

David J Segal

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1898434/publications.pdf>

Version: 2024-02-01

117
papers

7,961
citations

57752

44
h-index

51602

86
g-index

127
all docs

127
docs citations

127
times ranked

6851
citing authors

#	ARTICLE	IF	CITATIONS
1	Stimulation of Homologous Recombination through Targeted Cleavage by Chimeric Nucleases. <i>Molecular and Cellular Biology</i> , 2001, 21, 289-297.	2.3	564
2	Structure-based redesign of the dimerization interface reduces the toxicity of zinc-finger nucleases. <i>Nature Biotechnology</i> , 2007, 25, 786-793.	17.5	492
3	Toward controlling gene expression at will: Specific regulation of the <i>erbB-2/HER-2</i> promoter by using polydactyl zinc finger proteins constructed from modular building blocks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 14628-14633.	7.1	490
4	Toward controlling gene expression at will: Selection and design of zinc finger domains recognizing each of the 5'-GNN-3' DNA target sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 2758-2763.	7.1	412
5	Design of polydactyl zinc-finger proteins for unique addressing within complex genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 5525-5530.	7.1	297
6	Development of Zinc Finger Domains for Recognition of the 5'-ANN-3' Family of DNA Sequences and Their Use in the Construction of Artificial Transcription Factors. <i>Journal of Biological Chemistry</i> , 2001, 276, 29466-29478.	3.4	287
7	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. <i>Nature</i> , 2014, 507, 124-128.	27.8	271
8	Keep Your Fingers Off My DNA: Protein-Protein Interactions Mediated by C2H2 Zinc Finger Domains. <i>Cell Biochemistry and Biophysics</i> , 2008, 50, 111-131.	1.8	255
9	A genome-wide analysis of Cas9 binding specificity using ChIP-seq and targeted sequence capture. <i>Nucleic Acids Research</i> , 2015, 43, 3389-3404.	14.5	193
10	Targeted DNA demethylation of the <i>Arabidopsis</i> genome using the human TET1 catalytic domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2125-E2134.	7.1	190
11	Design, construction and in vitro testing of zinc finger nucleases. <i>Nature Protocols</i> , 2006, 1, 1329-1341.	12.0	177
12	Development of Zinc Finger Domains for Recognition of the 5'-CNN-3' Family DNA Sequences and Their Use in the Construction of Artificial Transcription Factors. <i>Journal of Biological Chemistry</i> , 2005, 280, 35588-35597.	3.4	166
13	Designing Transcription Factor Architectures for Drug Discovery. <i>Molecular Pharmacology</i> , 2004, 66, 1361-1371.	2.3	162
14	Evaluation of a Modular Strategy for the Construction of Novel Polydactyl Zinc Finger DNA-Binding Proteins. <i>Biochemistry</i> , 2003, 42, 2137-2148.	2.5	161
15	dCas9-based epigenome editing suggests acquisition of histone methylation is not sufficient for target gene repression. <i>Nucleic Acids Research</i> , 2017, 45, 9901-9916.	14.5	160
16	Custom Zinc-Finger Nucleases for Use in Human Cells. <i>Molecular Therapy</i> , 2005, 12, 610-617.	8.2	157
17	Quantitative analysis of TALE-DNA interactions suggests polarity effects. <i>Nucleic Acids Research</i> , 2013, 41, 4118-4128.	14.5	153
18	Insights into the molecular recognition of the 5'-GNN-3' family of DNA sequences by zinc finger domains 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 2000, 303, 489-502.	4.2	144

