David J Segal

List of Publications by Year
in descending order

117 papers	7,961 citations	66250 44 h-index	58552 86 g-index
127 all docs	127 docs citations	127 times ranked	7650 citing authors

#	Article	IF	Citations
1	Determinants of heritable gene silencing for KRAB-dCas9Â+ÂDNMT3 and Ezh2-dCas9Â+ÂDNMT3 hit-and-run epigenome editing. Nucleic Acids Research, 2022, 50, 3239-3253.	6.5	17
2	Imaging Unique DNA Sequences in Individual Cells Using a CRISPR-Cas9-Based, Split Luciferase Biosensor. Frontiers in Genome Editing, 2022, 4, 867390.	2.7	2
3	Aberrant promoter methylation contributes to LRIG1 silencing in basal/triple-negative breast cancer. British Journal of Cancer, 2022, 127, 436-448.	2.9	11
4	Early Developmental EEG and Seizure Phenotypes in a Full Gene Deletion of Ubiquitin Protein Ligase E3A Rat Model of Angelman Syndrome. ENeuro, 2021, 8, ENEURO.0345-20.2020.	0.9	20
5	Functional rescue in an Angelman syndrome model following treatment with lentivector transduced hematopoietic stem cells. Human Molecular Genetics, 2021, 30, 1067-1083.	1.4	25
6	The NIH Somatic Cell Genome Editing program. Nature, 2021, 592, 195-204.	13.7	84
7	Excessive Laughter-like Vocalizations, Microcephaly, and Translational Outcomes in the<i>Ube3a</i>Deletion Rat Model of Angelman Syndrome. Journal of Neuroscience, 2021, 41, 8801-8814.	1.7	13
8	An in vivo Cell-Based Delivery Platform for Zinc Finger Artificial Transcription Factors in Pre-clinical Animal Models. Frontiers in Molecular Neuroscience, 2021, 14, 789913.	1.4	2
9	Artificial escape from XCI by DNA methylation editing of the CDKL5 gene. Nucleic Acids Research, 2020, 48, 2372-2387.	6.5	30
10	Translational outcomes in a full gene deletion of ubiquitin protein ligase E3A rat model of Angelman syndrome. Translational Psychiatry, 2020, 10, 39.	2.4	50
11	Versatile 3â€² Functionalization of CRISPR Single Guide RNA. ChemBioChem, 2020, 21, 1633-1640.	1.3	10
12	Generation of a Novel Rat Model of Angelman Syndrome with a Complete <i>Ube3a</i> Gene Deletion. Autism Research, 2020, 13, 397-409.	2.1	28
13	Grand Challenges in Gene and Epigenetic Editing for Neurologic Disease. Frontiers in Genome Editing, 2020, 1, 1.	2.7	2
14	Editorial: Precise Genome Editing Techniques and Applications. Frontiers in Genetics, 2020, 11, 412.	1.1	5
15	Positron emission tomography imaging of novel AAV capsids maps rapid brain accumulation. Nature Communications, 2020, 11, 2102.	5.8	17
16	Abstract B05: Comprehensive functional modeling of pan-cancer risk SNP rs6983267 in human CRC cells via scarless CRISPR/Cas9 genome editing. , 2020, , .		0
17	Strategies for the Enrichment and Selection of Genetically Modified Cells. Trends in Biotechnology, 2019, 37, 56-71.	4.9	28
18	The Right Tools for the Right Job: CRISPR-pass Could Offer Safe Gene Correction for Many Disorders. Molecular Therapy, 2019, 27, 1346-1347.	3.7	1

