

Daniel Durocher

List of Publications by Year in descending order

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Version: 2024-02-01

126
papers

24,156
citations

14655

66
h-index

19190

118
g-index

143
all docs

143
docs citations

143
times ranked

26896
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Systematic identification of protein complexes in <i>Saccharomyces cerevisiae</i> by mass spectrometry. <i>Nature</i> , 2002, 415, 180-183. | 27.8 | 3,445 |
| 2 | The CRAPome: a contaminant repository for affinity purification mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736. | 19.0 | 1,353 |
| 3 | High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. <i>Cell</i> , 2015, 163, 1515-1526. | 28.9 | 1,339 |
| 4 | Orchestration of the DNA-Damage Response by the RNF8 Ubiquitin Ligase. <i>Science</i> , 2007, 318, 1637-1640. | 12.6 | 800 |
| 5 | RNF168 Binds and Amplifies Ubiquitin Conjugates on Damaged Chromosomes to Allow Accumulation of Repair Proteins. <i>Cell</i> , 2009, 136, 435-446. | 28.9 | 784 |
| 6 | A Cell Cycle-Dependent Regulatory Circuit Composed of 53BP1-RIF1 and BRCA1-CtIP Controls DNA Repair Pathway Choice. <i>Molecular Cell</i> , 2013, 49, 872-883. | 9.7 | 742 |
| 7 | The RIDDLE Syndrome Protein Mediates a Ubiquitin-Dependent Signaling Cascade at Sites of DNA Damage. <i>Cell</i> , 2009, 136, 420-434. | 28.9 | 673 |
| 8 | The cardiac transcription factors Nkx2-5 and GATA-4 are mutual cofactors. <i>EMBO Journal</i> , 1997, 16, 5687-5696. | 7.8 | 594 |
| 9 | 53BP1 is a reader of the DNA-damage-induced H2A Lys 15 ubiquitin mark. <i>Nature</i> , 2013, 499, 50-54. | 27.8 | 580 |
| 10 | The control of DNA repair by the cell cycle. <i>Nature Cell Biology</i> , 2017, 19, 1-9. | 10.3 | 549 |
| 11 | Regulation of DNA Damage Responses by Ubiquitin and SUMO. <i>Molecular Cell</i> , 2013, 49, 795-807. | 9.7 | 522 |
| 12 | DNA-PK, ATM and ATR as sensors of DNA damage: variations on a theme?. <i>Current Opinion in Cell Biology</i> , 2001, 13, 225-231. | 5.4 | 457 |
| 13 | The shieldin complex mediates 53BP1-dependent DNA repair. <i>Nature</i> , 2018, 560, 117-121. | 27.8 | 445 |
| 14 | A phosphatase complex that dephosphorylates γ -H2AX regulates DNA damage checkpoint recovery. <i>Nature</i> , 2006, 439, 497-501. | 27.8 | 439 |
| 15 | Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2719-2727. | 1.8 | 417 |
| 16 | The Molecular Basis of FHA Domain:Phosphopeptide Binding Specificity and Implications for Phospho-Dependent Signaling Mechanisms. <i>Molecular Cell</i> , 2000, 6, 1169-1182. | 9.7 | 412 |
| 17 | A mechanism for the suppression of homologous recombination in G1 cells. <i>Nature</i> , 2015, 528, 422-426. | 27.8 | 409 |
| 18 | The FHA Domain Is a Modular Phosphopeptide Recognition Motif. <i>Molecular Cell</i> , 1999, 4, 387-394. | 9.7 | 368 |

