

PERSONAL DATA

Name: **Alberto Ciccia, Ph.D.**
 Address: Columbia University Irving Medical Center
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 New York, NY 10032
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ACADEMIC APPOINTMENTS

01/2014 – 01/2020 Assistant Professor, Department of Genetics and Development, CUIMC
01/2014 – present Faculty, Training Program in Genetics and Development, CUIMC
01/2014 – present Faculty, Training Program in Cellular, Molecular and Biomedical Studies, CUIMC
01/2014 – present Member, Herbert Irving Comprehensive Cancer Center, CUIMC
01/2017 – present Member, Columbia Stem Cell Initiative, CUIMC
07/2020 – present Associate Professor, Department of Genetics and Development, CUIMC

EDUCATION

10/2000 Laurea (Master's Degree), Medical Biotechnology, University of Bologna, Italy
06/2006 Ph.D., Biochemistry, London Research Institute and University College London, UK
 PhD Thesis: The MUS81 Family of Proteins
 Advisor: Stephen West

TRAINING

06/2007 – 12/2013 Postdoctoral Fellow, Department of Genetics, Harvard Medical School, Boston, USA
 Advisor: Stephen Elledge

HONORS AND AWARDS

01/2008 EMBO Long-Term Fellowship
01/2015 Breast Cancer Alliance Young Investigator Award
02/2016 Ovarian Cancer Research Fund Liz Tilberis Award
07/2016 Susan G. Komen Career Catalyst Research Award
04/2018 Irma T. Hirschl Research Award
05/2018 Pershing Square Sohn Prize
06/2018 Schaefer Research Scholar Award
10/2020 Mary Kay Foundation Award
06/2022 Basser Center for BRCA Award
07/2023 CRI Lloyd J. Old STAR Award

ACADEMIC SERVICE

01/2014 – present *Ad hoc* Reviewer, Cell, Cell Cycle, Cell Reports, DNA Repair, eLife, FEBS Journal, Journal of Cell Biology, Molecular and Cell Biology, Molecular Cell, Nature, Nature Biotechnology, Nature Chemical Biology, Nature Communications, Oncogene, PLOS Biology, PNAS, Science, Science Signaling
10/2014 *Ad hoc* Reviewer, Medical Research Council, UK
08/2015 *Ad hoc* Reviewer, Villum Foundation, Denmark
10/2015 *Ad hoc* Reviewer, Israeli Ministry of Science, Technology and Space, Israel
02/2018 *Ad hoc* Reviewer, NIH, Cancer Etiology Study Section

04/2019 *Ad hoc Reviewer*, DoD Breast Cancer Research Program, Molecular Biology and Genetics Panel
10/2020 – 03/2023 **Panel Member**, NIH, Cancer Etiology Study Section
06/2023 – 06/2024 **Panel Member**, NIH, Basic Mechanisms of Cancer Health Disparities Study Section
03/2024 *Ad hoc Reviewer*, Novo Nordisk Foundation, Denmark
07/2024 **Panel Member**, Starr Cancer Consortium Scientific Review Board
04/2025 **Organizer**, Keystone Symposia Meeting, DNA Replication Gaps, Cancer and Disease, South Korea

PROFESSIONAL ORGANIZATIONS AND SOCIETIES

01/2014 – 07/2021 **Member**, The New York Academy of Sciences
10/2018 – present **Editorial Board Member**, Science Signaling, Cell Reports Methods

FELLOWSHIPS AND GRANT SUPPORT

Active Research Funding

Agency	NIH/NCI, R01CA197774
PI	Alberto Ciccia
Period	12/1/2015 – 11/31/2025
Title	Regulation of DNA synthesis in response to DNA damage
Agency	NIH/NCI, P01CA174653
PI	Jean Gautier (Alberto Ciccia, Co-Investigator)
Period	4/1/2020 – 3/31/2025
Title	DNA double-strand break repair, chromosome translocations and cancer
Agency	Cancer Research Institute
PI	Alberto Ciccia
Period	7/1/2023 – 6/30/2028
Title	High-throughput functional interrogation of the impact of DNA repair mutations on anti-tumor immunity
Agency	Ovarian Cancer Research Alliance
PI	Alberto Ciccia
Period	1/1/2024 - 12/31/2026
Title	Defining the impact of DNA repair variants on immune-based therapy of ovarian cancer at scale