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19	Imprinting effects of UBE3A loss on synaptic gene networks and Wnt signaling pathways. Human Molecular Genetics, 2019, 28, 3842-3852.	1.4	9
20	Live-Animal Epigenome Editing: Convergence of Novel Techniques. Trends in Genetics, 2019, 35, 527-541.	2.9	15
21	Ezh2-dCas9 and KRAB-dCas9 enable engineering of epigenetic memory in a context-dependent manner. Epigenetics and Chromatin, 2019, 12, 26.	1.8	101
22	Exploring the suitability of RanBP2-type Zinc Fingers for RNA-binding protein design. Scientific Reports, 2019, 9, 2484.	1.6	9
23	Targeted DNA demethylation of the <i>Arabidopsis</i> genome using the human TET1 catalytic domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2125-E2134.	3.3	190
24	Purified Protein Delivery to Activate an Epigenetically Silenced Allele in Mouse Brain. Methods in Molecular Biology, 2018, 1767, 227-239.	0.4	6
25	In Vivo Applications of Cell-Penetrating Zinc-Finger Transcription Factors. Methods in Molecular Biology, 2018, 1867, 239-251.	0.4	6
26	Pathogen-specific DNA sensing with engineered zinc finger proteins immobilized on a polymer chip. Analyst, The, 2018, 143, 4009-4016.	1.7	11
27	Unexpected binding behaviors of bacterial Argonautes in human cells cast doubts on their use as targetable gene regulators. PLoS ONE, 2018, 13, e0193818.	1.1	8
28	UBE3A: An E3 Ubiquitin Ligase With Genome-Wide Impact in Neurodevelopmental Disease. Frontiers in Molecular Neuroscience, 2018, 11, 476.	1.4	41
29	Abstract 394: Elucidating tissue-specific effects of the 8q24 multicancer risk locus via CRISPR/Cas9 scarless genome editing. , 2018, , .		0
30	A Method for Validating Mutations Associated with Malignant Hyperthermia using CRISPR/Cas9 and Dual Integrase Cassette Exchange. Biophysical Journal, 2017, 112, 98a.	0.2	0
31	UBE3A-mediated regulation of imprinted genes and epigenome-wide marks in human neurons. Epigenetics, 2017, 12, 982-990.	1.3	18
32	Methods for Scarless, Selection-Free Generation of Human Cells and Allele-Specific Functional Analysis of Disease-Associated SNPs and Variants of Uncertain Significance. Scientific Reports, 2017, 7, 15044.	1.6	8
33	dCas9-based epigenome editing suggests acquisition of histone methylation is not sufficient for target gene repression. Nucleic Acids Research, 2017, 45, 9901-9916.	6.5	160
34	Blood-brain barrier disruption for the delivery of non-infectious viral vectors and proteins, preliminary study. , 2017, , .		0
35	Blood-brain barrier disruption for the delivery of non-infectious viral vectors and proteins, preliminary study. , 2017, , .		0
36	Abstract 1445: Understanding the 8q24 colorectal cancer risk locus via CRISPR/Cas9 scarless genome editing. , 2017, , .		0

