

Frank Buchholz

List of Publications by Year in descending order

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Version: 2024-02-01

150
papers

14,186
citations

28190

55
h-index

22102

113
g-index

163
all docs

163
docs citations

163
times ranked

22042
citing authors

#	ARTICLE	IF	CITATIONS
1	Conformational dynamics promotes disordered regions from function-dispensable to essential in evolved site-specific DNA recombinases. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 989-1001.	1.9	4
2	Correction of a Factor VIII genomic inversion with designer-recombinases. <i>Nature Communications</i> , 2022, 13, 422.	5.8	14
3	Pairing of single mutations yields obligate Cre-type site-specific recombinases. <i>Nucleic Acids Research</i> , 2022, 50, 1174-1186.	6.5	10
4	DNA methylation-independent long-term epigenetic silencing with dCRISPR/Cas9 fusion proteins. <i>Life Science Alliance</i> , 2022, 5, e202101321.	1.3	3
5	RNAi-Mediated Screen of Primary AML Cells Nominates MDM4 as a Therapeutic Target in NK-AML with DNMT3A Mutations. <i>Cells</i> , 2022, 11, 854.	1.8	3
6	Loss of USP28 and SPINT2 expression promotes cancer cell survival after whole genome doubling. <i>Cellular Oncology (Dordrecht)</i> , 2022, 45, 103-119.	2.1	8
7	Antigen presentation safeguards the integrity of the hematopoietic stem cell pool. <i>Cell Stem Cell</i> , 2022, 29, 760-775.e10.	5.2	29
8	Different Effects of RNAi-Mediated Downregulation or Chemical Inhibition of NAMPT in an Isogenic IDH Mutant and Wild-Type Glioma Cell Model. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5787.	1.8	3
9	Efficient Correction of Oncogenic <i>KRAS</i> and <i>TP53</i> Mutations through CRISPR Base Editing. <i>Cancer Research</i> , 2022, 82, 3002-3015.	0.4	12
10	Efficient and gentle delivery of molecules into cells with different elasticity <i>via</i> Progressive Mechanoporation. <i>Lab on A Chip</i> , 2021, 21, 2437-2452.	3.1	16
11	The Paf1 complex positively regulates enhancer activity in mouse embryonic stem cells. <i>Life Science Alliance</i> , 2021, 4, e202000792.	1.3	15
12	A heterodimer of evolved designer-recombinases precisely excises a human genomic DNA locus. <i>Nucleic Acids Research</i> , 2020, 48, 472-485.	6.5	20
13	Nearest-neighbor amino acids of specificity-determining residues influence the activity of engineered Cre-type recombinases. <i>Scientific Reports</i> , 2020, 10, 13985.	1.6	6
14	Efficient Generation and Correction of Mutations in Human iPS Cells Utilizing mRNAs of CRISPR Base Editors and Prime Editors. <i>Genes</i> , 2020, 11, 511.	1.0	86
15	Zfp281 orchestrates interconversion of pluripotent states by engaging Ehmt1 and Zic2. <i>EMBO Journal</i> , 2020, 39, e102591.	3.5	20
16	Comparison of GeneChip, nCounter, and Real-Time PCR-Based Gene Expressions Predicting Locoregional Tumor Control after Primary and Postoperative Radiochemotherapy in Head and Neck Squamous Cell Carcinoma. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 801-810.	1.2	10
17	<i>MLLT6</i> maintains <i>PD-L1</i> expression and mediates tumor immune resistance. <i>EMBO Reports</i> , 2020, 21, e50155.	2.0	13
18	CRISPR/Cas9 as a tool to dissect cancer mutations. <i>Methods</i> , 2019, 164-165, 36-48.	1.9	5

