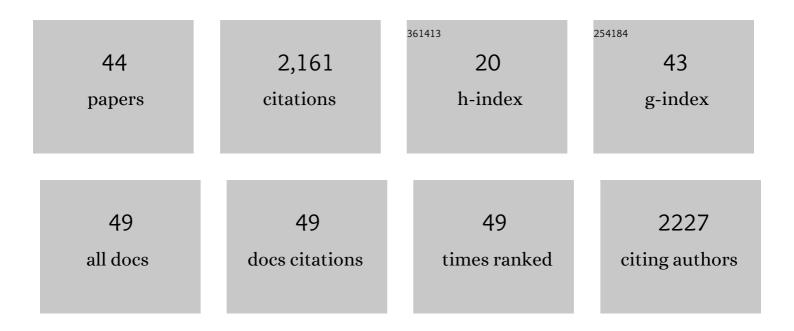
Steven S Plotkin

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	First Principles Calculation of Protein–Protein Dimer Affinities of ALS-Associated SOD1 Mutants. Frontiers in Molecular Biosciences, 2022, 9, 845013.	3.5	5
2	Misfolding-Associated Exposure of Natively Buried Residues in Mutant SOD1 Facilitates Binding to TRAF6. Journal of Molecular Biology, 2022, 434, 167697.	4.2	2
3	Optimizing Epitope Conformational Ensembles Using α-Synuclein Cyclic Peptide "Glycindel―Scaffolds: A Customized Immunogen Method for Generating Oligomer-Selective Antibodies for Parkinson's Disease. ACS Chemical Neuroscience, 2022, 13, 2261-2280.	3.5	7
4	A method for systematically ranking therapeutic drug candidates using multiple uncertain screening criteria. Statistical Methods in Medical Research, 2021, 30, 1502-1522.	1.5	5
5	Therapeutic targeting of the PI4K2A/PKR lysosome network is critical for misfolded protein clearance and survival in cancer cells. Oncogene, 2020, 39, 801-813.	5.9	16
6	Passive immunotherapies targeting Aβ and tau in Alzheimer's disease. Neurobiology of Disease, 2020, 144, 105010.	4.4	81
7	Epitope prediction for oligomerâ€selective antibodies in tau and Aβ. Alzheimer's and Dementia, 2020, 16, e045757.	0.8	0
8	TNF receptor–associated factor 6 interacts with ALS-linked misfolded superoxide dismutase 1 and promotes aggregation. Journal of Biological Chemistry, 2020, 295, 3808-3825.	3.4	16
9	Purification and Structural Characterization of Aggregation-Prone Human TDP-43 Involved in Neurodegenerative Diseases. IScience, 2020, 23, 101159.	4.1	19
10	Emerging Developments in Targeting Proteotoxicity in Neurodegenerative Diseases. CNS Drugs, 2019, 33, 883-904.	5.9	23
11	A Rationally Designed Humanized Antibody Selective for Amyloid Beta Oligomers in Alzheimer's Disease. Scientific Reports, 2019, 9, 9870.	3.3	35
12	Prion-Like Propagation of Protein Misfolding and Aggregation in Amyotrophic Lateral Sclerosis. Frontiers in Molecular Neuroscience, 2019, 12, 262.	2.9	101
13	CuATSM Protects Against the <i>In Vitro</i> Cytotoxicity of Wild-Type-Like Copper–Zinc Superoxide Dismutase Mutants but not Mutants That Disrupt Metal Binding. ACS Chemical Neuroscience, 2019, 10, 1555-1564.	3.5	21
14	A Rational Structured Epitope Defines a Distinct Subclass of Toxic Amyloid-beta Oligomers. ACS Chemical Neuroscience, 2018, 9, 1591-1606.	3.5	21
15	Soft Vibrational Modes Predict Breaking Events during Force-Induced Protein Unfolding. Biophysical Journal, 2018, 114, 562-569.	0.5	6
16	pH dependent membrane binding of the Solanum tuberosum plant specific insert: An in silico study. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 2608-2618.	2.6	4
17	Prediction of Misfolding-Specific Epitopes in SOD1 Using Collective Coordinates. Journal of Physical Chemistry B, 2018, 122, 11662-11676.	2.6	27
18	The unfolding mechanism of monomeric mutant SOD1 by simulated force spectroscopy. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1631-1642.	2.3	14

