# Glen E Kellogg

List of Publications by Year
in descending order

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Version: 2024-02-01

| | | 81743 | 110170 |
|---|---|---|---|
| 114 | 4,709 | 39 | 64 |
| papers | citations | h-index | g-index |

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|---|---|---|---|
| 115 | 115 | 115 | 4915 |
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | 3D Interaction Homology: Hydropathic Analyses of the â€œÏ€â€“Cationâ€•and â€œÏ€â€“Ï€â€•Interaction Motifs in Phenylalanine, Tyrosine, and Tryptophan Residues. Journal of Chemical Information and Modeling, 2021, 61, 2937-2956. | 2.5 | 11 |
| 2 | Structural understanding of 5-(4-hydroxy-phenyl)-N-(2-(5-methoxy-1H-indol-3-yl)-ethyl)-3-oxopentanamide as a neuroprotectant for Alzheimerâ€™s disease. Bioorganic and Medicinal Chemistry Letters, 2021, 43, 128081. | 1.0 | 1 |
| 3 | FOSL1 promotes metastasis of head and neck squamous cell carcinoma through super-enhancer-driven transcription program. Molecular Therapy, 2021, 29, 2583-2600. | 3.7 | 39 |
| 4 | 3D interaction homology: Hydropathic interaction environments of serine and cysteine are strikingly different and their roles adapt in membrane proteins. Current Research in Structural Biology, 2021, 3, 239-256. | 1.1 | 10 |
| 5 | 3D Interaction Homology: Computational Titration of Aspartic Acid, Glutamic Acid and Histidine Can Create pH-Tunable Hydropathic Environment Maps. Frontiers in Molecular Biosciences, 2021, 8, 773385. | 1.6 | 4 |
| 6 | Systematized Analysis of Secondary Structure Dependence of Key Structural Features of Residues in Soluble and Membrane-Bound Proteins. Journal of Structural Biology: X, 2021, 5, 100055. | 0.7 | 1 |
| 7 | Synthesis of novel 5-substituted-2-aminotetralin analogs: 5-HT1A and 5-HT7 G protein-coupled receptor affinity, 3D-QSAR and molecular modeling. Bioorganic and Medicinal Chemistry, 2020, 28, 115262. | 1.4 | 14 |
| 8 | 3D interaction homology: The hydropathic interaction environments of even alanine are diverse and provide novel structural insight. Journal of Structural Biology, 2019, 207, 183-198. | 1.3 | 8 |
| 9 | Functional diversification of the chemical landscapes of yeast Sec14-like phosphatidylinositol transfer protein lipid-binding cavities. Journal of Biological Chemistry, 2019, 294, 19081-19098. | 1.6 | 17 |
| 10 | Inhibiting Pneumococcal Surface Antigen A (PsaA) with Small Molecules Discovered through Virtual Screening: Steps toward Validating a Potential Target forStreptococcus pneumoniae. Chemistry and Biodiversity, 2018, 15, e1800234. | 1.0 | 8 |
| 11 | Exploring the binding mechanisms of diaminopimelic acid analogs to meso-diaminopimelate dehydrogenase by molecular modeling. Journal of Molecular Graphics and Modelling, 2018, 83, 100-111. | 1.3 | 3 |
| 12 | Ortho group activation of a bromopyrrole ester in Suzuki-Miyaura cross-coupling reactions: Application to the synthesis of new microtubule depolymerizing agents with potent cytotoxic activities. Bioorganic and Medicinal Chemistry, 2017, 25, 3206-3214. | 1.4 | 4 |
| 13 | The Roles of Water in the Protein Matrix: A Largely Untapped Resource for Drug Discovery. Journal of Medicinal Chemistry, 2017, 60, 6781-6827. | 2.9 | 111 |
| 14 | Diaminopimelic acid (DAP) analogs bearing isoxazoline moiety as selective inhibitors against meso-diaminopimelate dehydrogenase (m-Ddh) from Porphyromonas gingivalis. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 3840-3844. | 1.0 | 6 |
| 15 | Design, synthesis, and biological evaluation of substrate-competitive inhibitors of C-terminal Binding Protein (CtBP). Bioorganic and Medicinal Chemistry, 2016, 24, 2707-2715. | 1.4 | 21 |
| 16 | Crystal structure of carbonmonoxy sickle hemoglobin in R-state conformation. Journal of Structural Biology, 2016, 194, 446-450. | 1.3 | 30 |
