

# Darren J Hart

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4072356/publications.pdf>

Version: 2024-02-01

58  
papers

4,115  
citations

201674

27  
h-index

144013

57  
g-index

61  
all docs

61  
docs citations

61  
times ranked

4841  
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly of The Mitochondrial Complexâ€¦I Assembly Complex Suggests a Regulatory Role for Deflavination. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 4689-4697.	13.8	14
2	Assembly of The Mitochondrial Complexâ€¦I Assembly Complex Suggests a Regulatory Role for Deflavination. <i>Angewandte Chemie</i> , 2021, 133, 4739-4747.	2.0	0
3	Molecular basis of host-adaptation interactions between influenza virus polymerase PB2 subunit and ANP32A. <i>Nature Communications</i> , 2020, 11, 3656.	12.8	43
4	The K296-D320 region of recombinant levansucrase BA-SacB can affect the sensitivity of <i>Escherichia coli</i> host to sucrose. <i>Annals of Microbiology</i> , 2019, 69, 1147-1154.	2.6	2
5	Functional Metagenomic Technologies for the Discovery of Novel Enzymes for Biomass Degradation and Biofuel Production. <i>Bioenergy Research</i> , 2019, 12, 457-470.	3.9	23
6	A universal mini-vector and an annealing of PCR products (APP)-based cloning strategy for convenient molecular biological manipulations. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 978-982.	2.1	7
7	Auxin sensing is a property of an unstructured domain in the Auxin Response Factor ETTIN of <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2018, 8, 13563.	3.3	19
8	Three Novel <i>Escherichia coli</i> Vectors for Convenient and Efficient Molecular Biological Manipulations. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 6123-6131.	5.2	17
9	Expression and Characterization of Levansucrase from <i>Clostridium acetobutylicum</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 867-871.	5.2	25
10	A structural organization for the Disrupted in Schizophrenia 1 protein, identified by high-throughput screening, reveals distinctly folded regions, which are bisected by mental illness-related mutations. <i>Journal of Biological Chemistry</i> , 2017, 292, 6468-6477.	3.4	22
11	ESPRIT: A Method for Defining Soluble Expression Constructs in Poorly Understood Gene Sequences. <i>Methods in Molecular Biology</i> , 2017, 1586, 45-63.	0.9	9
12	Structural insights into the architecture of the <i>Shigella flexneri</i> virulence factor IcsA/VirG and motifs involved in polar distribution and secretion. <i>Journal of Structural Biology</i> , 2017, 198, 19-27.	2.8	21
13	Signal peptide-dependent protein translocation pathway is crucial for the sucrose sensitivity of SacB-expressing <i>Escherichia coli</i> . <i>Biochemical Engineering Journal</i> , 2017, 122, 71-74.	3.6	4
14	Mouse Rif1 is a regulatory subunit of protein phosphatase 1 (PP1). <i>Scientific Reports</i> , 2017, 7, 2119.	3.3	41
15	Structural Characterization of the SMRT Corepressor Interacting with Histone Deacetylase 7. <i>Scientific Reports</i> , 2017, 7, 3678.	3.3	14
16	The vaccinia virus DNA polymerase structure provides insights into the mode of processivity factor binding. <i>Nature Communications</i> , 2017, 8, 1455.	12.8	31
17	Investigating the Role of Large-Scale Domain Dynamics in Protein-Protein Interactions. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 54.	3.5	23
18	Secondary Structure Prediction of Protein Constructs Using Random Incremental Truncation and Vacuum-Ultraviolet CD Spectroscopy. <i>PLoS ONE</i> , 2016, 11, e0156238.	2.5	5

#	ARTICLE	IF	CITATIONS
19	Recent advances in universal TA cloning methods for use in function studies. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 551-556.	2.1	16
20	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , 2016, 24, 851-861.	3.3	21
21	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016, 61, 125-137.	9.7	123
22	Molecular Determinants for Nuclear Import of Influenza A PB2 by Importin $\hat{\pm}$ Isoforms 3 and 7. <i>Structure</i> , 2015, 23, 374-384.	3.3	87
23	Large-Scale Conformational Dynamics Control H5N1 Influenza Polymerase PB2 Binding to Importin $\hat{\pm}$ . <i>Journal of the American Chemical Society</i> , 2015, 137, 15122-15134.	13.7	49
24	Structural insight into cap-snatching and RNA synthesis by influenza polymerase. <i>Nature</i> , 2014, 516, 361-366.	27.8	376
25	Structural and Biophysical Characterization of Murine Rif1 C Terminus Reveals High Specificity for DNA Cruciform Structures. <i>Journal of Biological Chemistry</i> , 2014, 289, 13903-13911.	3.4	32
26	Structural Basis for the Oligomerization of the MADS Domain Transcription Factor SEPALLATA3 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 3603-3615.	6.6	97
27	Library methods for structural biology of challenging proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 2013, 23, 403-408.	5.7	19
28	Nucleoporin Nup50 Stabilizes Closed Conformation of Armadillo repeat 10 in Importin $\hat{\pm}$ 5. <i>Journal of Biological Chemistry</i> , 2012, 287, 2022-2031.	3.4	22
29	Structure of the Phosphatase Domain of the Cell Fate Determinant SpoIIIE from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2012, 415, 343-358.	4.2	27
30	Development of a Peptide that Selectively Activates Protein Phosphatase $\hat{\pm}$ 1 in Living Cells. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 10054-10059.	13.8	64
31	ORF-selector ESPRIT: A second generation library screen for soluble protein expression employing precise open reading frame selection. <i>Journal of Structural Biology</i> , 2011, 175, 189-197.	2.8	16
32	Library-based methods for identification of soluble expression constructs. <i>Methods</i> , 2011, 55, 38-43.	3.8	12
33	CoESPRIT: A Library-Based Construct Screening Method for Identification and Expression of Soluble Protein Complexes. <i>PLoS ONE</i> , 2011, 6, e16261.	2.5	15
34	Interaction of the Influenza A Virus Polymerase PB2 C-terminal Region with Importin $\hat{\pm}$ Isoforms Provides Insights into Host Adaptation and Polymerase Assembly. <i>Journal of Biological Chemistry</i> , 2011, 286, 10439-10448.	3.4	62
35	Structural studies of herpes virus terminase. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s25-s25.	0.3	0
36	Towards an atomic resolution understanding of the influenza virus replication machinery. <i>Current Opinion in Structural Biology</i> , 2010, 20, 104-113.	5.7	95

