

Article

Molecular Targets of Minor Cannabinoids in Breast Cancer: In Silico and In Vitro Studies

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Abstract: Background: Breast cancer therapy has been facing remarkable changes. Classic treatments are now combined with other therapies to improve efficacy and surpass resistance. Indeed, the emergence of resistance demands the development of novel therapeutic approaches. Due to key estrogen signaling, estrogen receptor-positive (ER⁺) breast cancer treatment has always been focused on aromatase inhibition and ER modulation. Lately, the effects of phytocannabinoids, mainly Δ^9 -tetrahydrocannabinol (THC) and cannabidiol (CBD), have been evaluated in different cancers, including breast. However, *Cannabis sativa* contains more than 120 phytocannabinoids less researched and understood. Methods: Here, we evaluated, both in silico and in vitro, the ability of 129 phytocannabinoids to modulate important molecular targets in ER⁺ breast cancer: aromatase, ER, and androgen receptor (AR). Results: In silico results suggested that some cannabinoids may inhibit aromatase and act as ER α antagonists. Nine selected cannabinoids showed, in vitro, potential to act either as ER antagonists with inverse agonist properties, or as ER agonists. Moreover, these cannabinoids were considered as weak aromatase inhibitors and AR antagonists with inverse agonist action. Conclusions: Overall, we present, for the first time, a comprehensive analysis of the actions of the phytocannabinoids in targets of ER⁺ breast tumors, pointing out their therapeutic potential in cancer and in other diseases.

Keywords: phytocannabinoids; medicinal cannabis; breast cancer; aromatase; estrogen receptor; androgen receptor



Citation: Almeida, C.F.; Palmeira, A.; Valente, M.J.; Correia-da-Silva, G.; Vinggaard, A.M.; Sousa, M.E.; Teixeira, N.; Amaral, C. Molecular Targets of Minor Cannabinoids in Breast Cancer: In Silico and In Vitro Studies. *Pharmaceuticals* **2024**, *17*, 1245. <https://doi.org/10.3390/ph17091245>

Academic Editor: Andrea Duranti

Received: 17 July 2024

Revised: 4 September 2024

Accepted: 18 September 2024

Published: 21 September 2024



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1. Introduction

Despite the continuous advances in drug development, breast cancer incidence keeps rising, having the main responsibility for all cancer-related death among women worldwide [1,2]. Due to their great heterogeneity, breast tumors are grouped in different subtypes, with most of them being classified as estrogen receptor-positive (ER⁺) [3–5]. This subtype overexpresses estrogen receptor alpha (ER α) and progesterone receptor (PR). Moreover, in these tumors, the enzyme aromatase is overexpressed, resulting in high rates of local estrogen production [4,6,7]. The elucidation of these targets was pivotal for the development of endocrine therapies, which prevent estrogen production or signaling, such as aromatase inhibitors (AIs), including Anastrozole (Ana), Letrozole (Let), and Exemestane

(Exe), as well as anti-estrogens, such as Tamoxifen and Fulvestrant (Figure 1) [8]. In fact, these drugs are part of the therapeutic strategy applied as first-line therapy, both in pre- and post-menopausal status [8–12]. Unfortunately, and despite their clinical success, these compounds are not only associated with adverse side effects, but also with the development of endocrine resistance, which compromises their effectiveness [13,14]. In view of that, alternative therapeutic approaches have been developed to improve treatment, including the introduction of new targeted therapies with novel drugs such as CDK4/6, mTOR, and PI3K inhibitors that are recommended in combination with endocrine therapy [11–17]. Indeed, the elucidation of the role of additional targets in the development of ER⁺ breast cancer represents a new hope for its treatment. One of the targets that has been considered is the androgen receptor (AR), which is expressed in 70–90% of ER⁺ breast tumors [13,18,19]. This receptor seems to cooperate with ER α and displays different functions depending on the hormonal and resistance status. In ER⁺ breast cancer cases, AR antagonizes ER α signaling, contributing to the decrease in cell proliferation and tumor growth [20]. On the other hand, in cases where resistance to endocrine therapy develops, and thus ER α activity is modified, AR switches its function from tumor suppressor to oncogenic in order to promote cell growth and survival. This emphasizes the existence of a hormone-dependent crosstalk between ER α and AR [21–24].

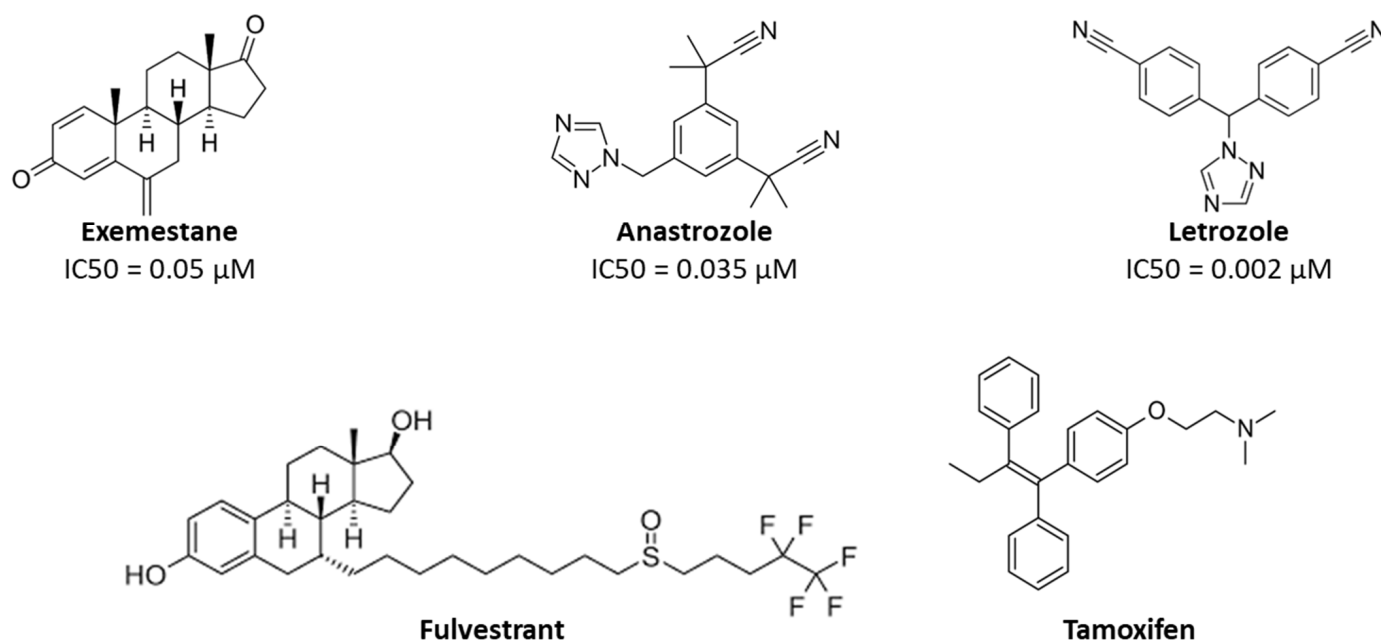


Figure 1. Chemical structures of the AIs, Ana, Let, and Exe, and the anti-estrogens Tamoxifen and Fulvestrant. The IC₅₀ values described for AIs are relative to aromatase and were evaluated in human placental microsomes [25,26].

