Ran Friedman

List of Publications by Year in Descending Order

78 papers	1,783 citations	21 h-index	39 g-index
86 ext. papers	2,074 ext. citations	4.2 avg, IF	5.3 L-index

#	Paper	IF	Citations
78	Rotating between ponatinib and imatinib temporarily increases the efficacy of imatinib as shown in a chronic myeloid leukaemia model.. *Scientific Reports*, **2022**, 12, 5164	4.9	1
77	The molecular mechanisms behind activation of FLT3 in acute myeloid leukemia and resistance to therapy by selective inhibitors.. *Biochimica Et Biophysica Acta: Reviews on Cancer*, **2021**, 1877, 188666	11.2	4
76	Activation of Abl1 Kinase Explored Using Well-Tempered Metadynamics Simulations on an Essential Dynamics Sampled Path. *Journal of Chemical Theory and Computation*, **2021**, 17, 7260-7270	6.4	3
75	Preferential Binding of Lanthanides to Methanol Dehydrogenase Evaluated with Density Functional Theory. *Journal of Physical Chemistry B*, **2021**, 125, 2251-2257	3.4	1
74	Combating drug resistance in acute myeloid leukaemia by drug rotations: the effects of quizartinib and pexidartinib. *Cancer Cell International*, **2021**, 21, 198	6.4	3
73	Understanding intermolecular interactions of large systems in ground state and excited state by using density functional based tight binding methods. *Journal of Chemical Physics*, **2021**, 154, 194106	3.9	4
72	Simulations Studies of Protein Kinases that are Molecular Targets in Cancer. *Israel Journal of Chemistry*, **2020**, 60, 667-680	3.4	6
71	Is breaking of a hydrogen bond enough to lead to drug resistance?. *Chemical Communications*, **2020**, 56, 6727-6730	5.8	5
70	The effects of combination treatments on drug resistance in chronic myeloid leukaemia: an evaluation of the tyrosine kinase inhibitors axitinib and asciminib. *BMC Cancer*, **2020**, 20, 397	4.8	10
69	Reverse engineering directed gene regulatory networks from transcriptomics and proteomics data of biomining bacterial communities with approximate Bayesian computation and steady-state signalling simulations. *BMC Bioinformatics*, **2020**, 21, 23	3.6	6
68	Deciphering the molecular mechanism of FLT3 resistance mutations. *FEBS Journal*, **2020**, 287, 3200-3220	5.7	10
67	Pattern and Dynamics of FLT3 Duplications. *Journal of Chemical Information and Modeling*, **2020**, 60, 4005-4020	5.4	4
66	Inferring time-dependent population growth rates in cell cultures undergoing adaptation. *BMC Bioinformatics*, **2020**, 21, 583	3.6	2
65	The catalytic activity of Abl1 single and compound mutations: Implications for the mechanism of drug resistance mutations in chronic myeloid leukaemia. *Biochimica Et Biophysica Acta - General Subjects*, **2019**, 1863, 732-741	4	13
64	Simulations of Biomolecules in Electrolyte Solutions. *Advanced Theory and Simulations*, **2019**, 2, 1800163	3.5	2
63	Stochastic modelling of tyrosine kinase inhibitor rotation therapy in chronic myeloid leukaemia. *BMC Cancer*, **2019**, 19, 508	4.8	8
62	Activation and Inactivation of the FLT3 Kinase: Pathway Intermediates and the Free Energy of Transition. *Journal of Physical Chemistry B*, **2019**, 123, 5385-5394	3.4	8

