



Review Article

The role of DNA damage response in chemo- and radio-resistance of cancer cells: Can DDR inhibitors solve the problem?

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ABSTRACT

Up to now, many improvements have been made in providing more therapeutic strategies for cancer patients. The lack of susceptibility to common therapies like chemo- and radio-therapy is one of the reasons why we need more methods in the field of cancer therapy. DNA damage response (DDR) is a set of mechanisms which identifies DNA lesions and triggers the repair process for restoring DNA after causing an arrest in the cell cycle. The ability of DDR in maintaining the genome stability and integrity can be favorable to cancerous cells which are exposed to radiation therapy or are treated with chemotherapeutic agents. When DDR mechanisms are error-free in cancer cells, they can escape the expected cellular death and display resistance to treatment. In this regard, targeting different components of DDR can help to increase the susceptibility of advanced tumors to chemo- and radio-therapy.

1. Introduction

DNA-damaging agents originating whether from endogenous or exogenous resources are known to threaten the viability of every cell of our body [1]. Besides to the cellular issues arising from the great number of mutations and genome instability, the lack of proper responses can establish generations of these defective cells and put our whole body in danger [1]. DNA damage response or DDR is a precise mechanism which contains sensing the lesions, establishing signals, and finally initiating repair processes by the means of these signals [2]. During DDR, cell cycle is also affected by the mediators of DDR and is temporarily stopped in order to inhibit the replication of a defective DNA [3]. In some cases, DNA deteriorations are irreparable and thus, cell death is the only option on the table [3].

In addition to normal cells, cancerous cells are also able to use the same mechanisms for their chemotherapy- and/or radiotherapy-induced damaged DNA. Until DDR is working properly in a cancerous cell, DNA damages would not lead to cell death and thus, treatment would not be considered successful [1]. This means that despite all the advantageous impacts of DDR, it stands in the way of overcoming a great challenge in cancer therapy: resistance to our common methods, chemo- and radio-therapy. Recently, a great number of researchers have worked on targeting distinct components of DDR for enhancing the efficacy of cytotoxic treatments [4]. In this paper, we review the process of DDR briefly and explain the role of its key players in decreasing the susceptibility of cancer cells to common therapeutic procedures. Additionally, the usage of DDR inhibitors on different types of cancer would be discussed for giving an insight for the treatment of advanced stages of this

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lethal disease.

2. DNA damage response

As mentioned before, the first step of DDR is the lesion detection and subsequent protein recruitment which prepares a context for DNA repair through five different pathways: base excision repair (BER), nucleotide excision repair (NER), mismatch repair (MMR), homologous recombination (HR) and non-homologous end joining repair (NHEJ) [5]. DDR starts with the activity of an enzyme named poly (ADP-ribose) polymerase 1 or PARP1 which has a tendency to DNA breaks and after its activations provides some protein-protein interactions in order to activate some other ingredients of this process [6]. Notwithstanding the substantial activity of PARP1 in DNA damage sensing, this enzyme is not the only involved protein in this process and in different repair pathways some other proteins also get engaged; for instance, xeroderma pigmentosum group C-complementing protein (XPC) in NER [7], apurinic-apyrimidinic (AP) endonuclease 1 in BER [8], and ATM in double-strand break repair [9].

When the DNA-binding domains of this enzyme are attached to the DNA lesion (independent of its sequence), they go through some structural transformations and thereby, affect the other domains of PARP1 which leads to the transmission of ADP-ribose units from donor NAD^+ to the acceptor protein or even the enzyme, itself [10]. Creating a chain composed of ADP-ribose units (PAR) helps the recruitment and activation of other proteins by the means of non-covalent linkages between their PAR-binding domains and the PAR chain [11]. In contrast to the advantages of PAR, if this polymer is not degraded by PAR glycohydrolase (PARG), DNA damage can be increased as a result of the enhanced accessibility and sensitivity to cytotoxicity [12,13]. Nevertheless, it seems that the importance of PARP1 is more highlighted in the single-stranded break repair (SSBR) [6]; hence, we would define more sensing mechanisms which are dedicated to each repair pathway in following sections:

2.1. Nucleotide excision repair (NER)

NER pathway which has the capacity of repairing helix-distorting DNA deteriorations is performed through either global genome repair (GG-NER) or transcription-coupled NER (TC-NER) [14]. The former one is triggered by a complex composed of three proteins: XPC, RAD23B and centrin 2 (CETN2) and the latter one is initiated by Cockayne syndrome (CS) protein A and B [15,16]. When the lesion detection is completed, the transcription factor II H (TFIIH) complex (which contains ten subunits) is formed in this site for providing a condition for the recruitment of XPA and replication protein A (RPA) [17–19]. Afterwards, two essential endonucleases, XPF-ERCC1 and XPG, which have the duty of incising both ends of the break are present by the help of XPA and RPA [20,21]. After the dual incision, the DNA gap is filled at the hand of a DNA polymerase (which can be δ , ϵ or κ) and two other proteins known as replication factor C (RFC) and proliferating cellular nuclear antigen (PCNA) [22]. Eventually, two complexes are applied beneficial to joining the repaired ends: (XRCC1)–DNA ligase III (LIG3) complex or flap endonuclease 1 (FEN1)–DNA ligase I (LIG1) complex [23,24].

2.2. Base excision repair (BER)

BER pathway is commonly adopted by a cell in response to deamination, alkylation, and more frequently oxidation of the DNA bases [25]. Interestingly, single-strand breaks are also commonly repaired through this method [25].

DNA glycosylases such as N-methylpurine-DNA glycosylase (MPG) [26], The nei-like 1 (NEIL1) and 8-oxoguanine DNA glycosylase (OGG1) [27] administer the first step of this mechanism: sensing [28]. Afterwards, DNA end processing is managed by the help of APE1 [29], Pol beta [30], and PNKP [31] in order to provide two error-free termini for

either Pol beta [32,33] or Pol δ/ϵ [34] to replace nucleotide(s) in the generated gap. After all, DNA ligation proceeds in a same way as NER [35].

2.3. Homologous recombination (HR)

HR along with NHEJ (which is more common in humans) are two major pathways that handle double-strand break (DSB) repair [36]. MRN complex which is formed by the gathering of MRE11, NBS1, and RAD50 has the most pivotal role in DSB detection [37]. DNA end resection in DSB repair is a bit more detailed than SSB repair and is composed of short- and long-scale phases managed by C-terminal binding protein (CtBP)-interacting protein (CtIP) and exonuclease 1 (EXO1), respectively [38,39]. DNA end resection in this mechanism results in the generation of a single-stranded DNA tail which then, is stabilized by RPA [38]. However, for proceeding the next step RPA should be removed by RAD52 and be replaced by RAD51 [40,41]. For extending the ends of the break, RAD51 should find a homology match by the use of the sister chromosome and then, connect this template DNA to the damaged one [36]. In a similar way as the previous repair pathways, polymerases synthesis an error-free DNA and ligases join the newly generated DNA ends [42,43]. During this process two important protein kinases are activated: ataxia telangiectasia mutated (ATM) is activated by the MRN complex and ATR is activated by RPA [25].

