ€Resolution Structural Characterization of a Helical α/βâ€Peptide Foldamer Bound to the Antiâ€Apoptotic Protein Bclâ€x _L . Angewandte Chemie - International Edition, 2009, 48, 4318-4322.	7.2	143

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19	Protective hinge in insulin opens to enable its receptor engagement. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3395-404.	3.3	142
20	Domain Reorientation and Rotation of an Intracellular Assembly Regulate Conduction in Kir Potassium Channels. Cell, 2010, 141, 1018-1029.	13.5	141
21	An evaluation of the performance of density functional theory, MP2, MP4, F4, G2(MP2) and G2 procedures in predicting gas-phase proton affinities. Chemical Physics Letters, 1994, 231, 345-351.	1.2	133
22	Structure/Function Characterization of μ-Conotoxin KIIIA, an Analgesic, Nearly Irreversible Blocker of Mammalian Neuronal Sodium Channels. Journal of Biological Chemistry, 2007, 282, 30699-30706.	1.6	132
23	Higher-Resolution Structure of the Human Insulin Receptor Ectodomain: Multi-Modal Inclusion of the Insert Domain. Structure, 2016, 24, 469-476.	1.6	129
24	Engineering a Stable and Selective Peptide Blocker of the Kv1.3 Channel in T Lymphocytes. Molecular Pharmacology, 2009, 75, 762-773.	1.0	128
25	Structural Studies of the Resistance of Influenza Virus Neuramindase to Inhibitors. Journal of Medicinal Chemistry, 2002, 45, 2207-2212.	2.9	125
26	Stabilizing the Pro-Apoptotic BimBH3 Helix (BimSAHB) Does Not Necessarily Enhance Affinity or Biological Activity. ACS Chemical Biology, 2013, 8, 297-302.	1.6	123
27	Unimolecular rearrangements connecting hydroxyethylidene (CH3-C-OH), acetaldehyde (CH3-CH:O), and vinyl alcohol (CH2:CH-OH). Journal of the American Chemical Society, 1991, 113, 6452-6458.	6.6	121
28	Inhibition of Plasmepsin V Activity Demonstrates Its Essential Role in Protein Export, PfEMP1 Display, and Survival of Malaria Parasites. PLoS Biology, 2014, 12, e1001897.	2.6	121
29	Novel Conotoxins fromConus striatusandConus kinoshitaiSelectively Block TTX-Resistant Sodium Channelsâ€. Biochemistry, 2005, 44, 7259-7265.	1.2	112
30	Apoptotic pore formation is associated with in-plane insertion of Bak or Bax central helices into the mitochondrial outer membrane. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4076-85.	3.3	111
31	A Malaria Parasite Formin Regulates Actin Polymerization and Localizes to the Parasite-Erythrocyte Moving Junction during Invasion. Cell Host and Microbe, 2008, 3, 188-198.	5.1	105
32	Structure and mechanism of a sub-family of enzymes related to N -acetylneuraminate lyase 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1997, 266, 381-399.	2.0	103
33	α/β-Peptide Foldamers Targeting Intracellular Protein–Protein Interactions with Activity in Living Cells. Journal of the American Chemical Society, 2015, 137, 11365-11375.	6.6	101
34	An aspartyl protease defines a novel pathway for export of Toxoplasma proteins into the host cell. ELife, 2015, 4, .	2.8	99
35	Analysis of inhibitor binding in influenza virus neuraminidase. Protein Science, 2001, 10, 689-696.	3.1	97
36	Structural resolution of a tandem hormone-binding element in the insulin receptor and its implications for design of peptide agonists. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6771-6776.	3.3	97

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37	Structural basis for plasmepsin V inhibition that blocks export of malaria proteins to human erythrocytes. Nature Structural and Molecular Biology, 2015, 22, 590-596.	3.6	93