| 17 | Biological Characterization of an Improved Pyrrole-Based Colchicine Site Agent Identified through Structure-Based Design. Molecular Pharmacology, 2016, 89, 287-296. | 1.0 | 9 |
| 18 | 3d interaction homology: The structurally known rotamers of tyrosine derive from a surprisingly limited set of information-rich hydropathic interaction environments described by maps. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1118-1136. | 1.5 | 10 |

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|---|---|---|---|
| 19 | Understanding Water and Its Many Roles in Biological Structure: Ways to Exploit a Resource for Drug Discovery. Methods in Pharmacology and Toxicology, 2015, , 85-110. | 0.1 | 0 |
| 20 | Molecular basis of E. coli l-threonine aldolase catalytic inactivation at low pH. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 278-283. | 1.1 | 7 |
| 21 | Anti-cytomegalovirus activity of the anthraquinone atanyl blue PRL. Antiviral Research, 2015, 114, 86-95. | 1.9 | 17 |
| 22 | Design, syntheses, and pharmacological characterization of 17-cyclopropylmethyl-3,14Î²-dihydroxy-4,5Î±-epoxy-6Î±-(isoquinoline-3â€²-carboxamido)morphinan analogues as opioid receptor ligands. Bioorganic and Medicinal Chemistry, 2015, 23, 1701-1715. | 1.4 | 19 |
| 23 | Identification of Small-Molecule Inhibitors against Meso-2, 6-Diaminopimelate Dehydrogenase from Porphyromonas gingivalis. PLoS ONE, 2015, 10, e0141126. | 1.1 | 13 |
| 24 | Formyl group activation of a bromopyrrole ester in Suzuki cross-coupling reactions: application to a formal synthesis of Polycitone AÂand B and Polycitrin A. Tetrahedron, 2014, 70, 2738-2745. | 1.0 | 4 |
| 25 | Intuitive, but not simple: Including explicit water molecules in proteinâ€“protein docking simulations improves model quality. Proteins: Structure, Function and Bioinformatics, 2014, 82, 916-932. | 1.5 | 18 |
| 26 | Predicting the molecular interactions of CRIP1aâ€“cannabinoid 1 receptor with integrated molecular modeling approaches. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 1158-1165. | 1.0 | 13 |
| 27 | Targeting Cystalysin, a Virulence Factor of Treponema denticolaâ€Supported Periodontitis. ChemMedChem, 2014, 9, 1501-1511. | 1.6 | 26 |
| 28 | Binding mode characterization of 6Î±- and 6Î²-N-heterocyclic substituted naltrexamine derivatives via docking in opioid receptor crystal structures and site-directed mutagenesis studies: Application of the â€˜messageâ€“addressâ€™ concept in development of mu opioid receptor selective antagonists. Bioorganic and Medicinal Chemistry, 2013, 21, 6405-6413. | 1.4 | 20 |
| 29 | Unintended consequences? Water molecules at biological and crystallographic proteinâ€“protein interfaces. Computational Biology and Chemistry, 2013, 47, 126-141. | 1.1 | 14 |
| 30 | How to Deal with Low-Resolution Target Structures: Using SAR, Ensemble Docking, Hydropathic Analysis, and 3D-QSAR to Definitively Map the Î±Î²-Tubulin Colchicine Site. Journal of Medicinal Chemistry, 2013, 56, 7382-7395. | 2.9 | 37 |
| 31 | Developing novel C-4 analogues of pyrrole-based antitubulin agents: weak but critical hydrogen bonding in the colchicine site. MedChemComm, 2013, 4, 417. | 3.5 | 17 |
| 32 | Fine tuning of the active site modulates specificity in the interaction of O-acetylserine sulfhydrylase isozymes with serine acetyltransferase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 169-181. | 1.1 | 35 |
| 33 | Structureâ€“Activity Relationships of Retro-dihydrochalcones Isolated from Tacca sp.. Journal of Natural Products, 2013, 76, 2189-2194. | 1.5 | 12 |
| 34 | Identification of quercitrin as an inhibitor of the p90 S6 ribosomal kinase (RSK): structure of its complex with the N-terminal domain of RSK2 at 1.8â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 266-275. | 2.5 | 15 |
| 35 | Isozyme-Specific Ligands for O-acetylserine sulfhydrylase, a Novel Antibiotic Target. PLoS ONE, 2013, 8, e77558. | 1.1 | 43 |