#	ARTICLE	IF	CITATIONS
19	Bind-n-Seq: high-throughput analysis of in vitro protein-DNA interactions using massively parallel sequencing. <i>Nucleic Acids Research</i> , 2009, 37, e151-e151.	14.5	125
20	Genome Engineering at the Dawn of the Golden Age. <i>Annual Review of Genomics and Human Genetics</i> , 2013, 14, 135-158.	6.2	109
21	Recombination Induced by Triple-Helix-Targeted DNA Damage in Mammalian Cells. <i>Molecular and Cellular Biology</i> , 1996, 16, 6820-6828.	2.3	107
22	Ezh2-dCas9 and KRAB-dCas9 enable engineering of epigenetic memory in a context-dependent manner. <i>Epigenetics and Chromatin</i> , 2019, 12, 26.	3.9	101
23	How specific is CRISPR/Cas9 really?. <i>Current Opinion in Chemical Biology</i> , 2015, 29, 72-78.	6.1	97
24	Custom DNA-binding proteins come of age: polydactyl zinc-finger proteins. <i>Current Opinion in Biotechnology</i> , 2001, 12, 632-637.	6.6	96
25	Direct detection of double-stranded DNA: molecular methods and applications for DNA diagnostics. <i>Molecular BioSystems</i> , 2006, 2, 551.	2.9	95
26	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. <i>Journal of Virology</i> , 2004, 78, 1301-1313.	3.4	89
27	Highly active zinc-finger nucleases by extended modular assembly. <i>Genome Research</i> , 2013, 23, 530-538.	5.5	88
28	DNA Sequence-Enabled Reassembly of the Green Fluorescent Protein. <i>Journal of the American Chemical Society</i> , 2005, 127, 10782-10783.	13.7	87
29	Structure of Aart, a Designed Six-finger Zinc Finger Peptide, Bound to DNA. <i>Journal of Molecular Biology</i> , 2006, 363, 405-421.	4.2	87
30	The NIH Somatic Cell Genome Editing program. <i>Nature</i> , 2021, 592, 195-204.	27.8	84
31	Site-Specific Detection of DNA Methylation Utilizing mCpG-SEER. <i>Journal of the American Chemical Society</i> , 2006, 128, 9761-9765.	13.7	78
32	Attenuation of HIV-1 Replication in Primary Human Cells with a Designed Zinc Finger Transcription Factor. <i>Journal of Biological Chemistry</i> , 2004, 279, 14509-14519.	3.4	77
33	The Protein-Binding Potential of C2H2 Zinc Finger Domains. <i>Cell Biochemistry and Biophysics</i> , 2008, 51, 9-19.	1.8	75
34	Guiding the Design of Synthetic DNA-Binding Molecules with Massively Parallel Sequencing. <i>Journal of the American Chemical Society</i> , 2012, 134, 17814-17822.	13.7	75
35	Design of novel sequence-specific DNA-binding proteins. <i>Current Opinion in Chemical Biology</i> , 2000, 4, 34-39.	6.1	68
36	Protein Delivery of an Artificial Transcription Factor Restores Widespread Ube3a Expression in an Angelman Syndrome Mouse Brain. <i>Molecular Therapy</i> , 2016, 24, 548-555.	8.2	67