38	High-Level ab Initio Molecular Orbital Calculations of Imine Formation. Journal of Physical Chemistry A, 1998, 102, 4930-4938.	1.1	90
39	Structural Basis for Broad Substrate Specificity in Higher Plant β-d-Glucan Glucohydrolases. Plant Cell, 2002, 14, 1033-1052.	3.1	89
40	Entropies and Free Energies of Protonation and Proton-Transfer Reactions. Journal of the American Chemical Society, 1997, 119, 9014-9020.	6.6	86
41	Quantitative in vivo Analyses Reveal Calcium-dependent Phosphorylation Sites and Identifies a Novel Component of the Toxoplasma Invasion Motor Complex. PLoS Pathogens, 2011, 7, e1002222.	2.1	85
42	Conformational Changes in Bcl-2 Pro-survival Proteins Determine Their Capacity to Bind Ligands. Journal of Biological Chemistry, 2009, 284, 30508-30517.	1.6	79
43	Active site modulation in the N-acetylneuraminate lyase sub-family as revealed by the structure of the inhibitor-complexed Haemophilus influenzae enzyme. Journal of Molecular Biology, 2000, 303, 405-421.	2.0	77
44	Gas-phase acidities: a comparison of density functional, MP2, MP4, F4, G2(MP2, SVP), G2(MP2) and G2 procedures. Chemical Physics Letters, 1995, 245, 123-128.	1.2	74
45	Catalytic Mechanisms and Reaction Intermediates along the Hydrolytic Pathway of a Plant β-D-glucan Glucohydrolase. Structure, 2001, 9, 1005-1016.	1.6	73
46	The SPRY domain of SSB-2 adopts a novel fold that presents conserved Par-4–binding residues. Nature Structural and Molecular Biology, 2006, 13, 77-84.	3.6	72
47	A minimized human insulin-receptor-binding motif revealed in a Conus geographus venom insulin. Nature Structural and Molecular Biology, 2016, 23, 916-920.	3.6	70
48	Conotoxins Containing Nonnatural Backbone Spacers: Cladistic-Based Design, Chemical Synthesis, and Improved Analgesic Activity. Chemistry and Biology, 2007, 14, 399-407.	6.2	69
49	Structure of the Analgesic μ-Conotoxin KIIIA and Effects on the Structure and Function of Disulfide Deletion. Biochemistry, 2009, 48, 1210-1219.	1.2	69
50	Rearrangement and dissociative reactions of the methanol radical cation (CH3OH.bul.+): a comparison of theory and experiment. Journal of the American Chemical Society, 1991, 113, 7903-7912.	6.6	68
51	Ethynol: a theoretical prediction of remarkably high gas-phase acidity. Journal of the American Chemical Society, 1989, 111, 8297-8299.	6.6	66
52	Evaluation of accurate gas-phase acidities. The Journal of Physical Chemistry, 1991, 95, 10549-10551.	2.9	66
53	Structureâ€Guided Rational Design of α/βâ€Peptide Foldamers with High Affinity for BCLâ€2 Family Prosurvival Proteins. ChemBioChem, 2013, 14, 1564-1572.	1.3	65
54	Harmonic force field, molecular structure, torsional potential, and possible isomerism of hydrogen sulfide (H2S2). The Journal of Physical Chemistry, 1988, 92, 347-353.	2.9	64

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55	New Theoretical and Experimental Proton Affinities for Methyl Halides and Diazomethane: A Revision of the Methyl Cation Affinity Scale. The Journal of Physical Chemistry, 1994, 98, 13099-13101.	2.9	63
56	Quinazoline Sulfonamides as Dual Binders of the Proteins B-Cell Lymphoma 2 and B-Cell Lymphoma Extra Long with Potent Proapoptotic Cell-Based Activity. Journal of Medicinal Chemistry, 2011, 54, 1914-1926.	2.9	62
57	Structural and Functional Diversities among μ-Conotoxins Targeting TTX-resistant Sodium Channels. Biochemistry, 2006, 45, 3723-3732.	1.2	61
58	Modulation of voltage-gated K ⁺ channels by the sodium channel β1 subunit. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18577-18582.	3.3	61
