

Darren J Hart

List of Publications by Year in descending order

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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	The cap-snatching endonuclease of influenza virus polymerase resides in the PA subunit. <i>Nature</i> , 2009, 458, 914-918.	27.8	630
2	The structural basis for cap binding by influenza virus polymerase subunit PB2. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 500-506.	8.2	436
3	Cooperative binding of two acetylation marks on a histone tail by a single bromodomain. <i>Nature</i> , 2009, 461, 664-668.	27.8	395
4	Structural insight into cap-snatching and RNA synthesis by influenza polymerase. <i>Nature</i> , 2014, 516, 361-366.	27.8	376
5	Structure and nuclear import function of the C-terminal domain of influenza virus polymerase PB2 subunit. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 229-233.	8.2	275
6	Influenza A Virus Polymerase: Structural Insights into Replication and Host Adaptation Mechanisms. <i>Journal of Biological Chemistry</i> , 2010, 285, 28411-28417.	3.4	170
7	Host Determinant Residue Lysine 627 Lies on the Surface of a Discrete, Folded Domain of Influenza Virus Polymerase PB2 Subunit. <i>PLoS Pathogens</i> , 2008, 4, e1000136.	4.7	165
8	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
9	Structure and inhibition of herpesvirus DNA packaging terminase nuclease domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16078-16083.	7.1	102
10	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
11	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
12	Molecular Determinants for Nuclear Import of Influenza A PB2 by Importin β Isoforms 3 and 7. <i>Structure</i> , 2015, 23, 374-384.	3.3	87
13	Functional protein microarrays for parallel characterisation of p53 mutants. <i>Proteomics</i> , 2004, 4, 1950-1958.	2.2	78
14	Development of a Peptide that Selectively Activates Protein Phosphatase ϵ in Living Cells. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 10054-10059.	13.8	64
15	Interaction of the Influenza A Virus Polymerase PB2 C-terminal Region with Importin β Isoforms Provides Insights into Host Adaptation and Polymerase Assembly. <i>Journal of Biological Chemistry</i> , 2011, 286, 10439-10448.	3.4	62
16	The salt dependence of DNA recognition by NF- κ 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
17	Implementation of semi-automated cloning and prokaryotic expression screening: the impact of SPINE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1103-1113.	2.5	56
18	ESPRIT: An automated, library-based method for mapping and soluble expression of protein domains from challenging targets. <i>Journal of Structural Biology</i> , 2010, 172, 66-74.	2.8	50

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19	Large-Scale Conformational Dynamics Control H5N1 Influenza Polymerase PB2 Binding to Importin β . Journal of the American Chemical Society, 2015, 137, 15122-15134.	13.7	49
20	Molecular basis of host-adaptation interactions between influenza virus polymerase PB2 subunit and ANP32A. Nature Communications, 2020, 11, 3656.	12.8	43
21	Mouse Rif1 is a regulatory subunit of protein phosphatase 1 (PP1). Scientific Reports, 2017, 7, 2119.	3.3	41
22	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
23	Expression of <i>Helicobacter pylori</i> CagA domains by library-based construct screening. FEBS Journal, 2009, 276, 816-824.	4.7	33
24	Structural and Biophysical Characterization of Murine Rif1 C Terminus Reveals High Specificity for DNA Cruciform Structures. Journal of Biological Chemistry, 2014, 289, 13903-13911.	3.4	32
25	The vaccinia virus DNA polymerase structure provides insights into the mode of processivity factor binding. Nature Communications, 2017, 8, 1455.	12.8	31
26	A Biophysical Characterisation of Factors Controlling Dimerisation and Selectivity in the NF- κ B and NFAT Families. Journal of Molecular Biology, 2004, 339, 1059-1075.	4.2	28
27	A new plasmid display technology for the in vitro selection of functional phenotype-“genotype linked proteins. Chemistry and Biology, 2001, 8, 951-965.	6.0	27
28	Structure of the Phosphatase Domain of the Cell Fate Determinant SpoIIIE from Bacillus subtilis. Journal of Molecular Biology, 2012, 415, 343-358.	4.2	27
29	Expression and Characterization of Levansucrase from <i>Clostridium acetobutylicum</i> . Journal of Agricultural and Food Chemistry, 2017, 65, 867-871.	5.2	25
30	Solubility survey of fragments of the neurofibromatosis type 1 protein neurofibromin. Protein Expression and Purification, 2009, 65, 30-37.	1.3	24
31	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
32	Investigating the Role of Large-Scale Domain Dynamics in Protein-Protein Interactions. Frontiers in Molecular Biosciences, 2016, 3, 54.	3.5	23
33	Functional Metagenomic Technologies for the Discovery of Novel Enzymes for Biomass Degradation and Biofuel Production. Bioenergy Research, 2019, 12, 457-470.	3.9	23
34	Analysis of the NF- κ B p50 dimer interface by diversity screening 1 Edited by J. Wells. Journal of Molecular Biology, 2001, 310, 563-575.	4.2	22
35	Nucleoporin Nup50 Stabilizes Closed Conformation of Armadillo repeat 10 in Importin β . Journal of Biological Chemistry, 2012, 287, 2022-2031.	3.4	22
36	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. Journal of Biological Chemistry, 2017, 292, 6468-6477.	3.4	22

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37	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
38	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
39	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
40	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
41	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
42	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
43	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
44	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
45	Structural Characterization of the SMRT Corepressor Interacting with Histone Deacetylase 7. <i>Scientific Reports</i> , 2017, 7, 3678.	3.3	14
46	Assembly of The Mitochondrial Complexâ€¦I Assembly Complex Suggests a Regulatory Role for De flavination. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 4689-4697.	13.8	14
47	Fabrication of Protein Function Microarrays for Systems-Oriented Proteomic Analysis. <i>Methods in Molecular Biology</i> , 2005, 310, 197-216.	0.9	13
48	Library-based methods for identification of soluble expression constructs. <i>Methods</i> , 2011, 55, 38-43.	3.8	12
49	An approach to prevent aggregation during the purification and crystallization of wild type acyl coenzyme A: Isopenicillin N acyltransferase from <i>Penicillium chrysogenum</i> . <i>Protein Expression and Purification</i> , 2005, 41, 61-67.	1.3	10
50	Expression of soluble, active fragments of the morphogenetic protein SpoIIE from <i>Bacillus subtilis</i> using a library-based construct screen. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 817-825.	2.1	10
51	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
52	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
53	Distamycin A affects the stability of NF- κ B p50-DNA complexes in a sequence-dependent manner. <i>Journal of Molecular Recognition</i> , 2002, 15, 19-26.	2.1	6
54	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

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55	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
56	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
57	Structural studies of herpes virus terminase. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s25-s25.	0.3	0
58	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