| 36 | Biological Characterization of 3-(2-amino-ethyl)-5-[3-(4-butoxyl-phenyl)-propylidene]-thiazolidine-2,4-dione (K145) as a Selective Sphingosine Kinase-2 Inhibitor and Anticancer Agent. PLoS ONE, 2013, 8, e56471. | 1.1 | 67 |

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|---|---|---|---|
| 37 | Correct Protonation States and Relevant Waters = Better Computational Simulations?. Current Pharmaceutical Design, 2013, 19, 4291-4309. | 0.9 | 7 |
| 38 | Structural modelling and mutagenesis of human cytomegalovirus alkaline nuclease UL98. Journal of General Virology, 2012, 93, 130-138. | 1.3 | 7 |
| 39 | Pyrrole-Based Antitubulin Agents: Two Distinct Binding Modalities Are Predicted for C-2 Analogues in the Colchicine Site. ACS Medicinal Chemistry Letters, 2012, 3, 53-57. | 1.3 | 20 |
| 40 | On the Specificity of Heparin/Heparan Sulfate Binding to Proteins. Anion-Binding Sites on Antithrombin and Thrombin Are Fundamentally Different. PLoS ONE, 2012, 7, e48632. | 1.1 | 45 |
| 41 | 3,5-Disubstituted-thiazolidine-2,4-dione analogs as anticancer agents: Design, synthesis and biological characterization. European Journal of Medicinal Chemistry, 2012, 47, 125-137. | 2.6 | 77 |
| 42 | Computational analysis of structure-based interactions and ligand properties can predict efflux effects on antibiotics. European Journal of Medicinal Chemistry, 2012, 52, 98-110. | 2.6 | 10 |
| 43 | Regio- and Stereoselective Syntheses of the Natural Product CCR5 Antagonist Anibamine and its Three Olefin Isomers. Journal of Organic Chemistry, 2011, 76, 7945-7952. | 1.7 | 16 |
| 44 | Editorial [Hot topic: Applying Induced Fit in Drug Discovery: Square Pegs and Round Holes? (Guest) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5<br>Medicinal Chemistry, 2011, 11, 131-132. | 1.0 | 2 |
| 45 | Applying an Empirical Hydropathic Forcefield in Refinement May Improve Low-Resolution Protein X-Ray Crystal Structures. PLoS ONE, 2011, 6, e15920. | 1.1 | 13 |
| 46 | Factors influencing protein tyrosine nitrationâ€"structure-based predictive models. Free Radical Biology and Medicine, 2011, 50, 749-762. | 1.3 | 40 |
| 47 | Premature Activation of the Paramyxovirus Fusion Protein before Target Cell Attachment with Corruption of the Viral Fusion Machinery. Journal of Biological Chemistry, 2011, 286, 37945-37954. | 1.6 | 34 |
| 48 | Using Active Site Mapping and Receptor-Based Pharmacophore Tools: Prelude to Docking and De Novo/Fragment-Based Ligand Design. Methods in Molecular Biology, 2011, 716, 39-54. | 0.4 | 8 |
| 49 | Bound Water at Protein-Protein Interfaces: Partners, Roles and Hydrophobic Bubbles as a Conserved Motif. PLoS ONE, 2011, 6, e24712. | 1.1 | 57 |
| 50 | A novel and efficient tool for locating and characterizing protein cavities and binding sites. Proteins: Structure, Function and Bioinformatics, 2010, 78, 825-842. | 1.5 | 53 |
| 51 | Hydrophobicity - Shake Flasks, Protein Folding and Drug Discovery. Current Topics in Medicinal Chemistry, 2010, 10, 67-83. | 1.0 | 111 |
| 52 | Nitration of the Tumor Suppressor Protein p53 at Tyrosine 327 Promotes p53 Oligomerization and Activation. Biochemistry, 2010, 49, 5331-5339. | 1.2 | 51 |
| 53 | Design of O-Acetylserine Sulfhydrylase Inhibitors by Mimicking Nature. Journal of Medicinal Chemistry, 2010, 53, 345-356. | 2.9 | 75 |
| 54 | Hydropathic analysis and biological evaluation of stilbene derivatives as colchicine site microtubule inhibitors with anti-leukemic activity. Journal of Enzyme Inhibition and Medicinal Chemistry, 2009, 24, 1237-1244. | 2.5 | 10 |

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| 55 | Web application for studying the free energy of binding and protonation states of proteinâ€“ligand complexes based on HINT. Journal of Computer-Aided Molecular Design, 2009, 23, 621-632. | 1.3 | 26 |