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37	Allele-Specific Reduction of the Mutant Huntingtin Allele Using Transcription Activator-Like Effectors in Human Huntington's Disease Fibroblasts. Cell Transplantation, 2016, 25, 677-686.	1.2	53
38	Effects on the transcriptome upon deletion of a distal element cannot be predicted by the size of the H3K27Ac peak in human cells. Nucleic Acids Research, 2016, 44, 4123-4133.	6.5	32
39	Protein Delivery of an Artificial Transcription Factor Restores Widespread Ube3a Expression in an Angelman Syndrome Mouse Brain. Molecular Therapy, 2016, 24, 548-555.	3.7	67
40	A genome-wide analysis of Cas9 binding specificity using ChIP-seq and targeted sequence capture. Nucleic Acids Research, 2015, 43, 3389-3404.	6.5	193
41	How specific is CRISPR/Cas9 really?. Current Opinion in Chemical Biology, 2015, 29, 72-78.	2.8	97
42	The Shelterin TIN2 Subunit Mediates Recruitment of Telomerase to Telomeres. PLoS Genetics, 2015, 11, e1005410.	1.5	47
43	Abstract 1117: Who's in the driver's seat? Identifying causative variants of colorectal cancer. , 2015, , .		0
44	Engineering Specificity Changes on a RanBP2 Zinc Finger that Binds Singleâ€Stranded RNA. Angewandte Chemie - International Edition, 2014, 53, 7848-7852.	7.2	5
45	The Functional Significance of Common Polymorphisms in Zinc Finger Transcription Factors. G3: Genes, Genomes, Genetics, 2014, 4, 1647-1655.	0.8	9
46	Conformational Elasticity can Facilitate TALEâ€“DNA Recognition. Advances in Protein Chemistry and Structural Biology, 2014, 94, 347-364.	1.0	5
47	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. Nature, 2014, 507, 124-128.	13.7	271
48	Carlos F. Barbas III (1964â€“2014): Visionary at the Interface of Chemistry and Biology. ACS Chemical Biology, 2014, 9, 1645-1646.	1.6	0
49	The prospect of molecular therapy for Angelman syndrome and other monogenic neurologic disorders. BMC Neuroscience, 2014, 15, 76.	0.8	24
50	Miz-1 Activates Gene Expression via a Novel Consensus DNA Binding Motif. PLoS ONE, 2014, 9, e101151.	1.1	14
51	Is there a telltale RH fingerprint in zinc fingers that recognizes methylated CpG dinucleotides?. Trends in Biochemical Sciences, 2013, 38, 421-422.	3.7	2
52	New Insights into DNA Recognition by Zinc Fingers Revealed by Structural Analysis of the Oncoprotein ZNF217. Journal of Biological Chemistry, 2013, 288, 10616-10627.	1.6	36
53	Quantitative analysis of TALEâ€“DNA interactions suggests polarity effects. Nucleic Acids Research, 2013, 41, 4118-4128.	6.5	153
54	Genome Engineering at the Dawn of the Golden Age. Annual Review of Genomics and Human Genetics, 2013, 14, 135-158.	2.5	109

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55	Highly active zinc-finger nucleases by extended modular assembly. Genome Research, 2013, 23, 530-538.	2.4	88
56	Transcription activator like effector (TALE)-directed piggyBac transposition in human cells. Nucleic Acids Research, 2013, 41, 9197-9207.	6.5	59
57	Bacteria herald a new era of gene editing. ELife, 2013, 2, e00563.	2.8	11
58	Chimeric piggyBac transposases for genomic targeting in human cells. Nucleic Acids Research, 2012, 40, 6978-6991.	6.5	46
59	Beyond the genome and into the clinic. Genome Medicine, 2012, 4, 78.	3.6	1
60	Guiding the Design of Synthetic DNA-Binding Molecules with Massively Parallel Sequencing. Journal of the American Chemical Society, 2012, 134, 17814-17822.	6.6	75
61	Dissecting the genetic architecture of coronary artery disease by genome engineering. BMC Proceedings, 2012, 6, .	1.8	0
62	Modular Assembly of RanBP2â€Type Zinc Finger Domains to Target Singleâ€Stranded RNA. Angewandte Chemie - International Edition, 2012, 51, 5371-5375.	7.2	7
63	Adding Fingers to an Engineered Zinc Finger Nuclease Can Reduce Activity. Biochemistry, 2011, 50, 5033-5041.	1.2	33
64	Zinc-finger nucleases transition to the CoDA. Nature Methods, 2011, 8, 53-55.	9.0	7
65	The prospects for designer single-stranded RNA-binding proteins. Nature Structural and Molecular Biology, 2011, 18, 256-261.	3.6	59
66	A zinc finger protein array for the visual detection of specific DNA sequences for diagnostic applications. Nucleic Acids Research, 2011, 39, e29-e29.	6.5	28
67	Toward a General Approach for RNA-Templated Hierarchical Assembly of Split-Proteins. Journal of the American Chemical Society, 2010, 132, 11692-11701.	6.6	39
68	Engineered Zinc Finger Proteins. Methods in Molecular Biology, 2010, , .	0.4	11
69	The Generation of Zinc Finger Proteins by Modular Assembly. Methods in Molecular Biology, 2010, 649, 3-30.	0.4	59
70	Seeing Genetic and Epigenetic Information Without DNA Denaturation Using Sequence-Enabled Reassembly (SEER). Methods in Molecular Biology, 2010, 649, 365-382.	0.4	1
71	Bind-n-Seq: high-throughput analysis of in vitro proteinâ€"DNA interactions using massively parallel sequencing. Nucleic Acids Research, 2009, 37, e151-e151.	6.5	125
72	Restricted spacer tolerance of a zinc finger nuclease with a six amino acid linker. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 3970-3972.	1.0	36