Past Support

Agency	Breast Cancer Alliance
PI	Alberto Ciccia
Period	2/1/2015 – 1/31/2017
Title	Exploiting DNA replication defects in breast cancer
Agency	NIH/NIGMS, R01 GM117064
PI	Alberto Ciccia
Period	9/2/2016 – 7/31/2020
Title	Transcriptional regulation by the DNA damage response
Agency	Ovarian Cancer Research Fund, Liz Tilberis Award
PI	Alberto Ciccia
Period	2/1/2016 – 1/31/2019
Title	Defining the molecular mechanisms of BRCA1-dependent tumor suppression

Agency	Susan G. Komen, Career Catalyst Research Grant
PI	Alberto Ciccia
Period	7/1/2016 – 6/30/2019
Title	Replication fork damage and breast cancer predisposition
Agency	Pershing Square Sohn Foundation
PI	Alberto Ciccia
Period	7/1/2018 – 6/30/2022
Title	Regulation of genome stability and innate immunity in breast cancer
Agency	Irma T. Hirschl Foundation
PI	Alberto Ciccia
Period	1/1/2018 – 12/31/2023
Title	Replication fork dynamics in BRCA1-deficient cells
Agency	NIH/NCI, R01CA227450
PI	Alberto Ciccia and Richard Baer
Period	1/1/2019 – 12/31/2023
Title	Restoring genome stability and tumor suppression in BRCA1-deficient cells
Agency	Mary Kay Foundation
PI	Alberto Ciccia
Period	7/1/2020 – 6/30/2022
Title	Large-scale functional analysis of BRCA1/2 single nucleotide variants
Agency	Basser Center
PI	Alberto Ciccia
Period	7/1/2022 – 6/30/2023
Title	Rev1-Pol ζ inhibition as a novel targeted therapy for BRCA1/2-mutant tumors
Agency	NIH/NIGMS, R01GM132604
PI	Dieter Egli (Alberto Ciccia, Co-Investigator)
Period	9/1/2020 – 8/31/2024
Title	DNA repair choice mediates somatic cell reprogramming

PUBLICATIONS

Peer-Reviewed Publications (* = corresponding author)

1. **Ciccia, A.**, Constantinou, A., and West, S. C. (2003). Identification and characterization of the human MUS81-EME1 endonuclease. *J. Biol. Chem.* 278(27), 25172-25178.
2. Abraham, J, Lemmers, B., Hande, M. P., Moynahan, M. E., Chahwan, C., **Ciccia, A.**, Essers, J., Hanada, K., Chahwan, R., Khaw, A. K., *et al.* (2003). EME1 is involved in DNA damage processing and maintenance of genomic stability in mammalian cells. *EMBO J.* 22, 6137-6147.
3. **Ciccia, A.**, Ling, C., Coulthard, R., Yan, Z., Xue, Y., Meetei, A.R., Laghmani el, H., Joenje, H., McDonald, N., de Winter, J.P., Wang, W., and West, S.C. (2007). Identification of FAAP24, a Fanconi anemia core complex protein that interacts with FANCM. *Mol. Cell* 25(3), 331-343.
4. Collis, S.J, **Ciccia, A.**, Deans, A.J., Horejsi, Z., Martin, J.S., Maslen, S.L., Skehel, J.M. Elledge S.J., West, S.C. and Boulton, S.J. (2008). FANCM and FAAP24 function in ATR-mediated checkpoint signaling independently of the Fanconi anemia core complex. *Mol. Cell* 32(3), 313- 324.

