

Alan R Davidson

List of Publications by Year in descending order

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106
papers

9,306
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36303

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docs citations

112
times ranked

7214
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of the tail assembly chaperone genes of T4-Like phages suggests a mechanism other than translational frameshifting for biogenesis of their encoded proteins. <i>Virology</i> , 2022, 566, 9-15.	2.4	3
2	Structural and Mechanistic Insight into CRISPR-Cas9 Inhibition by Anti-CRISPR Protein AcrIIC4. <i>Journal of Molecular Biology</i> , 2022, 434, 167420.	4.2	6
3	The small genome, virulent, non-contractile tailed bacteriophages that infect Enterobacteriales hosts. <i>Virology</i> , 2022, 573, 151-166.	2.4	4
4	Phage Proteins Required for Tail Fiber Assembly Also Bind Specifically to the Surface of Host Bacterial Strains. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	18
5	Anti-CRISPR AcrIE2 Binds the Type I-E CRISPR-Cas Complex But Does Not Block DNA Binding. <i>Journal of Molecular Biology</i> , 2021, 433, 166759.	4.2	11
6	Anti-CRISPR AcrIF9 functions by inducing the CRISPR-Cas complex to bind DNA non-specifically. <i>Nucleic Acids Research</i> , 2021, 49, 3381-3393.	14.5	22
7	A phage-encoded anti-activator inhibits quorum sensing in <i>Pseudomonas aeruginosa</i> . <i>Molecular Cell</i> , 2021, 81, 571-583.e6.	9.7	80
8	AcrIF9 tethers non-sequence specific dsDNA to the CRISPR RNA-guided surveillance complex. <i>Nature Communications</i> , 2020, 11, 2730.	12.8	27
9	Anti-CRISPRs: Protein Inhibitors of CRISPR-Cas Systems. <i>Annual Review of Biochemistry</i> , 2020, 89, 309-332.	11.1	91
10	<i>Listeria</i> Phages Induce Cas9 Degradation to Protect Lysogenic Genomes. <i>Cell Host and Microbe</i> , 2020, 28, 31-40.e9.	11.0	54
11	Anti-CRISPR AcrIIA5 Potently Inhibits All Cas9 Homologs Used for Genome Editing. <i>Cell Reports</i> , 2019, 29, 1739-1746.e5.	6.4	35
12	Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. <i>Cell</i> , 2019, 178, 1452-1464.e13.	28.9	105
13	Phage tail fibre assembly proteins employ a modular structure to drive the correct folding of diverse fibres. <i>Nature Microbiology</i> , 2019, 4, 1645-1653.	13.3	45
14	Inhibition of CRISPR-Cas9 ribonucleoprotein complex assembly by anti-CRISPR AcrIIC2. <i>Nature Communications</i> , 2019, 10, 2806.	12.8	50
15	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. <i>Journal of Molecular Biology</i> , 2019, 431, 336-350.	4.2	20
16	Anti-CRISPR: discovery, mechanism and function. <i>Nature Reviews Microbiology</i> , 2018, 16, 12-17.	28.6	288
17	<i>Pseudomonas aeruginosa</i> defends against phages through type IV pilus glycosylation. <i>Nature Microbiology</i> , 2018, 3, 47-52.	13.3	90
18	Type VI secretion system baseplate. <i>Nature Microbiology</i> , 2018, 3, 1330-1331.	13.3	1