#	ARTICLE	IF	CITATIONS
37	The prospects for designer single-stranded RNA-binding proteins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 256-261.	8.2	59
38	Transcription activator like effector (TALE)-directed piggyBac transposition in human cells. <i>Nucleic Acids Research</i> , 2013, 41, 9197-9207.	14.5	59
39	The Generation of Zinc Finger Proteins by Modular Assembly. <i>Methods in Molecular Biology</i> , 2010, 649, 3-30.	0.9	59
40	Sequence-Enabled Reassembly of \hat{I}^2 -Lactamase (SEER-LAC): A Sensitive Method for the Detection of Double-Stranded DNA. <i>Biochemistry</i> , 2006, 45, 3620-3625.	2.5	56
41	Split \hat{I}^2 -Lactamase Sensor for the Sequence-Specific Detection of DNA Methylation. <i>Analytical Chemistry</i> , 2007, 79, 6702-6708.	6.5	53
42	Allele-Specific Reduction of the Mutant Huntingtin Allele Using Transcription Activator-Like Effectors in Human Huntington's Disease Fibroblasts. <i>Cell Transplantation</i> , 2016, 25, 677-686.	2.5	53
43	Translational outcomes in a full gene deletion of ubiquitin protein ligase E3A rat model of Angelman syndrome. <i>Translational Psychiatry</i> , 2020, 10, 39.	4.8	50
44	Inhibition of Human Immunodeficiency Virus Type 1 Replication with Artificial Transcription Factors Targeting the Highly Conserved Primer-Binding Site. <i>Journal of Virology</i> , 2006, 80, 2873-2883.	3.4	49
45	Active integration: new strategies for transgenesis. <i>Transgenic Research</i> , 2007, 16, 333-339.	2.4	48
46	The Shelterin TIN2 Subunit Mediates Recruitment of Telomerase to Telomeres. <i>PLoS Genetics</i> , 2015, 11, e1005410.	3.5	47
47	The use of zinc finger peptides to study the role of specific factor binding sites in the chromatin environment. <i>Methods</i> , 2002, 26, 76-83.	3.8	46
48	Chimeric piggyBac transposases for genomic targeting in human cells. <i>Nucleic Acids Research</i> , 2012, 40, 6978-6991.	14.5	46
49	Endonuclease-induced, targeted homologous extrachromosomal recombination in <i>Xenopus</i> oocytes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 806-810.	7.1	44
50	Site-directed genome modification: nucleic acid and protein modules for targeted integration and gene correction. <i>Trends in Biotechnology</i> , 2005, 23, 399-406.	9.3	44
51	Site-directed genome modification: derivatives of DNA-modifying enzymes as targeting tools. <i>Trends in Biotechnology</i> , 2005, 23, 407-419.	9.3	43
52	Uranyl Acetate as a Direct Inhibitor of DNA-Binding Proteins. <i>Chemical Research in Toxicology</i> , 2007, 20, 784-789.	3.3	41
53	UBE3A: An E3 Ubiquitin Ligase With Genome-Wide Impact in Neurodevelopmental Disease. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 476.	2.9	41
54	Zinc fingers and a green thumb: manipulating gene expression in plants. <i>Current Opinion in Plant Biology</i> , 2003, 6, 163-168.	7.1	40

#	ARTICLE	IF	CITATIONS
55	Critical Parameters for Genome Editing Using Zinc Finger Nucleases. <i>Mini-Reviews in Medicinal Chemistry</i> , 2008, 8, 669-676.	2.4	40
56	Toward a General Approach for RNA-Templated Hierarchical Assembly of Split-Proteins. <i>Journal of the American Chemical Society</i> , 2010, 132, 11692-11701.	13.7	39
57	Restricted spacer tolerance of a zinc finger nuclease with a six amino acid linker. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2009, 19, 3970-3972.	2.2	36
58	New Insights into DNA Recognition by Zinc Fingers Revealed by Structural Analysis of the Oncoprotein ZNF217. <i>Journal of Biological Chemistry</i> , 2013, 288, 10616-10627.	3.4	36
59	Adding Fingers to an Engineered Zinc Finger Nuclease Can Reduce Activity. <i>Biochemistry</i> , 2011, 50, 5033-5041.	2.5	33
60	Effects on the transcriptome upon deletion of a distal element cannot be predicted by the size of the H3K27Ac peak in human cells. <i>Nucleic Acids Research</i> , 2016, 44, 4123-4133.	14.5	32
61	Artificial escape from XCI by DNA methylation editing of the CDKL5 gene. <i>Nucleic Acids Research</i> , 2020, 48, 2372-2387.	14.5	30
62	A zinc finger protein array for the visual detection of specific DNA sequences for diagnostic applications. <i>Nucleic Acids Research</i> , 2011, 39, e29-e29.	14.5	28
63	Strategies for the Enrichment and Selection of Genetically Modified Cells. <i>Trends in Biotechnology</i> , 2019, 37, 56-71.	9.3	28
64	Generation of a Novel Rat Model of Angelman Syndrome with a Complete <i>Ube3a</i> Gene Deletion. <i>Autism Research</i> , 2020, 13, 397-409.	3.8	28
65	Engineering zinc finger protein transcription factors to downregulate the epithelial glycoprotein-2 promoter as a novel anti-cancer treatment. <i>Molecular Carcinogenesis</i> , 2007, 46, 391-401.	2.7	27
66	Generation and Functional Analysis of Zinc Finger Nucleases. , 2008, 434, 277-290.		26
67	Functional rescue in an Angelman syndrome model following treatment with lentivector transduced hematopoietic stem cells. <i>Human Molecular Genetics</i> , 2021, 30, 1067-1083.	2.9	25
68	The prospect of molecular therapy for Angelman syndrome and other monogenic neurologic disorders. <i>BMC Neuroscience</i> , 2014, 15, 76.	1.9	24
69	Early Developmental EEG and Seizure Phenotypes in a Full Gene Deletion of Ubiquitin Protein Ligase E3A Rat Model of Angelman Syndrome. <i>ENeuro</i> , 2021, 8, ENEURO.0345-20.2020.	1.9	20
70	UBE3A-mediated regulation of imprinted genes and epigenome-wide marks in human neurons. <i>Epigenetics</i> , 2017, 12, 982-990.	2.7	18
71	Positron emission tomography imaging of novel AAV capsids maps rapid brain accumulation. <i>Nature Communications</i> , 2020, 11, 2102.	12.8	17
72	Determinants of heritable gene silencing for KRAB-dCas9+DNMT3 and Ezh2-dCas9+DNMT3 hit-and-run epigenome editing. <i>Nucleic Acids Research</i> , 2022, 50, 3239-3253.	14.5	17