59	Heats of Formation of Alkali and Alkaline Earth Oxides and Hydroxides:Â Some Dramatic Failures of the G2 Method. Journal of Physical Chemistry A, 1999, 103, 7522-7527.	1.1	58
60	Properties of GDP-mannose Pyrophosphorylase, a Critical Enzyme and Drug Target in Leishmania mexicana. Journal of Biological Chemistry, 2004, 279, 12462-12468.	1.6	58
61	Polymorphisms in Erythrocyte Binding Antigens 140 and 181 Affect Function and Binding but Not Receptor Specificity in <i>Plasmodium falciparum</i> . Infection and Immunity, 2009, 77, 1689-1699.	1.0	57
62	Conversion of Bim-BH3 from Activator to Inhibitor of Bak through Structure-Based Design. Molecular Cell, 2017, 68, 659-672.e9.	4.5	57
63	Structural Basis of Bclâ€x _L Recognition by a BH3â€Mimetic α/βâ€Peptide Generated by Sequenceâ€Based Design. ChemBioChem, 2011, 12, 2025-2032.	1.3	56
64	Membrane Core-Specific Antimicrobial Action of Cathelicidin LL-37 Peptide Switches Between Pore and Nanofibre Formation. Scientific Reports, 2016, 6, 38184.	1.6	56
65	The D-Diastereomer of ShK Toxin Selectively Blocks Voltage-gated K+ Channels and Inhibits T Lymphocyte Proliferation. Journal of Biological Chemistry, 2008, 283, 988-997.	1.6	54
66	Crystal structure of PfRh5, an essential P. falciparum ligand for invasion of human erythrocytes. ELife, 2014, 3, .	2.8	53
67	Bak apoptotic pores involve a flexible C-terminal region and juxtaposition of the C-terminal transmembrane domains. Cell Death and Differentiation, 2015, 22, 1665-1675.	5.0	51
68	A Conformational Study of 2-Oxanol:Â Insight into the Role of Ring Distortion on Enzyme-Catalyzed Glycosidic Bond Cleavage. Journal of the American Chemical Society, 1997, 119, 2699-2706.	6.6	50
69	Insight into the self-association of key enzymes from pathogenic species. European Biophysics Journal, 2005, 34, 469-476.	1.2	50
70	Identification of an activation site in Bak and mitochondrial Bax triggered by antibodies. Nature Communications, 2016, 7, 11734.	5.8	50
71	Two Essential Light Chains Regulate the MyoA Lever Arm To Promote <i>Toxoplasma</i> Gliding Motility. MBio, 2015, 6, e00845-15.	1.8	49
72	BAK core dimers bind lipids and can be bridged by them. Nature Structural and Molecular Biology, 2020, 27, 1024-1031	3.6	49

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73	Fish-hunting cone snail venoms are a rich source of minimized ligands of the vertebrate insulin receptor. ELife, 2019, 8, .	2.8	49
74	The ammonia dimer potential energy surface: resolution of the apparent discrepancy between theory and experiment?. Chemical Physics Letters, 1991, 183, 449-456.	1.2	48
75	Lactam-Stabilized Helical Analogues of the Analgesic μ-Conotoxin KIIIA. Journal of Medicinal Chemistry, 2011, 54, 7558-7566.	2.9	48
76	Characterization of the bifurcated structure of the water dimer. Journal of Chemical Physics, 1991, 95, 1825-1828.	1.2	46
77	Transition State Mimetics of the <i>Plasmodium</i> Export Element Are Potent Inhibitors of Plasmepsin V from <i>P. falciparum</i> and <i>P. vivax</i> . Journal of Medicinal Chemistry, 2014, 57, 7644-7662.	2.9	46
78	Solvation Effects on Zwitterion Formation. Journal of Physical Chemistry A, 1998, 102, 3985-3990.	1.1	45
79	Ethynamine: the remarkable acid-strengthening and base-weakening effect of the acetylenic linkage. A comparison with ethenamine and methylamine. Journal of the American Chemical Society, 1992, 114, 36-41.	6.6	44