#	ARTICLE	IF	CITATIONS
37	Structure and inhibition of herpesvirus DNA packaging terminase nuclease domain. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16078-16083.	7.1	102
38	Expression of soluble, active fragments of the morphogenetic protein SpoIIE from <i>Bacillus subtilis</i> using a library-based construct screen. Protein Engineering, Design and Selection, 2010, 23, 817-825.	2.1	10
39	Influenza A Virus Polymerase: Structural Insights into Replication and Host Adaptation Mechanisms. Journal of Biological Chemistry, 2010, 285, 28411-28417.	3.4	170
40	ESPRIT: An automated, library-based method for mapping and soluble expression of protein domains from challenging targets. Journal of Structural Biology, 2010, 172, 66-74.	2.8	50
41	Biological and Biophysical Properties of the Histone Deacetylase Inhibitor Suberoylanilide Hydroxamic Acid Are Affected by the Presence of Short Alkyl Groups on the Phenyl Ring. Journal of Medicinal Chemistry, 2010, 53, 1937-1950.	6.4	23
42	The cap-snatching endonuclease of influenza virus polymerase resides in the PA subunit. Nature, 2009, 458, 914-918.	27.8	630
43	Cooperative binding of two acetylation marks on a histone tail by a single bromodomain. Nature, 2009, 461, 664-668.	27.8	395
44	Expression of <i>Helicobacter pylori</i> CagA domains by library-based construct screening. FEBS Journal, 2009, 276, 816-824.	4.7	33
45	Solubility survey of fragments of the neurofibromatosis type 1 protein neurofibromin. Protein Expression and Purification, 2009, 65, 30-37.	1.3	24
46	The structural basis for cap binding by influenza virus polymerase subunit PB2. Nature Structural and Molecular Biology, 2008, 15, 500-506.	8.2	436
47	Host Determinant Residue Lysine 627 Lies on the Surface of a Discrete, Folded Domain of Influenza Virus Polymerase PB2 Subunit. PLoS Pathogens, 2008, 4, e1000136.	4.7	165
48	Structure and nuclear import function of the C-terminal domain of influenza virus polymerase PB2 subunit. Nature Structural and Molecular Biology, 2007, 14, 229-233.	8.2	275
49	Combinatorial library approaches for improving soluble protein expression in <i>Escherichia coli</i> . Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 19-26.	2.5	40
50	Implementation of semi-automated cloning and prokaryotic expression screening: the impact of SPINE. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1103-1113.	2.5	56
51	An approach to prevent aggregation during the purification and crystallization of wild type acyl coenzyme A: Isopenicillin N acyltransferase from <i>Penicillium chrysogenum</i> . Protein Expression and Purification, 2005, 41, 61-67.	1.3	10
52	Fabrication of Protein Function Microarrays for Systems-Oriented Proteomic Analysis. Methods in Molecular Biology, 2005, 310, 197-216.	0.9	13
53	Functional protein microarrays for parallel characterisation of p53 mutants. Proteomics, 2004, 4, 1950-1958.	2.2	78
54	A Biophysical Characterisation of Factors Controlling Dimerisation and Selectivity in the NF- $\kappa$ B and NFAT Families. Journal of Molecular Biology, 2004, 339, 1059-1075.	4.2	28

#	ARTICLE	IF	CITATIONS
55	Distamycin A affects the stability of NF- $\kappa$ B p50-DNA complexes in a sequence-dependent manner. <i>Journal of Molecular Recognition</i> , 2002, 15, 19-26.	2.1	6
56	Analysis of the NF- $\kappa$ B p50 dimer interface by diversity screening 1 Edited by J. Wells. <i>Journal of Molecular Biology</i> , 2001, 310, 563-575.	4.2	22
57	A new plasmid display technology for the in vitro selection of functional phenotype- $\kappa$ genotype linked proteins. <i>Chemistry and Biology</i> , 2001, 8, 951-965.	6.0	27
58	The salt dependence of DNA recognition by NF- $\kappa$ B p50: a detailed kinetic analysis of the effects on affinity and specificity. <i>Nucleic Acids Research</i> , 1999, 27, 1063-1069.	14.5	61