Michael J Schnieders

List of Publications by Year
in descending order

47	3,351	279798	265206
papers	citations	23	42
		h-index	g-index

53	53	53	4037
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Whole-genome sequencing reveals de-novo mutations associated with nonsyndromic cleft lip/palate. Scientific Reports, 2022, 12, .	3.3	11
2	Implicit Solvents for the Polarizable Atomic Multipole AMOEBA Force Field. Journal of Chemical Theory and Computation, 2021, 17, 2323-2341.	5.3	10
3	In Silico and In Vivo Analysis of Amino Acid Substitutions That Cause Laminopathies. International Journal of Molecular Sciences, 2021, 22, 11226.	4.1	7
4	Novel Intragenic *PAX6* Deletion in a Pedigree with Aniridia, Morbid Obesity, and Diabetes. Current Eye Research, 2020, 45, 91-96.	1.5	10
5	Characterization of a TP53 Somatic Variant of Unknown Function From an Ovarian Cancer Patient Using Organoid Culture and Computational Modeling. Clinical Obstetrics and Gynecology, 2020, 63, 109-119.	1.1	7
6	Nanophthalmos patient with a THR518MET mutation in MYRF, a case report. BMC Ophthalmology, 2020, 20, 388.	1.4	5
7	Structural Insights into Hearing Loss Genetics from Polarizable Protein Repacking. Biophysical Journal, 2019, 117, 602-612.	0.5	12
8	Scalable Indirect Free Energy Method Applied to Divalent Cation-Metalloprotein Binding. Journal of Chemical Theory and Computation, 2019, 15, 4602-4614.	5.3	4
9	A novel mutation (LEU396ARG) in OPA1 is associated with a severe phenotype in a large dominant optic atrophy pedigree. Eye, 2018, 32, 843-845.	2.1	2
10	Genomic Landscape and Mutational Signatures of Deafness-Associated Genes. American Journal of Human Genetics, 2018, 103, 484-497.	6.2	214
11	Tinker 8: Software Tools for Molecular Design. Journal of Chemical Theory and Computation, 2018, 14, 5273-5289.	5.3	403
12	Tinker-HP: a massively parallel molecular dynamics package for multiscale simulations of large complex systems with advanced point dipole polarizable force fields. Chemical Science, 2018, 9, 956-972.	7.4	190
13	Polarizable Amoeba Force Field Metadynamics with Minimization Predicts Missing Protein Loops. Biophysical Journal, 2017, 112, 55a.	0.5	0
14	The Use of Variant Maps to Explore Domain-Specific Mutations of FGFR1. Journal of Dental Research, 2017, 96, 1339-1345.	5.2	7
15	LADD syndrome with glaucoma is caused by a novel gene. Molecular Vision, 2017, 23, 179-184.	1.1	5
16	Protein Sequence Optimization with a Polarizable Force Field: Insights from PDZ Domains. Biophysical Journal, 2016, 110, 345a-346a.	0.5	0
17	Calculating binding free energies of host–guest systems using the AMOEBA polarizable force field. Physical Chemistry Chemical Physics, 2016, 18, 30261-30269.	2.8	44
18	Toward polarizable AMOEBA thermodynamics at fixed charge efficiency using a dual force field approach: application to organic crystals. Physical Chemistry Chemical Physics, 2016, 18, 30313-30322.	2.8	10

