Richard Fishel

List of Publications by Year
in descending order

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97 papers	15,683 citations	47006 47 h-index	39675 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. Scientific Reports, 2022, 12, 4082.	3.3	2
2	Retroviral prototype foamy virus intasome binding to a nucleosome target does not determine integration efficiency. Journal of Biological Chemistry, 2021, 296, 100550.	3.4	5
3	Linker domain function predicts pathogenic MLH1 missense variants. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	13
4	Evolutionary advantage of a dissociative search mechanism in DNA mismatch repair. Physical Review E, 2021, 103, 052404.	2.1	2
5	The mechanics of DNA mismatch repair sliding clamp progression in the prediction of clinically relevant HsMLH1 missense mutations. FASEB Journal, 2021, 35, .	0.5	0
6	Strategies for Targeting Retroviral Integration for Safer Gene Therapy: Advances and Challenges. Frontiers in Molecular Biosciences, 2021, 8, 662331.	3.5	16
7	Nucleosome DNA unwrapping does not affect prototype foamy virus integration efficiency or site selection. PLoS ONE, 2019, 14, e0212764.	2.5	8
8	MutL sliding clamps coordinate exonuclease-independent Escherichia coli mismatch repair. Nature Communications, 2019, 10, 5294.	12.8	20
9	Long repeating (TTAGGG) single-stranded DNA self-condenses into compact beaded filaments stabilized by G-quadruplex formation. Journal of Biological Chemistry, 2018, 293, 9473-9485.	3.4	22
10	MutS homolog sliding clamps shield the DNA from binding proteins. Journal of Biological Chemistry, 2018, 293, 14285-14294.	3.4	5
11	Mutation of TGFÎ²-RII eliminates NSAID cancer chemoprevention. Oncotarget, 2018, 9, 12554-12561.	1.8	10
12	Coordinating Multi-Protein Mismatch Repair by Managing Diffusion Mechanics on the DNA. Journal of Molecular Biology, 2018, 430, 4469-4480.	4.2	11
13	Plasticity of Multi-Protein Complexes. Journal of Molecular Biology, 2018, 430, 4441-4442.	4.2	3
14	Stochastic Processes and Component Plasticity Governing DNA Mismatch Repair. Journal of Molecular Biology, 2018, 430, 4456-4468.	4.2	13
15	Expression and purification of nuclease-free protocatechuate 3,4-dioxygenase for prolonged single-molecule fluorescence imaging. Analytical Biochemistry, 2018, 556, 78-84.	2.4	11
16	Dynamic unwrapping of nucleosomes by HsRAD51 that includes sliding and rotational motion of histone octamers. Nucleic Acids Research, 2017, 45, 685-698.	14.5	8
17	Enhanced gene targeting to evaluate Lynch syndrome alterations. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3918-3920.	7.1	1
18	Dynamic control of strand excision during human DNA mismatch repair. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3281-3286.	7.1	35

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19	Pseudomonas aeruginosa AmrZ Binds to Four Sites in the algD Promoter, Inducing DNA-AmrZ Complex Formation and Transcriptional Activation. Journal of Bacteriology, 2016, 198, 2673-2681.	2.2	22
20	The P seudomonas aeruginosa â€... AmrZ C â€terminal domain mediates tetramerization and is required for its activator and repressor functions. Environmental Microbiology Reports, 2016, 8, 85-90.	2.4	15
21	Cascading MutS and MutL sliding clamps control DNA diffusion to activate mismatch repair. Nature, 2016, 539, 583-587.	27.8	91
22	Retroviral intasomes search for a target DNA by 1D diffusion which rarely results in integration. Nature Communications, 2016, 7, 11409.	12.8	29
