Alan R Davidson

List of Publications by Year
in descending order

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106	9,306	36203	43802
papers	citations	51 h-index	91 g-index

112	112	112	7214
all docs	docs citations	times ranked	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. Virology, 2022, 566, 9-15.	1.1	3
2	Structural and Mechanistic Insight into CRISPR-Cas9 Inhibition by Anti-CRISPR Protein AcrIIC4. Journal of Molecular Biology, 2022, 434, 167420.	2.0	6
3	The small genome, virulent, non-contractile tailed bacteriophages that infect Enterobacteriales hosts. Virology, 2022, 573, 151-166.	1.1	4
4	Phage Proteins Required for Tail Fiber Assembly Also Bind Specifically to the Surface of Host Bacterial Strains. Journal of Bacteriology, 2021, 203, .	1.0	18
5	Anti-CRISPR AcrIE2 Binds the Type I-E CRISPR-Cas Complex But Does Not Block DNA Binding. Journal of Molecular Biology, 2021, 433, 166759.	2.0	11
6	Anti-CRISPR AcrIF9 functions by inducing the CRISPRâ€“Cas complex to bind DNA non-specifically. Nucleic Acids Research, 2021, 49, 3381-3393.	6.5	22
7	A phage-encoded anti-activator inhibits quorum sensing in Pseudomonas aeruginosa. Molecular Cell, 2021, 81, 571-583.e6.	4.5	80
8	AcrIF9 tethers non-sequence specific dsDNA to the CRISPR RNA-guided surveillance complex. Nature Communications, 2020, 11, 2730.	5.8	27
9	Anti-CRISPRs: Protein Inhibitors of CRISPR-Cas Systems. Annual Review of Biochemistry, 2020, 89, 309-332.	5.0	91
10	Listeria Phages Induce Cas9 Degradation to Protect Lysogenic Genomes. Cell Host and Microbe, 2020, 28, 31-40.e9.	5.1	54
11	Anti-CRISPR AcrIIA5 Potently Inhibits All Cas9 Homologs Used for Genome Editing. Cell Reports, 2019, 29, 1739-1746.e5.	2.9	35
12	Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. Cell, 2019, 178, 1452-1464.e13.	13.5	105
13	Phage tail fibre assembly proteins employ a modular structure to drive the correct folding of diverse fibres. Nature Microbiology, 2019, 4, 1645-1653.	5.9	45
14	Inhibition of CRISPR-Cas9 ribonucleoprotein complex assembly by anti-CRISPR AcrIIC2. Nature Communications, 2019, 10, 2806.	5.8	50
15	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. Journal of Molecular Biology, 2019, 431, 336-350.	2.0	20
16	Anti-CRISPR: discovery, mechanism and function. Nature Reviews Microbiology, 2018, 16, 12-17.	13.6	288
17	Pseudomonas aeruginosa defends against phages through type IV pilus glycosylation. Nature Microbiology, 2018, 3, 47-52.	5.9	90
18	Type VI secretion system baseplate. Nature Microbiology, 2018, 3, 1330-1331.	5.9	1

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19	Potent Cas9 Inhibition in Bacterial and Human Cells by AcrIIC4 and AcrIIC5 Anti-CRISPR Proteins. MBio, 2018, 9, .	1.8	80
20	A common trick for transferring bacterial DNA. Science, 2018, 362, 152-153.	6.0	14
21	A Unified Resource for Tracking Anti-CRISPR Names. CRISPR Journal, 2018, 1, 304-305.	1.4	94
22	Phage Morons Play an Important Role in Pseudomonas aeruginosa Phenotypes. Journal of Bacteriology, 2018, 200, .	1.0	53
23	Phages make a group decision. Nature, 2017, 541, 466-467.	13.7	16
24	Structure Reveals Mechanisms of Viral Suppressors that Intercept a CRISPR RNA-Guided Surveillance Complex. Cell, 2017, 169, 47-57.e11.	13.5	191
25	Cheese, phages and anti-CRISPRs. Nature Microbiology, 2017, 2, 1338-1339.	5.9	0
26	A Broad-Spectrum Inhibitor of CRISPR-Cas9. Cell, 2017, 170, 1224-1233.e15.	13.5	211
27	The Discovery, Mechanisms, and Evolutionary Impact of Anti-CRISPRs. Annual Review of Virology, 2017, 4, 37-59.	3.0	173
28	Disabling a Type I-E CRISPR-Cas Nuclease with a Bacteriophage-Encoded Anti-CRISPR Protein. MBio, 2017, 8, .	1.8	63
29	Inhibition of CRISPR-Cas systems by mobile genetic elements. Current Opinion in Microbiology, 2017, 37, 120-127.	2.3	30
30	Naturally Occurring Off-Switches for CRISPR-Cas9. Cell, 2016, 167, 1829-1838.e9.	13.5	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.	3.3	46
32	Inactivation of CRISPR-Cas systems by anti-CRISPR proteins in diverse bacterial species. Nature Microbiology, 2016, 1, 16085.	5.9	271
33	The solution structure of an anti-CRISPR protein. Nature Communications, 2016, 7, 13134.	5.8	48
34	Prophages mediate defense against phage infection through diverse mechanisms. ISME Journal, 2016, 10, 2854-2866.	4.4	363
35	Foreign DNA acquisition by the I-FÂCRISPRâ€“Cas system requires all components of the interference machinery. Nucleic Acids Research, 2015, 43, 10848-10860.	6.5	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.	2.0	34