Cannabinoids have demonstrated promising therapeutic actions in different pathological conditions, including epilepsy, asthma, sleep disorders, depression, and inflammation, and in the relief of chemotherapy-associated side effects [27–29]. Notably, various studies have attributed anti-proliferative, anti-angiogenic, and anti-invasive actions to cannabinoids in various cancer types [28,30–37]. In fact, the *in vitro* and *in vivo* effects of the two best known cannabinoids, Δ^9 -tetrahydrocannabinol (THC) and cannabidiol (CBD), were already explored in different cancer types, including breast cancers. Usually, the cannabinoids exert anti-tumor effects through the inhibition of cell growth, neovascularization, migration, adhesion, invasion, and metastasis, and also by promoting cell cycle arrest, autophagy, and apoptosis [33,38–57]. To date, the studies conducted on cannabinoids in breast cancer were mainly performed in triple-negative and HER2⁺ tumors [33,58–60]. Nevertheless, there is evidence that molecular pathways between cannabinoid receptors and estrogens or

androgens may overlap, which may impact ER⁺ breast cancer [60,61]. In 1997, Ruh et al. demonstrated that **THC** and **CBD** fail to act as ER agonists in MCF-7 cells [62]. Years later, it was demonstrated that **THC** impaired proliferation of MCF-7 cells by an ER- and AR-independent mechanism [63], and disrupted estrogen-signaling by up-regulating ER β [55]. More recently, our group has clarified the anti-cancer role of **CBD** and **THC**, and of the endocannabinoid anandamide (**AEA**) in MCF-7aro cells, unveiling their mechanism of action and their ability to modulate key targets, such as aromatase, ER α , and ER β [42,64,65]. Besides this, we have verified that **CBD** and **AEA** fit well at the aromatase binding site, inhibiting its activity by 78.6% and 61.0%, respectively, at 2 μ M, in human placental microsomes [64,65], whereas **THC** inhibited 25.6% [65]. Moreover, we recently demonstrated that **CBD** acts as an ER and AR antagonist, with inverse agonist properties at both receptors, depending on hormonal influence. Furthermore, this cannabinoid is able to improve AIs' anti-proliferative effects in ER⁺ breast cancer cells, with the combination of **CBD** with Exe having potential clinical value as an adjuvant therapy [44]. However, *Cannabis* contains several other phytocannabinoids. In fact, more than 500 different compounds were isolated from the plant and around 140 of them are phytocannabinoids. Regarding *Cannabis sativa*, 129 phytocannabinoids have been described whose therapeutic potential has not been fully understood. They are generally grouped in 11 different classes: the Δ^9 -**THC** type, Δ^8 -**THC** type, **CBD** type, cannabigerol (**CBG**) type, cannabinodiol (**CBND**) type, cannabielsoin (**CBE**) type, cannabicyclol (**CBL**) type, cannabichromene (**CBC**) type, cannabinol (**CBN**) type, cannabitrinol (**CBT**) type, and miscellaneous type [27,66–69]. All the cannabinoids included in the different classes share a similar C21 terpenophenolic backbone and their biosynthesis is mostly derived from the geranyl diphosphate (GPP) prenylation of either divarinolic acid or olivetolic acid, a reaction catalyzed by GPP olivetolate geranyltransferase. As a result, cannabigerovarinic acid (**CBGVA**) and cannabigerolic acid (**CBGA**) are produced, respectively. Through enzymatic and non-enzymatic transformations, **CBGVA** and **CBGA** originate the phytocannabinoids that constitute the five main classes described so far (Figure 2) [70,71]. The pharmacological interest about the minor phytocannabinoids has been growing and the anti-tumor properties of **CBG**, **CBN**, cannabidiolic acid (**CBDA**), cannabidiol-C4 (**CBDB**), and cannabichromenic acid (**CBCA**) were already addressed in diverse types of cancers, including breast [28,45,72–81]. So far, only the minor phytocannabinoids **CBG** and **CBN** have been studied in breast cancer models [75,76]. Taken together, we aimed to evaluate, in silico and in vitro, the ability of minor phytocannabinoids to interact with and modulate important targets in developing ER⁺ breast cancer, namely aromatase, ER α , and AR, to expand our knowledge on these compounds and substantiate the development of new therapeutic solutions. Moreover, we intend to characterize the potential multi-target actions of cannabinoids in this disease.