2.4. Non-homologous end joining (NHEJ)

Ku70/Ku80 (Ku) heterodimer is the detector of DSB in this procedure which after binding to DNA is able to recruit a multiprotein complex known as DNA-dependent protein kinase catalytic subunit (DNA-PKcs) [44]. The consequence of the recruitment and activation of this complex is the activation of a group of endo- or exonucleases such as Artemis which is the main enzyme in resecting the DNA ends [44,45]. The last phase of NHEJ, DNA ligation, is possible because of a “sleeve-like” structure which is established around the DNA by XRCC4 and XRCC4-like factor (XLF) to facilitate the performance of ligase IV [46–48]. Noteworthy, DNA gap filling in NHEJ occurs prior to the ligation by the use of Pol μ and Pol λ [49,50].

2.5. Mismatch repair (MMR)

This pathway is commonly used for repairing any mismatches that occur in bases due to replication errors or intermediates of the HR pathway [25]. Base mismatches and deletion/insertions are primarily recognized by two heterodimers: MutS α and MutS β [51]. In eukaryots, two dimers of the former complex include MSH2 and MSH6 and the dimers of the latter one contain MSH2 and MSH3 [51,52]. In eukaryots, after the lesion recognition, some other proteins named MutL get involved in MMR in order to show the right DNA strand (the nascent one) to exonucleases [53]. The excision process is performed afterwards by the help of PCNA and EXO1 which are recruited to the damaged site by MutL complex [25,54]. Eventually, polymerase δ and LIG1 fill the gap in the DNA and complete the MMR process [54].

3. DDR and radiotherapy failure

In general, radiation therapy is mostly known for causing base modifications and DNA breaks; although, DSBs seem to be the most important consequence of this treatment [2].

3.1. NHEJ and HR

14-3-3 σ is a member of the "14-3-3" protein family which its impacts on inducing invasion, EMT, and radio-resistance is of interest [55]. Recent investigations indicate that this protein is the bridge between DDR and radio-resistance. NHEJ is the major pathway which is prone to

be affected by 14-3-3 σ by the agency of elevating the expression levels of PARP1 and CHK2 [56]. In addition to affecting the expression, 14-3-3 σ also decreases the degradation of PARP1. Overall, the major effect of this protein is “up-regulating NHEJ repair while arresting cells in G2/M phase” [56].

CHK2 is a protein kinase which is a mediator in the ATM-dependent signaling and cell cycle arrest after ionizing radiation (IR)-induced DNA break. CHK2 executes its effects on cell cycle checkpoints through some proteins such as Cdc25, E2F1, BRCA1 and more importantly p53 [57, 58]. Takai et al. [59] are another group of researchers that demonstrated the important role of CHK2 in radiosensitivity. They found that CHK2 not only regulates the activity of p53 in transcriptional levels but also stabilize this tumor suppressor protein. They also revealed that after IR exposure to mice, apoptosis and G1/S arrest are impaired in the absence of CHK2 [59]. This suggests that despite CHK1, CHK2 inhibitors cannot be used in cancer patients for increasing the treatment efficacy. BRCA1 and 2 are two other proteins, which are responsible for both DNA repair and cell cycle control, are possibly causing radio-resistance [60]. BRCA1 is a key player in DSB repair which binds to CtIP and is able to switch the repair pathway from NHEJ to HR [61]. BRCA2 is also engaged in DSB repair and assists RAD51 to be replaced with RPA on the ssDNA in the HR pathway [62]. Additionally, BRCA1 is also able to increase radio-resistance by switching NHEJ to HR; this happens because NHEJ is an error-prone process which despite HR can increase genome instability in cancer cells [63]. Eenesos et al. [64] worked on BRAC1 and 2 women carriers and indicated that radiosensitivity is more observed in patients who carry the mutated versions of these genes.

ATM and ATR are also helping the failure of radiotherapy failure:

ATM induces radio-resistance mainly through zinc finger E-box binding homeobox 1 (ZEB 1) by stabilizing it and thereby, stabilizing CHK1 [65]. ZEB1 is essential for radio-resistance because of its regulatory effects on EMT. Interestingly, some parts of the ZEB1 function are related to CHK1 [65]. Another function of ATM is amplifying the DSB repair through phosphorylating the histone protein H2A.X. H2A.X phosphorylation is substantial because of its role in recruiting MRN complex, MDC1, ATM, and RNF8 [66]. On the other hand, the effect of ATM on checkpoint activation through stabilizing p53 and phosphorylating NBS1 cannot be neglected [67].

Several interesting features of ATR, such as conducting HR pathway, are also defining some parts of DDR roles in establishing radio-resistance in cancer cells [68]. Moreover, stalled replication fork stabilization, activating the intra-S checkpoint, administering the replication origin firing, and the activation of G2/M checkpoint are some other functions of ATR which their role in radio-resistance cannot be neglected [68]. Furthermore, assessing DNA-PKCS, p53, and PCNA after radiation therapy also showed that these proteins might be engaged in the response of lung cancer cells [69]. However, it seems that Ku70-Ku80 does not have an essential role in radio-sensitivity [69]. Overall, further investigations are required on these proteins. In nasopharyngeal carcinoma, PCNA's influence on radio sensibility is also approved by other researches [70,71].

3.2. BER and NER

In the BER point of view, examinations represent a lower radio-resistance when BER is impaired by some agents such as methoxyamine [72]. 5-Iodo-2'-deoxyuridine (IdUrd) cytotoxicity and radiosensitization can be enhanced by using BER inhibitors [72]. Considering APE1, there are some contradictory studies regarding the role of this BER component in radiosensitivity; for instance, Herring et al. [73] showed that APE1 expression in cervical carcinoma is related to radiosensitivity and can be used for predicting the treatment efficacy. Whereas, increased levels of Ape1/ref-1 complex provide a protection against radiation therapy in germ cell tumors [74]. XRCC1 which is involved in the last stage of both BER and NER pathways also has a relation to radio-resistance: XRCC1 mutant cells display more

susceptibility cytotoxicity after being treated with IdUrd [74]. In addition, polymorphism in XRCC1 gene also results in IR hypersensitivity [75].