80	G2(MP2,SVP) study of the relationship between the benzyl and tropyl radicals, and their cation analogues. Chemical Physics Letters, 1997, 279, 165-171.	1.2	44
81	Diverse Reactions of PhI(OTf) ₂ with Common 2-Electron Ligands: Complex Formation, Oxidation, and Oxidative Coupling. Inorganic Chemistry, 2012, 51, 13034-13040.	1.9	44
82	The energy difference between formaldehyde and hydroxymethylene radical cations: failure of unrestricted (UMP2) and restricted (RMP2) MÃ,ller—Plesset procedures. Chemical Physics Letters, 1992, 193, 386-394.	1.2	43
83	A Common Cross-species Function for the Double Epidermal Growth Factor-like Modules of the Highly Divergent Plasmodium Surface Proteins MSP-1 and MSP-8. Journal of Biological Chemistry, 2004, 279, 20147-20153.	1.6	43
84	Calculation of aqueous dissociation constants of 1,2,4-triazole and tetrazole: A comparison of solvation models. Physical Chemistry Chemical Physics, 2002, 4, 4314-4318.	1.3	42
85	Differences in the determinants of eplerenone, spironolactone and aldosterone binding to the mineralocorticoid receptor*. Clinical and Experimental Pharmacology and Physiology, 2004, 31, 704-709.	0.9	42
86	Structural Rationale for Low-Nanomolar Binding of Transition State Mimics to a Family GH3 β-d-Glucan Glucohydrolase from Barleyâ€,‡. Biochemistry, 2005, 44, 16529-16539.	1.2	42
87	Cortisol resistance in the New World revisited. Trends in Endocrinology and Metabolism, 2004, 15, 296-299.	3.1	40
88	Physiological restraint of Bak by Bcl-x _L is essential for cell survival. Genes and Development, 2016, 30, 1240-1250.	2.7	40
89	Structure of Leishmania mexicana Phosphomannomutase Highlights Similarities with Human Isoforms. Journal of Molecular Biology, 2006, 363, 215-227.	2.0	38
90	Ipratropium bromide versus long-acting beta-2 agonists for stable chronic obstructive pulmonary disease. The Cochrane Library, 2006, , CD006101.	1.5	38

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91	Domain structure and function of matrix metalloprotease 23 (MMP23): role in potassium channel trafficking. Cellular and Molecular Life Sciences, 2014, 71, 1191-1210.	2.4	38
92	Structural insights into BCL2 pro-survival protein interactions with the key autophagy regulator BECN1 following phosphorylation by STK4/MST1. Autophagy, 2019, 15, 785-795.	4.3	38
93	The Heat of Formation of Formaldimine. Australian Journal of Chemistry, 1992, 45, 285.	0.5	38
94	A Critical Region in the Mineralocorticoid Receptor for Aldosterone Binding and Activation by Cortisol: Evidence for a Common Mechanism Governing Ligand Binding Specificity in Steroid Hormone Receptors. Molecular Endocrinology, 2007, 21, 817-828.	3.7	37
95	Structure-Guided Rescaffolding of Selective Antagonists of BCL-X _L . ACS Medicinal Chemistry Letters, 2014, 5, 662-667.	1.3	37
96	Structure of a calcium-deficient form of influenza virus neuraminidase: implications for substrate binding. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 947-952.	2.5	36
97	Analysis of structure and function of the giant protein Pf332 in <i>Plasmodium falciparum</i> . Molecular Microbiology, 2009, 71, 48-65.	1.2	36
98	Psychological therapies for the treatment of anxiety disorders in chronic obstructive pulmonary disease. The Cochrane Library, 2017, 2017, CD010673.	1.5	36
99	A structurally minimized yet fully active insulin based on cone-snail venom insulin principles. Nature Structural and Molecular Biology, 2020, 27, 615-624.	3.6	36
100	Hexalithiobenzene: beauty is in the eye of the beholder. Chemical Physics Letters, 1993, 207, 403-406.	1.2	35