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19	Comparative RNAi Screens in Isogenic Human Stem Cells Reveal SMARCA4 as a Differential Regulator. <i>Stem Cell Reports</i> , 2019, 12, 1084-1098.	2.3	10
20	Independent validation of tumour volume, cancer stem cell markers and hypoxia-associated gene expressions for HNSCC after primary radiochemotherapy. <i>Clinical and Translational Radiation Oncology</i> , 2019, 16, 40-47.	0.9	32
21	Repeat FMISO-PET imaging weakly correlates with hypoxia-associated gene expressions for locally advanced HNSCC treated by primary radiochemotherapy. <i>Radiotherapy and Oncology</i> , 2019, 135, 43-50.	0.3	25
22	A Tug-of-War between Cell Shape and Polarity Controls Division Orientation to Ensure Robust Patterning in the Mouse Blastocyst. <i>Developmental Cell</i> , 2019, 51, 564-574.e6.	3.1	54
23	In-cell identification and measurement of RNA-protein interactions. <i>Nature Communications</i> , 2019, 10, 5317.	5.8	43
24	Assessment and site-specific manipulation of DNA (hydroxy-)methylation during mouse corticogenesis. <i>Life Science Alliance</i> , 2019, 2, e201900331.	1.3	20
25	Comparison of detection methods for HPV status as a prognostic marker for loco-regional control after radiochemotherapy in patients with HNSCC. <i>Radiotherapy and Oncology</i> , 2018, 127, 27-35.	0.3	17
26	Development and Validation of a Gene Signature for Patients with Head and Neck Carcinomas Treated by Postoperative Radio(chemo)therapy. <i>Clinical Cancer Research</i> , 2018, 24, 1364-1374.	3.2	45
27	Protein Dynamics in Complex DNA Lesions. <i>Molecular Cell</i> , 2018, 69, 1046-1061.e5.	4.5	128
28	MS Western, a Method of Multiplexed Absolute Protein Quantification is a Practical Alternative to Western Blotting. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 384-396.	2.5	32
29	A single reporter mouse line for Vika, Flp, Dre, and Cre-recombination. <i>Scientific Reports</i> , 2018, 8, 14453.	1.6	22
30	Analysis of Runx1 Using Induced Gene Ablation Reveals Its Essential Role in Pre-liver HSC Development and Limitations of an In Vivo Approach. <i>Stem Cell Reports</i> , 2018, 11, 784-794.	2.3	12
31	OC-0276: Combining different genomic signatures to improve the prognostic power for LRC after PORT-C in HNSCC. <i>Radiotherapy and Oncology</i> , 2018, 127, S140-S141.	0.3	0
32	Downregulation of PIK3CA via antibody-esiRNA-complexes suppresses human xenograft tumor growth. <i>PLoS ONE</i> , 2018, 13, e0200163.	1.1	6
33	Transcription factor Runx1 is pro-neurogenic in adult hippocampal precursor cells. <i>PLoS ONE</i> , 2018, 13, e0190789.	1.1	13
34	The long noncoding RNA lncR492 inhibits neural differentiation of murine embryonic stem cells. <i>PLoS ONE</i> , 2018, 13, e0191682.	1.1	16
35	STK3 is a therapeutic target for a subset of acute myeloid leukemias. <i>Oncotarget</i> , 2018, 9, 25458-25473.	0.8	10
36	The Apical Domain Is Required and Sufficient for the First Lineage Segregation in the Mouse Embryo. <i>Developmental Cell</i> , 2017, 40, 235-247.e7.	3.1	183