4. DDR inhibitors decrease radio-resistance

4.1. Targeting HR and NHEJ

CHK1 is another protein kinase that mediates the DDR-induced cell cycle arrest. Phosphorylation of this protein by ATR results in checkpoint activation by the means of Cdc25A inactivation [76]. In this regard, researchers have worked on utilizing CHK1 inhibitors for decreasing the resistance to radiation therapy; for instance, Engelke et al. [77] MK8776 on pancreatic cancer cells and indicated this inhibitor can reduce the resistance to chemoradiotherapy. However, they highlighted the function of CHK1 through HR pathway in this study. Furthermore, they also revealed that MK8776 increases DNA damage in cancer cells more than normal cells and hence, this inhibitor can be used along with gemcitabine-radiation for patients with locally advanced pancreatic cancer [77].

Due to the parts of ATR and ATM in establishing radio-resistance, numerous trials have tried their inhibitors on cancer cells. Sarkaria et al. and Blasina et al. are two of the first researcher groups which worked on targeting ATR and ATM for affecting the radio-resistance in tumor cells [78,79]. Previously, Gorecki et al. [80] used VX-970 or berzosertib which is a selective small-molecule for preventing the activity of ATR. “The results suggest that VX-970 is indeed a promising anticancer drug that can be used both as monotherapy and in combination with either chemotherapy or radiotherapy strategies” [80]. Toledo et al. [81] demonstrated that besides to the replicative stress, ATR inhibition is even more effective for treating cancer cells which have a p53 deficiency. In this exploration it was also revealed that NVP-BEZ235 which is commonly utilized for limiting the activity of mTOR and PI3K, can also be practical for inhibiting ATR, ATM, and DNA-PKcs [81]. Another study on chordoma represented RAD51 as the essential down-stream part of ATR/ATM signaling which executes the radio-resistant activities of these protein kinases [82]. MRE11 inhibitors are another group radio-sensitizer agents which are also effective on decreasing the resistance to chemotherapy [83]. In a study, pentamidine, a bisbenzamidine derivative, was used on Hela cells and the following was observed: decreased activity of ATM, accumulation of gamma-H2AX, and also reduced accumulation of NBS1 in the DSB site [83].

5. DDR roles in chemotherapy failure

PARP1 is one of the most interesting ingredients of DDR which takes part in chemo-resistance of the cancerous cells through distinct ways. BRD7 degradation is one of the ways by which PARP1 increases survival in tumors [84]. BRD7 is a tumor suppressor protein which has the capacity of impacting epithelial-mesenchymal transition (EMT) and Wnt signaling and inactivating HIF1 alpha/LDHA axis and thereby, inhibiting proliferation, progression, invasion, and metastasis of different cancer cells including breast, prostate, cervical, gastric, and colorectal cancers [85–91]. Hu et al. [84] demonstrated that “BRD7 is directly ribosylated by PARP1 which is then ubiquitinated by a PAR-binding E3 ubiquitin ligase RNF146, leading to degradation of BRD7 and survival of cancer cells”. Valanejad et al. [92] find another mechanism of PARP1-induced chemo-resistance in aggressive hepatoblastoma. They find that the PARP1- Ku80/Ku70 complex is responsible for cisplatin-resistance in these cells because of its linkage to aggressive liver cancer domains (ALCDs) which are specific to this cancer [92].

APE1/Ref-1 which is involved in BER process is also related to chemo-resistance; however, it functions through two distinct ways: increasing DDR and resistance and increasing the activity of p53 and sensitivity to therapy. Robertson and colleagues showed that in cases of higher Ape1/ref-1 complex expression, a 2-fold increase in repair

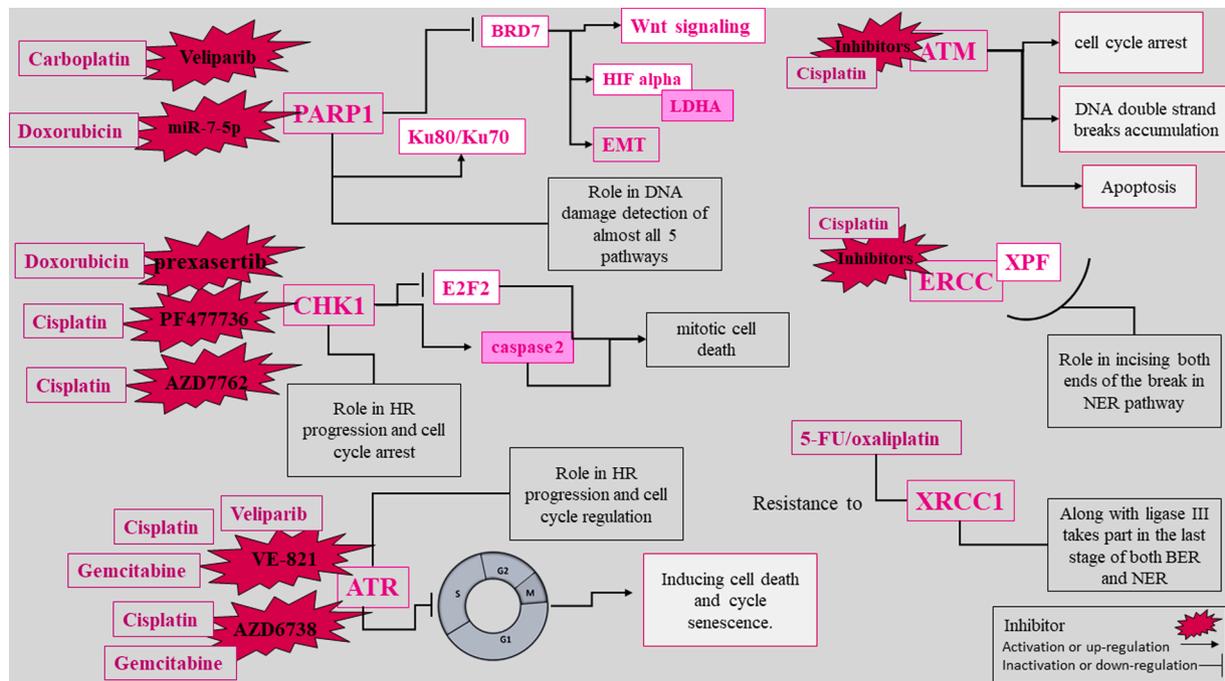


Fig. 2. Schematic representation of the essential components of DDR in chemo-resistance, their inhibitors, and the drugs to which they cause resistance.

Excision Repair, sensitizing melanoma cancer cells to cisplatin. Furthermore, it is indicated that these inhibitors do not sensitize cells that are Nucleotide Excision Repair-deficient [110]. Using non-coding RNAs is another favorable method in inhibiting the PARP1 functions: Lai and colleagues utilized miR-7-5p on cells with a resistance to Doxorubicin and found that this microRNA is able to impede HR repair through the downregulation of PARP1, BRCA1, and RAD51 [101].

