

Elizabeth M Meiering

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,090
citations

516710

16
h-index

501196

28
g-index

32
all docs

32
docs citations

32
times ranked

1584
citing authors

#	ARTICLE	IF	CITATIONS
1	Sonication of proteins causes formation of aggregates that resemble amyloid. <i>Protein Science</i> , 2008, 13, 3017-3027.	7.6	341
2	Decreased stability and increased formation of soluble aggregates by immature superoxide dismutase do not account for disease severity in ALS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2210-2215.	7.1	98
3	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. <i>ELife</i> , 2015, 4, e07296.	6.0	91
4	ALS-linked misfolded SOD1 species have divergent impacts on mitochondria. <i>Acta Neuropathologica Communications</i> , 2016, 4, 43.	5.2	57
5	Exploring the relationships between protein sequence, structure and solubility. <i>Current Opinion in Structural Biology</i> , 2017, 42, 136-146.	5.7	56
6	Effects of maturation on the conformational free-energy landscape of SOD1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2546-E2555.	7.1	48
7	Probing the free energy landscapes of ALS disease mutants of SOD1 by NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6939-E6945.	7.1	47
8	Destabilization of the dimer interface is a common consequence of diverse <sc>ALS</sc>-associated mutations in metal free <sc>SOD1</sc>. <i>Protein Science</i> , 2015, 24, 2081-2089.	7.6	40
9	Designed protein reveals structural determinants of extreme kinetic stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14605-14610.	7.1	33
10	Computational Modeling of Protein Stability: Quantitative Analysis Reveals Solutions to Pervasive Problems. <i>Structure</i> , 2020, 28, 717-726.e3.	3.3	33
11	Purification and characterization of recombinant <i>Thermotoga maritima</i> dihydrofolate reductase. <i>FEBS Journal</i> , 1998, 255, 628-637.	0.2	32
12	Many roads lead to Rome? Multiple modes of Cu,Zn superoxide dismutase destabilization, misfolding and aggregation in amyotrophic lateral sclerosis. <i>Essays in Biochemistry</i> , 2014, 56, 149-165.	4.7	27
13	The Threat of Instability: Neurodegeneration Predicted by Protein Destabilization and Aggregation Propensity. <i>PLoS Biology</i> , 2008, 6, e193.	5.6	25
14	Thermodynamics of Denaturation of Hisactophilin, a β^2 -Trefoil Protein. <i>Biochemistry</i> , 2001, 40, 3817-3827.	2.5	24
15	Temperature dependence of NMR chemical shifts: Tracking and statistical analysis. <i>Protein Science</i> , 2020, 29, 306-314.	7.6	23
16	Ensemble Modeling and Intracellular Aggregation of an Engineered Immunoglobulin-Like Domain. <i>Journal of Molecular Biology</i> , 2016, 428, 1365-1374.	4.2	18
17	Combined Isothermal Titration and Differential Scanning Calorimetry Define Three-State Thermodynamics of fALS-Associated Mutant Apo SOD1 Dimers and an Increased Population of Folded Monomer. <i>Biochemistry</i> , 2016, 55, 519-533.	2.5	18
18	TNF receptor-associated factor 6 interacts with ALS-linked misfolded superoxide dismutase 1 and promotes aggregation. <i>Journal of Biological Chemistry</i> , 2020, 295, 3808-3825.	3.4	16

#	ARTICLE	IF	CITATIONS
19	Spectrophotometric method for simultaneous measurement of zinc and copper in metalloproteins using 4-(2-pyridylazo)resorcinol. <i>Analytical Biochemistry</i> , 2019, 579, 44-56.	2.4	12
20	Wild-type and mutant SOD1 localizes to RNA-rich structures in cells and mice but does not bind RNA. <i>Journal of Neurochemistry</i> , 2021, 156, 524-538.	3.9	10
21	Evolution of magnetization due to asymmetric dimerization: theoretical considerations and application to aberrant oligomers formed by apoSOD1^{2SH}. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 5720-5728.	2.8	8
22	Using natural sequences and modularity to design common and novel protein topologies. <i>Current Opinion in Structural Biology</i> , 2016, 38, 26-36.	5.7	7
23	Asymmetric Anchoring Is Required for Efficient Î©-Loop Opening and Closing in Cytosolic Phosphoenolpyruvate Carboxykinase. <i>Biochemistry</i> , 2017, 56, 2106-2115.	2.5	7
24	Insight into the Autosomal-Dominant Inheritance Pattern of SOD1-Associated ALS from Native Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2020, 432, 5995-6002.	4.2	6
25	Methodological advances and strategies for high resolution structure determination of cellular protein aggregates. <i>Journal of Biological Chemistry</i> , 2022, 298, 102197.	3.4	6
26	A fine balance of hydrophobic-electrostatic communication pathways in a pH-switching protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	3
27	Design for Solubility May Reveal Induction of Amide Hydrogen/Deuterium Exchange by Protein Self-Association. <i>Journal of Molecular Biology</i> , 2022, 434, 167398.	4.2	1
28	High Resolution NMR H/D Exchange of Human Superoxide Dismutase Inclusion Bodies Reveals Significant Native Features Despite Structural Heterogeneity. <i>Angewandte Chemie - International Edition</i> , 2022, , .	13.8	1
29	Quenched hydrogen-deuterium amide exchange optimization for high-resolution structural analysis of cellular protein aggregates. <i>Analytical Biochemistry</i> , 2022, , 114675.	2.4	1
30	Editorial overview: Sequences and topology: Protein function - synthesizing information from sequence, structure and disorder. <i>Current Opinion in Structural Biology</i> , 2016, 38, vii-ix.	5.7	0
31	High Resolution NMR H/D Exchange of Human Superoxide Dismutase Inclusion Bodies Reveals Significant Native Features Despite Structural Heterogeneity. <i>Angewandte Chemie</i> , 0, , .	2.0	0