5. **Ciccia, A.**, Bredemeyer, A.L., Sowa, M.E., Terret, M.E., Jallepalli, P.V., Harper, J.W., and Elledge, S.J. (2009). The SIOD disorder protein SMARCAL1 is an RPA-interacting protein involved in replication fork restart. *Genes Dev.* 23(20), 2415-2425.
6. O'Connell, B.C., Adamson, B., Lydeard, J.R., Sowa, M.E., **Ciccia, A.**, Bredemeyer, A.L., Schlabach, M. Gygi, S.P., Elledge, S.J., and Harper, J.W. (2010). A genome-wide camptothecin sensitivity screen identifies a mammalian MMS22L-NFKBIL2 complex required for genomic stability. *Mol. Cell* 40(4), 645-657.
7. Meerbrey, K.L., Hu, G., Kessler, J.D., Roarty, K., Li, M.Z., Fang, J.E., Herschkowitz, J.I., Burrows, A.E., **Ciccia, A.**, Sun, T., *et al.* (2011). The pINDUCER lentiviral toolkit for inducible RNA interference in vitro and in vivo. *Proc. Natl. Acad. Sci. U S A* 108(9), 3665-3670.
8. Larman, H.B., Zhao, Z., Laserson, U., Li, M.Z., **Ciccia, A.**, Gakidis, M.A., Church, G.M., Kesari, S., Leproust, E.M., Solimini, N.L., Elledge, S.J. (2011). Autoantigen discovery with a synthetic human peptidome. *Nat. Biotechnol.* 29(6), 535-541.
9. Emanuele, M.J., **Ciccia, A.**, Elia, A.E., and Elledge, S.J. (2011). Proliferating cell nuclear antigen (PCNA)-associated KIAA0101/PAF15 protein is a cell cycle-regulated anaphase-promoting complex/cyclosome substrate. *Proc. Natl. Acad. Sci. U S A* 108(24), 9845-9850.
10. Hajdu, I., **Ciccia, A.**, Lewis, S.M., and Elledge, S.J. (2011). Wolf-Hirschhorn syndrome candidate 1 is involved in the cellular response to DNA damage. *Proc. Natl. Acad. Sci. U S A* 108(32), 13130-13134.
11. **Ciccia, A.**, Nimonkar, A.V., Hu, Y., Hajdu, I., Achar, Y.J., Izhar, L., Petit, S.A., Adamson, B., Yoon, J.C., Kowalczykowski, S.C., Livingston, D.M., Haracska, L., and Elledge, S.J. (2012). Polyubiquitinated PCNA recruits the ZRANB3 translocase to maintain genomic integrity after replication stress. *Mol. Cell* 47(3), 396-409.
12. Zhu, J., Larman, H.B., Gao, G., Somwar, R., Zhang, Z., Laserson, U., **Ciccia, A.**, Pavlova, N., Church, G., Zhang, W., Kesari, S., and Elledge, S.J. (2013). Protein interaction discovery using parallel analysis of translated ORFs (PLATO). *Nat. Biotechnol.* 31(4), 331-334.
- *13. **Ciccia, A.**#, Huang, J.W., Izhar, L., Sowa, M.E., Harper, J.W., and Elledge, S.J.# (2014). Treacher Collins syndrome TCOF1 protein cooperates with NBS1 in the DNA damage response. *Proc. Natl. Acad. Sci U S A* 111, 18631-18636.
Corresponding authors
14. Izhar, L., Adamson, B., **Ciccia, A.**, Lewis, J., Pontano-Vaites, L., Leng, Y., Liang, A.C., Westbrook, T.F., Harper, J.W., and Elledge, S.J. (2015). A systematic analysis of factors localized to damaged chromatin reveals PARP-dependent recruitment of transcription factors. *Cell Reports* 11(9), 1486-1500.
15. Kolinjivadi, A.M., Sannino, V., De Antoni, A., Zadorozhny, K., Kilkenny, M., Técher, H., Baldi, G., Shen, R., **Ciccia, A.**, Pellegrini, L., Krejci, L., Costanzo, V. (2017). SMARCAL1-mediated fork reversal triggers MRE11-dependent degradation of nascent DNA in the absence of BRCA2 and stable RAD51 nucleofilaments. *Mol. Cell* 67(5), 867-881.
16. Vujanovic, M., Krietsch, J., Raso, M.C., Terraneo, N., Zellweger, R., Schmid, J.A., Tagliatalata, A., Huang, J.W., Holland, C.L., Zwicky, K., Herrador, R., Jacobs, H., Cortez, D., **Ciccia, A.**, Penengo, L., Lopes, M. (2017). Replication fork slowing and reversal upon DNA damage require PCNA polyubiquitination and ZRANB3 DNA translocase activity. *Mol. Cell* 67(5), 882-890.
- *17. Billon, P., Bryant, E.E., Joseph, S.A., Nambiar, T.S., Hayward, S.B., Rothstein, R., **Ciccia, A.** (2017). CRISPR-mediated base editing enables efficient disruption of eukaryotic genes through induction of STOP codons. *Mol. Cell* 67(6), 1068-1079.