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19	Potent Cas9 Inhibition in Bacterial and Human Cells by AcrIIC4 and AcrIIC5 Anti-CRISPR Proteins. MBio, 2018, 9, .	4.1	80
20	A common trick for transferring bacterial DNA. Science, 2018, 362, 152-153.	12.6	14
21	A Unified Resource for Tracking Anti-CRISPR Names. CRISPR Journal, 2018, 1, 304-305.	2.9	94
22	Phage Morons Play an Important Role in Pseudomonas aeruginosa Phenotypes. Journal of Bacteriology, 2018, 200, .	2.2	53
23	Phages make a group decision. Nature, 2017, 541, 466-467.	27.8	16
24	Structure Reveals Mechanisms of Viral Suppressors that Intercept a CRISPR RNA-Guided Surveillance Complex. Cell, 2017, 169, 47-57.e11.	28.9	191
25	Cheese, phages and anti-CRISPRs. Nature Microbiology, 2017, 2, 1338-1339.	13.3	0
26	A Broad-Spectrum Inhibitor of CRISPR-Cas9. Cell, 2017, 170, 1224-1233.e15.	28.9	211
27	The Discovery, Mechanisms, and Evolutionary Impact of Anti-CRISPRs. Annual Review of Virology, 2017, 4, 37-59.	6.7	173
28	Disabling a Type I-E CRISPR-Cas Nuclease with a Bacteriophage-Encoded Anti-CRISPR Protein. MBio, 2017, 8, .	4.1	63
29	Inhibition of CRISPR-Cas systems by mobile genetic elements. Current Opinion in Microbiology, 2017, 37, 120-127.	5.1	30
30	Naturally Occurring Off-Switches for CRISPR-Cas9. Cell, 2016, 167, 1829-1838.e9.	28.9	345
31	Baseplate assembly of phage Mu: Defining the conserved core components of contractile-tailed phages and related bacterial systems. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10174-10179.	7.1	46
32	Inactivation of CRISPR-Cas systems by anti-CRISPR proteins in diverse bacterial species. Nature Microbiology, 2016, 1, 16085.	13.3	271
33	The solution structure of an anti-CRISPR protein. Nature Communications, 2016, 7, 13134.	12.8	48
34	Prophages mediate defense against phage infection through diverse mechanisms. ISME Journal, 2016, 10, 2854-2866.	9.8	363
35	Foreign DNA acquisition by the I-FACRISPR-Cas system requires all components of the interference machinery. Nucleic Acids Research, 2015, 43, 10848-10860.	14.5	88
36	A Comprehensive Membrane Interactome Mapping of Sho1p Reveals Fps1p as a Novel Key Player in the Regulation of the HOG Pathway in S. cerevisiae. Journal of Molecular Biology, 2015, 427, 2088-2103.	4.2	34

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37	Parasite Exposure Drives Selective Evolution of Constitutive versus Inducible Defense. <i>Current Biology</i> , 2015, 25, 1043-1049.	3.9	244
38	Multiple mechanisms for CRISPR-Cas inhibition by anti-CRISPR proteins. <i>Nature</i> , 2015, 526, 136-139.	27.8	325
39	The phage tail tape measure protein, an inner membrane protein and a periplasmic chaperone play connected roles in the genome injection process of <i>Escherichia coli</i> phage HK97. <i>Molecular Microbiology</i> , 2015, 96, 437-447.	2.5	89
40	When a virus is not a parasite: the beneficial effects of prophages on bacterial fitness. <i>Journal of Microbiology</i> , 2014, 52, 235-242.	2.8	210
41	To acquire or resist: the complex biological effects of CRISPR-Cas systems. <i>Trends in Microbiology</i> , 2014, 22, 218-225.	7.7	90
42	A New Group of Phage Anti-CRISPR Genes Inhibits the Type I-E CRISPR-Cas System of <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2014, 5, e00896.	4.1	224
43	Insights into Bacteriophage T5 Structure from Analysis of Its Morphogenesis Genes and Protein Components. <i>Journal of Virology</i> , 2014, 88, 1162-1174.	3.4	68
44	A Shifty Chaperone for Phage Tail Assembly. <i>Journal of Molecular Biology</i> , 2014, 426, 1001-1003.	4.2	9
45	Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. <i>Nature</i> , 2013, 493, 429-432.	27.8	689
46	A Conserved Spiral Structure for Highly Diverged Phage Tail Assembly Chaperones. <i>Journal of Molecular Biology</i> , 2013, 425, 2436-2449.	4.2	20
47	Tail Tip Proteins Related to Bacteriophage gpL Coordinate an Iron-Sulfur Cluster. <i>Journal of Molecular Biology</i> , 2013, 425, 2450-2462.	4.2	23
48	Structural and Functional Studies of gpX of <i>Escherichia coli</i> Phage P2 Reveal a Widespread Role for LysM Domains in the Baseplates of Contractile-Tailed Phages. <i>Journal of Bacteriology</i> , 2013, 195, 5461-5468.	2.2	18
49	The moron comes of age. <i>Bacteriophage</i> , 2012, 2, e23146.	1.9	52
50	The Importance of Conserved Features of Yeast Actin-Binding Protein 1 (Abp1p): The Conditional Nature of Essentiality. <i>Genetics</i> , 2012, 191, 1199-1211.	2.9	10
51	The Bacteriophage HK97 gp15 Moron Element Encodes a Novel Superinfection Exclusion Protein. <i>Journal of Bacteriology</i> , 2012, 194, 5012-5019.	2.2	107
52	The CRISPR/Cas Adaptive Immune System of <i>Pseudomonas aeruginosa</i> Mediates Resistance to Naturally Occurring and Engineered Phages. <i>Journal of Bacteriology</i> , 2012, 194, 5728-5738.	2.2	248
53	Kinetic consequences of native state optimization of surface-exposed electrostatic interactions in the Fyn SH3 domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 858-870.	2.6	42
54	A residue in helical conformation in the native state adopts a β -strand conformation in the folding transition state despite its high and canonical $\Delta\Delta G$ value. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1343-1349.	2.6	7