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|----|---|------|-----------|
| 19 | The FHA domain. FEBS Letters, 2002, 513, 58-66. | 2.8 | 358 |
| 20 | A Genetic Map of the Response to DNA Damage in Human Cells. Cell, 2020, 182, 481-496.e21. | 28.9 | 324 |
| 21 | Non-canonical inhibition of DNA damage-dependent ubiquitination by OTUB1. Nature, 2010, 466, 941-946. | 27.8 | 316 |
| 22 | 53BP1â€œRIF1â€œshieldin counteracts DSB resection through CST- and PolÎ±-dependent fill-in. Nature, 2018, 560, 112-116. | 27.8 | 313 |
| 23 | CRISPR screens identify genomic ribonucleotides as a source of PARP-trapping lesions. Nature, 2018, 559, 285-289. | 27.8 | 297 |
| 24 | Mitosis Inhibits DNA Double-Strand Break Repair to Guard Against Telomere Fusions. Science, 2014, 344, 189-193. | 12.6 | 280 |
| 25 | A Strategy for Modulation of Enzymes in the Ubiquitin System. Science, 2013, 339, 590-595. | 12.6 | 257 |
| 26 | MAD2L2 controls DNA repair at telomeres and DNA breaks by inhibiting 5â€² end resection. Nature, 2015, 521, 537-540. | 27.8 | 253 |
| 27 | Association of Distinct Mutational Signatures With Correlates of Increased Immune Activity in Pancreatic Ductal Adenocarcinoma. JAMA Oncology, 2017, 3, 774. | 7.1 | 221 |
| 28 | Xrcc4 physically links DNA end processing by polynucleotide kinase to DNA ligation by DNA ligase IV. EMBO Journal, 2004, 23, 3874-3885. | 7.8 | 218 |
| 29 | Structural and Functional Versatility of the FHA Domain in DNA-Damage Signaling by the Tumor Suppressor Kinase Chk2. Molecular Cell, 2002, 9, 1045-1054. | 9.7 | 207 |
| 30 | Saccharomyces cerevisiae Rad9 Acts as a Mec1 Adaptor to Allow Rad53 Activation. Current Biology, 2005, 15, 1364-1375. | 3.9 | 207 |
| 31 | Inhibition of 53BP1 favors homology-dependent DNA repair and increases CRISPRâ€œCas9 genome-editing efficiency. Nature Biotechnology, 2018, 36, 95-102. | 17.5 | 206 |
| 32 | An Allosteric Inhibitor of the Human Cdc34â€œUbiquitin-Conjugating Enzyme. Cell, 2011, 145, 1075-1087. | 28.9 | 203 |
| 33 | The structural basis of modified nucleosome recognition by 53BP1. Nature, 2016, 536, 100-103. | 27.8 | 201 |
| 34 | The TIP60 Complex Regulates Bivalent Chromatin Recognition by 53BP1 through Direct H4K20me Binding and H2AK15 Acetylation. Molecular Cell, 2016, 62, 409-421. | 9.7 | 198 |
| 35 | The Molecular Architecture of the Mammalian DNA Repair Enzyme, Polynucleotide Kinase. Molecular Cell, 2005, 17, 657-670. | 9.7 | 191 |
| 36 | Potent and Selective Inhibitors of the Inositol-requiring Enzyme 1 Endoribonuclease. Journal of Biological Chemistry, 2011, 286, 12743-12755. | 3.4 | 190 |

