

Richard Fishel

List of Publications by Year in descending order

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97
papers

15,683
citations

46918

47
h-index

39575

94
g-index

100
all docs

100
docs citations

100
times ranked

11860
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass COVID-19 patient screening using UvsX and UvsY mediated DNA recombination and high throughput parallel sequencing. <i>Scientific Reports</i> , 2022, 12, 4082.	1.6	2
2	Retroviral prototype foamy virus intasome binding to a nucleosome target does not determine integration efficiency. <i>Journal of Biological Chemistry</i> , 2021, 296, 100550.	1.6	5
3	Linker domain function predicts pathogenic MLH1 missense variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
4	Evolutionary advantage of a dissociative search mechanism in DNA mismatch repair. <i>Physical Review E</i> , 2021, 103, 052404.	0.8	2
5	The mechanics of DNA mismatch repair sliding clamp progression in the prediction of clinically relevant HsMLH1 missense mutations. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
6	Strategies for Targeting Retroviral Integration for Safer Gene Therapy: Advances and Challenges. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 662331.	1.6	16
7	Nucleosome DNA unwrapping does not affect prototype foamy virus integration efficiency or site selection. <i>PLoS ONE</i> , 2019, 14, e0212764.	1.1	8
8	MutL sliding clamps coordinate exonuclease-independent <i>Escherichia coli</i> mismatch repair. <i>Nature Communications</i> , 2019, 10, 5294.	5.8	20
9	Long repeating (TTAGGG) single-stranded DNA self-condenses into compact beaded filaments stabilized by G-quadruplex formation. <i>Journal of Biological Chemistry</i> , 2018, 293, 9473-9485.	1.6	22
10	MutS homolog sliding clamps shield the DNA from binding proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 14285-14294.	1.6	5
11	Mutation of TGF β 2-R11 eliminates NSAID cancer chemoprevention. <i>Oncotarget</i> , 2018, 9, 12554-12561.	0.8	10
12	Coordinating Multi-Protein Mismatch Repair by Managing Diffusion Mechanics on the DNA. <i>Journal of Molecular Biology</i> , 2018, 430, 4469-4480.	2.0	11
13	Plasticity of Multi-Protein Complexes. <i>Journal of Molecular Biology</i> , 2018, 430, 4441-4442.	2.0	3
14	Stochastic Processes and Component Plasticity Governing DNA Mismatch Repair. <i>Journal of Molecular Biology</i> , 2018, 430, 4456-4468.	2.0	13
15	Expression and purification of nuclease-free protocatechuate 3,4-dioxygenase for prolonged single-molecule fluorescence imaging. <i>Analytical Biochemistry</i> , 2018, 556, 78-84.	1.1	11
16	Dynamic unwrapping of nucleosomes by HsRAD51 that includes sliding and rotational motion of histone octamers. <i>Nucleic Acids Research</i> , 2017, 45, 685-698.	6.5	8
17	Enhanced gene targeting to evaluate Lynch syndrome alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3918-3920.	3.3	1
18	Dynamic control of strand excision during human DNA mismatch repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3281-3286.	3.3	35