#	ARTICLE	IF	CITATIONS
73	Live-Animal Epigenome Editing: Convergence of Novel Techniques. Trends in Genetics, 2019, 35, 527-541.	6.7	15
74	Miz-1 Activates Gene Expression via a Novel Consensus DNA Binding Motif. PLoS ONE, 2014, 9, e101151.	2.5	14
75	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.	3.6	13
76	Cold-Sensitive Mutants of Bacteriophage ϕ X174. II. Comparison of Two Cold-Sensitive Mutants. Journal of Virology, 1974, 14, 1115-1125.	3.4	13
77	Engineered Zinc Finger Proteins. Methods in Molecular Biology, 2010, , .	0.9	11
78	Pathogen-specific DNA sensing with engineered zinc finger proteins immobilized on a polymer chip. Analyst, The, 2018, 143, 4009-4016.	3.5	11
79	Bacteria herald a new era of gene editing. ELife, 2013, 2, e00563.	6.0	11
80	Aberrant promoter methylation contributes to LRIG1 silencing in basal/triple-negative breast cancer. British Journal of Cancer, 2022, 127, 436-448.	6.4	11
81	Systematic evaluation of split-fluorescent proteins for the direct detection of native and methylated DNA. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 3748-3751.	2.2	10
82	Versatile Ca^{2+} Functionalization of CRISPR Single Guide RNA. ChemBioChem, 2020, 21, 1633-1640.	2.6	10
83	The Functional Significance of Common Polymorphisms in Zinc Finger Transcription Factors. G3: Genes, Genomes, Genetics, 2014, 4, 1647-1655.	1.8	9
84	Imprinting effects of UBE3A loss on synaptic gene networks and Wnt signaling pathways. Human Molecular Genetics, 2019, 28, 3842-3852.	2.9	9
85	Exploring the suitability of RanBP2-type Zinc Fingers for RNA-binding protein design. Scientific Reports, 2019, 9, 2484.	3.3	9
86	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.	3.3	8
87	Unexpected binding behaviors of bacterial Argonautes in human cells cast doubts on their use as targetable gene regulators. PLoS ONE, 2018, 13, e0193818.	2.5	8
88	Processing of Targeted Psoralen Cross-Links in <i>Xenopus</i> Oocytes. Molecular and Cellular Biology, 1997, 17, 6645-6652.	2.3	7
89	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
90	Zinc-finger nucleases transition to the CoDA. Nature Methods, 2011, 8, 53-55.	19.0	7