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|----|--|------|-----------|
| 37 | The ubiquitous role of ubiquitin in the DNA damage response. <i>DNA Repair</i> , 2010, 9, 1229-1240. | 2.8 | 188 |
| 38 | PP4 is a $\hat{\Gamma}^3$ H2AX phosphatase required for recovery from the DNA damage checkpoint. <i>EMBO Reports</i> , 2008, 9, 1019-1026. | 4.5 | 179 |
| 39 | OTUB1 Co-opts Lys48-Linked Ubiquitin Recognition to Suppress E2 Enzyme Function. <i>Molecular Cell</i> , 2012, 45, 384-397. | 9.7 | 174 |
| 40 | Regulatory ubiquitylation in response to DNA double-strand breaks. <i>DNA Repair</i> , 2009, 8, 436-443. | 2.8 | 173 |
| 41 | Shieldin – the protector of <sc>DNA</sc> ends. <i>EMBO Reports</i> , 2019, 20, . | 4.5 | 169 |
| 42 | Systematic identification of fragile sites via genome-wide location analysis of $\hat{\Gamma}^3$ -H2AX. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 299-305. | 8.2 | 167 |
| 43 | Significant conservation of synthetic lethal genetic interaction networks between distantly related eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16653-16658. | 7.1 | 165 |
| 44 | A viral E3 ligase targets RNF8 and RNF168 to control histone ubiquitination and DNA damage responses. <i>EMBO Journal</i> , 2010, 29, 943-955. | 7.8 | 162 |
| 45 | A Genome-Wide Screen Identifies the Evolutionarily Conserved KEOPS Complex as a Telomere Regulator. <i>Cell</i> , 2006, 124, 1155-1168. | 28.9 | 158 |
| 46 | Elg1 Forms an Alternative PCNA-Interacting RFC Complex Required to Maintain Genome Stability. <i>Current Biology</i> , 2003, 13, 1583-1595. | 3.9 | 154 |
| 47 | Push back to respond better: regulatory inhibition of the DNA double-strand break response. <i>Nature Reviews Molecular Cell Biology</i> , 2013, 14, 661-672. | 37.0 | 154 |
| 48 | Identifying chemogenetic interactions from CRISPR screens with drugZ. <i>Genome Medicine</i> , 2019, 11, 52. | 8.2 | 127 |
| 49 | Tandem Protein Interaction Modules Organize the Ubiquitin-Dependent Response to DNA Double-Strand Breaks. <i>Molecular Cell</i> , 2012, 47, 383-395. | 9.7 | 124 |
| 50 | HELB Is a Feedback Inhibitor of DNA End Resection. <i>Molecular Cell</i> , 2016, 61, 405-418. | 9.7 | 119 |
| 51 | Rnf8 deficiency impairs class switch recombination, spermatogenesis, and genomic integrity and predisposes for cancer. <i>Journal of Experimental Medicine</i> , 2010, 207, 983-997. | 8.5 | 112 |
| 52 | MRE11 promotes AKT phosphorylation in direct response to DNA double-strand breaks. <i>Cell Cycle</i> , 2011, 10, 2218-2232. | 2.6 | 111 |
| 53 | Structure and mechanism of action of the hydroxy-aryl-aldehyde class of IRE1 endoribonuclease inhibitors. <i>Nature Communications</i> , 2014, 5, 4202. | 12.8 | 108 |
| 54 | The MMS22L-TONSL Complex Mediates Recovery from Replication Stress and Homologous Recombination. <i>Molecular Cell</i> , 2010, 40, 619-631. | 9.7 | 106 |