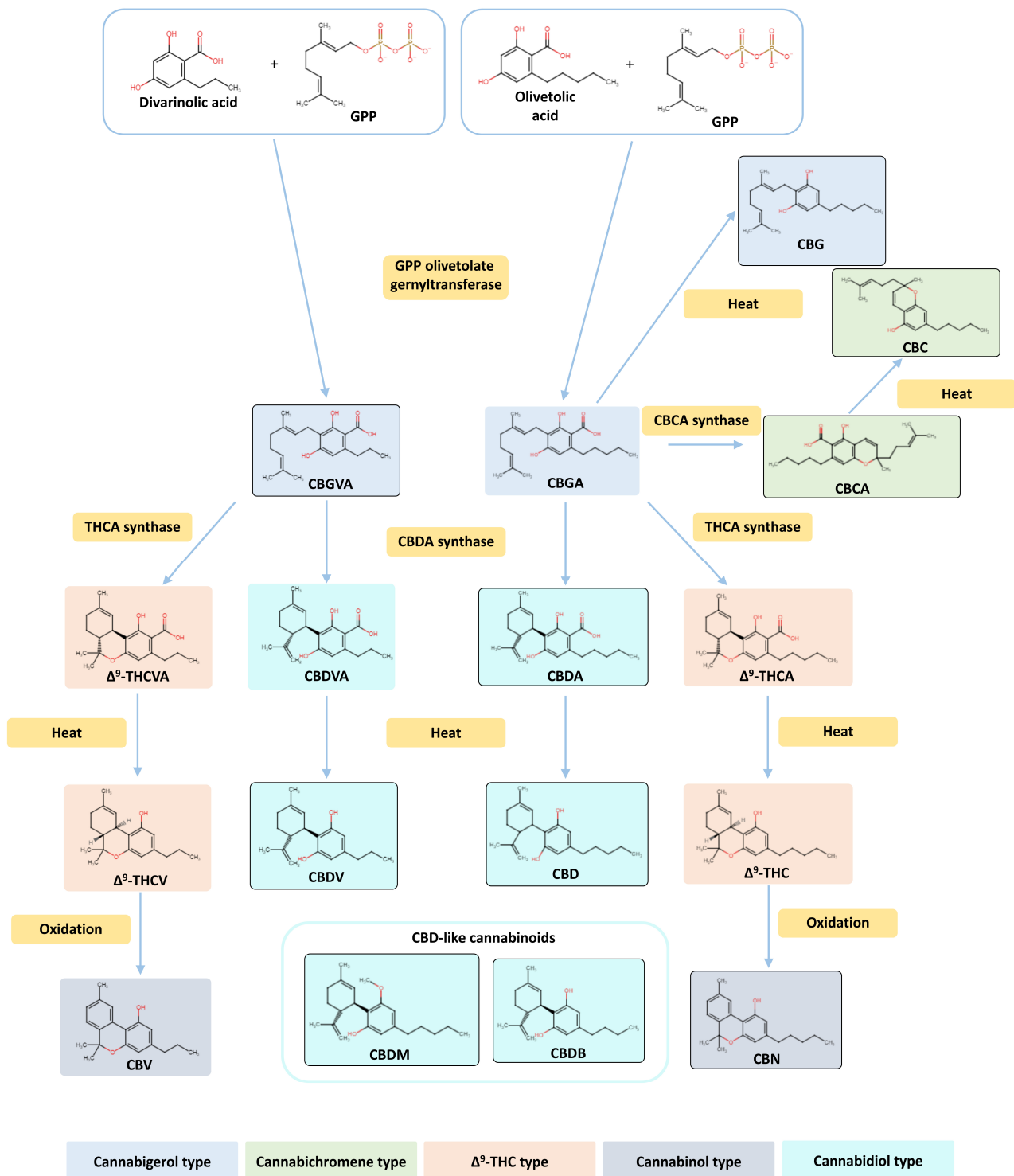


Figure 2. Biosynthetic pathway of phytocannabinoid and phytocannabinoid class representation. Structural and biosynthetic relationships of the nine minor cannabinoids studied in vitro: cannabigerol (CBG), cannabidivarin (CBDV), cannabinol (CBN), cannabidiol-C4 (CBDB), cannabidiolic acid (CBDA), cannabidiol monomethyl ether (CBDM), cannabichromenic acid (CBCA), cannabigerovarinic acid (CBGVA), and cannabichromene (CBC). The remaining phytocannabinoids involved in this pathway, namely cannabidiol (CBD), cannabigerolic acid (CBGA), Δ^9 -tetrahydrocannabivarinic acid (Δ^9 -THCVA), Δ^9 -tetrahydrocannabivarin (Δ^9 -THCV), Δ^9 -tetrahydrocannabinolic acid (Δ^9 -THCA), Δ^9 -tetrahydrocannabinol (THC), cannabivarin (CBV), and cannabidivarinic acid (CBDVA), are also presented. GPP: geranyl diphosphate.

2. Results

2.1. Molecular Docking Results

As previously stated, the therapeutic potential of almost all the 129 different phytocannabinoids from the *Cannabis sativa* plant is still unknown. In order to investigate their possible beneficial actions on ER⁺ breast cancer treatment, a molecular docking analysis on aromatase and ER α , two key targets responsible for the development of this disease [6], was performed. Our calculations revealed that 45 compounds are located in the aromatase binding site above the heme group and are stabilized by several residues, such as Arg115, Asp309, Phe221, Trp224, Met374, and Leu372 (Table 1, Supplementary Figure S1), previously reported as important for aromatase inhibition [82,83]. In fact, most of those cannabinoids belong to Δ^9 -THC, CBD, and miscellaneous types and showed the ability to establish hydrogen bonds with some residues, particularly with Asp309, a fundamental residue for the aromatase reaction [84,85]. According to our calculations, the compounds with the best energy score were cannabicyclol and (-)- Δ^7 -*trans*-(1*R*,3*R*,6*R*)-isotetrahydrocannabinol-C₅, both presenting a binding affinity of -9.8 kcal/mol.

Table 1. Phytocannabinoids presenting AI profiles. The information obtained from molecular docking of the 45 cannabinoids considered as promising AIs, such as the bind affinity score and the description of the most important interactions, is presented. The information regarding CBG and CBN is also presented.

Cannabinoid Name	Cannabinoid Class	Binding Affinity (kcal/mol)	Relevant Interactions
8-Oxo-(-)- Δ^9 - <i>trans</i> -tetrahydrocannabinol	Δ^9 -THC	-9.2	Hydrogen bonds with Arg115 and Leu477; hydrophobic interactions with Trp224 and Phe221
11-Acetoxy-(-)- Δ^9 - <i>trans</i> -tetrahydrocannabinolic acid A	Δ^9 -THC	-8.3	Hydrogen bonds with Arg115, Met374, Asp309, and Leu477; hydrophobic interactions with Phe221
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabivarinic acid	Δ^9 -THC	-7.1	Hydrogen bonds with the heme group, Leu372, and Leu477; hydrophobic interactions with Trp224 and Phe221
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinolic acid A-C ₄	Δ^9 -THC	-6.7	Hydrogen bonds with the heme group, Leu372, Met374, and Leu477; hydrophobic interactions with Trp224 and Phe221
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinolic acid B	Δ^9 -THC	-6.0	Hydrogen bonds with Asp309 and Leu477; hydrophobic interactions with Trp224 and Phe221
Δ^8 - <i>trans</i> -Tetrahydrocannabinolic acid A	Δ^9 -THC	-4.4	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinol	Δ^9 -THC	-3.8	Hydrogen bond with Asp309; hydrophobic interactions with Trp224 and Phe221
Cannabidiol (CBD)	Cannabidiol	-8.7	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
Cannabidiocol	Cannabidiol	-7.8	Hydrogen bonds with Asp309 and Leu477; hydrophobic interactions with Phe221
(-)-Cannabidivarin (CBDV)	Cannabidiol	-7.6	Hydrogen bonds with Asp309 and Leu477; hydrophobic interactions with Phe221
Cannabidiol monomethylether (CBDM)	Cannabidiol	-7.3	Hydrogen bonds with Asp309 and Ser478; hydrophobic interactions with Phe221
Cannabidiol-C ₄ (CBDB)	Cannabidiol	-6.9	Hydrogen bonds with Asp309 and Leu477; hydrophobic interactions with Phe221
Cannabidivarinic acid	Cannabidiol	-6.6	Hydrogen bonds with Asp309 and Leu477; hydrophobic interactions with Phe221
Cannabidiolic acid (CBDA)	Cannabidiol	-5.7	Hydrogen bonds with Asp309 and Leu477; hydrophobic interactions with Phe221
Cannabigerol (CBG)	Cannabigerol	-6.1	Hydrophobic interactions with Phe221 and Trp224
Cannabinerolic acid	Cannabigerol	-6.7	Hydrogen bond with Asp309; hydrophobic interactions with Trp224 and Phe221

Table 1. Cont.