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19	<i>Pseudomonas aeruginosa</i> AmrZ Binds to Four Sites in the <i>algD</i> Promoter, Inducing DNA-AmrZ Complex Formation and Transcriptional Activation. <i>Journal of Bacteriology</i> , 2016, 198, 2673-2681.	1.0	22
20	The <i>Pseudomonas aeruginosa</i> AmrZ C-terminal domain mediates tetramerization and is required for its activator and repressor functions. <i>Environmental Microbiology Reports</i> , 2016, 8, 85-90.	1.0	15
21	Cascading MutS and MutL sliding clamps control DNA diffusion to activate mismatch repair. <i>Nature</i> , 2016, 539, 583-587.	13.7	91
22	Retroviral intasomes search for a target DNA by 1D diffusion which rarely results in integration. <i>Nature Communications</i> , 2016, 7, 11409.	5.8	29
23	Mismatch Repair. , 2016, , 305-339.		1
24	An Efficient Site-Specific Method for Irreversible Covalent Labeling of Proteins with a Fluorophore. <i>Scientific Reports</i> , 2015, 5, 16883.	1.6	20
25	Mismatch Repair during Homologous and Homeologous Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a022657.	2.3	146
26	Widespread nuclease contamination in commonly used oxygen-scavenging systems. <i>Nature Methods</i> , 2015, 12, 901-902.	9.0	24
27	Mismatch Repair. <i>Journal of Biological Chemistry</i> , 2015, 290, 26395-26403.	1.6	181
28	Repair of Oxidative DNA Base Damage in the Host Genome Influences the HIV Integration Site Sequence Preference. <i>PLoS ONE</i> , 2014, 9, e103164.	1.1	12
29	Mismatch repair protein hMSH2-hMSH6 recognizes mismatches and forms sliding clamps within a D-loop recombination intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E316-25.	3.3	37
30	Single-molecule views of MutS on mismatched DNA. <i>DNA Repair</i> , 2014, 20, 82-93.	1.3	37
31	The mechanism of mismatch repair and the functional analysis of mismatch repair defects in Lynch syndrome. <i>Familial Cancer</i> , 2013, 12, 159-168.	0.9	65
32	The hMSH2(M688R) Lynch syndrome mutation may function as a dominant negative. <i>Carcinogenesis</i> , 2012, 33, 1647-1654.	1.3	8
33	Homologous Recombination in Eukaryotes. <i>Progress in Molecular Biology and Translational Science</i> , 2012, 110, 155-206.	0.9	28
34	ATP Alters the Diffusion Mechanics of MutS on Mismatched DNA. <i>Structure</i> , 2012, 20, 1264-1274.	1.6	87
35	The Base Excision Repair Pathway Is Required for Efficient Lentivirus Integration. <i>PLoS ONE</i> , 2011, 6, e17862.	1.1	38
36	MutS switches between two fundamentally distinct clamps during mismatch repair. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 379-385.	3.6	120

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37	A quantitative model of nucleosome dynamics. <i>Nucleic Acids Research</i> , 2011, 39, 8306-8313.	6.5	49
38	Human MSH2 (hMSH2) Protein Controls ATP Processing by hMSH2-hMSH6. <i>Journal of Biological Chemistry</i> , 2011, 286, 40287-40295.	1.6	33
39	MicroRNA-21 induces resistance to 5-fluorouracil by down-regulating human DNA MutS homolog 2 (hMSH2). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21098-21103.	3.3	333
40	Modulation of mismatch repair and genomic stability by miR-155. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6982-6987.	3.3	306
41	Single-Molecule Analysis Reveals the Kinetics and Physiological Relevance of MutL-ssDNA Binding. <i>PLoS ONE</i> , 2010, 5, e15496.	1.1	32
42	Sequence context effect for hMSH2-hMSH6 mismatch-dependent activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4177-4182.	3.3	59
43	Evidence that hMLH3 functions primarily in meiosis and in hMSH2-hMSH3 mismatch repair. <i>Cancer Biology and Therapy</i> , 2009, 8, 1411-1420.	1.5	24
44	Current and emerging trends in Lynch syndrome identification in women with endometrial cancer. <i>Gynecologic Oncology</i> , 2009, 114, 128-134.	0.6	97
45	DNA mismatch repair (MMR)-dependent 5-fluorouracil cytotoxicity and the potential for new therapeutic targets. <i>British Journal of Pharmacology</i> , 2009, 158, 679-692.	2.7	66
46	Enrichment and characterization of histones by two-dimensional hydroxyapatite/reversed-phase liquid chromatography-mass spectrometry. <i>Analytical Biochemistry</i> , 2009, 388, 47-55.	1.1	9
47	Nucleosome Remodeling by hMSH2-hMSH6. <i>Molecular Cell</i> , 2009, 36, 1086-1094.	4.5	62
48	Harnessing mismatch repair to model sporadic cancers. <i>Nature Methods</i> , 2008, 5, 225-226.	9.0	1
49	hMSH4-hMSH5 Adenosine Nucleotide Processing and Interactions with Homologous Recombination Machinery. <i>Journal of Biological Chemistry</i> , 2008, 283, 145-154.	1.6	44
50	DNA Damage-Dependent Acetylation and Ubiquitination of H2AX Enhances Chromatin Dynamics. <i>Molecular and Cellular Biology</i> , 2007, 27, 7028-7040.	1.1	327
51	Nitric Oxide-Donating Aspirin Derivatives Suppress Microsatellite Instability in Mismatch Repair-Deficient and Hereditary Nonpolyposis Colorectal Cancer Cells. <i>Cancer Research</i> , 2007, 67, 10966-10975.	0.4	47
52	Magnesium influences the discrimination and release of ADP by human RAD51. <i>DNA Repair</i> , 2006, 5, 704-717.	1.3	11
53	DNA Mismatch Repair-dependent Response to Fluoropyrimidine-generated Damage. <i>Journal of Biological Chemistry</i> , 2005, 280, 5516-5526.	1.6	108
54	Extreme Heterogeneity in the Molecular Events Leading to the Establishment of Chiasmata during Meiosis I in Human Oocytes. <i>American Journal of Human Genetics</i> , 2005, 76, 112-127.	2.6	151