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73	Systematic evaluation of split-fluorescent proteins for the direct detection of native and methylated DNA. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 3748-3751.	1.0	10
74	The Protein-Binding Potential of C2H2 Zinc Finger Domains. Cell Biochemistry and Biophysics, 2008, 51, 9-19.	0.9	75
75	Keep Your Fingers Off My DNA: Proteinâ€"Protein Interactions Mediated by C2H2 Zinc Finger Domains. Cell Biochemistry and Biophysics, 2008, 50, 111-131.	0.9	255
76	Generation and Functional Analysis of Zinc Finger Nucleases. , 2008, 434, 277-290.		26
77	Critical Parameters for Genome Editing Using Zinc Finger Nucleases. Mini-Reviews in Medicinal Chemistry, 2008, 8, 669-676.	1.1	40
78	Zinc-finger exercisesThe â€˜cutting edgeâ€™ of gene therapy â€¦ literally. Biochemist, 2008, 30, 10-13.	0.2	1
79	Split Î²-Lactamase Sensor for the Sequence-Specific Detection of DNA Methylation. Analytical Chemistry, 2007, 79, 6702-6708.	3.2	53
80	Uranyl Acetate as a Direct Inhibitor of DNA-Binding Proteins. Chemical Research in Toxicology, 2007, 20, 784-789.	1.7	41
81	Engineering zinc finger protein transcription factors to downregulate the epithelial glycoprotein-2 promoter as a novel anti-cancer treatment. Molecular Carcinogenesis, 2007, 46, 391-401.	1.3	27
82	Structure-based redesign of the dimerization interface reduces the toxicity of zinc-finger nucleases. Nature Biotechnology, 2007, 25, 786-793.	9.4	492
83	Active integration: new strategies for transgenesis. Transgenic Research, 2007, 16, 333-339.	1.3	48
84	Direct detection of double-stranded DNA: molecular methods and applications for DNA diagnostics. Molecular BioSystems, 2006, 2, 551.	2.9	95
85	Sequence-Enabled Reassembly of Î²-Lactamase (SEER-LAC):â€‰ A Sensitive Method for the Detection of Double-Stranded DNA. Biochemistry, 2006, 45, 3620-3625.	1.2	56
86	Site-Specific Detection of DNA Methylation Utilizing mCpG-SEER. Journal of the American Chemical Society, 2006, 128, 9761-9765.	6.6	78
87	Structure of Aart, a Designed Six-finger Zinc Finger Peptide, Bound to DNA. Journal of Molecular Biology, 2006, 363, 405-421.	2.0	87
88	Sequence-Enabled Reassembly (SEER) Peptides for the Detection of DNA Sequences. , 2006, , 214-215.		0
89	Design, construction and in vitro testing of zinc finger nucleases. Nature Protocols, 2006, 1, 1329-1341.	5.5	177
90	Inhibition of Human Immunodeficiency Virus Type 1 Replication with Artificial Transcription Factors Targeting the Highly Conserved Primer-Binding Site. Journal of Virology, 2006, 80, 2873-2883.	1.5	49