23	Mismatch Repair. , 2016, , 305-339.		1
24	An Efficient Site-Specific Method for Irreversible Covalent Labeling of Proteins with a Fluorophore. Scientific Reports, 2015, 5, 16883.	3.3	20
25	Mismatch Repair during Homologous and Homeologous Recombination. Cold Spring Harbor Perspectives in Biology, 2015, 7, a022657.	5.5	146
26	Widespread nuclease contamination in commonly used oxygen-scavenging systems. Nature Methods, 2015, 12, 901-902.	19.0	24
27	Mismatch Repair. Journal of Biological Chemistry, 2015, 290, 26395-26403.	3.4	181
28	Repair of Oxidative DNA Base Damage in the Host Genome Influences the HIV Integration Site Sequence Preference. PLoS ONE, 2014, 9, e103164.	2.5	12
29	Mismatch repair protein hMSH2â€“hMSH6 recognizes mismatches and forms sliding clamps within a D-loop recombination intermediate. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E316-25.	7.1	37
30	Single-molecule views of MutS on mismatched DNA. DNA Repair, 2014, 20, 82-93.	2.8	37
31	The mechanism of mismatch repair and the functional analysis of mismatch repair defects in Lynch syndrome. Familial Cancer, 2013, 12, 159-168.	1.9	65
32	The hMSH2(M688R) Lynch syndrome mutation may function as a dominant negative. Carcinogenesis, 2012, 33, 1647-1654.	2.8	8
33	Homologous Recombination in Eukaryotes. Progress in Molecular Biology and Translational Science, 2012, 110, 155-206.	1.7	28
34	ATP Alters the Diffusion Mechanics of MutS on Mismatched DNA. Structure, 2012, 20, 1264-1274.	3.3	87
35	The Base Excision Repair Pathway Is Required for Efficient Lentivirus Integration. PLoS ONE, 2011, 6, e17862.	2.5	38
36	MutS switches between two fundamentally distinct clamps during mismatch repair. Nature Structural and Molecular Biology, 2011, 18, 379-385.	8.2	120

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37	A quantitative model of nucleosome dynamics. Nucleic Acids Research, 2011, 39, 8306-8313.	14.5	49
38	Human MSH2 (hMSH2) Protein Controls ATP Processing by hMSH2-hMSH6. Journal of Biological Chemistry, 2011, 286, 40287-40295.	3.4	33
39	MicroRNA-21 induces resistance to 5-fluorouracil by down-regulating human DNA MutS homolog 2 (hMSH2). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21098-21103.	7.1	333
40	Modulation of mismatch repair and genomic stability by miR-155. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6982-6987.	7.1	306
41	Single-Molecule Analysis Reveals the Kinetics and Physiological Relevance of MutL-ssDNA Binding. PLoS ONE, 2010, 5, e15496.	2.5	32
42	Sequence context effect for hMSH2-hMSH6 mismatch-dependent activation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4177-4182.	7.1	59
43	Evidence that hMLH3 functions primarily in meiosis and in hMSH2-hMSH3 mismatch repair. Cancer Biology and Therapy, 2009, 8, 1411-1420.	3.4	24
44	Current and emerging trends in Lynch syndrome identification in women with endometrial cancer. Gynecologic Oncology, 2009, 114, 128-134.	1.4	97
45	DNA mismatch repair (MMR)â€dependent 5â€fluorouracil cytotoxicity and the potential for new therapeutic targets. British Journal of Pharmacology, 2009, 158, 679-692.	5.4	66
46	Enrichment and characterization of histones by two-dimensional hydroxyapatite/reversed-phase liquid chromatographyâ€“mass spectrometry. Analytical Biochemistry, 2009, 388, 47-55.	2.4	9
47	Nucleosome Remodeling by hMSH2-hMSH6. Molecular Cell, 2009, 36, 1086-1094.	9.7	62
48	Harnessing mismatch repair to model sporadic cancers. Nature Methods, 2008, 5, 225-226.	19.0	1