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37	Phylointeractomics reconstructs functional evolution of protein binding. <i>Nature Communications</i> , 2017, 8, 14334.	5.8	26
38	<scp>ZBTB</scp>48 is both a vertebrate telomere-binding protein and a transcriptional activator. <i>EMBO Reports</i> , 2017, 18, 929-946.	2.0	50
39	Purified Cas9 Fusion Proteins for Advanced Genome Manipulation. <i>Small Methods</i> , 2017, 1, 1600052.	4.6	11
40	Genome-scale single-cell mechanical phenotyping reveals disease-related genes involved in mitotic rounding. <i>Nature Communications</i> , 2017, 8, 1266.	5.8	52
41	Crystal structure of an engineered, HIV-specific recombinase for removal of integrated proviral DNA. <i>Nucleic Acids Research</i> , 2017, 45, 9726-9740.	6.5	8
42	Development of a genetic sensor that eliminates p53 deficient cells. <i>Nature Communications</i> , 2017, 8, 1463.	5.8	15
43	Inactivation of Cancer Mutations Utilizing CRISPR/Cas9. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	30
44	lncRNA Panct1 Maintains Mouse Embryonic Stem Cell Identity by Regulating TOBF1 Recruitment to Oct-Sox Sequences in Early G1. <i>Cell Reports</i> , 2017, 21, 3012-3021.	2.9	35
45	HPV status, cancer stem cell marker expression, hypoxia gene signatures and tumour volume identify good prognosis subgroups in patients with HNSCC after primary radiochemotherapy: A multicentre retrospective study of the German Cancer Consortium Radiation Oncology Group (DKTK-ROG). <i>Radiotherapy and Oncology</i> , 2016, 121, 364-373.	0.3	130
46	Independent validation of the prognostic value of cancer stem cell marker expression and hypoxia-induced gene expression for patients with locally advanced HNSCC after postoperative radiotherapy. <i>Clinical and Translational Radiation Oncology</i> , 2016, 1, 19-26.	0.9	22
47	Discovery of Nigri/nox and Panto/pox site-specific recombinase systems facilitates advanced genome engineering. <i>Scientific Reports</i> , 2016, 6, 30130.	1.6	27
48	Dissecting mechanisms of mouse embryonic stem cells heterogeneity through a model-based analysis of transcription factor dynamics. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20160167.	1.5	15
49	Cre Recombinase and Other Tyrosine Recombinases. <i>Chemical Reviews</i> , 2016, 116, 12785-12820.	23.0	104
50	Antiviral therapy of persistent viral infection using genome editing. <i>Current Opinion in Virology</i> , 2016, 20, 85-91.	2.6	11
51	Low Cancer Stem Cell Marker Expression and Low Hypoxia Identify Good Prognosis Subgroups in HPV(+) HNSCC after Postoperative Radiochemotherapy: A Multicenter Study of the DKTK-ROG. <i>Clinical Cancer Research</i> , 2016, 22, 2639-2649.	3.2	127
52	Antibody-coupled siRNA as an efficient method for in vivo mRNA knockdown. <i>Nature Protocols</i> , 2016, 11, 22-36.	5.5	39
53	Directed evolution of a recombinase that excises the provirus of most HIV-1 primary isolates with high specificity. <i>Nature Biotechnology</i> , 2016, 34, 401-409.	9.4	108
54	CRISPR/Cas9 nickase-mediated disruption of hepatitis B virus open reading frame S and X. <i>Scientific Reports</i> , 2015, 5, 13734.	1.6	97