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55	Long Noncontractile Tail Machines of Bacteriophages. <i>Advances in Experimental Medicine and Biology</i> , 2012, 726, 115-142.	1.6	101
56	A Conserved Residue in the Yeast Bem1p SH3 Domain Maintains the High Level of Binding Specificity Required for Function. <i>Journal of Biological Chemistry</i> , 2011, 286, 19470-19477.	3.4	9
57	Characterization of tetracycline modifying enzymes using a sensitive in vivo reporter system. <i>BMC Biochemistry</i> , 2010, 11, 34.	4.4	2
58	Phages have adapted the same protein fold to fulfill multiple functions in virion assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14384-14389.	7.1	37
59	The Crystal Structure of Bacteriophage HK97 gp6: Defining a Large Family of Head-Tail Connector Proteins. <i>Journal of Molecular Biology</i> , 2010, 395, 754-768.	4.2	62
60	A Comprehensive Analysis of Structural and Sequence Conservation in the TetR Family Transcriptional Regulators. <i>Journal of Molecular Biology</i> , 2010, 400, 847-864.	4.2	134
61	The Solution Structure of the C-Terminal Ig-like Domain of the Bacteriophage λ Tail Tube Protein. <i>Journal of Molecular Biology</i> , 2010, 403, 468-479.	4.2	46
62	Structural, Functional, and Bioinformatic Studies Demonstrate the Crucial Role of an Extended Peptide Binding Site for the SH3 Domain of Yeast Abp1p. <i>Journal of Biological Chemistry</i> , 2009, 284, 26918-26927.	3.4	36
63	The phage λ major tail protein structure reveals a common evolution for long-tailed phages and the type VI bacterial secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4160-4165.	7.1	243
64	Structure-Based Approach to the Photocontrol of Protein Folding. <i>Journal of the American Chemical Society</i> , 2009, 131, 2283-2289.	13.7	98
65	The induction of folding cooperativity by ligand binding drives the allosteric response of tetracycline repressor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22263-22268.	7.1	99
66	The osmolyte trimethylamine-N-oxide stabilizes the Fyn SH3 domain without altering the structure of its folding transition state. <i>Protein Science</i> , 2009, 18, 526-536.	7.6	22
67	The X-Ray Crystal Structure of the Phage λ Tail Terminator Protein Reveals the Biologically Relevant Hexameric Ring Structure and Demonstrates a Conserved Mechanism of Tail Termination among Diverse Long-Tailed Phages. <i>Journal of Molecular Biology</i> , 2009, 389, 938-951.	4.2	55
68	Recognition of Non-canonical Peptides by the Yeast Fus1p SH3 Domain: Elucidation of a Common Mechanism for Diverse SH3 Domain Specificities. <i>Journal of Molecular Biology</i> , 2008, 377, 889-901.	4.2	30
69	Ligand Recognition by ActR, a TetR-Like Regulator of Actinorhodin Export. <i>Journal of Molecular Biology</i> , 2008, 383, 753-761.	4.2	45
70	Theoretical and experimental demonstration of the importance of specific nonnative interactions in protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9999-10004.	7.1	120
71	A folding space odyssey. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2759-2760.	7.1	21
72	The Biologically Relevant Targets and Binding Affinity Requirements for the Function of the Yeast Actin-Binding Protein 1 Src-Homology 3 Domain Vary With Genetic Context. <i>Genetics</i> , 2007, 176, 193-208.	2.9	35