49	hMSH4-hMSH5 Adenosine Nucleotide Processing and Interactions with Homologous Recombination Machinery. Journal of Biological Chemistry, 2008, 283, 145-154.	3.4	44
50	DNA Damage-Dependent Acetylation and Ubiquitination of H2AX Enhances Chromatin Dynamics. Molecular and Cellular Biology, 2007, 27, 7028-7040.	2.3	327
51	Nitric Oxideâ€“Donating Aspirin Derivatives Suppress Microsatellite Instability in Mismatch Repairâ€“Deficient and Hereditary Nonpolyposis Colorectal Cancer Cells. Cancer Research, 2007, 67, 10966-10975.	0.9	47
52	Magnesium influences the discrimination and release of ADP by human RAD51. DNA Repair, 2006, 5, 704-717.	2.8	11
53	DNA Mismatch Repair-dependent Response to Fluoropyrimidine-generated Damage. Journal of Biological Chemistry, 2005, 280, 5516-5526.	3.4	108
54	Extreme Heterogeneity in the Molecular Events Leading to the Establishment of Chiasmata during Meiosis I in Human Oocytes. American Journal of Human Genetics, 2005, 76, 112-127.	6.2	151

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55	Lynch Syndrome: Form, Function, Proteins, and Basketball. Gastroenterology, 2005, 129, 751-755.	1.3	25
56	Lynch Syndrome: Form, Function, Proteins, and Basketball. Gastroenterology, 2005, 129, 751-755.	1.3	25
57	Mechanism of DNA Mismatch Repair from Bacteria to Human. , 2005, , .		0
58	MSI-Testing in Hereditary Non-Polyposis Colorectal Carcinoma (HNPCC). Disease Markers, 2004, 20, 225-236.	1.3	10
59	hXRCC2 Enhances ADP/ATP Processing and Strand Exchange by hRAD51. Journal of Biological Chemistry, 2004, 279, 30385-30394.	3.4	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. Cancer Research, 2004, 64, 3096-3102.	0.9	271
61	hMSH4-hMSH5 Recognizes Holliday Junctions and Forms a Meiosis-Specific Sliding Clamp that Embraces Homologous Chromosomes. Molecular Cell, 2004, 15, 437-451.	9.7	361
62	The Coordinated Functions of the E. coli MutS and MutL Proteins in Mismatch Repair. Molecular Cell, 2003, 12, 233-246.	9.7	259
63	Mismatch Repair and the Hereditary Non-polyposis Colorectal Cancer Syndrome (HNPCC). Cancer Investigation, 2002, 20, 102-109.	1.3	117
64	Activation of Human MutS Homologs by 8-Oxo-guanine DNA Damage. Journal of Biological Chemistry, 2002, 277, 8260-8266.	3.4	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. Molecular and Cellular Biology, 2002, 22, 4189-4201.	2.3	188
66	Biochemical Characterization of the Human RAD51 Protein. Journal of Biological Chemistry, 2002, 277, 14417-14425.	3.4	71
67	Biochemical Characterization of the Human RAD51 Protein. Journal of Biological Chemistry, 2002, 277, 14426-14433.	3.4	25
68	DNA Repair and Tumorigenesis: Lessons from Hereditary Cancer Syndromes. Cancer Biology and Therapy, 2002, 1, 477-485.	3.4	101
69	HNPCC mutations in hMSH2 result in reduced hMSH2-hMSH6 molecular switch functions. Cancer Cell, 2002, 1, 469-478.	16.8	59
70	BCR/ABL Regulates Mammalian RecA Homologs, Resulting in Drug Resistance. Molecular Cell, 2001, 8, 795-806.	9.7	290
71	Adenosine nucleotide modulates the physical interaction between hMSH2 and BRCA1. Oncogene, 2001, 20, 4640-4649.	5.9	57
72	The Interaction of DNA Mismatch Repair Proteins with Human Exonuclease I. Journal of Biological Chemistry, 2001, 276, 33011-33018.	3.4	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 theSaccharomyces cerevisiae mutant G-protein Gpa1G50V. Yeast, 2000, 16, 387-400.	1.7	13
75	BRCA1 and cell signaling. Oncogene, 2000, 19, 6152-6158.	5.9	80