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55	Lynch Syndrome: Form, Function, Proteins, and Basketball. <i>Gastroenterology</i> , 2005, 129, 751-755.	0.6	25
56	Lynch Syndrome: Form, Function, Proteins, and Basketball. <i>Gastroenterology</i> , 2005, 129, 751-755.	0.6	25
57	Mechanism of DNA Mismatch Repair from Bacteria to Human. , 2005, , .		0
58	MSI-Testing in Hereditary Non-Polyposis Colorectal Carcinoma (HNPCC). <i>Disease Markers</i> , 2004, 20, 225-236.	0.6	10
59	hXRCC2 Enhances ADP/ATP Processing and Strand Exchange by hRAD51. <i>Journal of Biological Chemistry</i> , 2004, 279, 30385-30394.	1.6	44
60	Deficiencies in Mouse Myh and Ogg1 Result in Tumor Predisposition and G to T Mutations in Codon 12 of the K-Ras Oncogene in Lung Tumors. <i>Cancer Research</i> , 2004, 64, 3096-3102.	0.4	271
61	hMSH4-hMSH5 Recognizes Holliday Junctions and Forms a Meiosis-Specific Sliding Clamp that Embraces Homologous Chromosomes. <i>Molecular Cell</i> , 2004, 15, 437-451.	4.5	361
62	The Coordinated Functions of the E. coli MutS and MutL Proteins in Mismatch Repair. <i>Molecular Cell</i> , 2003, 12, 233-246.	4.5	259
63	Mismatch Repair and the Hereditary Non-polyposis Colorectal Cancer Syndrome (HNPCC). <i>Cancer Investigation</i> , 2002, 20, 102-109.	0.6	117
64	Activation of Human MutS Homologs by 8-Oxo-guanine DNA Damage. <i>Journal of Biological Chemistry</i> , 2002, 277, 8260-8266.	1.6	149
65	Fusion Tyrosine Kinases Induce Drug Resistance by Stimulation of Homology-Dependent Recombination Repair, Prolongation of G ₂ /M Phase, and Protection from Apoptosis. <i>Molecular and Cellular Biology</i> , 2002, 22, 4189-4201.	1.1	188
66	Biochemical Characterization of the Human RAD51 Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 14417-14425.	1.6	71
67	Biochemical Characterization of the Human RAD51 Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 14426-14433.	1.6	25
68	DNA Repair and Tumorigenesis: Lessons from Hereditary Cancer Syndromes. <i>Cancer Biology and Therapy</i> , 2002, 1, 477-485.	1.5	101
69	HNPCC mutations in hMSH2 result in reduced hMSH2-hMSH6 molecular switch functions. <i>Cancer Cell</i> , 2002, 1, 469-478.	7.7	59
70	BCR/ABL Regulates Mammalian RecA Homologs, Resulting in Drug Resistance. <i>Molecular Cell</i> , 2001, 8, 795-806.	4.5	290
71	Adenosine nucleotide modulates the physical interaction between hMSH2 and BRCA1. <i>Oncogene</i> , 2001, 20, 4640-4649.	2.6	57
72	The Interaction of DNA Mismatch Repair Proteins with Human Exonuclease I. <i>Journal of Biological Chemistry</i> , 2001, 276, 33011-33018.	1.6	133

