

# Emre Brookes

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1124257/publications.pdf>

Version: 2024-02-01

55  
papers

2,023  
citations

331670

21  
h-index

276875

41  
g-index

57  
all docs

57  
docs citations

57  
times ranked

2648  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Disulfide-Stabilized A $\beta$ 2 that Forms Dimers but Does Not Form Fibrils. <i>Biochemistry</i> , 2022, 61, 252-264.	2.5	4
2	Biophysical characterisation of human LincRNA-p21 sense and antisense Alu inverted repeats. <i>Nucleic Acids Research</i> , 2022, 50, 5881-5898.	14.5	8
3	Multi-wavelength analytical ultracentrifugation of biopolymer mixtures and interactions. <i>Analytical Biochemistry</i> , 2022, 652, 114728.	2.4	10
4	Neuropathy-associated histidyl-tRNA synthetase variants attenuate protein synthesis in vitro and disrupt axon outgrowth in developing zebrafish. <i>FEBS Journal</i> , 2021, 288, 142-159.	4.7	13
5	The pH-Induced Selectivity Between Cysteine or Histidine Coordinated Heme in an Artificial Helical Metalloprotein. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 3974-3978.	13.8	10
6	The pH-Induced Selectivity Between Cysteine or Histidine Coordinated Heme in an Artificial Helical Metalloprotein. <i>Angewandte Chemie</i> , 2021, 133, 4020-4024.	2.0	2
7	Characterizing Drug-Polymer Interactions in Aqueous Solution with Analytical Ultracentrifugation. <i>Molecular Pharmaceutics</i> , 2021, 18, 246-256.	4.6	5
8	Nucleic acid binding by SAMHD1 contributes to the antiretroviral activity and is enhanced by the GpsN modification. <i>Nature Communications</i> , 2021, 12, 731.	12.8	26
9	Density Matching Multi-wavelength Analytical Ultracentrifugation to Measure Drug Loading of Lipid Nanoparticle Formulations. <i>ACS Nano</i> , 2021, 15, 5068-5076.	14.6	21
10	Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. <i>Nature Communications</i> , 2021, 12, 1988.	12.8	16
11	Human DDX17 Unwinds Rift Valley Fever Virus Non-Coding RNAs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 54.	4.1	20
12	Molecular Architecture of the Antiophidic Protein DM64 and its Binding Specificity to Myotoxin II From <i>Bothrops asper</i> Venom. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 787368.	3.5	2
13	A calibration disk for the correction of radial errors from chromatic aberration and rotor stretch in the Optima AUC analytical ultracentrifuge. <i>European Biophysics Journal</i> , 2020, 49, 701-709.	2.2	9
14	Multi-wavelength analytical ultracentrifugation as a tool to characterise protein-DNA interactions in solution. <i>European Biophysics Journal</i> , 2020, 49, 819-827.	2.2	10
15	Measuring compressibility in the optima AUC analytical ultracentrifuge. <i>European Biophysics Journal</i> , 2020, 49, 711-718.	2.2	4
16	Moving analytical ultracentrifugation software to a good manufacturing practices (GMP) environment. <i>PLoS Computational Biology</i> , 2020, 16, e1007942.	3.2	20
17	The BRPF1 bromodomain is a molecular reader of di-acetyllsine. <i>Current Research in Structural Biology</i> , 2020, 2, 104-115.	2.2	16
18	Nanoscale Structure Determination of Murray Valley Encephalitis and Powassan Virus Non-Coding RNAs. <i>Viruses</i> , 2020, 12, 190.	3.3	12

#	ARTICLE	IF	CITATIONS
19	Probing RNA-Protein Interactions and RNA Compaction by Sedimentation Velocity Analytical Ultracentrifugation. <i>Methods in Molecular Biology</i> , 2020, 2113, 281-317.	0.9	2
20	Moving analytical ultracentrifugation software to a good manufacturing practices (GMP) environment. , 2020, 16, e1007942.		0
21	Moving analytical ultracentrifugation software to a good manufacturing practices (GMP) environment. , 2020, 16, e1007942.		0
22	Crystallographic Structures of IlvN-Val/Ile Complexes: Conformational Selectivity for Feedback Inhibition of Aceto Hydroxy Acid Synthases. <i>Biochemistry</i> , 2019, 58, 1992-2008.	2.5	3
23	A Proteomic Screen of Neuronal Cell-Surface Molecules Reveals IgLONs as Structurally Conserved Interaction Modules at the Synapse. <i>Structure</i> , 2019, 27, 893-906.e9.	3.3	44
24	Structure-Function Studies of the <i>Bacillus subtilis</i> Ric Proteins Identify the Fe-S Cluster-Ligating Residues and Their Roles in Development and RNA Processing. <i>MBio</i> , 2019, 10, .	4.1	12
25	Multi-wavelength analytical ultracentrifugation of human serum albumin complexed with porphyrin. <i>European Biophysics Journal</i> , 2018, 47, 789-797.	2.2	16
26	General Model for Retroviral Capsid Pattern Recognition by TRIM5 Proteins. <i>Journal of Virology</i> , 2018, 92, .	3.4	24
27	Structural and functional characterisation of the entry point to pyocyanin biosynthesis in <i>Pseudomonas aeruginosa</i> defines a new 3-deoxy- <i>d</i> -arabino-heptulosonate 7-phosphate synthase subclass. <i>Bioscience Reports</i> , 2018, 38, .	2.4	14
28	Multi-speed sedimentation velocity simulations with UltraScan-III. <i>European Biophysics Journal</i> , 2018, 47, 815-823.	2.2	11
29	Two-dimensional grid optimization for sedimentation velocity analysis in the analytical ultracentrifuge. <i>European Biophysics Journal</i> , 2018, 47, 837-844.	2.2	4
30	The Usher Syndrome Type IIIB Histidyl-tRNA Synthetase Mutation Confers Temperature Sensitivity. <i>Biochemistry</i> , 2017, 56, 3619-3631.	2.5	19
31	Spectral and Hydrodynamic Analysis of West Nile Virus RNA-Protein Interactions by Multiwavelength Sedimentation Velocity in the Analytical Ultracentrifuge. <i>Analytical Chemistry</i> , 2017, 89, 862-870.	6.5	24
32	2D analysis of polydisperse core-shell nanoparticles using analytical ultracentrifugation. <i>Analyst</i> , 2017, 142, 206-217.	3.5	25
33	Pih1p-Tah1p Puts a Lid on Hexameric AAA+ ATPases Rvb1/2p. <i>Structure</i> , 2017, 25, 1519-1529.e4.	3.3	22
34	Structure of a pentameric virion-associated fiber with a potential role in Orsay virus entry to host cells. <i>PLoS Pathogens</i> , 2017, 13, e1006231.	4.7	11
35	US-SOMO HPLC-SAXS module: dealing with capillary fouling and extraction of pure component patterns from poorly resolved SEC-SAXS data. <i>Journal of Applied Crystallography</i> , 2016, 49, 1827-1841.	4.5	86
36	KDM2B Recruitment of the Polycomb Group Complex, PRC1.1, Requires Cooperation between PCGF1 and BCORL1. <i>Structure</i> , 2016, 24, 1795-1801.	3.3	49

