Troy W Whitfield

List of Publications by Year
in descending order

29 papers	17,821 citations	361413 20 h-index	454955 30 g-index
30 all docs	30 docs citations	30 times ranked	37181 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	5.5	762
3	Simulating Monovalent and Divalent Ions in Aqueous Solution Using a Drude Polarizable Force Field. Journal of Chemical Theory and Computation, 2010, 6, 774-786.	5.3	401
4	Functional analysis of transcription factor binding sites in human promoters. Genome Biology, 2012, 13, R50.	9.6	136
5	Understanding the Dielectric Properties of Liquid Amides from a Polarizable Force Field. Journal of Physical Chemistry B, 2008, 112, 3509-3521.	2.6	122
6	Genomic occupancy of Runx2 with global expression profiling identifies a novel dimension to control of osteoblastogenesis. Genome Biology, 2014, 15, R52.	9.6	122
7	Theoretical Study of Aqueous Solvation of K^+ Comparing ab Initio, Polarizable, and Fixed-Charge Models. Journal of Chemical Theory and Computation, 2007, 3, 2068-2082.	5.3	87
8	Demethylated HSATII DNA and HSATII RNA Foci Sequester PRC1 and MeCP2 into Cancer-Specific Nuclear Bodies. Cell Reports, 2017, 18, 2943-2956.	6.4	76
9	Identification of functional modules that correlate with phenotypic difference: the influence of network topology. Genome Biology, 2010, 11, R23.	9.6	67
10	Quantum Drude oscillator model of atoms and molecules: Many-body polarization and dispersion interactions for atomistic simulation. Physical Review B, 2013, 87, .	3.2	65
11	Chromatin dynamics regulate mesenchymal stem cell lineage specification and differentiation to osteogenesis. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 438-449.	1.9	55
12	Genome-Wide Studies Reveal that H3K4me3 Modification in Bivalent Genes Is Dynamically Regulated during the Pluripotent Cell Cycle and Stabilized upon Differentiation. Molecular and Cellular Biology, 2016, 36, 615-627.	2.3	53
13	Generalized parallel sampling. Physica A: Statistical Mechanics and Its Applications, 2002, 305, 157-171.	2.6	49
14	Liquid NMA: A surprisingly realistic model for hydrogen bonding motifs in proteins. Chemical Physics Letters, 2005, 414, 210-214.	2.6	36
15	A Combined Experimental and Theoretical Study of Ion Solvation in Liquid N-Methylacetamide. Journal of the American Chemical Society, 2010, 132, 10847-10856.	13.7	35
16	Genome-wide co-occupancy of AML1-ETO and N-CoR defines the t(8;21) AML signature in leukemic cells. BMC Genomics, 2015, 16, 309.	2.8	30
17	A unified formalism for many-body polarization and dispersion: The quantum Drude model applied to fluid xenon. Chemical Physics Letters, 2006, 424, 409-413.	2.6	29
18	The bone-specific Runx2-P1 promoter displays conserved three-dimensional chromatin structure with the syntenic Supt3h promoter. Nucleic Acids Research, 2014, 42, 10360-10372.	14.5	28

#	Article	IF	Citations
19	Epigenetic landscape during osteoblastogenesis defines a differentiation-dependent Runx2 promoter region. Gene, 2014, 550, 1-9.	2.2	28
20	Elucidating the Interdependence of Drug Resistance from Combinations of Mutations. Journal of Chemical Theory and Computation, 2017, 13, 5671-5682.	5.3	27
21	Characterizing Protein–Ligand Binding Using Atomistic Simulation and Machine Learning: Application to Drug Resistance in HIV-1 Protease. Journal of Chemical Theory and Computation, 2020, 16, 1284-1299.	5.3	19
22	Low variance energy estimators for systems of quantum Drude oscillators: Treating harmonic path integrals with large separations of time scales. Journal of Chemical Physics, 2007, 126, 074104.	3.0	17
23	Synonymous Mutations at the Beginning of the Influenza A Virus Hemagglutinin Gene Impact Experimental Fitness. Journal of Molecular Biology, 2018, 430, 1098-1115.	4.2	16
24	Molecular Determinants of Epistasis in HIV-1 Protease: Elucidating the Interdependence of L89V and L90M Mutations in Resistance. Biochemistry, 2019, 58, 3711-3726.	2.5	15
25	Constrained Mutational Sampling of Amino Acids in HIV-1 Protease Evolution. Molecular Biology and Evolution, 2019, 36, 798-810.	8.9	10
26	A machine learning approach for the prediction of protein surface loop flexibility. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2467-2474.	2.6	8
27	Uncertainty of path integral averages at low temperature. Journal of Chemical Physics, 2001, 115, 6834-6840.	3.0	4
28	Gravitational smoothing as a global optimization strategy. Journal of Computational Chemistry, 2002, 23, 1100-1103.	3.3	4
29	Structural Basis of the Disorder in the Tandem Zinc Finger Domain of the RNA-Binding Protein Tristetraprolin. Journal of Chemical Theory and Computation, 2016, 12, 4717-4725.	5.3	2