#	ARTICLE	IF	CITATIONS
91	Modular Assembly of RanBP2-Type Zinc Finger Domains to Target Single-Stranded RNA. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 5371-5375.	13.8	7
92	Purified Protein Delivery to Activate an Epigenetically Silenced Allele in Mouse Brain. <i>Methods in Molecular Biology</i> , 2018, 1767, 227-239.	0.9	6
93	In Vivo Applications of Cell-Penetrating Zinc-Finger Transcription Factors. <i>Methods in Molecular Biology</i> , 2018, 1867, 239-251.	0.9	6
94	Engineering Specificity Changes on a RanBP2 Zinc Finger that Binds Single-Stranded RNA. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 7848-7852.	13.8	5
95	Conformational Elasticity can Facilitate TALE-DNA Recognition. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 94, 347-364.	2.3	5
96	Editorial: Precise Genome Editing Techniques and Applications. <i>Frontiers in Genetics</i> , 2020, 11, 412.	2.3	5
97	Crystallization and preliminary X-ray crystallographic analysis of Aart, a designed six-finger zinc-finger peptide, bound to DNA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 573-576.	0.7	3
98	The promise of gene editing: so close and yet so perilously far. <i>Frontiers in Genome Editing</i> , 0, 4, .	5.2	3
99	Is there a telltale RH fingerprint in zinc fingers that recognizes methylated CpG dinucleotides?. <i>Trends in Biochemical Sciences</i> , 2013, 38, 421-422.	7.5	2
100	Grand Challenges in Gene and Epigenetic Editing for Neurologic Disease. <i>Frontiers in Genome Editing</i> , 2020, 1, 1.	5.2	2
101	An in vivo Cell-Based Delivery Platform for Zinc Finger Artificial Transcription Factors in Pre-clinical Animal Models. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 789913.	2.9	2
102	Imaging Unique DNA Sequences in Individual Cells Using a CRISPR-Cas9-Based, Split Luciferase Biosensor. <i>Frontiers in Genome Editing</i> , 2022, 4, 867390.	5.2	2
103	Beyond the genome and into the clinic. <i>Genome Medicine</i> , 2012, 4, 78.	8.2	1
104	The Right Tools for the Right Job: CRISPR-pass Could Offer Safe Gene Correction for Many Disorders. <i>Molecular Therapy</i> , 2019, 27, 1346-1347.	8.2	1
105	Seeing Genetic and Epigenetic Information Without DNA Denaturation Using Sequence-Enabled Reassembly (SEER). <i>Methods in Molecular Biology</i> , 2010, 649, 365-382.	0.9	1
106	Zinc-finger exercisesThe "cutting edge"™ of gene therapy literally. <i>Biochemist</i> , 2008, 30, 10-13.	0.5	1
107	Sequence-Enabled Reassembly (SEER) Peptides for the Detection of DNA Sequences. , 2006, , 214-215.		0
108	973. SEquence-Enabled Reassembly of β -Lactamase (SEER-LAC): A Sensitive Method for the Detection of Double-Stranded DNA. <i>Molecular Therapy</i> , 2006, 13, S374.	8.2	0

#	ARTICLE	IF	CITATIONS
109	Dissecting the genetic architecture of coronary artery disease by genome engineering. BMC Proceedings, 2012, 6, .	1.6	0
110	Carlos F. Barbas III (1964–2014): Visionary at the Interface of Chemistry and Biology. ACS Chemical Biology, 2014, 9, 1645-1646.	3.4	0
111	A Method for Validating Mutations Associated with Malignant Hyperthermia using CRISPR/Cas9 and Dual Integrase Cassette Exchange. Biophysical Journal, 2017, 112, 98a.	0.5	0
112	Blood-brain barrier disruption for the delivery of non-infectious viral vectors and proteins, preliminary study. , 2017, , .		0
113	Blood-brain barrier disruption for the delivery of non-infectious viral vectors and proteins, preliminary study. , 2017, , .		0
114	Abstract 1117: Who's in the driver's seat? Identifying causative variants of colorectal cancer. , 2015, , .		0
115	Abstract 1445: Understanding the 8q24 colorectal cancer risk locus via CRISPR/Cas9 scarless genome editing. , 2017, , .		0
116	Abstract 394: Elucidating tissue-specific effects of the 8q24 multicancer risk locus via CRISPR/Cas9 scarless genome editing. , 2018, , .		0
117	Abstract B05: Comprehensive functional modeling of pan-cancer risk SNP rs6983267 in human CRC cells via scarless CRISPR/Cas9 genome editing. , 2020, , .		0