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|----|---|------|-----------|
| 55 | Combinatorial interactions regulating cardiac transcription. , 1998, 22, 250-262. | | 91 |
| 56 | Synthetic Lethality in Cancer Therapeutics: The Next Generation. <i>Cancer Discovery</i> , 2021, 11, 1626-1635. | 9.4 | 91 |
| 57 | Atomic Structure of the KEOPS Complex: An Ancient Protein Kinase-Containing Molecular Machine. <i>Molecular Cell</i> , 2008, 32, 259-275. | 9.7 | 87 |
| 58 | APLF (C2orf13) facilitates nonhomologous end-joining and undergoes ATM-dependent hyperphosphorylation following ionizing radiation. <i>DNA Repair</i> , 2008, 7, 292-302. | 2.8 | 83 |
| 59 | Nucleosome Acidic Patch Promotes RNF168- and RING1B/BMI1-Dependent H2AX and H2A Ubiquitination and DNA Damage Signaling. <i>PLoS Genetics</i> , 2014, 10, e1004178. | 3.5 | 83 |
| 60 | DNA damage signalling targets the kinetochore to promote chromatin mobility. <i>Nature Cell Biology</i> , 2016, 18, 281-290. | 10.3 | 82 |
| 61 | A consensus set of genetic vulnerabilities to ATR inhibition. <i>Open Biology</i> , 2019, 9, 190156. | 3.6 | 81 |
| 62 | Functional characterization of a PROTAC directed against BRAF mutant V600E. <i>Nature Chemical Biology</i> , 2020, 16, 1170-1178. | 8.0 | 80 |
| 63 | BRCA1 Haploinsufficiency Is Masked by RNF168-Mediated Chromatin Ubiquitylation. <i>Molecular Cell</i> , 2019, 73, 1267-1281.e7. | 9.7 | 78 |
| 64 | Perinuclear tethers license telomeric DSBs for a broad kinesin- and NPC-dependent DNA repair process. <i>Nature Communications</i> , 2015, 6, 7742. | 12.8 | 76 |
| 65 | De novo telomere formation is suppressed by the Mec1-dependent inhibition of Cdc13 accumulation at DNA breaks. <i>Genes and Development</i> , 2010, 24, 502-515. | 5.9 | 73 |
| 66 | Genomic Instability, Defective Spermatogenesis, Immunodeficiency, and Cancer in a Mouse Model of the RIDDLE Syndrome. <i>PLoS Genetics</i> , 2011, 7, e1001381. | 3.5 | 73 |
| 67 | Rad6-Rad18 Mediates a Eukaryotic SOS Response by Ubiquitinating the 9-1-1 Checkpoint Clamp. <i>Cell</i> , 2008, 133, 601-611. | 28.9 | 72 |
| 68 | A Genomewide Suppressor and Enhancer Analysis of <i>cdc13-1</i> Reveals Varied Cellular Processes Influencing Telomere Capping in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2008, 180, 2251-2266. | 2.9 | 70 |
| 69 | The RNF8/RNF168 ubiquitin ligase cascade facilitates class switch recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 809-814. | 7.1 | 70 |
| 70 | Endogenous DNA 3' Blocks Are Vulnerabilities for BRCA1 and BRCA2 Deficiency and Are Reversed by the APE2 Nuclease. <i>Molecular Cell</i> , 2020, 78, 1152-1165.e8. | 9.7 | 69 |
| 71 | Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. <i>Nucleic Acids Research</i> , 2013, 41, 6332-6346. | 14.5 | 68 |
| 72 | ZMYM3 regulates BRCA1 localization at damaged chromatin to promote DNA repair. <i>Genes and Development</i> , 2017, 31, 260-274. | 5.9 | 65 |

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|----|---|------|-----------|
| 73 | Analysis of the Histone H3.1 Interactome: A Suitable Chaperone for the Right Event. <i>Molecular Cell</i> , 2015, 60, 697-709. | 9.7 | 61 |
| 74 | CCNE1 amplification is synthetic lethal with PKMYT1 kinase inhibition. <i>Nature</i> , 2022, 604, 749-756. | 27.8 | 60 |
| 75 | Ccr4 contributes to tolerance of replication stress through control of CRT1 mRNA poly(A) tail length. <i>Journal of Cell Science</i> , 2006, 119, 5178-5192. | 2.0 | 57 |
| 76 | Interaction Proteomics Identify NEURL4 and the HECT E3 Ligase HERC2 as Novel Modulators of Centrosome Architecture. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014233. | 3.8 | 57 |
| 77 | A Screen for Suppressors of Gross Chromosomal Rearrangements Identifies a Conserved Role for PLP in Preventing DNA Lesions. <i>PLoS Genetics</i> , 2007, 3, e134. | 3.5 | 55 |
| 78 | Control of homologous recombination by the HROBâ€“MCM8â€“MCM9 pathway. <i>Genes and Development</i> , 2019, 33, 1397-1415. | 5.9 | 55 |
| 79 | The CIP2Aâ€“TOPBP1 axis safeguards chromosome stability and is a synthetic lethal target for BRCA-mutated cancer. <i>Nature Cancer</i> , 2021, 2, 1357-1371. | 13.2 | 55 |
| 80 | The F-Box Protein Dia2 Overcomes Replication Impedance to Promote Genome Stability in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2006, 174, 1709-1727. | 2.9 | 53 |
| 81 | ATM and CDK2 control chromatin remodeler CSB to inhibit RIF1 in DSB repair pathway choice. <i>Nature Communications</i> , 2017, 8, 1921. | 12.8 | 51 |
| 82 | γH2AX as a Checkpoint Maintenance Signal. <i>Cell Cycle</i> , 2006, 5, 1376-1381. | 2.6 | 50 |
| 83 | CDC5 Inhibits the Hyperphosphorylation of the Checkpoint Kinase Rad53, Leading to Checkpoint Adaptation. <i>PLoS Biology</i> , 2010, 8, e1000286. | 5.6 | 50 |
| 84 | Reading chromatin signatures after DNA double-strand breaks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160280. | 4.0 | 49 |
| 85 | Proteomic analysis of the human KEOPS complex identifies C14ORF142 as a core subunit homologous to yeast Gon7. <i>Nucleic Acids Research</i> , 2017, 45, 805-817. | 14.5 | 49 |
| 86 | The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. <i>ELife</i> , 2017, 6, . | 6.0 | 44 |
| 87 | Chromatin and DNA repair: the benefits of relaxation. <i>Nature Cell Biology</i> , 2006, 8, 9-10. | 10.3 | 39 |
| 88 | Uroporphyrinogen Decarboxylase Is a Radiosensitizing Target for Head and Neck Cancer. <i>Science Translational Medicine</i> , 2011, 3, 67ra7. | 12.4 | 32 |
| 89 | DNA repair pathway choiceâ€”a PTIP of the hat to 53BP1. <i>EMBO Reports</i> , 2013, 14, 665-666. | 4.5 | 31 |
| 90 | The FHA Domain in DNA Repair and Checkpoint Signaling. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2000, 65, 423-432. | 1.1 | 31 |