| 56 | Development of water soluble derivatives of cis-3, 4â€², 5-trimethoxy-3â€²-aminostilbene for optimization and use in cancer therapy. Investigational New Drugs, 2009, 27, 41-52. | 1.2 | 10 |
| 57 | Design, synthesis and biological evaluation of novel stilbene-based antitumor agents. Bioorganic and Medicinal Chemistry, 2009, 17, 512-522. | 1.4 | 27 |
| 58 | Synthesis, structureâ€“affinity relationships, and modeling of AMDA analogs at 5-HT2A and H1 receptors: Structural factors contributing to selectivity. Bioorganic and Medicinal Chemistry, 2009, 17, 6496-6504. | 1.4 | 22 |
| 59 | Structureâ€“activity relationship (SAR) studies of 3-(2-amino-ethyl)-5-(4-ethoxy-benzylidene)-thiazolidine-2,4-dione: Development of potential substrate-specific ERK1/2 inhibitors. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 6042-6046. | 1.0 | 39 |
| 60 | Comparative Docking Study of Anibamine as the First Natural Product CCR5 Antagonist in CCR5 Homology Models. Journal of Chemical Information and Modeling, 2009, 49, 120-132. | 2.5 | 34 |
| 61 | Energyâ€based prediction of amino acidâ€nucleotide base recognition. Journal of Computational Chemistry, 2008, 29, 1955-1969. | 1.5 | 44 |
| 62 | Stilbene derivatives that are colchicine site microtubule inhibitors have antileukemic activity and minimal systemic toxicity. American Journal of Hematology, 2008, 83, 390-397. | 2.0 | 21 |
| 63 | Docking and hydropathic scoring of polysubstituted pyrrole compounds with antitubulin activity. Bioorganic and Medicinal Chemistry, 2008, 16, 2235-2242. | 1.4 | 42 |
| 64 | Novel inhibitors of anthrax edema factor. Bioorganic and Medicinal Chemistry, 2008, 16, 7225-7233. | 1.4 | 38 |
| 65 | Target Flexibility: An Emerging Consideration in Drug Discovery and Design. Journal of Medicinal Chemistry, 2008, 51, 6237-6255. | 2.9 | 280 |
| 66 | Robust Classification of â€œRelevantâ€•Water Molecules in Putative Protein Binding Sites. Journal of Medicinal Chemistry, 2008, 51, 1063-1067. | 2.9 | 93 |
| 67 | Molecular Modeling: Considerations for the Design of Pharmaceuticals and Biopharmaceuticals. , 2008, , 267-291. | | 0 |
| 68 | A LC-Electrospray Tandem MS Method for the Analysis of Naltrexone in Canine Plasma Employing a Molecular Model to Demonstrate the Absence of Internal Standard Deuterium Isotope Effects. Journal of Chromatographic Science, 2007, 45, 694-700. | 0.7 | 14 |
| 69 | A Second Receptor Binding Site on Human Parainfluenza Virus Type 3 Hemagglutinin-Neuraminidase Contributes to Activation of the FusionMechanism. Journal of Virology, 2007, 81, 3216-3228. | 1.5 | 87 |
| 70 | Tyrosine Nitration of IÎºBÎ±:â€‰ A Novel Mechanism for NF-ÎºB Activation<sup>,</sup>. Biochemistry, 2007, 46, 11671-11683. | 1.2 | 88 |
| 71 | Complexity in Modeling and Understanding Protonation States: Computational Titration of HIVâ€1 â€Proteaseâ€“Inhibitor Complexes. Chemistry and Biodiversity, 2007, 4, 2564-2577. | 1.0 | 10 |
| 72 | Hydropathic Analysis and Comparison of KcsA and Shaker Potassium Channels. Chemistry and Biodiversity, 2007, 4, 2578-2592. | 1.0 | 4 |

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| 73 | The consequences of scoring docked ligand conformations using free energy correlations. European Journal of Medicinal Chemistry, 2007, 42, 921-933. | 2.6 | 58 |
| 74 | Energetics of the protein-DNA-water interaction. BMC Structural Biology, 2007, 7, 4. | 2.3 | 57 |
| 75 | Autophagic cell death, polyploidy and senescence induced in breast tumor cells by the substituted pyrrole JG-03-14, a novel microtubule poison. Biochemical Pharmacology, 2007, 74, 981-991. | 2.0 | 72 |
| 76 | Mapping the Energetics of Waterâ€"Protein and Waterâ€"Ligand Interactions with the â€œNaturalâ€•HINT Forcefield: Predictive Tools for Characterizing the Roles of Water in Biomolecules. Journal of Molecular Biology, 2006, 358, 289-309. | 2.0 | 85 |