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55	RNAi profiling of primary human AML cells identifies ROCK1 as a therapeutic target and nominates fasudil as an antileukemic drug. <i>Blood</i> , 2015, 125, 3760-3768.	0.6	53
56	Systems Analyses Reveal Shared and Diverse Attributes of Oct4 Regulation in Pluripotent Cells. <i>Cell Systems</i> , 2015, 1, 141-151.	2.9	15
57	Antibody-Mediated Delivery of Anti-KRAS-siRNA In Vivo Overcomes Therapy Resistance in Colon Cancer. <i>Clinical Cancer Research</i> , 2015, 21, 1383-1394.	3.2	95
58	The iBeetle large-scale RNAi screen reveals gene functions for insect development and physiology. <i>Nature Communications</i> , 2015, 6, 7822.	5.8	139
59	Targeting Human Long Noncoding Transcripts by Endoribonuclease-Prepared siRNAs. <i>Journal of Biomolecular Screening</i> , 2015, 20, 1018-1026.	2.6	12
60	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. <i>Cell</i> , 2015, 163, 712-723.	13.5	1,132
61	Stage-Specific Binding Profiles of Cohesin in Resting and Activated B Lymphocytes Suggest a Role for Cohesin in Immunoglobulin Class Switching and Maturation. <i>PLoS ONE</i> , 2014, 9, e111748.	1.1	8
62	Universal Tre (uTre) recombinase specifically targets the majority of HIV-1 isolates. <i>Journal of the International AIDS Society</i> , 2014, 17, 19706.	1.2	10
63	Runx1 is required for progression of CD41+ embryonic precursors into HSCs but not prior to this. <i>Development (Cambridge)</i> , 2014, 141, 3319-3323.	1.2	36
64	G-107 Pronounced antiviral activity of next-generation LTR-specific Tre-recombinase. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 67, 70.	0.9	0
65	Interplay of Acetyltransferase EP300 and the Proteasome System in Regulating Heat Shock Transcription Factor 1. <i>Cell</i> , 2014, 156, 975-985.	13.5	130
66	Mitotic Cell Shape - RNA Interference Screening for Genes Involved in Mechanics using Atomic Force Microscopy. <i>Biophysical Journal</i> , 2014, 106, 787a.	0.2	0
67	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. <i>Molecular Cell</i> , 2014, 56, 389-399.	4.5	88
68	Another Brick in the Wall: RNAi Screens Identify New Barriers in iPSC Reprogramming. <i>Cell Stem Cell</i> , 2014, 15, 116-118.	5.2	3
69	Quantitative interaction screen of telomeric repeat-containing RNA reveals novel TERRA regulators. <i>Genome Research</i> , 2013, 23, 2149-2157.	2.4	69
70	The histone demethylase UTX regulates stem cell migration and hematopoiesis. <i>Blood</i> , 2013, 121, 2462-2473.	0.6	93
71	Engineered DNA modifying enzymes: Components of a future strategy to cure HIV/AIDS. <i>Antiviral Research</i> , 2013, 97, 211-217.	1.9	8
72	Designing Efficient and Specific Endoribonuclease-Prepared siRNAs. <i>Methods in Molecular Biology</i> , 2013, 942, 193-204.	0.4	15

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73	Vika/vox, a novel efficient and specific Cre/loxP-like site-specific recombination system. <i>Nucleic Acids Research</i> , 2013, 41, e37-e37.	6.5	50
74	HOT1 is a mammalian direct telomere repeat-binding protein contributing to telomerase recruitment. <i>EMBO Journal</i> , 2013, 32, 1681-1701.	3.5	74
75	Highly Significant Antiviral Activity of HIV-1 LTR-Specific Tre-Recombinase in Humanized Mice. <i>PLoS Pathogens</i> , 2013, 9, e1003587.	2.1	55
76	Engineering of a target site-specific recombinase by a combined evolution- and structure-guided approach. <i>Nucleic Acids Research</i> , 2013, 41, 2394-2403.	6.5	31
77	Interaction between AP-5 and the hereditary spastic paraplegia proteins SPG11 and SPG15. <i>Molecular Biology of the Cell</i> , 2013, 24, 2558-2569.	0.9	95
78	A genome-wide RNAi screen identifies proteins modulating aberrant FLT3-ITD signaling. <i>Leukemia</i> , 2013, 27, 2301-2310.	3.3	8
79	Runx1 is essential at two stages of early murine B-cell development. <i>Blood</i> , 2013, 122, 413-423.	0.6	47
80	Combined RNAi and localization for functionally dissecting long noncoding RNAs. <i>Nature Methods</i> , 2012, 9, 360-362.	9.0	62
81	3D Profile-Based Approach to Proteome-Wide Discovery of Novel Human Chemokines. <i>PLoS ONE</i> , 2012, 7, e36151.	1.1	6
82	Polycomb group ring finger 1 cooperates with Runx1 in regulating differentiation and self-renewal of hematopoietic cells. <i>Blood</i> , 2012, 119, 4152-4161.	0.6	42
83	From RNAi Screens to Molecular Function in Embryonic Stem Cells. <i>Stem Cell Reviews and Reports</i> , 2012, 8, 32-42.	5.6	13
84	Excision of HIV-1 Proviral DNA by Recombinant Cell Permeable Tre-Recombinase. <i>PLoS ONE</i> , 2012, 7, e31576.	1.1	27
85	A systematic RNAi synthetic interaction screen reveals a link between p53 and snRNP assembly. <i>Nature Cell Biology</i> , 2011, 13, 809-818.	4.6	74
86	In vitro evolution and analysis of HIV-1 LTR-specific recombinases. <i>Methods</i> , 2011, 53, 102-109.	1.9	27
87	High-throughput RNAi screening in mammalian cells with esiRNAs. <i>Methods</i> , 2011, 53, 424-429.	1.9	13
88	RAD21 Cooperates with Pluripotency Transcription Factors in the Maintenance of Embryonic Stem Cell Identity. <i>PLoS ONE</i> , 2011, 6, e19470.	1.1	109
89	Ribosome biogenesis and p53: Who is regulating whom?. <i>Cell Cycle</i> , 2011, 10, 3417-3418.	1.3	5
90	An RNA Interference Phenotypic Screen Identifies a Role for FGF Signals in Colon Cancer Progression. <i>PLoS ONE</i> , 2011, 6, e23381.	1.1	23