- *18. Tagliatela, A., Alvarez, S., Leuzzi, G., Sannino, V., Ranjha, L., Huang, J.W., Madubata, C., Anand, R., Levy, B., Rabadan, R., Cejka, P., Costanzo, V., **Ciccia, A.** (2017). Restoration of replication fork stability in BRCA1- and BRCA2-deficient cells by inactivation of SNF2-family fork remodelers. *Mol. Cell* 68(2), 414-430.
19. Billing, D., Horiguchi, M., Wu-Baer, F., Tagliatela, A., Leuzzi, G., Alvarez, S., Jiang, W., Zha, S., Szabolcs, M., Lin, C.-S., **Ciccia, A.**, and Baer, R. (2018). The BRCT domains of the BARD1 and BRCA1 tumor suppressors differentially regulate homology-directed repair of DNA breaks and protection of stalled replication forks. *Mol. Cell* 72(1), 127-139.
- *20. Nambiar, T.S., Billon, P., Diedenhofen, G., Hayward, S.B., Tagliatela, A., Cai, K., Huang, J.W., Leuzzi, G., Cuella-Martin, R., Palacios, A., Gupta, A., Egli, D., **Ciccia, A.** (2019). Stimulation of CRISPR-mediated homology-directed repair by an engineered RAD18 variant. *Nat. Commun.* 10, 3395
- *21. Billon, P., Nambiar, T.S., Hayward, S.B., Zafra, M.P., Schatoff, E.M., Oshima, K., Dunbar, A., Wong, M., Breinig, M., Park, Y.C., Tschaharganeh, D.F., Levine, R.L., Baer, R., Ferrando, A.A., Dow, L.E., **Ciccia, A.** (2020). Detection of marker-free precision genome editing and genetic variation through the capture of genomic signatures. *Cell Reports* 30(10), 3280-3295.
- *22. Huang, J.W., Tagliatela, A., Acharya, A., Nambiar, T.S., Cuella-Martin, Leuzzi, G., R., Hayward, S.B., Joseph, S.A., Brunette, G.J., Anand, R., Soni, R.K., Clark, N.L., Bernstein, K.A., Cejka, P., and **Ciccia, A.** (2020). MCM8IP activates the MCM8-9 helicase to promote DNA synthesis and homologous recombination upon DNA damage. *Nat. Commun.* 11, 2948 PMID: PMC7290032.
- *23. Cuella-Martin, R., Hayward, S.B., Fan, X., Chen, X., Huang, J.W., Tagliatela, A., Leuzzi, G., Zhao, J., Rabadan, R., Lu, C., Shen, Y., and **Ciccia, A.** (2021). Functional interrogation of DNA damage response variants with base editing screens. *Cell* 184(4), 1081-1097.
- *24. Tagliatela, A., Leuzzi, G., Sannino, V., Cuella-Martin, R., Huang, J.W., Wu-Baer, F., Baer, R., Costanzo, V., and **Ciccia, A.** (2021). REV1-Pol ζ maintains the viability of homologous recombination-deficient cancer cells through mutagenic repair of PRIMPOL-dependent ssDNA gaps. *Mol. Cell* 81(19), 4008-4025.
25. Martinez-Pastor, B., Silveira, G.G., Clarke, T.L., Chung, D., Gu, Y., Cosentino, C., Davidow, L.S., Mata, G., Hassanieh, S., Salsman, J., **Ciccia, A.**, Bae, N., Bedford, M.T., Megias, D., Rubin, L.L., Efeyan, A., Dellaire, G., and Mostoslavsky, R. (2021). Assessing kinetics and recruitment of DNA repair factors using high content screens. *Cell Reports* 37(13), 110176.
26. Halder, S., Ranjha, L., Tagliatela, A., **Ciccia, A.** and Cejka, P. (2022). Strand annealing and motor driven activities of SMARCAL1 and ZRANB3 are stimulated by RAD51 and the paralogue complex. *Nucleic Acids Res.* 50(14), 8008-8022.
27. Palmerola, K.L., Amrane, S., De Los Angeles, A., Xu, S., Wang, N., de Pinho, J., Zuccaro, M.V., Tagliatela, A., Massey, D.J., Turocy, J., Robles, A., Subbiah, A., Prosser, B., Lobo, R., **Ciccia, A.**, Koren, A., Baslan, T., and Egli, D. (2022). Replication stress impairs chromosome segregation and preimplantation development in human embryos. *Cell* 185(16), 2988-3007.
28. Li, Y., Goldberg, E.M., Chen, X., McGuire, J.T., Leuzzi, G., Karagiannis, D., Tate, T., Farhangdoost, N., Horth, C., Dai, E., Li, Z., Zhang, Z., Izar, B., Que, J., **Ciccia, A.**, Majewski, J., Yoon, A.J., Ailles, L., Mendelsohn, C.L., and Lu, C. (2022). Histone methylation antagonism drives tumor immune evasion in squamous cell carcinomas. *Mol. Cell* 82(20), 3901-3918.
29. Conte, M.I., Poli, M.C., Tagliatela, A., Leuzzi, G., Chinn, I.K., Salinas, S.A., Rey-Jurado, E., Olivares, N., Veramendi-Espinoza, L., **Ciccia, A.**, Lupski, J.R., Aldave Becerra, J.C., Mace, E.M., Orange, J.S. (2022). Partial loss-