| 77 | Water: How to evaluate its contribution in protein-ligand interactions. International Journal of Quantum Chemistry, 2006, 106, 647-651. | 1.0 | 12 |
| 78 | Tools for building a comprehensive modeling system for virtual screening under real biological conditions: The Computational Titration algorithm. Journal of Molecular Graphics and Modelling, 2006, 24, 434-439. | 1.3 | 18 |
| 79 | Paramyxovirus Receptor-Binding Molecules: Engagement of One Site on the Hemagglutinin-Neuraminidase Protein Modulates Activity at the Second Site. Journal of Virology, 2006, 80, 1204-1213. | 1.5 | 57 |
| 80 | A computational tool to optimize ligand selectivity between two similar biomacromolecular targets. Journal of Computer-Aided Molecular Design, 2005, 19, 69-82. | 1.3 | 12 |
| 81 | A molecular model to explain paclitaxel and docetaxel sensitivity changes through adduct formation with primary amines in electrospray ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 2005, 19, 1221-1226. | 0.7 | 14 |
| 82 | Homology Model of the CDK1/cyclin B Complex. Journal of Biomolecular Structure and Dynamics, 2005, 22, 493-502. | 2.0 | 37 |
| 83 | Free Energy of Ligand Binding to Protein: Evaluation of the Contribution of Water Molecules by Computational Methods. Current Medicinal Chemistry, 2004, 11, 3093-3118. | 1.2 | 89 |
| 84 | Evaluation of Deuterium Isotope Effects in Normal-Phase LC-MS-MS Separations Using a Molecular Modeling Approach. Journal of Chromatographic Science, 2004, 42, 383-387. | 0.7 | 60 |
| 85 | The Importance of Being Exhaustive. Optimization of Bridging Structural Water Molecules and Water Networks in Models of Biological Systems. Chemistry and Biodiversity, 2004, 1, 98-105. | 1.0 | 40 |
| 86 | Getting it right: modeling of pH, solvent and â€œnearlyâ€•everything else in virtual screening of biological targets. Journal of Molecular Graphics and Modelling, 2004, 22, 479-486. | 1.3 | 32 |
| 87 | 1,2-Dithiole-3-Ones as Potent Inhibitors of the Bacterial 3-Ketoacyl Acyl Carrier Protein Synthase III (FabH). Antimicrobial Agents and Chemotherapy, 2004, 48, 3093-3102. | 1.4 | 88 |
| 88 | ComputationalÂTitrationÂAnalysisÂofÂaÂMultiproticÂHIV-1ÂProteaseâ^'LigandÂComplex. Journal of the American Chemical Society, 2004, 126, 11764-11765. | 6.6 | 34 |
| 89 | A Computational Model for Anthracycline Binding to DNA:Â Tuning Groove-Binding Intercalators for Specific Sequences. Journal of Medicinal Chemistry, 2004, 47, 1360-1374. | 2.9 | 47 |
| 90 | Simple, Intuitive Calculations of Free Energy of Binding for Proteinâ^'Ligand Complexes. 3. The Free Energy Contribution of Structural Water Molecules in HIV-1 Protease Complexes. Journal of Medicinal Chemistry, 2004, 47, 4507-4516. | 2.9 | 112 |

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| 91 | 3D QSAR in modern drug design. , 2003, , 223-241. | | 14 |
| 92 | Simple, Intuitive Calculations of Free Energy of Binding for Proteinâ˜Ligand Complexes. 2. Computational Titration and pH Effects in Molecular Models of Neuraminidaseâ˜Inhibitor Complexes. Journal of Medicinal Chemistry, 2003, 46, 4487-4500. | 2.9 | 77 |
| 93 | Hydropathic analysis of the free energy differences in anthracycline antibiotic binding to DNA. Nucleic Acids Research, 2003, 31, 4410-4416. | 6.5 | 24 |
| 94 | Simple, Intuitive Calculations of Free Energy of Binding for Proteinâ˜Ligand Complexes. 1. Models without Explicit Constrained Water. Journal of Medicinal Chemistry, 2002, 45, 2469-2483. | 2.9 | 131 |
| 95 | Which aminoglycoside ring is most important for binding? a hydropathic analysis of gentamicin, paromomycin, and analogues. Bioorganic and Medicinal Chemistry Letters, 2001, 11, 119-122. | 1.0 | 23 |