Cannabinoid Name	Cannabinoid Class	Binding Affinity (kcal/mol)	Relevant Interactions
Camagerol	Cannabigerol	−6.6	Hydrogen bonds with Asp309, Arg115, and Met374
(-)-6,7- <i>cis</i> -Epoxy-cannabigerolic acid	Cannabigerol	−6.3	Hydrogen bonds with Asp309, Leu477, and Arg115; hydrophobic interactions with Trp224
Cannabigerovarinic acid (CBGVA)	Cannabigerol	−5.8	Hydrogen bond with Asp309
5-Acetyl-4-hydroxy cannabigerol	Cannabigerol	−5.1	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
(-)-6,7- <i>trans</i> -Epoxy-cannabigerolic acid	Cannabigerol	−5.4	Hydrogen bonds with Asp309 and Leu477; hydrophobic interactions with Trp224
Cannabielsoic acid B-C ₃	Cannabielsoin	−6.0	Hydrogen bonds with the heme group and Asp309
Cannabielsoin acid A	Cannabielsoin	−5.9	Hydrogen bonds with Asp309 and Arg115
Cannabielsoin acid B	Cannabielsoin	−5.1	Hydrogen bond with Asp309; hydrophobic interactions with Trp224 and Phe221
Cannabicyclol	Cannabicyclol	−9.8	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
Cannabicyclovarin	Cannabicyclol	−9.3	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
Cannabicyclic acid	Cannabicyclol	−5.5	Hydrogen bond with Leu477
Cannabichromevarin	Cannabichromene	−7.1	Hydrogen bond with Asp309
Cannabichromenic acid (CBCA)	Cannabichromen	−6.4	Hydrogen bond with Asp309; hydrophobic interactions with Trp224
Cannabichromene (CBC)	Cannabichromene	−6.0	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
(-)-7-Hydroxycannabichromene	Cannabichromen	−5.5	Hydrogen bonds with the heme group and Asp309; hydrophobic interactions with Phe221
Cannabichromevarinic acid	Cannabichromene	−5.2	Hydrogen bond with Arg115
Cannabinol (CBN)	Cannabinol	−5.9	Hydrogen bond with Leu477; hydrophobic interactions with Phe221 and Trp224
8-Hydroxycannabinol	Cannabinol	−7.9	Hydrogen bonds with Asp309 and Arg115
Cannabiorcol-C ₁	Cannabinol	−6.6	Hydrogen bond with Asp309; hydrophobic interactions with Trp224 and Phe221
8-Hydroxycannabinolic acid A	Cannabinol	−4.8	Hydrogen bonds with Asp309 and Arg115; hydrophobic interactions with Trp224 and Phe221
(-)- <i>trans</i> -Cannabitrinol-OEt-C ₅ *	Cannabitrinol	−3.9	Hydrogen bonds with Asp309, Arg115, and Leu477; hydrophobic interactions with Phe221
(-)- <i>trans</i> -Cannabitrinol-OEt-C ₃ *	Cannabitrinol	−3.5	Hydrogen bonds with Asp309 and Ser478; hydrophobic interactions with Phe221
(-)- Δ^7 - <i>trans</i> -(1R,3R,6R)-isotetrahydrocannabinol-C ₅	Miscellaneous	−9.8	Hydrogen bonds with the heme group and Asp309; hydrophobic interactions with Trp224 and Phe221
Cannabimovone	Miscellaneous	−8.4	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
Cannabichromanone C	Miscellaneous	−7.8	Hydrogen bonds with Asp309 and Arg115; hydrophobic interactions with Phe221
Dehydrocannabifuran	Miscellaneous	−7.3	Hydrogen bond with Asp309; hydrophobic interactions with Phe221
Cannabichromanone B	Miscellaneous	−7.0	Hydrogen bonds with the heme group and Asp309; hydrophobic interactions with Phe221
(-)-(7R)-Cannabicumarononic acid	Miscellaneous	−6.5	Hydrogen bonds with Asp309 and Met374; hydrophobic interactions with Trp224 and Phe221
8-Hydroxy-isohexahydrocannabivarin	Miscellaneous	−6.0	Hydrogen bonds with the heme group and Asp309; hydrophobic interactions with Trp224 and Phe221
Cannabicumaronome-C ₅	Miscellaneous	−6.0	Hydrogen bonds with the heme group and Asp309; hydrophobic interactions with Phe221
Cannabichromanone-C ₃	Miscellaneous	−5.4	Hydrogen bonds with the heme group and Asp309; hydrophobic interactions with Phe221

* Et = ethyl.

Regarding ER α , we analyzed the docking positions and the energy scores and selected 85 compounds of the 129 cannabinoids as the best candidates to act as ER α antagonists (Table 2, Supplementary Figure S2). The cannabinoids selected belong mainly to Δ^9 -THC, CBG, CBC, and miscellaneous classes and all of them bind in the vicinity of the residues Val534, Leu525, Glu353, Arg394, Phe404, Met421, His524, and Asp351, being mainly stabilized by hydrophobic interactions. The cannabinoid with the best binding affinity was cannabioxepane, which presented a value of -9.2 kcal/mol.

Table 2. Phytocannabinoids presenting ER α antagonist profiles. The information obtained from molecular docking for the 85 cannabinoids considered as promising ER α antagonists, such as the bind affinity score and the description of the most important interactions, is presented. The information regarding CBG and CBN is also presented.