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73	Sequence analysis of the mismatch repair gene hMSH6 in the germline of patients with familial and sporadic colorectal cancer. , 2000, 85, 606-613.		53
74	The GTP hydrolysis defect of the <i>Saccharomyces cerevisiae</i> mutant G-protein Gpa1G50V. <i>Yeast</i> , 2000, 16, 387-400.	0.8	13
75	BRCA1 and cell signaling. <i>Oncogene</i> , 2000, 19, 6152-6158.	2.6	80
76	The Effect of O6-Methylguanine DNA Adducts on the Adenosine Nucleotide Switch Functions of hMSH2-hMSH6 and hMSH2-hMSH3. <i>Journal of Biological Chemistry</i> , 2000, 275, 27851-27857.	1.6	38
77	A Human REV7 Homolog That Interacts with the Polymerase ϵ Catalytic Subunit hREV3 and the Spindle Assembly Checkpoint Protein hMAD2. <i>Journal of Biological Chemistry</i> , 2000, 275, 4391-4397.	1.6	170
78	The Role of Mismatched Nucleotides in Activating the hMSH2-hMSH6 Molecular Switch. <i>Journal of Biological Chemistry</i> , 2000, 275, 3922-3930.	1.6	103
79	Colorectal carcinomas with high microsatellite instability: Defining a distinct immunologic and molecular entity with respect to prognostic markers. <i>Human Pathology</i> , 2000, 31, 1506-1514.	1.1	76
80	Cytochrome c and dATP-mediated Oligomerization of Apaf-1 Is a Prerequisite for Procaspase-9 Activation. <i>Journal of Biological Chemistry</i> , 1999, 274, 17941-17945.	1.6	432
81	The Interaction of the Human MutL Homologues in Hereditary Nonpolyposis Colon Cancer. <i>Journal of Biological Chemistry</i> , 1999, 274, 6336-6341.	1.6	153
82	Dissociation of Mismatch Recognition and ATPase Activity by hMSH2-hMSH3. <i>Journal of Biological Chemistry</i> , 1999, 274, 21659-21664.	1.6	90
83	Severe Attenuation of the B Cell Immune Response in Msh2-deficient Mice. <i>Journal of Experimental Medicine</i> , 1999, 189, 471-482.	4.2	80
84	Signaling mismatch repair in cancer. <i>Nature Medicine</i> , 1999, 5, 1239-1241.	15.2	126
85	Female embryonic lethality in Msh2 Δ -Trp53 nullizygous mice is strain dependent. <i>Mammalian Genome</i> , 1999, 10, 1020-1022.	1.0	16
86	Molecular diagnostics of cancer predisposition: hereditary non-polyposis colorectal carcinoma and mismatch repair defects. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 1999, 1423, O1-O10.	3.3	30
87	hMSH2-hMSH6 Forms a Hydrolysis-Independent Sliding Clamp on Mismatched DNA. <i>Molecular Cell</i> , 1999, 3, 255-261.	4.5	338
88	Increased Hypermutation at G and C Nucleotides in Immunoglobulin Variable Genes from Mice Deficient in the MSH2 Mismatch Repair Protein. <i>Journal of Experimental Medicine</i> , 1998, 187, 1745-1751.	4.2	170
89	Interactions of Human hMSH2 with hMSH3 and hMSH2 with hMSH6: Examination of Mutations Found in Hereditary Nonpolyposis Colorectal Cancer. <i>Molecular and Cellular Biology</i> , 1998, 18, 6616-6623.	1.1	123
90	MutS homologs in mammalian cells. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 105-113.	1.5	150

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91	The Human Mismatch Recognition Complex hMSH2-hMSH6 Functions as a Novel Molecular Switch. <i>Cell</i> , 1997, 91, 995-1005.	13.5	336
92	Female embryonic lethality in mice nullizygous for both Msh2 and p53. <i>Nature Genetics</i> , 1997, 17, 114-118.	9.4	67
93	The mismatch-repair protein hMSH2 binds selectively to DNA adducts of the anticancer drug cisplatin. <i>Chemistry and Biology</i> , 1996, 3, 579-589.	6.2	167
94	Identification of mismatch repair genes and their role in the development of cancer. <i>Current Opinion in Genetics and Development</i> , 1995, 5, 382-395.	1.5	293
95	Mutation in the DNA mismatch repair gene homologue hMLH 1 is associated with hereditary non-polyposis colon cancer. <i>Nature</i> , 1994, 368, 258-261.	13.7	2,001
96	Multiple Pathways Leading to Genomic Instability and Tumorigenesis. <i>Annals of the New York Academy of Sciences</i> , 1994, 726, 165-177.	1.8	20
97	The human mutator gene homolog MSH2 and its association with hereditary nonpolyposis colon cancer. <i>Cell</i> , 1993, 75, 1027-1038.	13.5	2,706