7. Conclusions

Notwithstanding the improvements in the field of cancer and the establishment of novel methods such as immunotherapy, gene therapy, and using nanocarriers, still, resistance to therapy is one of the most complicated and effortful obstacles in the way of excluding cancer from the list of leading causes of death. DDR is a set of mechanisms by which a damaged cell sustains its genome stability and integrity along with its survival and viability. As much as these mechanisms are beneficial for every cell of our body, they can be disservice when it comes to cancer therapy. This suggests that targeting the components of DDR is a promising method in this field for enhancing the efficacy of common methods including chemo- and radio-therapy.

As we reviewed in this paper, PARP1, ATM, and ATR are some of the resistance-related proteins involved in DDR which are considered great candidates for being targeted in diverse types of cancer (summarized in Figs.1 and 2). Recently, using DDR inhibitors for cancer treatment has attracted the attention of clinicians and it is expected that in the coming years, this method would be utilized in a greater scale specially for patients who are suffering from an advanced-stage cancer.

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References

- [1] M.J. O'Connor, Targeting the DNA damage response in cancer, *Mol. Cell* 60 (2015) 547–560.
- [2] M. Goldstein, M.B. Kastan, The DNA damage response: implications for tumor responses to radiation and chemotherapy, *Annu. Rev. Med.* 66 (2015) 129–143.
- [3] S.P. Jackson, J. Bartek, The DNA-damage response in human biology and disease, *Nature* 461 (2009) 1071–1078.
- [4] J. Mateo, C.J. Lord, V. Serra, A. Tutt, J. Balmaña, M. Castroviejo-Bermejo, C. Cruz, A. Oaknin, S.B. Kaye, J.S. de Bono, A decade of clinical development of PARP inhibitors in perspective, *Ann. Oncol.* 30 (2019) 1437–1447.
- [5] L.R. Gomes, C.F.M. Menck, G.S. Leandro, Autophagy roles in the modulation of DNA repair pathways, *Int. J. Mol. Sci.* 18 (2017).
- [6] A. Ray Chaudhuri, A. Nussenzweig, The multifaceted roles of PARP1 in DNA repair and chromatin remodelling, *Nat. Rev. Mol. Cell Biol.* 18 (2017) 610–621.
- [7] M. Robu, R.G. Shah, N. Petitclerc, J. Brind'Amour, F. Kandan-Kulangara, G. M. Shah, Role of poly(ADP-ribose) polymerase-1 in the removal of UV-induced DNA lesions by nucleotide excision repair, *Proc. Natl. Acad. Sci. U.S.A.* 110 (2013) 1658–1663.
- [8] H.K. Wong, M. Muftuoglu, G. Beck, S.Z. Imam, V.A. Bohr, D.M. Wilson 3rd, Cockayne syndrome B protein stimulates apurinic endonuclease 1 activity and protects against agents that introduce base excision repair intermediates, *Nucleic Acids Res.* 35 (2007) 4103–4113.
- [9] J.F. Haince, S. Kozlov, V.L. Dawson, T.M. Dawson, M.J. Hendzel, M.F. Lavin, G. G. Poirier, Ataxia telangiectasia mutated (ATM) signaling network is modulated by a novel poly(ADP-ribose)-dependent pathway in the early response to DNA-damaging agents, *J. Biol. Chem.* 282 (2007) 16441–16453.
- [10] J.M. Pascal, The comings and goings of PARP-1 in response to DNA damage, *DNA Repair* 71 (2018) 177–182.