| 96 | Computationally accessible method for estimating free energy changes resulting from site-specific mutations of biomolecules: Systematic model building and structural/hydropathic analysis of deoxy and oxy hemoglobins. Proteins: Structure, Function and Bioinformatics, 2001, 42, 355-377. | 1.5 | 45 |
| 97 | Very empirical treatment of solvation and entropy: a force field derived from log Po/w. Journal of Computer-Aided Molecular Design, 2001, 15, 381-393. | 1.3 | 54 |
| 98 | HINT predictive analysis of binding between retinol binding protein and hydrophobic ligands. Bioorganic and Medicinal Chemistry Letters, 2000, 10, 2129-2132. | 1.0 | 13 |
| 99 | Hydrophobicity: is LogPo/w more than the sum of its parts?. European Journal of Medicinal Chemistry, 2000, 35, 651-661. | 2.6 | 236 |
| 100 | Computational Methodology for Estimating Changes in Free Energies of Biomolecular Association upon Mutation. The Importance of Bound Water in Dimerâ˜Tetramer Assembly for Î²37 Mutant Hemoglobinsâ€. Biochemistry, 2000, 39, 1622-1633. | 1.2 | 42 |
| 101 | Use of 3D QSAR Methodology for Data Mining the National Cancer Institute Repository of Small Molecules: Application to HIV-1 Reverse Transcriptase Inhibition. Methods, 1998, 14, 255-263. | 1.9 | 18 |
| 102 | Identification and hydropathic characterization of structural features affecting sequence specificity for doxorubicin intercalation into DNA double-stranded polynucleotides. Nucleic Acids Research, 1998, 26, 4721-4732. | 6.5 | 64 |
| 103 | All-Atom Models for the Non-Nucleoside Binding Site of HIV-1 Reverse Transcriptase Complexed with Inhibitors:Â A 3D QSAR Approachâ€. Journal of Medicinal Chemistry, 1996, 39, 1645-1650. | 2.9 | 53 |
| 104 | E-state fields: Applications to 3D QSAR. Journal of Computer-Aided Molecular Design, 1996, 10, 513-520. | 1.3 | 86 |
| 105 | Differences in hydropathic properties of ligand binding at four independent sites in wheat germ agglutininâ€oligosaccharide crystal complexes. Protein Science, 1996, 5, 1466-1476. | 3.1 | 91 |
| 106 | The effect of physical organic properties on hydrophobic fields. Journal of Computer-Aided Molecular Design, 1994, 8, 41-49. | 1.3 | 33 |
| 107 | Evaluating docked complexes with the HINT exponential function and empirical atomic hydrophobicities. Journal of Computer-Aided Molecular Design, 1994, 8, 299-306. | 1.3 | 52 |
| 108 | Effect of distamycin on chlorambucil-induced mutagenesis in pZ189: evidence of a role for minor groove alkylation at adenine N-3. Mutagenesis, 1994, 9, 133-139. | 1.0 | 15 |

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| 109 | Allosteric modifiers of hemoglobin. 2. Crystallographically determined binding sites and hydrophobic binding/interaction analysis of novel hemoglobin oxygen effectors. Journal of Medicinal Chemistry, 1991, 34, 758-767. | 2.9 | 123 |
| 110 | HINT: A new method of empirical hydrophobic field calculation for CoMFA. Journal of Computer-Aided Molecular Design, 1991, 5, 545-552. | 1.3 | 303 |
| 111 | Molecular metals with widely tunable band filling. Structure/stoichiometry/counterion relationships in the electrochemistry of a cofacially joined polymeric phthalocyanine metal. Journal of the American Chemical Society, 1989, 111, 5259-5271. | 6.6 | 38 |
| 112 | Molecular metals with widely tunable band filling. Response of the collective properties of a phthalocyanine molecular metal to drastic excursions in partial oxidation state and charge-compensating counterions. Journal of the American Chemical Society, 1989, 111, 5271-5284. | 6.6 | 20 |
| 113 | Additions and Corrections. Electronic Structure Factors of Carbon-Hydrogen Bond Activation. The Photoelectron Spectroscopy of (Cyclohexenyl) manganese Tricarbonyl. Journal of the American Chemical Society, 1986, 108, 7134-7134. | 6.6 | 0 |
| 114 | Ligand additivity in the valence photoelectron spectroscopy of phosphine-substituted molybdenum carbonyls. Inorganic Chemistry, 1984, 23, 4361-4365. | 1.9 | 29 |