Cannabinoid Name	Cannabinoid Class	Binding Affinity (kcal/mol)	Relevant Interactions
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabihexol	Δ^9 -THC	-8.5	Close to Asp351; hydrophobic interactions with Trp383
α -Terpenyl (-)- Δ^9 - <i>trans</i> -tetrahydrocannabinolate	Δ^9 -THC	-8.0	Close to Asp351; hydrophobic interactions with Phe404
11-Acetoxy-(-)- Δ^9 - <i>trans</i> -tetrahydrocannabinolic acid A	Δ^9 -THC	-7.8	Hydrogen bonds with Glu353 and Arg394; close to Asp351; hydrophobic interactions with Phe404
8-oxo-(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinol	Δ^9 -THC	-7.8	Close to Asp351; hydrophobic interactions with Trp383
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabiphorol	Δ^9 -THC	-7.8	Close to Asp351; hydrophobic interactions with Trp383
4-Terpenyl (-)- Δ^9 - <i>trans</i> -tetrahydrocannabinolate	Δ^9 -THC	-7.3	Hydrogen bond with Asp351; hydrophobic interactions with Trp383
Δ^9 -Tetrahydrocannabinol (THC)	Δ^9 -THC	-7.1	Close to Asp351; hydrophobic interactions with Trp383
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinol-C ₄	Δ^9 -THC	-7.0	Close to Asp351; hydrophobic interactions with Trp383
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinol	Δ^9 -THC	-6.5	Hydrogen bond with Asp351; hydrophobic interactions with Trp383
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinolic acid A-C ₄	Δ^9 -THC	-5.4	Hydrogen bonds with Val534 and Asp351; hydrophobic interactions with Trp383
(-)- Δ^8 - <i>trans</i> -Tetrahydrocannabinol	Δ^8 -THC	-8.4	Close to Asp351; hydrophobic interactions with Trp383
10 β -Hydroxy- Δ^8 -tetrahydrocannabinol	Δ^8 -THC	-8.1	Hydrogen bond with Glu353; close to Asp351; hydrophobic interactions with Trp383
10 α -Hydroxy- Δ^8 -tetrahydrocannabinol	Δ^8 -THC	-7.4	Close to Asp351; hydrophobic interactions with Trp383
10 α - α -Hydroxy- <i>o</i> -oxo- Δ^8 -tetrahydrocannabinol	Δ^8 -THC	-6.4	Close to Asp351; hydrophobic interactions with Trp383
Cannabidiolic acid	Cannabidiol	-8.3	Close to Asp351; hydrophobic interactions with Trp383
Cannabidiol-C ₄	Cannabidiol	-7.8	Close to Asp351; hydrophobic interactions with Trp383
(-)-Cannabidivarin	Cannabidiol	-7.6	Close to Asp351; hydrophobic interactions with Trp383
Cannabidiol monomethyl ether	Cannabidiol	-7.4	Close to Asp351; hydrophobic interactions with Trp383
Cannabidiol (CBD)	Cannabidiol	-7.3	Close to Asp351; hydrophobic interactions with Trp383

Table 2. Cont.

Cannabinoid Name	Cannabinoid Class	Binding Affinity (kcal/mol)	Relevant Interactions
Cannabidihexol	Cannabidiol	−6.8	Close to Asp351; hydrophobic interactions with Trp383
Cannabigerol	Cannabigerol	−6.9	Possible hydrogen bond with His 524; close to Asp351
γ -Eudesmyl-cannabigerolate	Cannabigerol	−7.7	Close to Asp351; hydrophobic interactions with Trp383
Cannabineroic acid	Cannabigerol	−7.7	Hydrogen bonds with His524 and Glu353; close to Asp351; hydrophobic interactions with Trp383
5-Acetyl-4-hydroxy-cannabigerol	Cannabigerol	−7.0	Hydrogen bonds with His524 and Glu353; close to Asp351; hydrophobic interactions with Trp383 and Phe404
(-)-6,7- <i>trans</i> -Epoxy-cannabigerolic acid	Cannabigerol	−6.9	Hydrogen bonds with His524 and Ala350; close to Asp351; hydrophobic interactions with Trp383 and Phe404
(-)-6,7- <i>cis</i> -Epoxy-cannabigerolic acid	Cannabigerol	−6.9	Hydrogen bonds with His524 and Ala350; close to Asp351; hydrophobic interactions with Trp383 and Phe404
Monomethyl ether of (E)-cannabigerol	Cannabigerol	−6.8	Close to Asp351; hydrophobic interactions with Trp383
Sesquicannabigerol	Cannabigerol	−6.5	Hydrogen bonds with Asp351, Asn532, and Val534; hydrophobic interactions with Trp383
(-)-6,7- <i>trans</i> -Epoxy-cannabigerol	Cannabigerol	−6.4	Close to Asp351; hydrophobic interactions with Trp383
Cannabigerolic acid	Cannabigerol	−6.3	Close to Asp351; hydrophobic interactions with Trp383
Cannabigerovarinic acid	Cannabigerol	−6.3	Hydrogen bonds with Asp351 and Val534; hydrophobic interactions with Trp383
Camagerol	Cannabigerol	−6.0	Hydrogen bonds with Asp351 and Asn532
Monomethyl ether of cannabigerolic acid	Cannabigerol	−5.9	Close to Asp351; hydrophobic interactions with Trp383
(-)-6,7- <i>cis</i> -Epoxy-cannabigerol	Cannabigerol	−5.1	Close to Asp351; hydrophobic interactions with Trp383
Cannabinodiol	Cannabinodiol	−8.1	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
Cannabinodivirin	Cannabinodiol	−7.8	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
Cannabielsoin	Cannabielsoin	−8.1	Close to Asp351; hydrophobic interactions with Trp383
Cannabielsoin acid B	Cannabielsoin	−6.0	Hydrogen bond with His524; close to Asp351; hydrophobic interactions with Phe404
Cannabielsoin acid A	Cannabielsoin	−5.2	Hydrogen bonds with His524 and Ala350; close to Asp351; hydrophobic interactions with Trp383
Cannabicyclol	Cannabicyclol	−8.9	Close to Asp351; hydrophobic interactions with Trp383
Cannabicycloic acid	Cannabicyclol	−8.7	Hydrogen bond with His524; hydrophobic interactions with Trp383
Cannabicyclovarin	Cannabicyclol	−7.8	Close to Asp351; hydrophobic interactions with Trp383
(-)-7-Hydroxycannabichromene	Cannabichromen	−8.5	Close to Asp351; hydrophobic interactions with Phe404
(±)-4-Acetoxycannabichromene	Cannabichromene	−7.8	Hydrogen bond with Met421; close to Asp351; hydrophobic interactions with Trp383 and Phe404

Table 2. Cont.