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37	Parasite Exposure Drives Selective Evolution of Constitutive versus Inducible Defense. Current Biology, 2015, 25, 1043-1049.	1.8	244
38	Multiple mechanisms for CRISPRâ€“Cas inhibition by anti-CRISPR proteins. Nature, 2015, 526, 136-139.	13.7	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 <scp>E</scp>.â€‰coli phage <scp>HK</scp>97. Molecular Microbiology, 2015, 96, 437-447.	1.2	89
40	When a virus is not a parasite: the beneficial effects of prophages on bacterial fitness. Journal of Microbiology, 2014, 52, 235-242.	1.3	210
41	To acquire or resist: the complex biological effects of CRISPRâ€“Cas systems. Trends in Microbiology, 2014, 22, 218-225.	3.5	90
42	A New Group of Phage Anti-CRISPR Genes Inhibits the Type I-E CRISPR-Cas System of Pseudomonas aeruginosa. MBio, 2014, 5, e00896.	1.8	224
43	Insights into Bacteriophage T5 Structure from Analysis of Its Morphogenesis Genes and Protein Components. Journal of Virology, 2014, 88, 1162-1174.	1.5	68
44	A Shifty Chaperone for Phage Tail Assembly. Journal of Molecular Biology, 2014, 426, 1001-1003.	2.0	9
45	Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. Nature, 2013, 493, 429-432.	13.7	689
46	A Conserved Spiral Structure for Highly Diverged Phage Tail Assembly Chaperones. Journal of Molecular Biology, 2013, 425, 2436-2449.	2.0	20
47	Tail Tip Proteins Related to Bacteriophage Î» gpL Coordinate an Iron-Sulfur Cluster. Journal of Molecular Biology, 2013, 425, 2450-2462.	2.0	23
48	Structural and Functional Studies of gpX of Escherichia coli Phage P2 Reveal a Widespread Role for LysM Domains in the Baseplates of Contractile-Tailed Phages. Journal of Bacteriology, 2013, 195, 5461-5468.	1.0	18
49	The moron comes of age. Bacteriophage, 2012, 2, e23146.	1.9	52
50	The Importance of Conserved Features of Yeast Actin-Binding Protein 1 (Abp1p): The Conditional Nature of Essentiality. Genetics, 2012, 191, 1199-1211.	1.2	10
51	The Bacteriophage HK97 gp15 Moron Element Encodes a Novel Superinfection Exclusion Protein. Journal of Bacteriology, 2012, 194, 5012-5019.	1.0	107
52	The CRISPR/Cas Adaptive Immune System of Pseudomonas aeruginosa Mediates Resistance to Naturally Occurring and Engineered Phages. Journal of Bacteriology, 2012, 194, 5728-5738.	1.0	248
53	Kinetic consequences of native state optimization of surfaceâ€exposed electrostatic interactions in the Fyn SH3 domain. Proteins: Structure, Function and Bioinformatics, 2012, 80, 858-870.	1.5	42
54	A residue in helical conformation in the native state adopts a Î²â€strand conformation in the folding transition state despite its high and canonical Ï•â€value. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1343-1349.	1.5	7

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55	Long Noncontractile Tail Machines of Bacteriophages. Advances in Experimental Medicine and Biology, 2012, 726, 115-142.	0.8	101
56	A Conserved Residue in the Yeast Bem1p SH3 Domain Maintains the High Level of Binding Specificity Required for Function. Journal of Biological Chemistry, 2011, 286, 19470-19477.	1.6	9
57	Characterization of tetracycline modifying enzymes using a sensitive in vivo reporter system. BMC Biochemistry, 2010, 11, 34.	4.4	2
58	Phages have adapted the same protein fold to fulfill multiple functions in virion assembly. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14384-14389.	3.3	37
59	The Crystal Structure of Bacteriophage HK97 gp6: Defining a Large Family of Headâ€“Tail Connector Proteins. Journal of Molecular Biology, 2010, 395, 754-768.	2.0	62
60	A Comprehensive Analysis of Structural and Sequence Conservation in the TetR Family Transcriptional Regulators. Journal of Molecular Biology, 2010, 400, 847-864.	2.0	134
61	The Solution Structure of the C-Terminal Ig-like Domain of the Bacteriophage Î» Tail Tube Protein. Journal of Molecular Biology, 2010, 403, 468-479.	2.0	46
62	Structural, Functional, and Bioinformatic Studies Demonstrate the Crucial Role of an Extended Peptide Binding Site for the SH3 Domain of Yeast Abp1p. Journal of Biological Chemistry, 2009, 284, 26918-26927.	1.6	36
63	The phage Î» major tail protein structure reveals a common evolution for long-tailed phages and the type VI bacterial secretion system. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4160-4165.	3.3	243
64	Structure-Based Approach to the Photocontrol of Protein Folding. Journal of the American Chemical Society, 2009, 131, 2283-2289.	6.6	98
65	The induction of folding cooperativity by ligand binding drives the allosteric response of tetracycline repressor. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22263-22268.	3.3	99
66	The osmolyte trimethylamineâ€Nâ€oxide stabilizes the Fyn SH3 domain without altering the structure of its folding transition state. Protein Science, 2009, 18, 526-536.	3.1	22
67	The X-Ray Crystal Structure of the Phage Î» Tail Terminator Protein Reveals the Biologically Relevant Hexameric Ring Structure and Demonstrates a Conserved Mechanism of Tail Termination among Diverse Long-Tailed Phages. Journal of Molecular Biology, 2009, 389, 938-951.	2.0	55
68	Recognition of Non-canonical Peptides by the Yeast Fus1p SH3 Domain: Elucidation of a Common Mechanism for Diverse SH3 Domain Specificities. Journal of Molecular Biology, 2008, 377, 889-901.	2.0	30
69	Ligand Recognition by ActR, a TetR-Like Regulator of Actinorhodin Export. Journal of Molecular Biology, 2008, 383, 753-761.	2.0	45
70	Theoretical and experimental demonstration of the importance of specific nonnative interactions in protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9999-10004.	3.3	120
71	A folding space odyssey. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2759-2760.	3.3	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. Genetics, 2007, 176, 193-208.	1.2	35