61	Specific Ion and Concentration Effects in Acetate Solutions with Na , K and Cs. *ChemPhysChem*, **2019**, 20, 1006-1010	3.2	1
60	Conformational modifications induced by internal tandem duplications on the FLT3 kinase and juxtamembrane domains. *Physical Chemistry Chemical Physics*, **2019**, 21, 18467-18476	3.6	5
59	Oxidative hotspots on actin promote skeletal muscle weakness in rheumatoid arthritis. *JCI Insight*, **2019**, 5,	9.9	10
58	Clustering of atomic displacement parameters in bovine trypsin reveals a distributed lattice of atoms with shared chemical properties. *Scientific Reports*, **2019**, 9, 19281	4.9	4
57	Membrane-Ion Interactions. *Journal of Membrane Biology*, **2018**, 251, 453-460	2.3	16
56	Computer simulations of the signalling network in FLT3 -acute myeloid leukaemia - indications for an optimal dosage of inhibitors against FLT3 and CDK6. *BMC Bioinformatics*, **2018**, 19, 155	3.6	6
55	A computational study of hedgehog signalling involved in basal cell carcinoma reveals the potential and limitation of combination therapy. *BMC Cancer*, **2018**, 18, 569	4.8	8
54	An interactive computer lab of the galvanic cell for students in biochemistry. *Biochemistry and Molecular Biology Education*, **2018**, 46, 58-65	1.3	0
53	Understanding Conformational Dynamics of Complex Lipid Mixtures Relevant to Biology. *Journal of Membrane Biology*, **2018**, 251, 609-631	2.3	26
52	Protein-ion Interactions: Simulations of Bovine Serum Albumin in Physiological Solutions of NaCl, KCl and LiCl. *Israel Journal of Chemistry*, **2017**, 57, 403-412	3.4	13
51	Palbociclib can overcome mutations in cyclin dependent kinase 6 that break hydrogen bonds between the drug and the protein. *Protein Science*, **2017**, 26, 870-879	6.3	16
50	Interaction Energies in Complexes of Zn and Amino Acids: A Comparison of Ab Initio and Force Field Based Calculations. *Journal of Physical Chemistry A*, **2017**, 121, 2643-2654	2.8	15
49	Dilution of whisky - the molecular perspective. *Scientific Reports*, **2017**, 7, 6489	4.9	18
48	The molecular mechanism behind resistance of the kinase FLT3 to the inhibitor quizartinib. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 2143-2152	4.2	18
47	Computer simulations of alkali-acetate solutions: Accuracy of the forcefields in difference concentrations. *Journal of Chemical Physics*, **2017**, 147, 194102	3.9	7
46	Biological Membranes in Extreme Conditions: Simulations of Anionic Archaeal Tetraether Lipid Membranes. *PLoS ONE*, **2016**, 11, e0155287	3.7	13
45	Sensitivity Analysis of the NPM-ALK Signalling Network Reveals Important Pathways for Anaplastic Large Cell Lymphoma Combination Therapy. *PLoS ONE*, **2016**, 11, e0163011	3.7	9
44	Drug resistance in cancer: molecular evolution and compensatory proliferation. *Oncotarget*, **2016**, 7, 11746-55	3.3	46

43	Transcriptomic analysis reveals how a lack of potassium ions increases Sulfolobus acidocaldarius sensitivity to pH changes. *Microbiology (United Kingdom)*, **2016**, 162, 1422-1434	2.9	14
42	Biological Membranes in Extreme Conditions: Anionic Tetraether Lipid Membranes and Their Interactions with Sodium and Potassium. *Journal of Physical Chemistry B*, **2016**, 120, 10628-10634	3.4	7
41	Membrane Protein Structure, Function, and Dynamics: a Perspective from Experiments and Theory. *Journal of Membrane Biology*, **2015**, 248, 611-40	2.3	101
40	Acute Toxicity-Supported Chronic Toxicity Prediction: A k-Nearest Neighbor Coupled Read-Across Strategy. *International Journal of Molecular Sciences*, **2015**, 16, 11659-77	6.3	13
39	S100A4 and its role in metastasis □computational integration of data on biological networks. *Molecular BioSystems*, **2015**, 11, 2238-46		12
38	Terahertz radiation induces non-thermal structural changes associated with Fr□lich condensation in a protein crystal. *Structural Dynamics*, **2015**, 2, 054702	3.2	37
37	S100A4 and its role in metastasis □simulations of knockout and amplification of epithelial growth factor receptor and matrix metalloproteinases. *Molecular BioSystems*, **2015**, 11, 2247-54		18
36	Structural and computational insights into the versatility of cadmium binding to proteins. *Dalton Transactions*, **2014**, 43, 2878-87	4.3	23
35	BCR-ABL1 compound mutations combining key kinase domain positions confer clinical resistance to ponatinib in Ph chromosome-positive leukemia. *Cancer Cell*, **2014**, 26, 428-442	24.3	233
34	Wild type and mutants of the HET-s(218-289) prion show different flexibility at fibrillar ends: a simulation study. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 399-404	4.2	5
33	Electrolyte Solutions and Specific Ion Effects on Interfaces. *Journal of Chemical Education*, **2013**, 90, 1018-1023	2.4	12
32	How warfarin□s structural diversity influences its phospholipid bilayer membrane permeation. *Journal of Physical Chemistry B*, **2013**, 117, 2384-95	3.4	14
31	Interaction energies between metal ions (Zn2+ and Cd2+) and biologically relevant ligands. *International Journal of Quantum Chemistry*, **2013**, 113, 2554-2562	2.1	13
30	Molecular modelling and simulations in cancer research. *Biochimica Et Biophysica Acta: Reviews on Cancer*, **2013**, 1836, 1-14	11.2	33
29	Drug resistance missense mutations in cancer are subject to evolutionary constraints. *PLoS ONE*, **2013**, 8, e82059	3.7	20
28	Ions and the protein surface revisited: extensive molecular dynamics simulations and analysis of protein structures in alkali-chloride solutions. *Journal of Physical Chemistry B*, **2011**, 115, 9213-23	3.4	30
27	Surfactant effects on amyloid aggregation kinetics. *Journal of Molecular Biology*, **2011**, 414, 303-12	6.5	20
26	Aggregation of amyloids in a cellular context: modelling and experiment. *Biochemical Journal*, **2011** , 438, 415-26	3.8	45