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19	As Simple As Possible, but Not Simpler: Exploring the Fidelity of Coarse-Grained Protein Models for Simulated Force Spectroscopy. PLoS Computational Biology, 2016, 12, e1005211.	3.2	32
20	P4â€299: A Computational Method to Predict Diseaseâ€Specific Epitopes in Aβ, and its Application to Oligomerâ€Selective Antibodies for Alzheimer'S Immunotherapy. Alzheimer's and Dementia, 2016, 12, P1148.	0.8	1
21	Protein Transfer Free Energy Obeys Entropy-Enthalpy Compensation. Journal of Physical Chemistry B, 2015, 119, 14130-14144.	2.6	14
22	Intercellular propagated misfolding of wild-type Cu/Zn superoxide dismutase occurs via exosome-dependent and -independent mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3620-3625.	7.1	373
23	SOD1 exhibits allosteric frustration to facilitate metal binding affinity. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3871-3876.	7.1	46
24	Mechanical Probes of SOD1 Predict Systematic Trends in Metal and Dimer Affinity of ALS-Associated Mutants. Journal of Molecular Biology, 2013, 425, 850-874.	4.2	24
25	Polymer Uncrossing and Knotting in Protein Folding, and Their Role in Minimal Folding Pathways. PLoS ONE, 2013, 8, e53642.	2.5	7
26	A theory for the anisotropic and inhomogeneous dielectric properties of proteins. Physical Chemistry Chemical Physics, 2011, 13, 6286.	2.8	38
27	Toward a Mechanism of Prion Misfolding and Structural Models of PrP ^{Sc} : Current Knowledge and Future Directions. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2011, 74, 154-160.	2.3	15
28	Improved Measures for the Shape of a Disordered Polymer To Test a Mean-Field Theory of Collapse. Macromolecules, 2011, 44, 6182-6197.	4.8	16
29	Intermolecular transmission of superoxide dismutase 1 misfolding in living cells. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16398-16403.	7.1	234
30	Electrostatics in the stability and misfolding of the prion protein: salt bridges, self energy, and solvationThis paper is one of a selection of papers published in this special issue entitled "Canadian Society of Biochemistry, Molecular & amp; Cellular Biology 52nd Annual Meeting — Protein Folding: Principles and Diseasesâ€and has undergone the Journal's usual peer review process Biochemistry and	2.0	32
31	Cell Biology, 2010, 88, 371-381. Immunological mimicry of PrPC-PrPSc interactions: antibody-induced PrP misfolding. Protein Engineering, Design and Selection, 2009, 22, 523-529.	2.1	21
32	Structural alignment using the generalized Euclidean distance between conformations. International Journal of Quantum Chemistry, 2009, 109, 3217-3228.	2.0	5
33	Minimal Folding Pathways for Coarse-Grained Biopolymer Fragments. Biophysical Journal, 2008, 95, 5496-5507.	0.5	4
34	Minimal distance transformations between links and polymers: principles and examples. Journal of Physics Condensed Matter, 2008, 20, 244133.	1.8	4
35	Generalization of distance to higher dimensional objects. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14899-14904.	7.1	10
36	The effects of nonnative interactions on protein folding rates: Theory and simulation. Protein Science, 2004, 13, 1750-1766.	7.6	158

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37	Buffed energy landscapes: Another solution to the kinetic paradoxes of protein folding. Proceedings of the United States of America, 2003, 100, 4417-4422.	7.1	29
38	Structural and energetic heterogeneity in protein folding. I. Theory. Journal of Chemical Physics, 2002, 116, 5263.	3.0	32
39	Understanding protein folding with energy landscape theory Part II: Quantitative aspects. Quarterly Reviews of Biophysics, 2002, 35, 205-286.	5.7	91
40	Understanding protein folding with energy landscape theory Part I: Basic concepts. Quarterly Reviews of Biophysics, 2002, 35, 111-167.	5.7	179
41	Speeding protein folding beyond the G? model: How a little frustration sometimes helps. Proteins: Structure, Function and Bioinformatics, 2001, 45, 337-345.	2.6	61
42	Non-Markovian Configurational Diffusion and Reaction Coordinates for Protein Folding. Physical Review Letters, 1998, 80, 5015-5018.	7.8	96
43	Statistical mechanics of a correlated energy landscape model for protein folding funnels. Journal of Chemical Physics, 1997, 106, 2932-2948.	3.0	145
44	Correlated energy landscape model for finite, random heteropolymers. Physical Review E, 1996, 53, 6271-6296.	2.1	88