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19	Hypomorphic mutations in *TRNT1* cause retinitis pigmentosa with erythrocytic microcytosis. Human Molecular Genetics, 2016, 25, 44-56.	2.9	64
20	High-Throughput Genetic Testing for Thrombotic Microangiopathies and C3 Glomerulopathies. Journal of the American Society of Nephrology: JASN, 2016, 27, 1245-1253.	6.1	89
21	*PDZD7* and hearing loss: More than just a modifier. American Journal of Medical Genetics, Part A, 2015, 167, 2957-2965.	1.2	54
22	Polarizable Molecular Dynamics in a Polarizable Continuum Solvent. Journal of Chemical Theory and Computation, 2015, 11, 623-634.	5.3	45
23	Scalable Evaluation of Polarization Energy and Associated Forces in Polarizable Molecular Dynamics: II. Toward Massively Parallel Computations Using Smooth Particle Mesh Ewald. Journal of Chemical Theory and Computation, 2015, 11, 2589-2599.	5.3	53
24	Dead-End Elimination with a Polarizable Force Field Repacks PCNA Structures. Biophysical Journal, 2015, 109, 816-826.	0.5	24
25	Absolute Organic Crystal Thermodynamics: Growth of the Asymmetric Unit into a Crystal via Alchemy. Journal of Chemical Theory and Computation, 2014, 10, 2781-2791.	5.3	24
26	Scalable Evaluation of Polarization Energy and Associated Forces in Polarizable Molecular Dynamics: I. Toward Massively Parallel Direct Space Computations. Journal of Chemical Theory and Computation, 2014, 10, 1638-1651.	5.3	76
27	Biomolecular Structure Refinement & Prediction using Dead-End Elimination with a Polarizable Force Field. Biophysical Journal, 2014, 106, 407a.	0.5	1
28	Computational Insights for the Discovery of Non-ATP Competitive Inhibitors of MAP Kinases. Current Pharmaceutical Design, 2012, 18, 1173-1185.	1.9	19
29	Biomolecular electrostatics and solvation: a computational perspective. Quarterly Reviews of Biophysics, 2012, 45, 427-491.	5.7	152
30	Bayesian Modeling of Crystallographic Disorder. Biophysical Journal, 2012, 102, 225a.	0.5	0
31	Pharmaceutical Applications of the Polarizable Amoeba Potential, Including Protein-Ligand Binding Affinity and Drug Solubility, using the Force Field X Software. Biophysical Journal, 2012, 102, 409a-410a.	0.5	0
32	The Structure, Thermodynamics, and Solubility of Organic Crystals from Simulation with a Polarizable Force Field. Journal of Chemical Theory and Computation, 2012, 8, 1721-1736.	5.3	77
33	Polarizable Atomic Multipole X-Ray Refinement: Particle Mesh Ewald Electrostatics for Macromolecular Crystals. Journal of Chemical Theory and Computation, 2011, 7, 1141-1156.	5.3	40
34	Reintroducing Electrostatics into Macromolecular Crystallographic Refinement: Application to Neutron Crystallography and DNA Hydration. Structure, 2011, 19, 523-533.	3.3	36
35	Polarizable atomic multipole X-ray refinement: weighting schemes for macromolecular diffraction. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 957-965.	2.5	24
36	Assessment of protein structure refinement in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 74-90.	2.6	87

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37	A smooth and differentiable bulk-solvent model for macromolecular diffraction. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1024-1031.	2.5	19
38	X-Ray Crystallography Refinement as Ewald Intended: From Drug Design to Ribosome Crystals. Biophysical Journal, 2010, 98, 177a.	0.5	0
39	Polarizable Atomic Multipole X-Ray Refinement: Hydration Geometry and Application to Macromolecules. Biophysical Journal, 2010, 98, 2984-2992.	0.5	29
40	Current Status of the AMOEBA Polarizable Force Field. Journal of Physical Chemistry B, 2010, 114, 2549-2564.	2.6	1,093
41	Trypsin-ligand binding free energy calculation with AMOEBA. , 2009, 2009, 2328-31.		9
42	Trypsin–ligand binding free energies from explicit and implicit solvent simulations with polarizable potential. Journal of Computational Chemistry, 2009, 30, 1701-1711.	3.3	96
43	Assessment of the protein–structure refinement category in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 66-80.	2.6	65
44	Polarizable atomic multipole X-ray refinement: application to peptide crystals. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 952-965.	2.5	49
45	Polarizable atomic multipole solutes in a Poisson-Boltzmann continuum. Journal of Chemical Physics, 2007, 126, 124114.	3.0	79
46	Polarizable Atomic Multipole Solutes in a Generalized Kirkwood Continuum. Journal of Chemical Theory and Computation, 2007, 3, 2083-2097.	5.3	66
47	A SURGICAL GUIDE TO ACCURATELY PLACE PINS OR NAILS WITHIN THE FEMORAL HEAD. Journal of Musculoskeletal Research, 1999, 03, 233-237.	0.2	1