Joseph A. Marsh

List of Publications by Year
in descending order

73 papers	5,739 citations	94433 37 h-index	88630 70 g-index
87 all docs	87 docs citations	87 times ranked	8097 citing authors

#	Article	IF	Citations
1	Sensitivity of secondary structure propensities to sequence differences between Î±- and Î³-synuclein: Implications for fibrillation. Protein Science, 2006, 15, 2795-2804.	7.6	648
2	Structure, Dynamics, Assembly, and Evolution of Protein Complexes. Annual Review of Biochemistry, 2015, 84, 551-575.	11.1	351
3	Sequence Determinants of Compaction in Intrinsically Disordered Proteins. Biophysical Journal, 2010, 98, 2383-2390.	0.5	342
4	Kinetic Analysis of Protein Stability Reveals Age-Dependent Degradation. Cell, 2016, 167, 803-815.e21.	28.9	259
5	Structure/Function Implications in a Dynamic Complex of the Intrinsically Disordered Sic1 with the Cdc4 Subunit of an SCF Ubiquitin Ligase. Structure, 2010, 18, 494-506.	3.3	239
6	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. Cell, 2013, 153, 461-470.	28.9	215
7	Principles of assembly reveal a periodic table of protein complexes. Science, 2015, 350, aaa2245.	12.6	198
8	Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. Structure, 2011, 19, 859-867.	3.3	174
9	Structure and Disorder in an Unfolded State under Nondenaturing Conditions from Ensemble Models Consistent with a Large Number of Experimental Restraints. Journal of Molecular Biology, 2009, 391, 359-374.	4.2	144
10	Characterization of disordered proteins with ENSEMBLE. Bioinformatics, 2013, 29, 398-399.	4.1	141
11	SMCHD1 mutations associated with a rare muscular dystrophy can also cause isolated arhinia and Bosma arhinia microphthalmia syndrome. Nature Genetics, 2017, 49, 238-248.	21.4	131
12	Mutations in COPA lead to abnormal trafficking of STING to the Golgi and interferon signaling. Journal of Experimental Medicine, 2020, 217, .	8.5	130
13	Interrogation of Mammalian Protein Complex Structure, Function, and Membership Using Genome-Scale Fitness Screens. Cell Systems, 2018, 6, 555-568.e7.	6.2	126
14	Using deep mutational scanning to benchmark variant effect predictors and identify disease mutations. Molecular Systems Biology, 2020, 16, e9380.	7.2	120
15	Structural Diversity in Free and Bound States of Intrinsically Disordered Protein Phosphatase 1 Regulators. Structure, 2010, 18, 1094-1103.	3.3	110
16	Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. Nature Genetics, 2019, 51, 96-105.	21.4	110
17	Improved Structural Characterizations of the drkN SH3 Domain Unfolded State Suggest a Compact Ensemble with Native-like and Non-native Structure. Journal of Molecular Biology, 2007, 367, 1494-1510.	4.2	109
18	Ensemble modeling of protein disordered states: Experimental restraint contributions and validation. Proteins: Structure, Function and Bioinformatics, 2012, 80, 556-572.	2.6	107