101	Three-dimensional Structure of the Barley β-d-Glucan Glucohydrolase in Complex with a Transition State Mimic. Journal of Biological Chemistry, 2004, 279, 4970-4980.	1.6	35
102	Structural Insights into the Protease-like Antigen Plasmodium falciparum SERA5 and Its Noncanonical Active-Site Serine. Journal of Molecular Biology, 2009, 392, 154-165.	2.0	35
103	Determinants of spironolactone binding specificity in the mineralocorticoid receptor. Journal of Molecular Endocrinology, 2003, 31, 573-582.	1.1	34
104	Insights into Duffy Binding-like Domains through the Crystal Structure and Function of the Merozoite Surface Protein MSPDBL2 from Plasmodium falciparum. Journal of Biological Chemistry, 2012, 287, 32922-32939.	1.6	34
105	Molecular evolution of the switch for progesterone and spironolactone from mineralocorticoid receptor agonist to antagonist. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18578-18583.	3.3	34
106	Quality of Life in Asthma: A Comparison of Community and Hospital Asthma Patients. Journal of Asthma, 2001, 38, 205-214.	0.9	33
107	De-Novo Designed Library of Benzoylureas as Inhibitors of BCL-X _L : Synthesis, Structural and Biochemical Characterization. Journal of Medicinal Chemistry, 2014, 57, 1323-1343.	2.9	33
108	Solution Structure of Ectodomains of the Insulin Receptor Family: The Ectodomain of the Type 1 Insulin-Like Growth Factor Receptor Displays Asymmetry of Ligand Binding Accompanied by Limited Conformational Change. Journal of Molecular Biology, 2009, 394, 878-892.	2.0	32

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109	Insulin Mimetic Peptide Disrupts the Primary Binding Site of the Insulin Receptor. Journal of Biological Chemistry, 2016, 291, 15473-15481.	1.6	31
110	BCL-2 family protein BOK is a positive regulator of uridine metabolism in mammals. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15469-15474.	3.3	31
111	Refined calculations of the structures and stabilities of the formyl (HCO+) and isoformyl (COH+) cations. Chemical Physics Letters, 1992, 197, 573-580.	1.2	29
112	Heat of Formation of thetert-Butyl Radical. Journal of Physical Chemistry A, 1998, 102, 10787-10790.	1.1	28
113	Modelling the structure of the fusion protein from human respiratory syncytial virus. Protein Engineering, Design and Selection, 2002, 15, 365-371.	1.0	28
114	Structure of glyceraldehyde-3-phosphate dehydrogenase fromPlasmodium falciparum. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1213-1221.	2.5	28
115	Spiroleucettadine: synthetic studies and investigations towards structural revision. Tetrahedron Letters, 2007, 48, 2199-2203.	0.7	28
116	The vinylidene-acetylene rearrangement. A phantom minimum on the MP2 potential energy surface. Chemical Physics Letters, 1992, 188, 589-594.	1.2	27
117	Refined thermochemistry for the methanol radical cation (CH3OH.cntdot.+) and its distonic isomer (CH2OH2.cntdot.+). The Journal of Physical Chemistry, 1992, 96, 5804-5807.	2.9	26
118	Further Insights into the Effects of Pre-organizing the BimBH3 Helix. ACS Chemical Biology, 2014, 9, 838-839.	1.6	26
119	Nâ€ŧerminally extended analogues of the K ⁺ channel toxin from <i>StichodactylaÂhelianthus</i> as potent and selective blockers of the voltageâ€gated potassium channel Kv1.3. FEBS Journal, 2015, 282, 2247-2259.	2.2	26
120	Characterization of the Two Fundamental Conformations of Benzoylureas and Elucidation of the Factors That Facilitate Their Conformational Interchange. Journal of Organic Chemistry, 2009, 74, 6511-6525.	1.7	25