Cannabinoid Name	Cannabinoid Class	Binding Affinity (kcal/mol)	Relevant Interactions
Cannabichromenic acid	Cannabichromen	−7.7	Close to Asp351; hydrophobic interactions with Trp383
2-Methyl-2-(4-methyl-2-pentyl)-7-propyl-2H-1-benzopyran-5-ol	Cannabichromene	−7.6	Close to Asp351; hydrophobic interactions with Phe404
Cannabichromevarin	Cannabichromen	−7.6	Close to Asp351; hydrophobic interactions with Phe404
Cannabichromevarinic acid	Cannabichromene	−7.6	Hydrogen bond with Asp351; hydrophobic interactions with Trp383
(-)-3''-Hydroxy- Δ^4 '-cannabichromene	Cannabichromen	−7.2	Close to Asp351; hydrophobic interactions with Trp383
Cannabichromene	Cannabichromene	−7.0	Close to Asp351; hydrophobic interactions with Trp383
Cannabinol	Cannabinol	−8.9	Hydrophobic interactions with Trp383 and Phe404
Cannabinol methyl ether	Cannabinol	−8.4	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
Cannabinol-C ₄	Cannabinol	−6.6	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
(10S)-Hydroxycannabinol	Cannabinol	−6.4	Hydrogen bond with Val534; close to Asp351; hydrophobic interactions with Trp383 and Phe404
8-Hydroxycannabinol	Cannabinol	−6.0	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
8-Hydroxycannabinolic acid A	Cannabinol	−5.4	Hydrogen bond with Val524; hydrophobic interaction with Phe404
(+)- <i>trans</i> -Cannabitriol-C ₃	Cannabitriol	−7.7	Close to Asp351; hydrophobic interactions with Trp383
(+)- <i>cis</i> -Cannabitriol-C ₅	Cannabitriol	−7.6	Close to Asp351; hydrophobic interactions with Trp383
(-)- <i>cis</i> -Cannabitriol-C ₅	Cannabitriol	−7.6	Close to Asp351; hydrophobic interactions with Trp383
(+)- <i>trans</i> -Cannabitriol-C ₅	Cannabitriol	−7.5	Close to Asp351; hydrophobic interactions with Trp383
(-)- <i>trans</i> -Cannabitriol-OEt-C ₃ *	Cannabitriol	−7.5	Hydrogen bond with His524; close to Asp351; hydrophobic interactions with Trp383
(-)- <i>trans</i> -Cannabitriol-C ₅	Cannabitriol	−6.8	Hydrogen bond with Met421; close to Asp351; hydrophobic interactions with Trp383
Cannabitriol	Cannabitriol	−6.5	Close to Asp351; hydrophobic interactions with Trp383
Cannabixepane	Miscellaneous	−9.2	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
(-)- Δ^9 - <i>cis</i> -(6aS,10aR)-Tetrahydrocannabinol	Miscellaneous	−8.7	Close to Asp351; hydrophobic interactions with Trp383
Dehydrocannabifuran	Miscellaneous	−8.5	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
Cannabifuran	Miscellaneous	−8.1	Close to Asp351; hydrophobic interactions with Trp383 and Phe404
10 α -Hydroxyhexahydrocannabinol	Miscellaneous	−8.0	Close to Asp351; hydrophobic interactions with Trp383
2-Geranyl-5-hydroxy-3-n-pentyl-1,4-benzoquinone	Miscellaneous	−7.9	Close to Asp351; hydrophobic interactions with Trp383
9 α -Hydroxyhexahydrocannabinol	Miscellaneous	−7.9	Close to Asp351; hydrophobic interactions with Trp383

Table 2. Cont.

Cannabinoid Name	Cannabinoid Class	Binding Affinity (kcal/mol)	Relevant Interactions
10-Oxo- $\Delta^{6a(10a)}$ -tetrahydrocannabinol	Miscellaneous	−7.7	Close to Asp351; hydrophobic interactions with Trp383
Cannabichromanone D	Miscellaneous	−7.7	Close to Asp351; hydrophobic interactions with Trp383
Cannabichromanone-C ₃	Miscellaneous	−7.5	Hydrogen bond with His524; close to Asp351; hydrophobic interactions with Trp383
Cannabicomaronome-C ₅	Miscellaneous	−7.2	Close to Asp351; hydrophobic interactions with Trp383
Cannabimovone	Miscellaneous	−7.2	Close to Asp351; hydrophobic interactions with Trp383
9 β , 10 β -Epoxyhexahydrocannabinol	Miscellaneous	−7.0	Close to Asp351; hydrophobic interactions with Trp383
10 α -Hydroxy- $\Delta^{9,11}$ -hexahydrocannabinol	Miscellaneous	−7.0	Close to Asp351; hydrophobic interactions with Trp383
10 α R-Hydroxyhexahydrocannabinol	Miscellaneous	−6.7	Close to Asp351; hydrophobic interactions with Trp383
Cannabichromanone C	Miscellaneous	−6.7	Hydrogen bond with Val534; close to Asp351; hydrophobic interactions with Phe404
(-)- Δ^7 - <i>trans</i> -(1R,3R,6R)-Isotetrahydrocannabinol-C ₅	Miscellaneous	−6.6	Hydrogen bond with His524; close to Asp351
9 α -Hydroxy-10-oxo- $\Delta^{6a,10a}$ -tetrahydrocannabinol	Miscellaneous	−6.6	Close to Asp351; hydrophobic interactions with Trp383
4-Acetoxy-2-geranyl-5-hydroxy-3-n-pentylphenol	Miscellaneous	−6.4	Close to Asp351; hydrophobic interactions with Phe404
7-Oxo-9 α -hydroxyhexahydrocannabinol	Miscellaneous	−6.4	Close to Asp351; hydrophobic interactions with Trp383
(-)-Cannabitetrol	Miscellaneous	−6.4	Close to Asp351; hydrophobic interactions with Trp383
(-)-(7R)-Cannabicomaronic acid	Miscellaneous	−6.4	Close to Asp351; hydrophobic interactions with Trp383
Cannabichromanone B	Miscellaneous	−6.4	Close to Asp351; hydrophobic interactions with Phe404
(-)-Cannabiripsol-C ₅	Miscellaneous	−6.2	Close to Asp351; hydrophobic interactions with Trp383

* Et = ethyl.

Considering the overall results observed for these two targets, 36 out of the 129 phytocannabinoids were simultaneously considered as potential AIs and ER α antagonists (Table 3, Supplementary Figure S3). However, only 7 out of those 36 selected cannabinoids, namely **CBDV**, **CBDB**, **CBDA**, **CBDM**, **CBCA**, **CBGVA**, and **CBC** (Figure 2), are commercially available and, thus, were selected for in vitro studies. Furthermore, two other cannabinoids, **CBG** and **CBN** (Figure 2), that did not show potential to act as AIs or ER α antagonists, but have growing pharmacological interest and have been studied in other breast cancer subtypes [75,76], were also included in our study. Figure 2 highlights their structural and biosynthetic relationships. The docking positions of the nine selected minor cannabinoids in aromatase, as well as the most important residues for their binding, are represented in Figure 3.

Table 3. Phytocannabinoids presenting dual functions: AI and ER α antagonist profiles. Information about the binding affinity score of the 36 cannabinoids on aromatase and ER α is presented. The information regarding CBG and CBN is also presented.