- of-function mutations in GINS4 lead to NK cell deficiency with neutropenia. *JCI Insight* 7(21):e154948. doi: 10.1172/jci.insight.154948.
30. Wang, Y.C., Kelso, A.A., Karamafrooz, A., Chen, Y.H., Chen, W.K., Cheng, C.T., Qi, Y., Gu, L., Malkas, L., Tagliatalata, A., Kung, H.J., Moldovan, G.L., **Ciccia, A.**, Stark, J.M., Ann, D.K. (2023). Arginine shortage induces replication stress and confers genotoxic resistance by inhibiting histone H4 translation and promoting PCNA ubiquitination. *Cell Reports* 42(4):112296. Doi:10.1016/j.celrep.2023.112296.
31. Moore, C.E., Yalcindag, S.E., Czeladko, H., Ravindranathan, R., Wijesekara Hanthi, Y., Levy, J.C., Sannino, V., Schindler, D., **Ciccia, A.**, Costanzo, V., and Elia A.E.H. (2023). RFWD3 promotes ZRANB3 recruitment to regulate the remodeling of stalled replication forks. *J Cell Biol.* 222(5):e202106022. doi: 10.1083/jcb.202106022.
32. Schwartzman, J.M., Forsyth, G., Walch, H., Chatila, W., Tagliatalata, A., Lee, B.J., Zhu, X., Gershtik, S., Cimino, F.V., Santella, A., Menghrajani, K., **Ciccia, A.**, Koche, R., Sánchez-Vega, F., Zha, S., and Thompson, C.B. (2023). Oncogenic IDH mutations increase heterochromatin-related replication stress without impacting homologous recombination. *Mol. Cell* 83(13):2347-2356.e8. doi: 10.1016/j.molcel.2023.05.026.
33. Chen, X., Li, Y., Zhu, F., Xu, X., Estrella, B., Pazos, M.A. 2nd, McGuire, J.T., Karagiannis, D., Sahu, V., Mustafokulov, M., Scuoppo, C., Sánchez-Rivera, F.J., Soto-Feliciano, Y.M., Pasqualucci, L., **Ciccia, A.**, Amengual J.E., and Lu, C. (2023). Context-defined cancer co-dependency mapping identifies a functional interplay between PRC2 and MLL-MEN1 complex in lymphoma. *Nat. Commun.* 14(1):4259. doi: 10.1038/s41467-023-39990-5.
- *34. Leuzzi, G., Vasciaveo, A., Tagliatalata, A., Chen, X., Firestone, T.M., Hickman, A.R., Mao, W., Thakar, T., Vaitianskova, A., Huang, J.W., Cuella-Martin, R., Hayward, S.B., Kesner, J.S., Ghasemzadeh, A., Nambiar, T.S., Ho, P., Rialdi, A., Hebrard, M., Li, Y., Gao, J., Gopinath, S., Adeleke, O.A., Venters, B., Drake, C.G., Baer, R., Izar, B., Guccione, E., Keogh, M.C., Guerois, R., Sun, L., Lu, C., Califano, A., and **Ciccia, A.** (2024). SMARCA1 is a dual regulator of innate immune signaling and PD-L1 expression that promotes tumor immune evasion. *Cell* 187: 1-21.
35. Georgieva, D., Wang, N., Tagliatalata, A., Jerabek, S., Reczek, C.R., Lim, P.X., Sung, J., Du, Q., Horiguchi, M., Jasin, M., **Ciccia, A.**, Baer, R., and Egli, D. (2024). BRCA1 and 53BP1 regulate reprogramming efficiency by mediating DNA repair pathway choice at replication-associated double-strand breaks. *Cell Reports* 43(4): 114006. doi: <https://doi.org/10.1016/j.celrep.2024.114006>.
36. Acharya, A., Bret, H., Huang, J.W., Mütze, M., Göse, M., Kissling, V., Seidel, R., **Ciccia, A.**, Guérois, R., Cejka, P. (2024). Mechanism of DNA unwinding by hexameric MCM8-9 in complex with HROB. *Nat. Commun.* 15(1):3584. doi: 10.1038/s41467-024-47936-8.
37. Lee, J., Lee, J., Sohn, E.J., Tagliatalata, A., O'Sullivan, R.J., **Ciccia, A.**, and Min J. (2024). Extrachromosomal Telomere DNA Derived from Excessive Strand Displacements. *Proc Natl Acad Sci U S A.* 121(19):e2318438121. doi: 10.1073/pnas.2318438121.
38. Walsh, Z.H., Shah, P., Kothapalli, N., Shah, S.B., Nikolenyi, G., Brodtman, D.Z., Leuzzi, G., Rogava, M., Mu, M., Ho, P., Abuzaid, S., Vasan, N., AlQuraishi, M., Milner, J.D., **Ciccia, A.**, Melms, J.C., and Izar, B. (2024). Mapping variant effects on anti-tumor hallmarks of primary human T cells with base-editing screens. *Nat. Biotechnol.* doi: 10.1038/s41587-024-02235-x.
39. IGVF Consortium. (2024). Deciphering the impact of genomic variation on function. *Nature.* 633(8028):47-57. doi: 10.1038/s41586-024-07510-0.
40. Gu, J., Iyer, A., Wesley, B., Tagliatalata, A., Leuzzi, G., Hangai, S., Decker, A., Gu, R., Klickstein, N., Shuai, Y., Jankovic, K., Parker-Burns, L., Jin, Y., Zhang, J.Y., Hong, J., Niu, S., Chou, J., Landau, D.A., Azizi, E., Chan, E.M., **Ciccia, A.**, Gaublot, J.T. (2024). CRISPRmap: Sequencing-free optical pooled screens mapping multi-omic phenotypes in cells and tissue. *Nat. Biotechnol.* doi: 10.1038/s41587-024-02386-x.