121	Crystal Structure of a BCL-W Domain-Swapped Dimer: Implications for the Function of BCL-2 Family Proteins. Structure, 2011, 19, 1467-1476.	1.6	25
122	Intracellular Trafficking of the KV1.3 Potassium Channel Is Regulated by the Prodomain of a Matrix Metalloprotease. Journal of Biological Chemistry, 2013, 288, 6451-6464.	1.6	25
123	Aromatic Anchor at an Invariant Hormone-Receptor Interface. Journal of Biological Chemistry, 2014, 289, 34709-34727.	1.6	25
124	Extending Halogen-based Medicinal Chemistry to Proteins. Journal of Biological Chemistry, 2016, 291, 27023-27041.	1.6	25
125	Atomic radii: Incorporation of solvation effects. Journal of Computational Chemistry, 1998, 19, 1482-1493.	1.5	24
126	Substrate-Assisted Catalysis in Sialic Acid Aldolase. Journal of Organic Chemistry, 1999, 64, 945-949.	1.7	24

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127	Bronchoscopic lung volume reduction procedures for chronic obstructive pulmonary disease. The Cochrane Library, 2017, 2, CD012158.	1.5	24
128	Asthma, Inhaled Corticosteroid Use, and Bone Mass in Prepubertal Children. Journal of Asthma, 2000, 37, 603-611.	0.9	23
129	Ab initio molecular orbital calculations on sulphur compounds. Computational and Theoretical Chemistry, 1983, 105, 385-392.	1.5	22
130	Isomers and transition structures of diazene. The Journal of Physical Chemistry, 1993, 97, 10513-10514.	2.9	22
131	Structure of vinyl alcohol: a resolution of the discrepancy between theory and experiment. Journal of the American Chemical Society, 1990, 112, 7525-7528.	6.6	21
132	Crystal structure and immunological properties of the first annexin from <i>SchistosomaÂmansoni</i> : insights into the structural integrity of the schistosomal tegument. FEBS Journal, 2014, 281, 1209-1225.	2.2	21
133	Solvation parameters for amino acids. Journal of Computational Chemistry, 1999, 20, 428-442.	1.5	20
134	Development of recombinant protein-based influenza vaccine. Journal of Chromatography A, 2006, 1136, 48-56.	1.8	20
135	Neutralization-reionization and ab initio study of the CH2î—»CHSOH â‡,, CH3CHî—»Sî—»O rearrangement. International Journal of Mass Spectrometry and Ion Processes, 1990, 101, 283-300.	1.9	19
136	Potential energy surfaces describing ion complexes containing molecular hydrogen. Journal of Chemical Physics, 1992, 97, 1191-1210.	1.2	19
137	Catalytic mechanism and cofactor preference of dihydrodipicolinate reductase from methicillin-resistant Staphylococcus aureus. Archives of Biochemistry and Biophysics, 2011, 512, 167-174.	1.4	19
138	Short-acting bronchodilators for the management of acute exacerbations of chronic obstructive pulmonary disease in the hospital setting: systematic review. Systematic Reviews, 2018, 7, 213.	2.5	19
139	An ab initio study of many isomers of S2O2. A combined theoretical and experimental analysis of the harmonic force field and molecular structure of cis-planar OSSO. Chemical Physics, 1990, 141, 335-353.	0.9	18
140	Theoretical and experimental structures of vinyl fluoride and vinyl alcohol. Journal of Chemical Physics, 1992, 97, 6113-6120.	1.2	18
141	From Cyclohexane to 2-Hydroxy-3-oxanone:Â A Conformation Study. Journal of Physical Chemistry A, 1998, 102, 3756-3761.	1.1	18
142	Structural analysis of phosphorylationâ€associated interactions of human MCC with Scribble PDZ domains. FEBS Journal, 2019, 286, 4910-4925.	2.2	18
143	Predicting aqueous solubility by QSPR modeling. Journal of Molecular Graphics and Modelling, 2021, 106, 107901.	1.3	18