Cannabinoid Name	Cannabinoid Class	Binding Affinity—Aromatase (kcal/mol)	Binding Affinity—ER α (kcal/mol)
8-Oxo-(-)- Δ^9 - <i>trans</i> -tetrahydrocannabinol	Δ^9 -THC	-9.2	-7.8
11-Acetoxy-(-)- Δ^9 - <i>trans</i> -tetrahydrocannabinolic acid A	Δ^9 -THC	-8.3	-7.8
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinolic acid A-C ₄	Δ^9 -THC	-6.7	-5.4
(-)- Δ^9 - <i>trans</i> -Tetrahydrocannabinol	Δ^9 -THC	-3.8	-6.5
Cannabidiol (CBD)	Cannabidiol	-8.7	-7.3
(-)-Cannabidivarin (CBDV)	Cannabidiol	-7.6	-7.6
Cannabidiol monomethylether (CBDME)	Cannabidiol	-7.3	-7.4
Cannabidiol-C ₄ (CBDDB)	Cannabidiol	-6.9	-7.8
Cannabidiolic acid (CBDA)	Cannabidiol	-5.7	-8.3
Cannabimerolic acid	Cannabigerol	-6.7	-7.7
Camagerol	Cannabigerol	-6.6	-6.0
(-)-6,7- <i>cis</i> -Epoxy-cannabigerolic acid	Cannabigerol	-6.3	-6.9
Cannabigerol (CBG)	Cannabigerol	-6.1	-6.9
Cannabigerovarinic acid (CBGVA)	Cannabigerol	-5.8	-6.3
(-)-6,7- <i>trans</i> -Epoxy-cannabigerolic acid	Cannabigerol	-5.4	-6.9
5-Acetyl-4-hydroxy-cannabigerol	Cannabigerol	-5.1	-7.0
Cannabielsoin acid A	Cannabielsoin	-5.9	-5.2
Cannabielsoin acid B	Cannabielsoin	-5.1	-6.0
Cannabicyclol	Cannabicyclol	-9.8	-8.9
Cannabicyclovarin	Cannabicyclol	-9.3	-7.8
Cannabicyclic acid	Cannabicyclol	-5.5	-8.7
Cannabichromevarin	Cannabichromene	-7.1	-7.6
Cannabichromenic acid (CBCA)	Cannabichromene	-6.4	-7.7
Cannabichromene (CBC)	Cannabichromene	-6.0	-7.0
(-)-7-Hydroxycannabichromene	Cannabichromene	-5.5	-8.5
Cannabichromevarinic acid	Cannabichromene	-5.2	-7.6
8-Hydroxycannabinol	Cannabinol	-7.9	-6.0
Cannabinol (CBN)	Cannabinol	-5.9	-8.9
8-Hydroxycannabinolic acid A	Cannabinol	-4.8	-5.4
(-)- <i>trans</i> -Cannabitrinol-OEt-C ₃ *	Cannabitrinol	-3.5	-7.5
(-)- Δ^7 - <i>trans</i> -(1R,3R,6R)-isotetrahydrocannabinol-C ₅	Miscellaneous	-9.8	-6.6
Cannabimovone	Miscellaneous	-8.4	-7.2
Cannabichromanone C	Miscellaneous	-7.8	-6.7
Dehydrocannabifuran	Miscellaneous	-7.3	-8.5
Cannabichromanone B	Miscellaneous	-7.0	-6.4
(-)-(7R)-Cannabicumarononic acid	Miscellaneous	-6.5	-6.4
Cannabicumaronome-C ₅	Miscellaneous	-6.0	-7.2
Cannabichromanone-C ₃	Miscellaneous	-5.4	-7.5

* Et = ethyl.

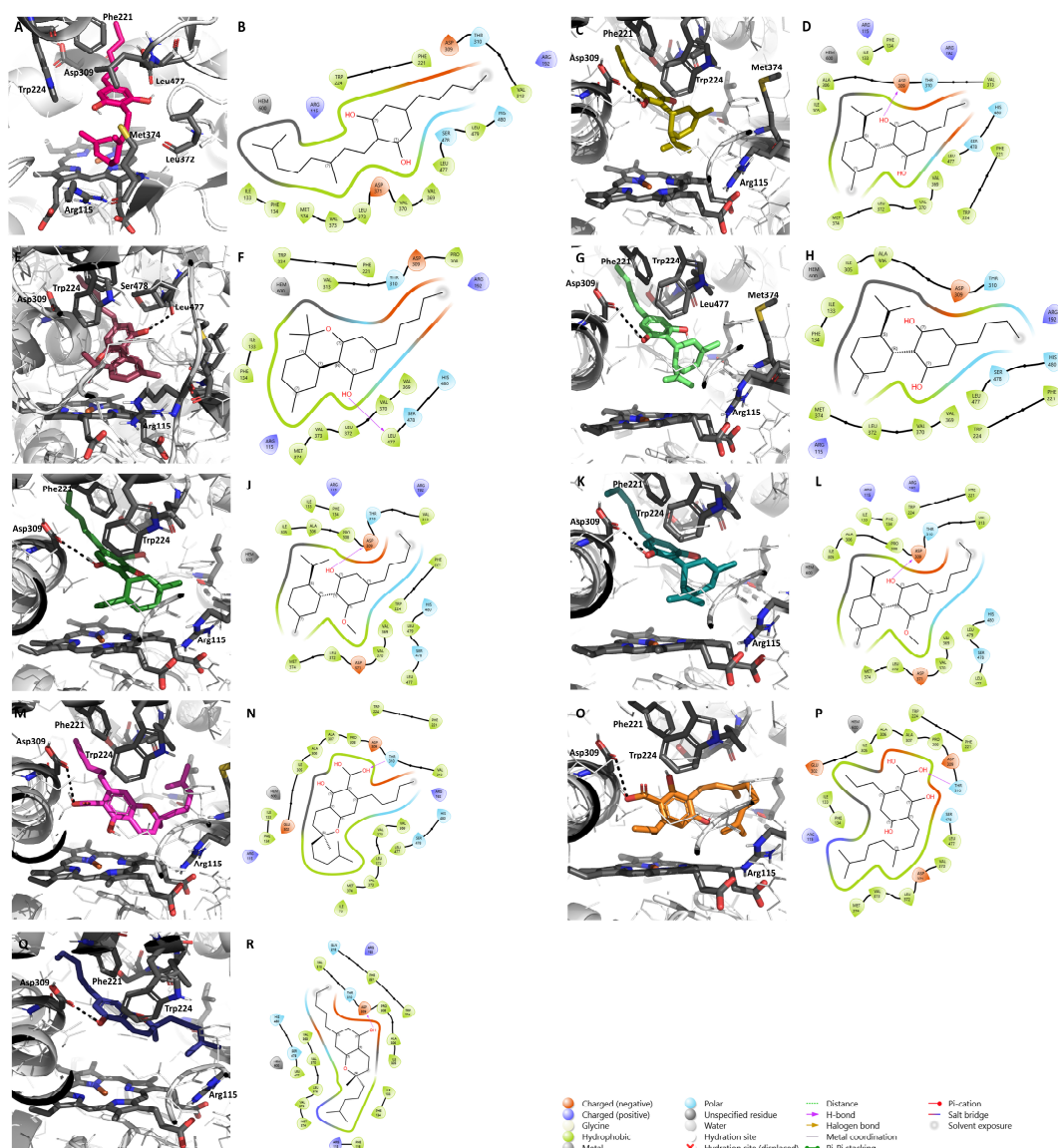


Figure 3. Molecular docking of the nine minor cannabinoids, **CBG (A,B)**, **CBDV (C,D)**, **CBN (E,F)**, **CBDB (G,H)**, **CBDA (I,J)**, **CBDM (K,L)**, **CBCA (M,N)**, **CBGVA (O,P)**, and **CBC (Q,R)**, in aromatase. The images represent both 2D and 3D aromatase/cannabinoid interactions. Aromatase structure has the PDB code 3S79 and is represented in as cartoon. The main amino acid residues of the target, including Asp309, Phe221, Trp224, Arg115, Leu372, Leu477, Ser478, and Met374, as well as the heme group, are shown as gray sticks, while the cannabinoids are shown as different colorful sticks. Hydrogen bonds are represented as black dashed lines in the 3D representations and as purple arrows in the 2D maps.