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73	$\hat{\Delta}$ -Value analysis of a three-state protein folding pathway by NMR relaxation dispersion spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15717-15722.	7.1	49
74	The NMR Structure of the gpU Tail-terminator Protein from Bacteriophage Lambda: Identification of Sites Contributing to Mg(II)-mediated Oligomerization and Biological Function. Journal of Molecular Biology, 2007, 365, 175-186.	4.2	28
75	Protein Folding Kinetics Provides a Context-independent Assessment of $\hat{\Delta}$ ² -Strand Propensity in the Fyn SH3 Domain. Journal of Molecular Biology, 2007, 373, 764-774.	4.2	13
76	Immunoglobulin-like domains on bacteriophage: weapons of modest damage?. Current Opinion in Microbiology, 2007, 10, 382-387.	5.1	86
77	Computational design of the Fyn SH3 domain with increased stability through optimization of surface charge-charge interactions. Protein Science, 2007, 16, 2694-2702.	7.6	56
78	Abp1p and Fyn SH3 Domains Fold through Similar Low-Populated Intermediate States. Biochemistry, 2006, 45, 10175-10183.	2.5	41
79	Ig-Like Domains on Bacteriophages: A Tale of Promiscuity and Deceit. Journal of Molecular Biology, 2006, 359, 496-507.	4.2	169
80	Two-way Interdomain Signal Transduction in Tetracycline Repressor. Journal of Molecular Biology, 2006, 361, 382-389.	4.2	22
81	Identification of a Collapsed Intermediate with Non-native Long-range Interactions on the Folding Pathway of a Pair of Fyn SH3 Domain Mutants by NMR Relaxation Dispersion Spectroscopy. Journal of Molecular Biology, 2006, 363, 958-976.	4.2	77
82	Protein stabilization by specific binding of guanidinium to a functional arginine-binding surface on an SH3 domain. Protein Science, 2006, 15, 162-170.	7.6	46
83	Multiple Sequence Alignment as a Guideline for Protein Engineering Strategies. , 2006, 340, 171-182.		9
84	The family feud: do proteins with similar structures fold via the same pathway?. Current Opinion in Structural Biology, 2005, 15, 42-49.	5.7	90
85	Dramatic acceleration of protein folding by stabilization of a nonnative backbone conformation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7954-7959.	7.1	79
86	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. Nature, 2004, 430, 586-590.	27.8	445
87	The analysis of protein folding kinetic data produced in protein engineering experiments. Methods, 2004, 34, 41-50.	3.8	47
88	Protein-Protein Interaction Affinity Plays a Crucial Role in Controlling the Sho1p-Mediated Signal Transduction Pathway in Yeast. Molecular Cell, 2004, 14, 813-823.	9.7	67
89	The Relationship Between Conservation, Thermodynamic Stability, and Function in the SH3 Domain Hydrophobic Core. Journal of Molecular Biology, 2003, 333, 641-655.	4.2	64
90	Residues participating in the protein folding nucleus do not exhibit preferential evolutionary conservation. Journal of Molecular Biology, 2002, 316, 225-233.	4.2	57

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91	The Solution Structure of the Bacteriophage λ Head-Tail Joining Protein, gpII. Journal of Molecular Biology, 2002, 318, 1395-1404.	4.2	38
92	Protein Folding Kinetics Beyond the Φ Value: Using Multiple Amino Acid Substitutions to Investigate the Structure of the SH3 Domain Folding Transition State. Journal of Molecular Biology, 2002, 320, 389-402.	4.2	75
93	Hydrophobic core packing in the SH3 domain folding transition state. Nature Structural Biology, 2002, 9, 126-130.	9.7	139
94	Dramatic stabilization of an SH3 domain by a single substitution: roles of the folded and unfolded states ¹¹ Edited by C. R. Matthews. Journal of Molecular Biology, 2001, 307, 913-928.	4.2	75
95	The solution structure of bacteriophage λ protein W, a small morphogenetic protein possessing a novel fold ¹¹ Edited by P. E. Wright. Journal of Molecular Biology, 2001, 308, 9-14.	4.2	41
96	Mechanisms for Intragenic Complementation at the Human Argininosuccinate Lyase Locus. Biochemistry, 2001, 40, 15581-15590.	2.5	22
97	The identification of conserved interactions within the SH3 domain by alignment of sequences and structures. Protein Science, 2000, 9, 2170-2180.	7.6	148
98	The design of a hyperstable mutant of the Abp1p SH3 domain by sequence alignment analysis. Protein Science, 2000, 9, 2457-2469.	7.6	58
99	Thermodynamic and Functional Characterization of Protein W from Bacteriophage λ . Journal of Biological Chemistry, 2000, 275, 18879-18886.	3.4	18
100	Evolutionary conservation in protein folding kinetics. Journal of Molecular Biology, 2000, 298, 303-312.	4.2	80
101	Analysis of covariation in an SH3 domain sequence alignment: applications in tertiary contact prediction and the design of compensating hydrophobic core substitutions. Journal of Molecular Biology, 2000, 303, 433-446.	4.2	109
102	Functional importance of regions in Escherichia coli elongation factor NusA that interact with RNA polymerase, the bacteriophage lambda N protein and RNA. Molecular Microbiology, 1999, 34, 523-537.	2.5	50
103	A simple in vivo assay for increased protein solubility. Protein Science, 1999, 8, 1908-1911.	7.6	153
104	Domain exchange experiments in duck α -crystallins: Functional and evolutionary implications. Protein Science, 1999, 8, 529-537.	7.6	5
105	Mutagenesis of a Buried Polar Interaction in an SH3 Domain: A Sequence Conservation Provides the Best Prediction of Stability Effects. Biochemistry, 1998, 37, 16172-16182.	2.5	92
106	One Anti-CRISPR to Rule Them All: Potent Inhibition of Cas9 Homologs Used for Genome Editing. SSRN Electronic Journal, 0, , .	0.4	1