144	Industry, air quality, cigarette smoke and rates of respiratory illness in Port Adelaide. Australian and New Zealand Journal of Public Health, 1999, 23, 657-660.	0.8	17

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145	Cochrane Review: Mass media interventions for preventing smoking in young people. Evidence-Based Child Health: A Cochrane Review Journal, 2012, 7, 86-144.	2.0	17
146	Interaction of Small Ionic Species With Phospholipid Membranes: The Role of Metal Coordination. Frontiers in Materials, 2019, 5, .	1.2	17
147	The cyclization of N-butylpent-4-enylaminyl revisited: a combined theoretical and experimental study â€. Perkin Transactions II RSC, 2000, , 425-431.	1.1	16
148	Leishmania major CorA-like magnesium transporters play a critical role in parasite development and virulence. International Journal for Parasitology, 2009, 39, 713-723.	1.3	16
149	The effect of N-methylation on transition state mimetic inhibitors of the <i>Plasmodium</i> protease, plasmepsin V. MedChemComm, 2015, 6, 437-443.	3.5	16
150	Predicting the Enthalpy and Gibbs Energy of Sublimation by QSPR Modeling. Scientific Reports, 2018, 8, 9779.	1.6	15
151	Theoretical and experimental structures of vinyl chloride and vinyl bromide. Journal of Chemical Physics, 1993, 98, 3952-3959.	1.2	14
152	Structure–Activity Relationship Study Reveals the Molecular Basis for Specific Sensing of Hydrophobic Amino Acids by the Campylobacter jejuni Chemoreceptor Tlp3. Biomolecules, 2020, 10, 744.	1.8	14
153	A constricted opening in Kir channels does not impede potassium conduction. Nature Communications, 2020, 11, 3024.	5.8	14
154	Ionized methyl formate (CH3OCHO.ovrhdot.+) and its distonic isomer (.ovrhdot.CH2OC+HOH). Journal of the American Chemical Society, 1992, 114, 1151-1156.	6.6	13
155	The Role of Virtual Screening in Computer Aided Structure-Based Drug Design. Australian Journal of Chemistry, 2004, 57, 1029.	0.5	13
156	Structure-guided design of a novel class of benzyl-sulfonate inhibitors for influenza virus neuraminidase. Biochemical Journal, 2006, 399, 215-223.	1.7	13
157	Consequences of Two Different Amino-Acid Substitutions at the Same Codon in KRT14 Indicate Definitive Roles of Structural Distortion in Epidermolysis Bullosa Simplex Pathogenesis. Journal of Investigative Dermatology, 2011, 131, 1869-1876.	0.3	13
158	Truncated Latrunculins as Actin Inhibitors Targeting <i>Plasmodium falciparum</i> Motility and Host Cell Invasion. Journal of Medicinal Chemistry, 2016, 59, 10994-11005.	2.9	13
159	Heat of formation for the hydroxymethylene radical cation: the importance of reverse activation energy. The Journal of Physical Chemistry, 1989, 93, 7759-7760.	2.9	12
160	Solution structure of an ultra-stable single-chain insulin analog connects protein dynamics to a novel mechanism of receptor binding. Journal of Biological Chemistry, 2018, 293, 69-88.	1.6	12
161	Two-year efficacy of varenicline tartrate and counselling for inpatient smoking cessation (STOP) Tj ETQq1 1 0.7	84314 rgE 1.1	BT /Qverlock 1
162	Conformational preferences ofXONO2 systems (X = H, F, Cl, CH3) fromab initio techniques. Journal of Computational Chemistry, 1991, 12, 565-574.	1.5	11

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163	Calculation of aqueous proton dissociation constants of quinoline and hydroxyquinolines: A comparison of solvation models. Physical Chemistry Chemical Physics, 2000, 2, 5383-5388.	1.3	11
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