- [11] J. Krietsch, M. Rouleau, É. Pic, C. Ethier, T.M. Dawson, V.L. Dawson, J.Y. Masson, G.G. Poirier, J.P. Gagné, Reprogramming cellular events by poly(ADP-ribose)-binding proteins, *Mol. Aspects Med.* 34 (2013) 1066–1087.
- [12] Y. Zhou, X. Feng, D.W. Koh, Enhanced DNA accessibility and increased DNA damage induced by the absence of poly(ADP-ribose) hydrolysis, *Biochemistry* 49 (2010) 7360–7366.
- [13] D.W. Koh, A.M. Lawler, M.F. Poitras, M. Sasaki, S. Wattler, M.C. Nehls, T. Stöger, G.G. Poirier, V.L. Dawson, T.M. Dawson, Failure to degrade poly(ADP-ribose) causes increased sensitivity to cytotoxicity and early embryonic lethality, *Proc. Natl. Acad. Sci. U.S.A.* 101 (2004) 17699–17704.
- [14] G. Spivak, Nucleotide excision repair in humans, *DNA Repair* 36 (2015) 13–18.
- [15] P.C. Hanawalt, G. Spivak, Transcription-coupled DNA repair: two decades of progress and surprises, *Nature reviews, Mol. Cell Biol.* 9 (2008) 958–970.
- [16] E. Renaud, L. Miccoli, N. Zagal, D.S. Biard, C.T. Craescu, A.J. Rainbow, J. F. Angulo, Differential contribution of XPC, RAD23A, RAD23B and CENTRIN 2 to the UV-response in human cells, *DNA Repair* 10 (2011) 835–847.
- [17] T. Matsuda, M. Saijo, I. Kuraoka, T. Kobayashi, Y. Nakatsu, A. Nagai, T. Enjoji, C. Masutani, K. Sugawara, F. Hanaoka, et al., DNA repair protein XPA binds replication protein A (RPA), *J. Biol. Chem.* 270 (1995) 4152–4157.
- [18] C.H. Park, D. Mu, J.T. Reardon, A. Sancar, The general transcription-repair factor TFIIH is recruited to the excision repair complex by the XPA protein independent of the TFIIIE transcription factor, *J. Biol. Chem.* 270 (1995) 4896–4902.
- [19] O. Kolesnikova, L. Radu, A. Poterszman, TFIIH: A multi-subunit complex at the cross-roads of transcription and DNA repair, *Adv. Protein Chem. Struct. Biol.* 115 (2019) 21–67.
- [20] O.V. Tsodikov, D. Ivanov, B. Orelli, L. Staresinic, I. Shoshani, R. Oberman, O. D. Schärer, G. Wagner, T. Ellenberger, Structural basis for the recruitment of ERCC1-XPF to nucleotide excision repair complexes by XPA, *EMBO J.* 26 (2007) 4768–4776.
- [21] Z. He, L.A. Henricksen, M.S. Wold, C.J. Ingles, RPA involvement in the damage-recognition and incision steps of nucleotide excision repair, *Nature* 374 (1995) 566–569.
- [22] T. Ogi, S. Limsirichaikul, R.M. Overmeer, M. Volker, K. Takenaka, R. Cloney, Y. Nakazawa, A. Niimi, Y. Miki, N.G. Jaspers, L.H. Mullenders, S. Yamashita, M. I. Foustieri, A.R. Lehmann, Three DNA polymerases, recruited by different mechanisms, carry out NER repair synthesis in human cells, *Mol. Cell* 37 (2010) 714–727.
- [23] J. Moser, H. Kool, I. Giakzidis, K. Caldecott, L.H. Mullenders, M.I. Foustieri, Sealing of chromosomal DNA nicks during nucleotide excision repair requires XRCC1 and DNA ligase III alpha in a cell-cycle-specific manner, *Mol. Cell* 27 (2007) 311–323.
- [24] S.J. Araújo, F. Tirode, F. Coin, H. Pospiech, J.E. Syväoja, M. Stucki, U. Hübscher, J.M. Egly, R.D. Wood, Nucleotide excision repair of DNA with recombinant human proteins: definition of the minimal set of factors, active forms of TFIIH, and modulation by CAK, *Genes Dev.* 14 (2000) 349–359.
- [25] T. Iyama, D.M. Wilson 3rd, DNA repair mechanisms in dividing and non-dividing cells, *DNA Repair* 12 (2013) 620–636.
- [26] F. Miao, M. Bouziane, R. Dammann, C. Masutani, F. Hanaoka, G. Pfeifer, T. R. O'Connor, 3-Methyladenine-DNA glycosylase (MPG protein) interacts with human RAD23 proteins, *J. Biol. Chem.* 275 (2000) 28433–28438.
- [27] T.K. Hazra, J.W. Hill, T. Izumi, S. Mitra, Multiple DNA glycosylases for repair of 8-oxoguanine and their potential in vivo functions, *Prog. Nucleic Acid Res. Mol. Biol.* 68 (2001) 193–205.
- [28] M. Dizdaroglu, Base-excision repair of oxidative DNA damage by DNA glycosylases, *Mutat. Res. Mol. Mech. Mutagen.* 591 (2005) 45–59.
- [29] B. Demple, J.S. Sung, Molecular and biological roles of Ape1 protein in mammalian base excision repair, *DNA Repair* 4 (2005) 1442–1449.
- [30] R.A. Bennett, D.M. Wilson 3rd, D. Wong, B. Demple, Interaction of human apurinic endonuclease and DNA polymerase beta in the base excision repair pathway, *Proc. Natl. Acad. Sci. U.S.A.* 94 (1997) 7166–7169.
- [31] L. Wiederhold, J.B. Leppard, P. Kedar, F. Karimi-Busheri, A. Rasouli-Nia, M. Weinfeld, A.E. Tomkinson, T. Izumi, R. Prasad, S.H. Wilson, S. Mitra, T. K. Hazra, AP endonuclease-independent DNA base excision repair in human cells, *Mol. Cell* 15 (2004) 209–220.
- [32] M. Çağlayan, Pol β gap filling, DNA ligation and substrate-product channeling during base excision repair opposite oxidized 5-methylcytosine modifications, *DNA Repair (Amst.)* 95 (2020), 102945.
- [33] M. Çağlayan, J.K. Horton, D.P. Dai, D.F. Stefanick, S.H. Wilson, Oxidized nucleotide insertion by pol β confounds ligation during base excision repair, *Nat. Commun.* 8 (2017) 14045.
- [34] M. Stucki, B. Pascucci, E. Parlanti, P. Fortini, S.H. Wilson, U. Hübscher, E. Dogliotti, Mammalian base excision repair by DNA polymerases delta and epsilon, *Oncogene* 17 (1998) 835–843.
- [35] J. Fan, D.M. Wilson 3rd, Protein-protein interactions and posttranslational modifications in mammalian base excision repair, *Free Radic. Biol. Med.* 38 (2005) 1121–1138.
- [36] A. Piazza, W.D. Heyer, Homologous recombination and the formation of complex genomic rearrangements, *Trends Cell Biol.* 29 (2019) 135–149.
- [37] M. Jasin, R. Rothstein, Repair of strand breaks by homologous recombination, *Cold Spring Harb. Perspect. Biol.* 5 (2013), a012740.
- [38] L.S. Symington, Mechanism and regulation of DNA end resection in eukaryotes, *Crit. Rev. Biochem. Mol. Biol.* 51 (2016) 195–212.