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91	MISSION esiRNA for RNAi Screening in Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2010, , .	0.2	12
92	PhenoFam-gene set enrichment analysis through protein structural information. <i>BMC Bioinformatics</i> , 2010, 11, 254.	1.2	6
93	A domesticated transposon mediates the effects of a single nucleotide polymorphism responsible for enhanced muscle growth. <i>EMBO Reports</i> , 2010, 11, 305-311.	2.0	53
94	Systems survey of endocytosis by multiparametric image analysis. <i>Nature</i> , 2010, 464, 243-249.	13.7	407
95	SeLOX—a locus of recombination site search tool for the detection and directed evolution of site-specific recombination systems. <i>Nucleic Acids Research</i> , 2010, 38, W293-W298.	6.5	20
96	A Genome-Scale DNA Repair RNAi Screen Identifies SPG48 as a Novel Gene Associated with Hereditary Spastic Paraplegia. <i>PLoS Biology</i> , 2010, 8, e1000408.	2.6	164
97	Systematic Analysis of Human Protein Complexes Identifies Chromosome Segregation Proteins. <i>Science</i> , 2010, 328, 593-599.	6.0	465
98	Dre recombinase, like Cre, is a highly efficient site-specific recombinase in <i>E. coli</i> , mammalian cells and mice. <i>DMM Disease Models and Mechanisms</i> , 2009, 2, 508-515.	1.2	254
99	SKAnking with Ska3: Essential role of Ska3 in cell division revealed by combined phenotypic profiling. <i>Cell Cycle</i> , 2009, 8, 3435-3437.	1.3	10
100	Three LIF-dependent signatures and gene clusters with atypical expression profiles, identified by transcriptome studies in mouse ES cells and early derivatives. <i>BMC Genomics</i> , 2009, 10, 73.	1.2	29
101	HAUS, the 8-Subunit Human Augmin Complex, Regulates Centrosome and Spindle Integrity. <i>Current Biology</i> , 2009, 19, 816-826.	1.8	231
102	Comparative profiling identifies C13orf3 as a component of the Ska complex required for mammalian cell division. <i>EMBO Journal</i> , 2009, 28, 1453-1465.	3.5	89
103	Engineering DNA processing enzymes for the postgenomic era. <i>Current Opinion in Biotechnology</i> , 2009, 20, 383-389.	3.3	14
104	A Genome-Scale RNAi Screen for Oct4 Modulators Defines a Role of the Paf1 Complex for Embryonic Stem Cell Identity. <i>Cell Stem Cell</i> , 2009, 4, 403-415.	5.2	252
105	The Symplekin/ZONAB Complex Inhibits Intestinal Cell Differentiation by the Repression of AML1/Runx1. <i>Gastroenterology</i> , 2009, 137, 156-164.e3.	0.6	33
106	The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. <i>PLoS ONE</i> , 2009, 4, e6804.	1.1	54
107	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. <i>Nature Methods</i> , 2008, 5, 409-415.	9.0	568
108	Systems biology of mammalian cell division. <i>Cell Cycle</i> , 2008, 7, 2123-2128.	1.3	13