#	Article	IF	Citations
19	Evolution of condensin and cohesin complexes driven by replacement of Kite by Hawk proteins. Current Biology, 2017, 27, R17-R18.	3.9	98
20	Probing the diverse landscape of protein flexibility and binding. Current Opinion in Structural Biology, 2012, 22, 643-650.	5.7	94
21	Operon Gene Order Is Optimized for Ordered Protein Complex Assembly. Cell Reports, 2016, 14, 679-685.	6.4	91
22	Protein Flexibility Facilitates Quaternary Structure Assembly and Evolution. PLoS Biology, 2014, 12, e1001870.	5.6	89
23	Alpha Helices Are More Robust to Mutations than Beta Strands. PLoS Computational Biology, 2016, 12, e1005242.	3.2	85
24	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. Genes and Development, 2019, 33, 1031-1047.	5.9	83
25	The Role of Salt Bridges, Charge Density, and Subunit Flexibility in Determining Disassembly Routes of Protein Complexes. Structure, 2013, 21, 1325-1337.	3.3	82
26	A Restricted Repertoire of De Novo Mutations in ITPR1 Cause Gillespie Syndrome with Evidence for Dominant-Negative Effect. American Journal of Human Genetics, 2016, 98, 981-992.	6.2	81
27	The emergence of protein complexes: quaternary structure, dynamics and allostery. Biochemical Society Transactions, 2012, 40, 475-491.	3.4	75
28	How do proteins gain new domains?. Genome Biology, 2010, 11, 126.	9.6	70
29	Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. BioEssays, 2014, 36, 209-218.	2.5	68
30	Calculation of Residual Dipolar Couplings from Disordered State Ensembles Using Local Alignment. Journal of the American Chemical Society, 2008, 130, 7804-7805.	13.7	67
31	Identification of pathogenic missense mutations using protein stability predictors. Scientific Reports, 2020, 10, 15387.	3.3	66
32	Buried and Accessible Surface Area Control Intrinsic Protein Flexibility. Journal of Molecular Biology, 2013, 425, 3250-3263.	4.2	62
33	Regulation, evolution and consequences of cotranslational protein complex assembly. Current Opinion in Structural Biology, 2017, 42, 90-97.	5.7	62
34	Intrinsic lipid binding activity of <scp>ATG</scp> 16L1 supports efficient membrane anchoring and autophagy. EMBO Journal, 2019, 38, .	7.8	59
35	The role of protein complexes in human genetic disease. Protein Science, 2019, 28, 1400-1411.	7.6	53
36	Synuclein-Î³ Targeting Peptide Inhibitor that Enhances Sensitivity of Breast Cancer Cells to Antimicrotubule Drugs. Cancer Research, 2007, 67, 626-633.	0.9	52

#	Article	IF	Citations
37	Functional determinants of protein assembly into homomeric complexes. Scientific Reports, 2017, 7, 4932.	3.3	52
38	Structural and evolutionary versatility in protein complexes with uneven stoichiometry. Nature Communications, 2015, 6, 6394.	12.8	48
39	Structural Signature of the MYPT1â˜PP1 Interaction. Journal of the American Chemical Society, 2011, 133, 73-80.	13.7	44
40	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. Nature Structural and Molecular Biology, 2018, 25, 279-288.	8.2	43
41	Recurrent heterozygous PAX6 missense variants cause severe bilateral microphthalmia via predictable effects on DNAâ€“protein interaction. Genetics in Medicine, 2020, 22, 598-609.	2.4	43
42	Diverse Molecular Mechanisms Underlying Pathogenic Protein Mutations: Beyond the Loss-of-Function Paradigm. Annual Review of Genomics and Human Genetics, 2022, 23, 475-498.	6.2	41
43	Longitudinal dynamics of clonal hematopoiesis identifies gene-specific fitness effects. Nature Medicine, 2022, 28, 1439-1446.	30.7	36
44	Heterozygous lamin B1 and lamin B2 variants cause primary microcephaly and define a novel laminopathy. Genetics in Medicine, 2021, 23, 408-414.	2.4	35
45	Ligand-Binding-Site Structure Shapes Allosteric Signal Transduction and the Evolution of Allostery in Protein Complexes. Molecular Biology and Evolution, 2019, 36, 1711-1727.	8.9	33
46	Co-translational assembly of protein complexes. Biochemical Society Transactions, 2015, 43, 1221-1226.	3.4	32
47	Novel pathogenic mutations in C1QTNF5 support a dominant negative disease mechanism in late-onset retinal degeneration. Scientific Reports, 2017, 7, 12147.	3.3	30
48	A WDR35-dependent coat protein complex transports ciliary membrane cargo vesicles to cilia. ELife, 2021, 10, .	6.0	29
49	Oxygen as a Paramagnetic Probe of Clustering and Solvent Exposure in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2007, 129, 1826-1835.	13.7	28
50	Interpreting protein variant effects with computational predictors and deep mutational scanning. DMM Disease Models and Mechanisms, 2022, 15, .	2.4	25
51	Mouse Idh3a mutations cause retinal degeneration and reduced mitochondrial function. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	23
52	PRIM1 deficiency causes a distinctive primordial dwarfism syndrome. Genes and Development, 2020, 34, 1520-1533.	5.9	20
53	The properties of human disease mutations at protein interfaces. PLoS Computational Biology, 2022, 18, e1009858.	3.2	19
54	Ligand Binding Site Structure Influences the Evolution of Protein Complex Function and Topology. Cell Reports, 2018, 22, 3265-3276.	6.4	18