- [39] A.A. Sartori, C. Lukas, J. Coates, M. Mistrík, S. Fu, J. Bartek, R. Baer, J. Lukas, S. P. Jackson, Human CtIP promotes DNA end resection, *Nature* 450 (2007) 509–514.
- [40] J. San Filippo, P. Sung, H. Klein, Mechanism of eukaryotic homologous recombination, *Annu. Rev. Biochem.* 77 (2008) 229–257.
- [41] A. Nogueira, M. Fernandes, R. Catarino, R. Medeiros, RAD52 functions in homologous recombination and its importance on genomic integrity maintenance and cancer therapy, *Cancers* 11 (2019).
- [42] W.C. Griffin, M.A. Trakselis, The MCM8/9 complex: a recent recruit to the roster of helicases involved in genome maintenance, *DNA Repair* 76 (2019) 1–10.
- [43] J. Li, D.L. Holzschu, T. Sugiyama, PCNA is efficiently loaded on the DNA recombination intermediate to modulate polymerase δ, η, and ζ activities, *Proc. Natl. Acad. Sci. U.S.A.* 110 (2013) 7672–7677.
- [44] H.H.Y. Chang, N.R. Pannunzio, N. Adachi, M.R. Lieber, Non-homologous DNA end joining and alternative pathways to double-strand break repair, *Nature reviews, Molecular cell biology* 18 (2017) 495–506.
- [45] A.A. Goodarzi, Y. Yu, E. Riballo, P. Douglas, S.A. Walker, R. Ye, C. Härer, C. Marchetti, N. Morrice, P.A. Jeggo, S.P. Lees-Miller, DNA-PK autophosphorylation facilitates Artemis endonuclease activity, *EMBO J.* 25 (2006) 3880–3889.
- [46] C.A. Koch, R. Agyei, S. Galicia, P. Metelnikov, P. O'Donnell, A. Starostine, M. Weinfeld, D. Durocher, Xrcc4 physically links DNA end processing by polynucleotide kinase to DNA ligation by DNA ligase IV, *EMBO J.* 23 (2004) 3874–3885.
- [47] M.A. Recuero-Checa, A.S. Doré, E. Arias-Palomo, A. Rivera-Calzada, S.H. Scheres, J.D. Maman, L.H. Pearl, O. Llorca, Electron microscopy of Xrcc4 and the DNA ligase IV-Xrcc4 DNA repair complex, *DNA Repair* 8 (2009) 1380–1389.
- [48] P. Ahnesorg, P. Smith, S.P. Jackson, XLF interacts with the XRCC4-DNA ligase IV complex to promote DNA nonhomologous end-joining, *Cell* 124 (2006) 301–313.
- [49] P. Andrade, M.J. Martín, R. Juárez, F. López de Saro, L. Blanco, Limited terminal transferase in human DNA polymerase mu defines the required balance between accuracy and efficiency in NHEJ, *Proc. Natl. Acad. Sci. U.S.A.* 106 (2009) 16203–16208.
- [50] J.P. Capp, F. Boudsocq, P. Bertrand, A. Laroche-Clary, P. Pourquier, B.S. Lopez, C. Cazaux, J.S. Hoffmann, Y. Canitrot, The DNA polymerase lambda is required for the repair of non-compatible DNA double strand breaks by NHEJ in mammalian cells, *Nucleic Acids Res.* 34 (2006) 2998–3007.
- [51] A.A. Larrea, S.A. Lujan, T.A. Kunkel, SnapShot: DNA mismatch repair, *Cell* 141 (730) (2010) e731.
- [52] T.A. Kunkel, D.A. Erie, DNA mismatch repair, *Annu. Rev. Biochem.* 74 (2005) 681–710.
- [53] P. Modrich, Mechanisms in eukaryotic mismatch repair, *J. Biol. Chem.* 281 (2006) 30305–30309.
- [54] P. Hsieh, K. Yamane, DNA mismatch repair: molecular mechanism, cancer, and ageing, *Mech. Ageing Dev.* 129 (2008) 391–407.
- [55] Z. Li, J.Y. Liu, J.T. Zhang, 14-3-3sigma, the double-edged sword of human cancers, *Am. J. Transl. Res.* 1 (2009) 326–340.
- [56] Y. Chen, Z. Li, Z. Dong, J. Beebe, K. Yang, L. Fu, J.T. Zhang, 14-3-3σ Contributes to Radioresistance By Regulating DNA Repair and Cell Cycle via PARP1 and CHK2, *Mol. Cancer Res.* 15 (2017) 418–428.
- [57] J. Smith, L.M. Tho, N. Xu, D.A. Gillespie, The ATM-Chk2 and ATR-Chk1 pathways in DNA damage signaling and cancer, *Adv. Cancer Res.* 108 (2010) 73–112.
- [58] J. Bartek, J. Falck, J. Lukas, CHK2 kinase—a busy messenger, *Nature reviews, Mol. Cell Biol.* 2 (2001) 877–886.
- [59] H. Takai, K. Naka, Y. Okada, M. Watanabe, N. Harada, S. Saito, C.W. Anderson, E. Appella, M. Nakanishi, H. Suzuki, K. Nagashima, H. Sawa, K. Ikeda, N. Motoyama, Chk2-deficient mice exhibit radioresistance and defective p53-mediated transcription, *EMBO J.* 21 (2002) 5195–5205.
- [60] M. Takaoka, Y. Miki, BRCA1 gene: function and deficiency, *Int. J. Clin. Oncol.* 23 (2018) 36–44.
- [61] M.H. Yun, K. Hiom, CtIP-BRCA1 modulates the choice of DNA double-strand-break repair pathway throughout the cell cycle, *Nature* 459 (2009) 460–463.
- [62] R.B. Jensen, A. Carreira, S.C. Kowalczykowski, Purified human BRCA2 stimulates RAD51-mediated recombination, *Nature* 467 (2010) 678–683.
- [63] A.K. Byrum, A. Vindigni, N. Mosammam, Defining and Modulating 'BRCAness', *Trends Cell Biol.* 29 (2019) 740–751.
- [64] B. Ernestos, P. Nikolaos, G. Koulis, R. Eleni, B. Konstantinos, G. Alexandra, K. Michael, Increased chromosomal radiosensitivity in women carrying BRCA1/BRCA2 mutations assessed with the G2 assay, *Int. J. Radiat. Oncol. Biol. Phys.* 76 (2010) 1199–1205.
- [65] P. Zhang, Y. Wei, L. Wang, B.G. Debeb, Y. Yuan, J. Zhang, J. Yuan, M. Wang, D. Chen, Y. Sun, W.A. Woodward, Y. Liu, D.C. Dean, H. Liang, Y. Hu, K.K. Ang, M. C. Hung, J. Chen, L. Ma, ATM-mediated stabilization of ZEB1 promotes DNA damage response and radioresistance through CHK1, *Nat. Cell Biol.* 16 (2014) 864–875.
- [66] A. Kinner, W. Wu, C. Staudt, G. Iliakis, Gamma-H2AX in recognition and signaling of DNA double-strand breaks in the context of chromatin, *Nucleic Acids Res.* 36 (2008) 5678–5694.
- [67] A.M. Weber, A.J. Ryan, ATM and ATR as therapeutic targets in cancer, *Pharmacol. Ther.* 149 (2015) 124–138.
- [68] Z. Qiu, N.L. Oleinick, J. Zhang, ATR/CHK1 inhibitors and cancer therapy, *Radiother. Oncol.* 126 (2018) 450–464.
- [69] P.L. Dai, X.S. Du, Y. Hou, L. Li, Y.X. Xia, L. Wang, H.X. Chen, L. Chang, W.H. Li, Different proteins regulated apoptosis, proliferation and metastasis of lung adenocarcinoma after radiotherapy at different time, *Cancer Manag. Res.* 12 (2020) 2437–2447.
- [70] H.Y. Mo, C.Q. Zhang, K.T. Feng, F. Zhang, M.H. Hong, Z.Y. Sun, [Expression of P53 and PCNA in nasopharyngeal carcinoma and their relation with clinical