25	Wordom: a user-friendly program for the analysis of molecular structures, trajectories, and free energy surfaces. *Journal of Computational Chemistry*, **2011**, 32, 1183-94	3.5	187
24	Soluble Protofibrils as Metastable Intermediates in Simulations of Amyloid Fibril Degradation Induced by Lipid Vesicles. *Journal of Physical Chemistry Letters*, **2010**, 1, 471-474	6.4	20
23	On the orientation of the catalytic dyad in aspartic proteases. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1575-82	4.2	11
22	Discovery of plasmepsin inhibitors by fragment-based docking and consensus scoring. *ChemMedChem*, **2009**, 4, 1317-26	3.7	44
21	Amyloid aggregation on lipid bilayers and its impact on membrane permeability. *Journal of Molecular Biology*, **2009**, 387, 407-15	6.5	119
20	Proton Transfer on the Molecular Surface of Proteins and Model Systems. *Israel Journal of Chemistry*, **2009**, 49, 149-153	3.4	5
19	Diffusion of anionic and neutral GFP derivatives through plasmodesmata in epidermal cells of Nicotiana benthamiana. *Protoplasma*, **2008**, 234, 13-23	3.4	21
18	Pepsinogen-like activation intermediate of plasmepsin II revealed by molecular dynamics analysis. *Proteins: Structure, Function and Bioinformatics*, **2008**, 73, 814-27	4.2	16
17	Myosin V movement: lessons from molecular dynamics studies of IQ peptides in the lever arm. *Biochemistry*, **2007**, 46, 14524-36	3.2	2
16	Minimum energy pathways for proton transfer between adjacent sites exposed to water. *Journal of Physical Chemistry B*, **2007**, 111, 6059-70	3.4	22
15	Molecular dynamics simulations of palmitate entry into the hydrophobic pocket of the fatty acid binding protein. *FEBS Letters*, **2007**, 581, 1243-7	3.8	34
14	The protonation state of the catalytic aspartates in plasmepsin II. *FEBS Letters*, **2007**, 581, 4120-4	3.8	26
13	The dynamics of proton transfer between adjacent sites. *Photochemical and Photobiological Sciences*, **2006**, 5, 531-7	4.2	16
12	Fatty acid binding proteins: same structure but different binding mechanisms? Molecular dynamics simulations of intestinal fatty acid binding protein. *Biophysical Journal*, **2006**, 90, 1535-45	2.9	35
11	A molecular dynamics study of the effect of Ca2+ removal on calmodulin structure. *Biophysical Journal*, **2006**, 90, 3842-50	2.9	35
10	A molecular dynamics study and free energy analysis of complexes between the Mlc1p protein and two IQ motif peptides. *Biophysical Journal*, **2006**, 91, 2436-50	2.9	30
9	The mechanism of proton transfer between adjacent sites on the molecular surface. *Biochimica Et Biophysica Acta - Bioenergetics*, **2006**, 1757, 931-41	4.6	17
8	Molecular dynamics study of a calmodulin-like protein with an IQ peptide: spontaneous refolding of the protein around the peptide. *Proteins: Structure, Function and Bioinformatics*, **2006**, 64, 133-46	4.2	3

7	The mechanism of proton transfer between adjacent sites exposed to water. *Journal of Physical Chemistry B*, **2005**, 109, 11379-88	3.4	20
6	Molecular dynamics of a protein surface: ion-residues interactions. *Biophysical Journal*, **2005**, 89, 768-81	2.9	62
5	Application of classical molecular dynamics for evaluation of proton transfer mechanism on a protein. *Biochimica Et Biophysica Acta - Bioenergetics*, **2005**, 1710, 67-77	4.6	21
4	Molecular dynamics simulations of the adipocyte lipid binding protein reveal a novel entry site for the ligand. *Biochemistry*, **2005**, 44, 4275-83	3.2	32
3	Protein surface dynamics: interaction with water and small solutes. *Journal of Biological Physics*, **2005**, 31, 433-52	1.6	7
2	The role of small intraprotein cavities in the catalytic cycle of bacteriorhodopsin. *Biophysical Journal*, **2003**, 85, 886-96	2.9	19
1	Computational studies of protein–drug binding affinity changes upon mutations in the drug target. *Wiley Interdisciplinary Reviews: Computational Molecular Science*,e1563	7.9	3