#	ARTICLE	IF	CITATIONS
37	BMI1 regulates PRC1 architecture and activity through homo- and hetero-oligomerization. <i>Nature Communications</i> , 2016, 7, 13343.	12.8	52
38	A new mode of SAM domain mediated oligomerization observed in the CASKIN2 neuronal scaffolding protein. <i>Cell Communication and Signaling</i> , 2016, 14, 17.	6.5	11
39	Cryo-EM reveals a novel octameric integrase structure for betaretroviral intasome function. <i>Nature</i> , 2016, 530, 358-361.	27.8	88
40	Analytical Ultracentrifugation Data Analysis with UltraScan-III. , 2016, , 119-143.		62
41	Next-Generation AUC. <i>Methods in Enzymology</i> , 2015, 562, 27-47.	1.0	33
42	Next-Generation AUC Adds a Spectral Dimension. <i>Methods in Enzymology</i> , 2015, 562, 1-26.	1.0	32
43	Aspheric Solute Ions Modulate Gold Nanoparticle Interactions in an Aqueous Solution: An Optimal Way To Reversibly Concentrate Functionalized Nanoparticles. <i>Journal of Physical Chemistry B</i> , 2015, 119, 15502-15508.	2.6	8
44	Structural and Mechanistic Insights into the Latrophilin3-FLRT3 Complex that Mediates Glutamatergic Synapse Development. <i>Structure</i> , 2015, 23, 1665-1677.	3.3	42
45	Structural basis of HIV-1 capsid recognition by PF74 and CPSF6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18625-18630.	7.1	215
46	A Parametrically Constrained Optimization Method for Fitting Sedimentation Velocity Experiments. <i>Biophysical Journal</i> , 2014, 106, 1741-1750.	0.5	56
47	Characterization of Size, Anisotropy, and Density Heterogeneity of Nanoparticles by Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 7688-7695.	6.5	74
48	Fibrinogen species as resolved by HPLC-SAXS data processing within the UltraScan Solution Modeler (US-SOMO) enhanced SAS module. <i>Journal of Applied Crystallography</i> , 2013, 46, 1823-1833.	4.5	57
49	A two-dimensional spectrum analysis for sedimentation velocity experiments of mixtures with heterogeneity in molecular weight and shape. <i>European Biophysics Journal</i> , 2010, 39, 405-414.	2.2	198
50	The implementation of SOMO (SOlution MOdeller) in the UltraScan analytical ultracentrifugation data analysis suite: enhanced capabilities allow the reliable hydrodynamic modeling of virtually any kind of biomacromolecule. <i>European Biophysics Journal</i> , 2010, 39, 423-435.	2.2	111
51	Developments in the US-SOMO Bead Modeling Suite: New Features in the Direct Residue-Bead Method, Improved Grid Routines, and Influence of Accessible Surface Area Screening. <i>Macromolecular Bioscience</i> , 2010, 10, 746-753.	4.1	55
52	Methods for the Design and Analysis of Sedimentation Velocity and Sedimentation Equilibrium Experiments with Proteins. <i>Current Protocols in Protein Science</i> , 2010, 60, Unit 7.13.	2.8	82
53	Chapter 4 Analysis of Heterogeneity in Molecular Weight and Shape by Analytical Ultracentrifugation Using Parallel Distributed Computing. <i>Methods in Enzymology</i> , 2009, 454, 87-113.	1.0	35
54	Sedimentation velocity analysis of highly heterogeneous systems. <i>Analytical Biochemistry</i> , 2004, 335, 279-288.	2.4	232

#	ARTICLE	IF	CITATIONS
55	Preformed GroES oligomers are not required as functional cochaperonins. The Protein Journal, 1997, 16, 661-668.	1.1	5