- stage, VCA/IgA, EA/IgA, radiation sensibility, and pognosis], Ai zheng = Aizheng = Chinese journal of cancer 23 (2004) 1551–1554.
- [71] Y. Okuno, Y. Nishimura, I. Kashu, K. Ono, M. Hiraoka, Prognostic values of proliferating cell nuclear antigen (PCNA) and Ki-67 for radiotherapy of oesophageal squamous cell carcinomas, *Br. J. Cancer* 80 (1999) 387–395.
- [72] P. Taverna, H.S. Hwang, J.E. Schupp, T. Radivoyevitch, N.N. Session, G. Reddy, D.A. Zarling, T.J. Kinsella, Inhibition of base excision repair potentiates iododeoxyuridine-induced cytotoxicity and radiosensitization, *Cancer Res.* 63 (2003) 838–846.
- [73] C.J. Herring, C.M. West, D.P. Wilks, S.E. Davidson, R.D. Hunter, P. Berry, G. Forster, J. MacKinnon, J.A. Rafferty, R.H. Elder, J.H. Hendry, G.P. Margison, Levels of the DNA repair enzyme human apurinic/apyrimidinic endonuclease (APE1, APEX, Ref-1) are associated with the intrinsic radiosensitivity of cervical cancers, *Br. J. Cancer* 78 (1998) 1128–1133.
- [74] K.A. Robertson, H.A. Bullock, Y. Xu, R. Tritt, E. Zimmerman, T.M. Ulbright, R. S. Foster, L.H. Einhorn, M.R. Kelley, Altered expression of Ape1/ref-1 in germ cell tumors and overexpression in NT2 cells confers resistance to bleomycin and radiation, *Cancer Res.* 61 (2001) 2220–2225.
- [75] J.J. Hu, T.R. Smith, M.S. Miller, H.W. Mohrenweiser, A. Golden, L.D. Case, Amino acid substitution variants of APE1 and XRCC1 genes associated with ionizing radiation sensitivity, *Carcinogenesis* 22 (2001) 917–922.
- [76] A.N. Blackford, S.P. Jackson, ATM, ATR, and DNA-PK: The Trinity at the Heart of the DNA Damage Response, *Mol. Cell* 66 (2017) 801–817.
- [77] C.G. Engelke, L.A. Parsels, Y. Qian, Q. Zhang, D. Karnak, J.R. Robertson, D. M. Tanska, D. Wei, M.A. Davis, J.D. Parsels, L. Zhao, J.K. Greenson, T. S. Lawrence, J. Maybaum, M.A. Morgan, Sensitization of pancreatic cancer to chemoradiation by the Chk1 inhibitor MK8776, *Clin. Cancer Res.* 19 (2013) 4412–4421.
- [78] A. Blasina, B.D. Price, G.A. Turenne, C.H. McGowan, Caffeine inhibits the checkpoint kinase ATM, *Curr. Biol.* 9 (1999) 1135–1138.
- [79] J.N. Sarkaria, E.C. Busby, R.S. Tibbetts, P. Roos, Y. Taya, L.M. Karnitz, R. T. Abraham, Inhibition of ATM and ATR kinase activities by the radiosensitizing agent, caffeine, *Cancer Res.* 59 (1999) 4375–4382.
- [80] L. Gorecki, M. Andrs, M. Rezacova, J. Korabecny, Discovery of ATR kinase inhibitor berzosertib (VX-970, M6620): Clinical candidate for cancer therapy, *Pharmacol. Ther.* 210 (2020), 107518.
- [81] L.I. Toledo, M. Murga, R. Zur, R. Soría, A. Rodriguez, S. Martinez, J. Oyarzabal, J. Pastor, J.R. Bischoff, O. Fernandez-Capetillo, A cell-based screen identifies ATR inhibitors with synthetic lethal properties for cancer-associated mutations, *Nat. Struct. Mol. Biol.* 18 (2011) 721–727.
- [82] C. Zhang, B. Wang, L. Li, Y. Li, P. Li, G. Lv, Radioresistance of chordoma cells is associated with the ATM/ATR pathway, in which RAD51 serves as an important downstream effector, *Exp. Ther. Med.* 14 (2017) 2171–2179.
- [83] J. Kobayashi, A. Kato, Y. Ota, R. Ohba, K. Komatsu, Bisbenzimidazole derivative, pentamidine represses DNA damage response through inhibition of histone H2A acetylation, *Mol. Cancer* 9 (2010) 34.
- [84] K. Hu, W. Wu, Y. Li, L. Lin, D. Chen, H. Yan, X. Xiao, H. Chen, Z. Chen, Y. Zhang, S. Xu, Y. Guo, H.P. Koeffler, E. Song, D. Yin, Poly(ADP-ribosyl)ation of BRD7 by PARP1 confers resistance to DNA-damaging chemotherapeutic agents, *EMBO Rep.* 20 (2019).
- [85] Y. Liang, B. Dong, J. Shen, C. Ma, Z. Ma, Clinical significance of bromodomain-containing protein 7 and its association with tumor progression in prostate cancer, *Oncol. Lett.* 17 (2019) 849–856.
- [86] W. Niu, Y. Luo, X. Wang, Y. Zhou, H. Li, H. Wang, Y. Fu, S. Liu, S. Yin, J. Li, R. Zhao, Y. Liu, S. Fan, Z. Li, W. Xiong, X. Li, G. Li, C. Ren, M. Tan, M. Zhou, Retraction Note: BRD7 inhibits the Warburg effect and tumor progression through inactivation of HIF1 α /LDHA axis in breast cancer, *Cell Death Dis.* 10 (2019) 640.
- [87] W. Niu, Y. Luo, Y. Zhou, M. Li, C. Wu, Y. Duan, H. Wang, S. Fan, Z. Li, W. Xiong, X. Li, G. Li, C. Ren, H. Li, M. Zhou, BRD7 suppresses invasion and metastasis in breast cancer by negatively regulating YB1-induced epithelial-mesenchymal transition, *J. Exp. Clin. Cancer Res.* 39 (2020) 30.
- [88] H. Wang, Y. Xie, BRD7-mediated miR-3148 inhibits progression of cervical cancer by targeting Wnt3a/ β -Catenin pathway, *Reprod. Sci.* 27 (2020) 877–887.
- [89] X.M. Zhang, X.Y. Wang, S.R. Sheng, J.R. Wang, J. Li, Expression of tumor related genes NGX6, NAG-7, BRD7 in gastric and colorectal cancer, *World J. Gastroenterol.* 9 (2003) 1729–1733.
- [90] Y. Liu, R. Zhao, Y. Wei, M. Li, H. Wang, W. Niu, Y. Zhou, Y. Qiu, S. Fan, Y. Zhan, W. Xiong, Y. Zhou, X. Li, Z. Li, G. Li, M. Zhou, BRD7 expression and c-Myc activation forms a double-negative feedback loop that controls the cell proliferation and tumor growth of nasopharyngeal carcinoma by targeting oncogenic miR-141, *J. Exp. Clin. Cancer Res.* 37 (2018) 64.
- [91] W. Niu, Y. Luo, X. Wang, Y. Zhou, H. Li, H. Wang, Y. Fu, S. Liu, S. Yin, J. Li, R. Zhao, Y. Liu, S. Fan, Z. Li, W. Xiong, X. Li, G. Li, C. Ren, M. Tan, M. Zhou, BRD7 inhibits the Warburg effect and tumor progression through inactivation of HIF1 α /LDHA axis in breast cancer, *Cell Death Dis.* 9 (2018) 519.