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73	Î¦-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.	3.3	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.	2.0	28
75	Protein Folding Kinetics Provides a Context-independent Assessment of Î²-Strand Propensity in the Fyn SH3 Domain. Journal of Molecular Biology, 2007, 373, 764-774.	2.0	13
76	Immunoglobulin-like domains on bacteriophage: weapons of modest damage?. Current Opinion in Microbiology, 2007, 10, 382-387.	2.3	86
77	Computational design of the Fyn SH3 domain with increased stability through optimization of surface chargeâ€“charge interactions. Protein Science, 2007, 16, 2694-2702.	3.1	56
78	Abp1p and Fyn SH3 Domains Fold through Similar Low-Populated Intermediate Statesâ€. Biochemistry, 2006, 45, 10175-10183.	1.2	41
79	Ig-Like Domains on Bacteriophages: A Tale of Promiscuity and Deceit. Journal of Molecular Biology, 2006, 359, 496-507.	2.0	169
80	Two-way Interdomain Signal Transduction in Tetracycline Repressor. Journal of Molecular Biology, 2006, 361, 382-389.	2.0	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.	2.0	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.	3.1	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.	2.6	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.	3.3	79
86	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. Nature, 2004, 430, 586-590.	13.7	445
87	The analysis of protein folding kinetic data produced in protein engineering experiments. Methods, 2004, 34, 41-50.	1.9	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.	4.5	67
89	The Relationship Between Conservation, Thermodynamic Stability, and Function in the SH3 Domain Hydrophobic Core. Journal of Molecular Biology, 2003, 333, 641-655.	2.0	64
90	Residues participating in the protein folding nucleus do not exhibit preferential evolutionary conservation. Journal of Molecular Biology, 2002, 316, 225-233.	2.0	57

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91	The Solution Structure of the Bacteriophage Î» Headâ€“Tail Joining Protein, gpFII. Journal of Molecular Biology, 2002, 318, 1395-1404.	2.0	38
92	Protein Folding Kinetics Beyond the Î¦ 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.	2.0	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 states11Edited by C. R. Matthews. Journal of Molecular Biology, 2001, 307, 913-928.	2.0	75
95	The solution structure of bacteriophage Î» protein W, a small morphogenetic protein possessing a novel fold11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 308, 9-14.	2.0	41
96	Mechanisms for Intragenic Complementation at the Human Argininosuccinate Lyase Locus. Biochemistry, 2001, 40, 15581-15590.	1.2	22
97	The identification of conserved interactions within the SH3 domain by alignment of sequences and structures. Protein Science, 2000, 9, 2170-2180.	3.1	148
98	The design of a hyperstable mutant of the Abp1p SH3 domain by sequence alignment analysis. Protein Science, 2000, 9, 2457-2469.	3.1	58
99	Thermodynamic and Functional Characterization of Protein W from Bacteriophage Î». Journal of Biological Chemistry, 2000, 275, 18879-18886.	1.6	18
100	Evolutionary conservation in protein folding kinetics. Journal of Molecular Biology, 2000, 298, 303-312.	2.0	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.	2.0	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.	1.2	50
103	A simple in vivo assay for increased protein solubility. Protein Science, 1999, 8, 1908-1911.	3.1	153
104	Domain exchange experiments in duck dâ€crystallins: Functional and evolutionary implications. Protein Science, 1999, 8, 529-537.	3.1	5
105	Mutagenesis of a Buried Polar Interaction in an SH3 Domain:Â Sequence Conservation Provides the Best Prediction of Stability Effectsâ€. Biochemistry, 1998, 37, 16172-16182.	1.2	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