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|-----|--|------|-----------|
| 91 | FAM72A antagonizes UNG2 to promote mutagenic repair during antibody maturation. <i>Nature</i> , 2021, 600, 324-328. | 27.8 | 29 |
| 92 | Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. <i>Nature Communications</i> , 2021, 12, 4496. | 12.8 | 28 |
| 93 | Srs2 enables checkpoint recovery by promoting disassembly of DNA damage foci from chromatin. <i>DNA Repair</i> , 2011, 10, 1213-1222. | 2.8 | 26 |
| 94 | Structural and functional characterization of KEOPS dimerization by Pcc1 and its role in t ^{sup} 6 biosynthesis. <i>Nucleic Acids Research</i> , 2016, 44, 6971-6980. | 14.5 | 26 |
| 95 | Mapping DNA damage-dependent genetic interactions in yeast via party mating and barcode fusion genetics. <i>Molecular Systems Biology</i> , 2018, 14, e7985. | 7.2 | 25 |
| 96 | RM1 Promotes DNA Replication Fork Progression and Recovery from Replication Fork Stress. <i>Molecular and Cellular Biology</i> , 2012, 32, 3054-3064. | 2.3 | 24 |
| 97 | Excess PolÎ functions in response to replicative stress in homologous recombination-proficient cancer cells. <i>Biology Open</i> , 2016, 5, 1485-1492. | 1.2 | 22 |
| 98 | Genome-scale chemogenomic CRISPR screens in human cells using the TKOv3 library. <i>STAR Protocols</i> , 2021, 2, 100321. | 1.2 | 22 |
| 99 | A sharp Pif1-dependent threshold separates DNA double-strand breaks from critically short telomeres. <i>ELife</i> , 2017, 6, . | 6.0 | 22 |
| 100 | A substrate binding model for the KEOPS tRNA modifying complex. <i>Nature Communications</i> , 2020, 11, 6233. | 12.8 | 21 |
| 101 | SHLD 2 promotes class switch recombination by preventing inactivating deletions within the Igh locus. <i>EMBO Reports</i> , 2020, 21, e49823. | 4.5 | 20 |
| 102 | The CIP2A-TOPBP1 complex safeguards chromosomal stability during mitosis. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 20 |
| 103 | Structural basis of Rad53 kinase activation by dimerization and activation segment exchange. <i>Cellular Signalling</i> , 2014, 26, 1825-1836. | 3.6 | 16 |
| 104 | DNA Repair Has a New FAN1 Club. <i>Molecular Cell</i> , 2010, 39, 167-169. | 9.7 | 14 |
| 105 | RIF1 acts in DNA repair through phosphopeptide recognition of 53BP1. <i>Molecular Cell</i> , 2022, 82, 1359-1371.e9. | 9.7 | 14 |
| 106 | Localization of the Catf1 transcription factor gene to mouse Chromosome 19. <i>Mammalian Genome</i> , 1995, 6, 147-148. | 2.2 | 13 |
| 107 | A siRNA-Based Screen for Genes Involved in Chromosome End Protection. <i>PLoS ONE</i> , 2011, 6, e21407. | 2.5 | 12 |
| 108 | Two redundant ubiquitin-dependent pathways of BRCA1 localization to DNA damage sites. <i>EMBO Reports</i> , 2021, 22, e53679. | 4.5 | 11 |