- [92] L. Valanejad, A. Cast, M. Wright, K.D. Bissig, R. Karns, M.T. Weirauch, N. Timchenko, PARP1 activation increases expression of modified tumor suppressors and pathways underlying development of aggressive hepatoblastoma, *Commun. Biol.* 1 (2018) 67.
- [93] L.B. Meira, D.L. Cheo, R.E. Hammer, D.K. Burns, A. Reis, E.C. Friedberg, Genetic interaction between HAP1/REF-1 and p53, *Nat. Genet.* 17 (1997) 145.
- [94] L. Jayaraman, K.G. Murthy, C. Zhu, T. Curran, S. Xanthoudakis, C. Prives, Identification of redox/repair protein Ref-1 as a potent activator of p53, *Genes Dev.* 11 (1997) 558–570.
- [95] J. Stoehlmacher, V. Ghaderi, S. Iobal, S. Groshen, D. Tsao-Wei, D. Park, H.J. Lenz, A polymorphism of the XRCC1 gene predicts for response to platinum based treatment in advanced colorectal cancer, *Anticancer Res.* 21 (2001) 3075–3079.
- [96] Z. Zhang, X. Dou, H. Yang, L. Jia, K. Qin, X. Gao, B. Yang, W. Zhang, C. Qin, F. Zhang, B. Shan, Association of expression of p53, livin, ERCC1, BRCA1 and PARP1 in epithelial ovarian cancer tissue with drug resistance and prognosis, *Pathol. Res. Pract.* 216 (2020), 152794.
- [97] A.J. Chalmers, The potential role and application of PARP inhibitors in cancer treatment, *Br. Med. Bull.* 89 (2009) 23–40.
- [98] M. Rose, J.T. Burgess, K. O'Byrne, D.J. Richard, E. Bolderson, PARP inhibitors: clinical relevance, mechanisms of action and tumor resistance, *Front. Cell Dev. Biol.* 8 (2020).
- [99] G. Somlo, P.H. Frankel, B.K. Arun, C.X. Ma, A.A. Garcia, T. Cigler, L.V. Cream, H. A. Harvey, J.A. Sparano, R. Nanda, H.K. Chew, T.J. Moynihan, L.T. Vahdat, M. P. Goetz, J.H. Beumer, A. Hurria, J. Mortimer, R. Piekarz, S. Sand, J. Herzog, L. R. Van Tongeren, K.V. Ferry-Galow, A.P. Chen, C. Ruel, E.M. Newman, D. R. Gandara, J.N. Weitzel, Efficacy of the PARP inhibitor veliparib with carboplatin or as a single agent in patients with germline BRCA1- or BRCA2-associated metastatic breast cancer: California cancer consortium trial NCT01149083, *Clin. Cancer Res.* 23 (2017) 4066–4076.
- [100] H.S. Han, V. Diéras, M. Robson, M. Palácová, P.K. Marcom, A. Jager, I. Bondarenko, D. Citrin, M. Campone, M.L. Telli, S.M. Domchek, M. Friedlander, B. Kaufman, J.E. Garber, Y. Shparyk, E. Chmielowska, E.H. Jakobsen, V. Kalamani, W. Gradishar, C.K. Ratajczak, C. Nickner, Q. Qin, J. Qian, S. P. Shepherd, S.J. Isakoff, S. Puhalla, Veliparib with temozolomide or carboplatin/paclitaxel versus placebo with carboplatin/paclitaxel in patients with BRCA1/2 locally recurrent/metastatic breast cancer: randomized phase II study, *Ann. Oncol.* 29 (2018) 154–161.
- [101] J. Lai, H. Yang, Y. Zhu, M. Ruan, Y. Huang, Q. Zhang, MiR-7-5p-mediated downregulation of PARP1 impacts DNA homologous recombination repair and resistance to doxorubicin in small cell lung cancer, *BMC Cancer* 19 (2019) 602.
- [102] Y. Sun, J. Wu, X. Dong, J. Zhang, C. Meng, G. Liu, MicroRNA-506-3p increases the response to PARP inhibitors and cisplatin by targeting EZH2/ β -catenin in serous ovarian cancers, *Transl. Oncol.* 14 (2020), 100987-100987.
- [103] B.-J. Hwang, G. Adhikary, R.L. Eckert, A.L. Lu, Chk1 inhibition as a novel therapeutic strategy in melanoma, *Oncotarget* 9 (2018) 30450–30464.
- [104] W.-H. Hsu, X. Zhao, J. Zhu, I.-K. Kim, G. Rao, J. McCutcheon, S.-T. Hsu, B. Teicher, B. Kallakury, A. Dowlati, Y.-W. Zhang, G. Giaccone, Checkpoint kinase 1 inhibition enhances cisplatin cytotoxicity and overcomes cisplatin resistance in SCLC by promoting mitotic cell death, *J. Thorac. Oncol.* 14 (2019) 1032–1045.
- [105] M. Kwok, N. Davies, A. Agathangelou, E. Smith, C. Oldreive, E. Petermann, G. Stewart, J. Brown, A. Lau, G. Pratt, H. Parry, M. Taylor, P. Moss, P. Hillmen, T. Stankovic, ATR inhibition induces synthetic lethality and overcomes chemoresistance in TP53- or ATM-defective chronic lymphocytic leukemia cells, *Blood* 127 (2016) 582–595.
- [106] C.J. Huntoon, K.S. Flatten, A.E. Wahner Hendrickson, A.M. Huehls, S.L. Sutor, S. H. Kaufmann, L.M. Karnitz, ATR inhibition broadly sensitizes ovarian cancer cells to chemotherapy independent of BRCA status, *Cancer Res.* 73 (2013) 3683–3691.
- [107] F.P. Vendetti, A. Lau, S. Schamus, T.P. Conrads, M.J. O'Connor, C.J. Bakkenist, The orally active and bioavailable ATR kinase inhibitor AZD6738 potentiates the anti-tumor effects of cisplatin to resolve ATM-deficient non-small cell lung cancer in vivo, *Oncotarget* 6 (2015) 44289–44305.
- [108] N. Albarakati, T.M. Abdel-Fatah, R. Doherty, R. Russell, D. Agarwal, P. Moseley, C. Perry, A. Arora, N. Alsubhi, C. Seedhouse, E.A. Rakha, A. Green, G. Ball, S. Chan, C. Caldas, I.O. Ellis, S. Madhusudan, Targeting BRCA1-BER deficient breast cancer by ATM or DNA-PKcs blockade either alone or in combination with cisplatin for personalized therapy, *Mol. Oncol.* 9 (2015) 204–217.
- [109] S.G. Boccard, S.V. Marand, S. Geraci, L. Pycroft, F.R. Berger, L.A. Pelletier, Inhibition of DNA-repair genes Ercc1 and Mgmt enhances temozolomide efficacy in gliomas treatment: a pre-clinical study, *Oncotarget* 6 (2015) 29456–29468.
- [110] E.M. McNeil, K.R. Astell, A.M. Ritchie, S. Shave, D.R. Houston, P. Bakrania, H. M. Jones, P. Khurana, C. Wallace, T. Chapman, M.A. Wear, M.D. Walkinshaw, B. Saxty, D.W. Melton, Inhibition of the ERCC1-XPF structure-specific endonuclease to overcome cancer chemoresistance, *DNA Repair* 31 (2015) 19–28.