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109	Molecular Evolution of the Tre Recombinase. <i>Journal of Visualized Experiments</i> , 2008, , .	0.2	3
110	HIV-1 Proviral DNA Excision Using an Evolved Recombinase. <i>Science</i> , 2007, 316, 1912-1915.	6.0	193
111	RUNX1 DNA-Binding Mutants, Associated with Minimally Differentiated Acute Myelogenous Leukemia, Disrupt Myeloid Differentiation. <i>Cancer Research</i> , 2007, 67, 537-545.	0.4	30
112	Genome-scale RNAi profiling of cell division in human tissue culture cells. <i>Nature Cell Biology</i> , 2007, 9, 1401-1412.	4.6	270
113	Genome-wide resources of endoribonuclease-prepared short interfering RNAs for specific loss-of-function studies. <i>Nature Methods</i> , 2007, 4, 337-344.	9.0	167
114	Tandem affinity purification of functional TAP-tagged proteins from human cells. <i>Nature Protocols</i> , 2007, 2, 1145-1151.	5.5	57
115	Production of Endoribonuclease-Prepared Short Interfering RNAs (esiRNAs) for Specific and Effective Gene Silencing in Mammalian Cells. <i>Cold Spring Harbor Protocols</i> , 2007, 2007, pdb.prot4824.	0.2	9
116	Minimizing the risk of reporting false positives in large-scale RNAi screens. <i>Nature Methods</i> , 2006, 3, 777-779.	9.0	417
117	Enzymatically prepared RNAi libraries. <i>Nature Methods</i> , 2006, 3, 696-700.	9.0	69
118	Protein phosphatase 2A protects centromeric sister chromatid cohesion during meiosis I. <i>Nature</i> , 2006, 441, 53-61.	13.7	419
119	AML1 deletion in adult mice causes splenomegaly and lymphomas. <i>Oncogene</i> , 2006, 25, 929-939.	2.6	109
120	RNAi in embryonic stem cells. <i>Stem Cell Reviews and Reports</i> , 2006, 2, 11-18.	5.6	11
121	RNAi in Embryonic Stem Cells. <i>Stem Cell Reviews and Reports</i> , 2006, 2, 11-18.	5.6	0
122	Production of endoribonuclease-prepared short interfering RNAs for gene silencing in mammalian cells. <i>Nature Methods</i> , 2005, 2, 779-784.	9.0	76
123	Downregulation of Apaf-1 and caspase-3 by RNA interference in human glioma cells: Consequences for erucylphosphocholine-induced apoptosis. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2005, 10, 1163-1174.	2.2	23
124	RNA interference in postimplantation mouse embryos. , 2005, , 207-219.		0
125	Selective Expression of the Cre Recombinase in Late-Stage Thymocytes Using the Distal Promoter of the <i>Lck</i> Gene. <i>Journal of Immunology</i> , 2005, 174, 6725-6731.	0.4	111
126	RNA interference rescue by bacterial artificial chromosome transgenesis in mammalian tissue culture cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2396-2401.	3.3	88