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|-----|---|------|-----------|
| 109 | DNA Repair: DNA Polymerase η and Rev1 Break in. <i>Current Biology</i> , 2006, 16, R296-R299. | 3.9 | 9 |
| 110 | Dun1 Counts on Rad53 to Be Turned On. <i>Molecular Cell</i> , 2008, 31, 1-2. | 9.7 | 9 |
| 111 | Bacterial signal transduction: a fascinating glimpse at the origins of phospho-dependent signal transduction. <i>Trends in Microbiology</i> , 2003, 11, 67-68. | 7.7 | 6 |
| 112 | Problems with Co-Funding in Canada. <i>Science</i> , 2005, 308, 1867b-1867b. | 12.6 | 6 |
| 113 | Telomere Protection: An Act of God. <i>Current Biology</i> , 2006, 16, R544-R546. | 3.9 | 6 |
| 114 | 53BP1 Goes Back to Its p53 Roots. <i>Molecular Cell</i> , 2016, 64, 3-4. | 9.7 | 5 |
| 115 | Combinatorial interactions regulating cardiac transcription. <i>Genesis</i> , 1998, 22, 250-262. | 2.1 | 4 |
| 116 | OTUB1 Co-opts Lys48-Linked Ubiquitin Recognition to Suppress E2 Enzyme Function. <i>Molecular Cell</i> , 2012, 46, 549. | 9.7 | 3 |
| 117 | Global cellular response to chemical perturbation of PLK4 activity and abnormal centrosome number. <i>ELife</i> , 0, 11, . | 6.0 | 2 |
| 118 | Engineering a DNA damage response without DNA damage. <i>Genome Biology</i> , 2008, 9, 227. | 9.6 | 1 |
| 119 | DNA Damage Sensing and Signaling. , 2009, , 1-24. | | 1 |
| 120 | RNF8-Independent Lys63 Poly-Ubiquitylation Prevents Genomic Instability in Response to Replication-Associated DNA Damage. <i>PLoS ONE</i> , 2014, 9, e89997. | 2.5 | 1 |
| 121 | The FHA Domain. , 2005, , 143-162. | | 0 |
| 122 | PP4 is a γ H2AX phosphatase required for recovery from the DNA damage checkpoint. <i>EMBO Reports</i> , 2008, 9, 1251-1251. | 4.5 | 0 |
| 123 | Rnf8 deficiency impairs class switch recombination, spermatogenesis, and genomic integrity and predisposes for cancer. <i>Journal of Cell Biology</i> , 2010, 189, i6-i6. | 5.2 | 0 |
| 124 | Regulatory ubiquitylation during the response to DNA double-strand breaks. <i>FASEB Journal</i> , 2013, 27, 334.3. | 0.5 | 0 |
| 125 | R tino des et bases mol culaires des malformations cardiaques cong nitales. <i>Medecine/Sciences</i> , 1995, 11, 132. | 0.2 | 0 |
| 126 | Abstract PL03-03: Navigating gene-gene and drug-gene interaction landscapes underpinning the DNA damage response. , 2019, , . | | 0 |