Reviews and Editorials

1. **Ciccia, A.**, McDonald, N., and West, S.C. (2008). Structural and functional relationships of the XPF/MUS81 family of proteins. *Annu. Rev. Biochem.* 77, 259-287.
2. **Ciccia, A.**, and Elledge, S.J. (2010). The DNA damage response: making it safe to play with knives. *Mol. Cell* 40(2) 179-204.
- *3. **Ciccia, A.** # and Symington, L.S. # (2016). Stressing out about RAD52. *Mol. Cell* 64(6), 1017-1019.
Corresponding authors
- *4. Joseph, S.A., Taglialatela, A., Leuzzi, G., Huang, J.W., Cuella-Martin, R. and **Ciccia, A.** (2020). Time for remodeling: SNF2-family DNA translocases in human health and disease. *DNA Repair* 95, 102943.
- *5. Leuzzi, G., Taglialatela, A., and **Ciccia, A.** (2020). HATtracting nucleases to stalled forks. *Mol. Cell* 80(2):177-180.
- *6. Hayward, S.B., and **Ciccia, A.** (2021). Towards a CRISPeR understanding of homologous recombination with high-throughput functional genomics. *Curr. Opin. Genet. Dev.* 71, 171-181.
- *7. Nambiar, T.S., Baudrier, L., Billon, P., and **Ciccia, A.** (2022). CRISPR-based genome editing through the lens of DNA repair. *Mol. Cell* 82(2):348-388.
8. **Ciccia, A.**, Greenberg, R.A., Lees-Miller, S.P., and Nussenzweig, A. (2022). A genetic roadmap to the response to genotoxic agents in human cells. *Fac. Rev.* 11:35.
9. Klapp, V., Alvarez-Abril, B., Leuzzi, G., Kroemer, G., **Ciccia, A.**, and Galluzzi, L. (2023). The DNA Damage Response and Inflammation in Cancer. *Cancer Discov.* 13(7):1521-1545.
- *10. Vaitsiankova, A., Thakar, T., and **Ciccia, A.** (2023). Base-editing screens illuminate variants effect in human hematopoiesis. *Cell Rep. Methods* 3(7):100541.