Grant S Stewart

List of Publications by Year
in descending order

36 papers	3,872 citations	430874 18 h-index	377865 34 g-index
38 all docs	38 docs citations	38 times ranked	5068 citing authors

#	Article	IF	Citations
1	Cancer-Associated SF3B1 Mutations Confer a BRCA-Like Cellular Phenotype and Synthetic Lethality to PARP Inhibitors. Cancer Research, 2022, 82, 819-830.	0.9	16
2	RECON syndrome is a genome instability disorder caused by mutations in the DNA helicase RECQL1. Journal of Clinical Investigation, 2022, 132, .	8.2	21
3	H3K4 methylation by SETD1A/BOD1L facilitates RIF1-dependent NHEJ. Molecular Cell, 2022, 82, 1924-1939.e10.	9.7	16
4	MYBL2 and ATM suppress replication stress in pluripotent stem cells. EMBO Reports, 2021, 22, e51120.	4.5	15
5	Bi-allelic MCM10 variants associated with immune dysfunction and cardiomyopathy cause telomere shortening. Nature Communications, 2021, 12, 1626.	12.8	22
6	Replication of the Mammalian Genome by Replisomes Specific for Euchromatin and Heterochromatin. Frontiers in Cell and Developmental Biology, 2021, 9, 729265.	3.7	4
7	Arginine methylation and ubiquitylation crosstalk controls DNA end-resection and homologous recombination repair. Nature Communications, 2021, 12, 6313.	12.8	16
8	ATRX proximal protein associations boast roles beyond histone deposition. PLoS Genetics, 2021, 17, e1009909.	3.5	9
9	The Promotion of Genomic Instability in Human Fibroblasts by Adenovirus 12 Early Region 1B 55K Protein in the Absence of Viral Infection. Viruses, 2021, 13, 2444.	3.3	0
10	DONSON and FANCM associate with different replisomes distinguished by replication timing and chromatin domain. Nature Communications, 2020, 11, 3951.	12.8	26
11	Warsaw Breakage Syndrome associated DDX11 helicase resolves G-quadruplex structures to support sister chromatid cohesion. Nature Communications, 2020, 11, 4287.	12.8	33
12	Germline RBBP8 variants associated with early-onset breast cancer compromise replication fork stability. Journal of Clinical Investigation, 2020, 130, 4069-4080.	8.2	12
13	Bi-allelic Variants in TONSL Cause SPONASTRIME Dysplasia and a Spectrum of Skeletal Dysplasia Phenotypes. American Journal of Human Genetics, 2019, 104, 422-438.	6.2	27
14	Hypomorphic Mutations in TONSL Cause SPONASTRIME Dysplasia. American Journal of Human Genetics, 2019, 104, 439-453.	6.2	16
15	PALB2 variant status in hematological malignancies â€“ a potential therapeutic target?. Leukemia and Lymphoma, 2019, 60, 1823-1826.	1.3	1
16	Degradation of a Novel DNA Damage Response Protein, Tankyrase 1 Binding Protein 1, following Adenovirus Infection. Journal of Virology, 2018, 92, .	3.4	19
17	Analysis of novel missense ATR mutations reveals new splicing defects underlying Seckel syndrome. Human Mutation, 2018, 39, 1847-1853.	2.5	10
18	Histone Methylation by SETD1A Protects Nascent DNA through the Nucleosome Chaperone Activity of FANCD2. Molecular Cell, 2018, 71, 25-41.e6.	9.7	87

#	Article	IF	Citations
19	MYBL2 Supports DNA Double Strand Break Repair in Hematopoietic Stem Cells. Cancer Research, 2018, 78, 5767-5779.	0.9	30
20	PRMT5-Dependent Methylation of the TIP60 Coactivator RUVBL1 Is a Key Regulator of Homologous Recombination. Molecular Cell, 2017, 65, 900-916.e7.	9.7	106
21	Mutations in DONSON disrupt replication fork stability and cause microcephalic dwarfism. Nature Genetics, 2017, 49, 537-549.	21.4	81
22	USP7 inhibition alters homologous recombination repair and targets CLL cells independently of ATM/p53 functional status. Blood, 2017, 130, 156-166.	1.4	60
23	Reduced Contractility and Motility of Prostatic Cancer-Associated Fibroblasts after Inhibition of Heat Shock Protein 90. Cancers, 2016, 8, 77.	3.7	15
24	Measuring the effects of fractionated radiation therapy in a 3D prostate cancer model system using SERS nanosensors. Analyst, The, 2016, 141, 5056-5061.	3.5	14
25	TRAIP promotes DNA damage response during genome replication and is mutated in primordial dwarfism. Nature Genetics, 2016, 48, 36-43.	21.4	74
26	A Hypomorphic PALB2 Allele Gives Rise to an Unusual Form of FA-N Associated with Lymphoid Tumour Development. PLoS Genetics, 2016, 12, e1005945.	3.5	19
27	BOD1L Is Required to Suppress Deleterious Resection of Stressed Replication Forks. Molecular Cell, 2015, 59, 462-477.	9.7	146
28	Alchemix, p53 and topoisomerase. Aging, 2015, 7, 601-602.	3.1	0
29	Identification of the First ATRIPâ€“Deficient Patient and Novel Mutations in ATR Define a Clinical Spectrum for ATRâ€“ATRIP Seckel Syndrome. PLoS Genetics, 2012, 8, e1002945.	3.5	104
30	Serotype-Specific Inactivation of the Cellular DNA Damage Response during Adenovirus Infection. Journal of Virology, 2011, 85, 2201-2211.	3.4	60
31	53BP1-dependent robust localized KAP-1 phosphorylation is essential for heterochromatic DNA double-strand break repair. Nature Cell Biology, 2010, 12, 177-184.	10.3	289
32	Adenovirus 12 E4orf6 inhibits ATR activation by promoting TOPBP1 degradation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12251-12256.	7.1	71
33	The RIDDLE Syndrome Protein Mediates a Ubiquitin-Dependent Signaling Cascade at Sites of DNA Damage. Cell, 2009, 136, 420-434.	28.9	673
34	MDC1 is a mediator of the mammalian DNA damage checkpoint. Nature, 2003, 421, 961-966.	27.8	789
35	Ataxia without telangiectasia revisited: Update on genetic findings in two brothers with an ataxia-telangiectasia-like disorder. Movement Disorders, 2001, 16, 788-789.	3.9	4
36	The DNA Double-Strand Break Repair Gene hMRE11 Is Mutated in Individuals with an Ataxia-Telangiectasia-like Disorder. Cell, 1999, 99, 577-587.	28.9	986