#	Article	IF	Citations
55	Biallelic variants in DNA2 cause microcephalic primordial dwarfism. Human Mutation, 2019, 40, 1063-1070.	2.5	16
56	The genetic basis and evolution of red blood cell sickling in deer. Nature Ecology and Evolution, 2018, 2, 367-376.	7.8	14
57	Signalling assemblies: the odds of symmetry. Biochemical Society Transactions, 2017, 45, 599-611.	3.4	9
58	ER stress-induced aggresome trafficking of HtrA1 protects against proteotoxicity. Journal of Molecular Cell Biology, 2017, 9, 516-532.	3.3	9
59	Ligands and Receptors with Broad Binding Capabilities Have Common Structural Characteristics: An Antibiotic Design Perspective. Journal of Medicinal Chemistry, 2019, 62, 9357-9374.	6.4	9
60	Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195.	3.2	9
61	Finding Diagnostically Useful Patterns in Quantitative Phenotypic Data. American Journal of Human Genetics, 2019, 105, 933-946.	6.2	8
62	Structural Determinants of Sleeping Beauty Transposase Activity. Molecular Therapy, 2016, 24, 1369-1377.	8.2	7
63	Fast and Accurate Resonance Assignment of Small-to-Large Proteins by Combining Automated and Manual Approaches. PLoS Computational Biology, 2015, 11, e1004022.	3.2	6
64	Characterization of a novel RP2-OSTF1 interaction and its implication for actin remodeling. Journal of Cell Science, 2018, 131, .	2.0	6
65	Rheumatoid factor positive polyarticular juvenile idiopathic arthritis associated with a novel COPA mutation. Rheumatology, 2021, 60, e171-e173.	1.9	6
66	Ligand Binding Site Structure Shapes Folding, Assembly and Degradation of Homomeric Protein Complexes. Journal of Molecular Biology, 2019, 431, 3871-3888.	4.2	5
67	Experimental Characterization of Protein Complex Structure, Dynamics, and Assembly. Methods in Molecular Biology, 2018, 1764, 3-27.	0.9	4
68	Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. Molecular Metabolism, 2022, 61, 101509.	6.5	3
69	Computational Modelling of Protein Complex Structure and Assembly. Methods in Molecular Biology, 2018, 1764, 347-356.	0.9	2
70	A Graph-Based Approach for Detecting Sequence Homology in Highly Diverged Repeat Protein Families. Methods in Molecular Biology, 2019, 1851, 251-261.	0.9	2
71	Evolution of protein interfaces in multimers and fibrils. Journal of Chemical Physics, 2019, 150, 225102.	3.0	1
72	Editorial overview: Sequences and topology: Dynamic sequences and topologies of proteins. Current Opinion in Structural Biology, 2018, 50, vii-viii.	5.7	0

#	Article	IF	Citations
73	Novel biallelic USH2A variants in a patient with usher syndrome type IIA- a case report. BMC Ophthalmology, 2022, 22, 140.	1.4	0