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91	973. SEquence-Enabled Reassembly of Î²- Lactamase (SEER-LAC): A Sensitive Method for the Detection of Double-Stranded DNA. Molecular Therapy, 2006, 13, S374.	3.7	0
92	Site-directed genome modification: derivatives of DNA-modifying enzymes as targeting tools. Trends in Biotechnology, 2005, 23, 407-419.	4.9	43
93	Crystallization and preliminary X-ray crystallographic analysis of Aart, a designed six-finger zinc-finger peptide, bound to DNA. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 573-576.	0.7	3
94	Development of Zinc Finger Domains for Recognition of the 5â€²-CNN-3â€² Family DNA Sequences and Their Use in the Construction of Artificial Transcription Factors. Journal of Biological Chemistry, 2005, 280, 35588-35597.	1.6	166
95	Custom Zinc-Finger Nucleases for Use in Human Cells. Molecular Therapy, 2005, 12, 610-617.	3.7	157
96	Site-directed genome modification: nucleic acid and protein modules for targeted integration and gene correction. Trends in Biotechnology, 2005, 23, 399-406.	4.9	44
97	DNA Sequence-Enabled Reassembly of the Green Fluorescent Protein. Journal of the American Chemical Society, 2005, 127, 10782-10783.	6.6	87
98	Fusion Proteins Consisting of Human Immunodeficiency Virus Type 1 Integrase and the Designed Polydactyl Zinc Finger Protein E2C Direct Integration of Viral DNA into Specific Sites. Journal of Virology, 2004, 78, 1301-1313.	1.5	89
99	Attenuation of HIV-1 Replication in Primary Human Cells with a Designed Zinc Finger Transcription Factor. Journal of Biological Chemistry, 2004, 279, 14509-14519.	1.6	77
100	Designing Transcription Factor Architectures for Drug Discovery. Molecular Pharmacology, 2004, 66, 1361-1371.	1.0	162
101	Zinc fingers and a green thumb: manipulating gene expression in plants. Current Opinion in Plant Biology, 2003, 6, 163-168.	3.5	40
102	Evaluation of a Modular Strategy for the Construction of Novel Polydactyl Zinc Finger DNA-Binding Proteinsâ€. Biochemistry, 2003, 42, 2137-2148.	1.2	161
103	The use of zinc finger peptides to study the role of specific factor binding sites in the chromatin environment. Methods, 2002, 26, 76-83.	1.9	46
104	Custom DNA-binding proteins come of age: polydactyl zinc-finger proteins. Current Opinion in Biotechnology, 2001, 12, 632-637.	3.3	96
105	Development of Zinc Finger Domains for Recognition of the 5â€²-ANN-3â€² Family of DNA Sequences and Their Use in the Construction of Artificial Transcription Factors. Journal of Biological Chemistry, 2001, 276, 29466-29478.	1.6	287
106	From catalytic asymmetric synthesis to the transcriptional regulation of genes: In vivo and in vitro evolution of proteins. Advances in Protein Chemistry, 2001, 55, 317-366.	4.4	7
107	Stimulation of Homologous Recombination through Targeted Cleavage by Chimeric Nucleases. Molecular and Cellular Biology, 2001, 21, 289-297.	1.1	564
108	Design of novel sequence-specific DNA-binding proteins. Current Opinion in Chemical Biology, 2000, 4, 34-39.	2.8	68

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109	Insights into the molecular recognition of the 5â€²-GNN-3â€² family of DNA sequences by zinc finger domains 1 1Edited by M. Yaniv. Journal of Molecular Biology, 2000, 303, 489-502.	2.0	144
110	Toward controlling gene expression at will: Selection and design of zinc finger domains recognizing each of the 5'-GNN-3' DNA target sequences. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 2758-2763.	3.3	412
111	Toward controlling gene expression at will: Specific regulation of the erbB-2/HER-2 promoter by using polydactyl zinc finger proteins constructed from modular building blocks. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 14628-14633.	3.3	490
112	Processing of Targeted Psoralen Cross-Links in <i>Xenopus</i> Oocytes. Molecular and Cellular Biology, 1997, 17, 6645-6652.	1.1	7
113	Design of polydactyl zinc-finger proteins for unique addressing within complex genomes. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 5525-5530.	3.3	297
114	Recombination Induced by Triple-Helix-Targeted DNA Damage in Mammalian Cells. Molecular and Cellular Biology, 1996, 16, 6820-6828.	1.1	107
115	Endonuclease-induced, targeted homologous extrachromosomal recombination in Xenopus oocytes.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 806-810.	3.3	44
116	Cold-Sensitive Mutants of Bacteriophage Ï†X174. II. Comparison of Two Cold-Sensitive Mutants. Journal of Virology, 1974, 14, 1115-1125.	1.5	13
117	The promise of gene editing: so close and yet so perilously far. Frontiers in Genome Editing, 0, 4, .	2.7	3