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127	Functional Genomic Analysis of Cell Division by Endoribonuclease-Prepared siRNAs. <i>Cell Cycle</i> , 2005, 4, 561-564.	1.3	30
128	Correlation-based Method for Automatic Mitotic Cell Detection in Phase Contrast Microscopy. <i>Advances in Soft Computing</i> , 2005, , 627-634.	0.4	12
129	Alternative Approaches for Efficient Inhibition of Hepatitis C Virus RNA Replication by Small Interfering RNAs. <i>Journal of Virology</i> , 2004, 78, 3436-3446.	1.5	158
130	DEQOR: a web-based tool for the design and quality control of siRNAs. <i>Nucleic Acids Research</i> , 2004, 32, W113-W120.	6.5	140
131	An endoribonuclease-prepared siRNA screen in human cells identifies genes essential for cell division. <i>Nature</i> , 2004, 432, 1036-1040.	13.7	369
132	Tissue-specific RNA interference in post-implantation mouse embryos using directional electroporation and whole embryo culture. <i>Differentiation</i> , 2004, 72, 92-102.	1.0	28
133	Production of siRNA In Vitro by Enzymatic Digestion of Double-Stranded RNA. , 2004, , .		1
134	RNA interference: gene silencing in the fast lane. <i>Seminars in Cancer Biology</i> , 2003, 13, 259-265.	4.3	36
135	Crystal structure of a wild-type Cre recombinase-loxP synapse reveals a novel spacer conformation suggesting an alternative mechanism for DNA cleavage activation. <i>Nucleic Acids Research</i> , 2003, 31, 5449-5460.	6.5	67
136	Tissue-specific RNA interference in postimplantation mouse embryos with endoribonuclease-prepared short interfering RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14236-14240.	3.3	148
137	Short RNA duplexes produced by hydrolysis with <i>Escherichia coli</i> RNase III mediate effective RNA interference in mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9942-9947.	3.3	285
138	Codon-improved Cre recombinase (iCre) expression in the mouse. <i>Genesis</i> , 2002, 32, 19-26.	0.8	350
139	loxP-Directed Cloning: Use of Cre Recombinase as a Universal Restriction Enzyme. <i>BioTechniques</i> , 2001, 31, 906-918.	0.8	11
140	Alteration of Cre recombinase site specificity by substrate-linked protein evolution. <i>Nature Biotechnology</i> , 2001, 19, 1047-1052.	9.4	147
141	High-efficiency deleter mice show that FLPe is an alternative to Cre-loxP. <i>Nature Genetics</i> , 2000, 25, 139-140.	9.4	1,073
142	Inducible chromosomal translocation of AML1 and ETO genes through Cre/loxP-mediated recombination in the mouse. <i>EMBO Reports</i> , 2000, 1, 133-139.	2.0	105
143	A new logic for DNA engineering using recombination in <i>Escherichia coli</i> . <i>Nature Genetics</i> , 1998, 20, 123-128.	9.4	1,123
144	Improved properties of FLP recombinase evolved by cycling mutagenesis. <i>Nature Biotechnology</i> , 1998, 16, 657-662.	9.4	374

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145	Comparative kinetic analysis of FLP and cre recombinases: mathematical models for DNA binding and recombination. <i>Journal of Molecular Biology</i> , 1998, 284, 363-384.	2.0	142
146	Inducible expression based on regulated recombination: a single vector strategy for stable expression in cultured cells. <i>Nucleic Acids Research</i> , 1998, 26, 3263-3269.	6.5	19
147	A Novel Family of Cys-Cys, His-Cys Zinc Finger Transcription Factors Expressed in Developing Nervous System and Pituitary Gland. <i>Journal of Biological Chemistry</i> , 1996, 271, 10723-10730.	1.6	60
148	Different thermostabilities of FLP and Cre recombinases: implications for applied site-specific recombination. <i>Nucleic Acids Research</i> , 1996, 24, 4256-4262.	6.5	165
149	A simple assay to determine the functionality of Cre or FLP recombination targets in genomic manipulation constructs. <i>Nucleic Acids Research</i> , 1996, 24, 3118-3119.	6.5	87
150	LncRNA <i>Panct1</i> Maintains Mouse Embryonic Stem Cell Identity by Regulating TOBF1 Recruitment to Oct-Sox Sequences in Early G1. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0