76	The Effect of O6-Methylguanine DNA Adducts on the Adenosine Nucleotide Switch Functions of hMSH2-hMSH6 and hMSH2-hMSH3. Journal of Biological Chemistry, 2000, 275, 27851-27857.	3.4	38
77	A Human REV7 Homolog That Interacts with the Polymerase Î¶ Catalytic Subunit hREV3 and the Spindle Assembly Checkpoint Protein hMAD2. Journal of Biological Chemistry, 2000, 275, 4391-4397.	3.4	170
78	The Role of Mismatched Nucleotides in Activating the hMSH2-hMSH6 Molecular Switch. Journal of Biological Chemistry, 2000, 275, 3922-3930.	3.4	103
79	Colorectal carcinomas with high microsatellite instability: Defining a distinct immunologic and molecular entity with respect to prognostic markers. Human Pathology, 2000, 31, 1506-1514.	2.0	76
80	Cytochrome c and dATP-mediated Oligomerization of Apaf-1 Is a Prerequisite for Procaspase-9 Activation. Journal of Biological Chemistry, 1999, 274, 17941-17945.	3.4	432
81	The Interaction of the Human MutL Homologues in Hereditary Nonpolyposis Colon Cancer. Journal of Biological Chemistry, 1999, 274, 6336-6341.	3.4	153
82	Dissociation of Mismatch Recognition and ATPase Activity by hMSH2-hMSH3. Journal of Biological Chemistry, 1999, 274, 21659-21664.	3.4	90
83	Severe Attenuation of the B Cell Immune Response in Msh2-deficient Mice. Journal of Experimental Medicine, 1999, 189, 471-482.	8.5	80
84	Signaling mismatch repair in cancer. Nature Medicine, 1999, 5, 1239-1241.	30.7	126
85	Female embryonic lethality in Msh2Â–Trp53 nullizygous mice is strain dependent. Mammalian Genome, 1999, 10, 1020-1022.	2.2	16
86	Molecular diagnostics of cancer predisposition: hereditary non-polyposis colorectal carcinoma and mismatch repair defects. Biochimica Et Biophysica Acta: Reviews on Cancer, 1999, 1423, O1-O10.	7.4	30
87	hMSH2â€“hMSH6 Forms a Hydrolysis-Independent Sliding Clamp on Mismatched DNA. Molecular Cell, 1999, 3, 255-261.	9.7	338
88	Increased Hypermutation at G and C Nucleotides in Immunoglobulin Variable Genes from Mice Deficient in the MSH2 Mismatch Repair Protein. Journal of Experimental Medicine, 1998, 187, 1745-1751.	8.5	170
89	Interactions of Human hMSH2 with hMSH3 and hMSH2 with hMSH6: Examination of Mutations Found in Hereditary Nonpolyposis Colorectal Cancer. Molecular and Cellular Biology, 1998, 18, 6616-6623.	2.3	123
90	MutS homologs in mammalian cells. Current Opinion in Genetics and Development, 1997, 7, 105-113.	3.3	150

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91	The Human Mismatch Recognition Complex hMSH2-hMSH6 Functions as a Novel Molecular Switch. Cell, 1997, 91, 995-1005.	28.9	336
92	Female embryonic lethality in mice nullizygous for both Msh2 and p53. Nature Genetics, 1997, 17, 114-118.	21.4	67
93	The mismatch-repair protein hMSH2 binds selectively to DNA adducts of the anticancer drug cisplatin. Chemistry and Biology, 1996, 3, 579-589.	6.0	167
94	Identification of mismatch repair genes and their role in the development of cancer. Current Opinion in Genetics and Development, 1995, 5, 382-395.	3.3	293
95	Mutation in the DNA mismatch repair gene homologue hMLH 1 is associated with hereditary non-polyposis colon cancer. Nature, 1994, 368, 258-261.	27.8	2,001
96	Multiple Pathways Leading to Genomic Instabiligy and Tumorigenesis. Annals of the New York Academy of Sciences, 1994, 726, 165-177.	3.8	20
97	The human mutator gene homolog MSH2 and its association with hereditary nonpolyposis colon cancer. Cell, 1993, 75, 1027-1038.	28.9	2,706