The binding of these compounds to ER α is depicted in Figure 4. **CBD (Figure 4J)** was also included for molecular docking comparison, as it acts as an ER antagonist with inverse agonist properties [44]. As target flexibility is important for the ligand/ER α binding, and in order to better understand the energetic stability and conformational pattern of the ligand/target complexes, a 10 ns MD simulation was performed based on the most stable complex structures derived from the docking studies presented in Figure 4. After the MD run, all the ligands remained in the active site in locations similar to the ones presented at the beginning of the simulation (Supplementary Figure S4). In fact, the protein–ligand complexes were clearly overlapping, demonstrating the stability of the complexes and the lack of significant conformational changes related to the ligand binding. Furthermore, the

MD simulations indicate that the complex structures are in a stable state as the potential energy at the end of the simulation is lower than the initial conformations, indicating more stability of the system (Supplementary Figure S4). As demonstrated by RMSD plots, all the ligands were stable after 2–6 ns with an RMSD value of around 2 Å, and the complex backbone acquired a stable trajectory beyond 2–6 ns with an RMSD value of 2.5–3 Å (Supplementary Figure S4).

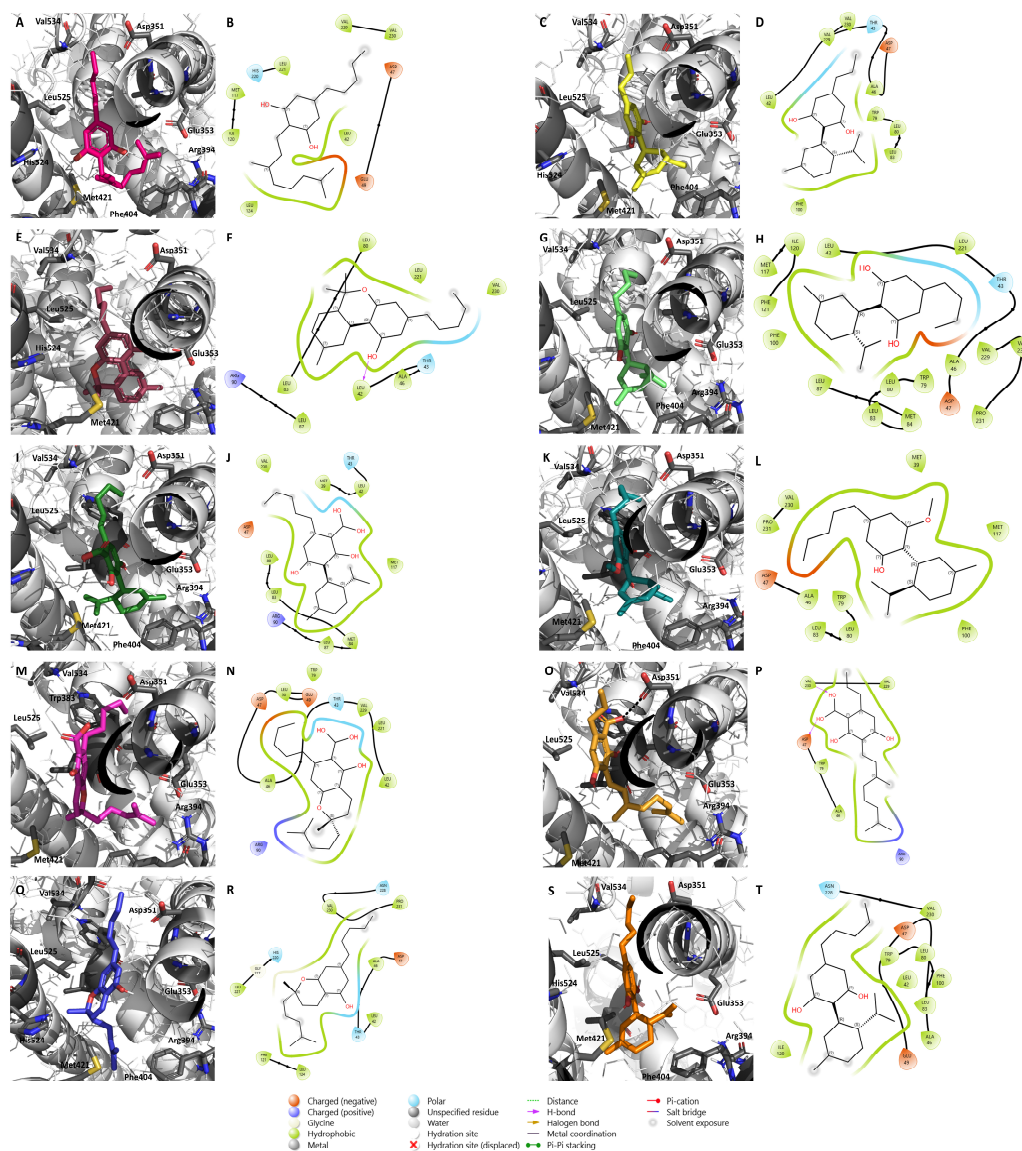


Figure 4. Molecular docking of the nine minor cannabinoids, CBG (A,B), CBDV (C,D), CBN (E,F), CBD (G,H), CBDM (K,L), CBCA (M,N), CBGVA (O,P), and CBC (Q,R), as well as CBD (S,T), in ER α . The images represent both 2D and 3D ER α /cannabinoid interactions. ER α structure was generated by the authors and is represented as cartoon. The main amino acid residues of the target, including Asp351, Glu353, Arg394, Phe404, Met421, His 524, Leu525, Val534, and Trp383, are shown as gray sticks, while the cannabinoids are shown as different colorful sticks. Hydrogen bonds are represented as black dashed lines in the 3D representations and as purple arrows in the 2D maps.

The complete MD simulation study was carried out for 10 ns, during which the ligand lost some of the interactions established in the pre-MD docked pose (Figure 4), and established new ones, as evident from Figure 5.

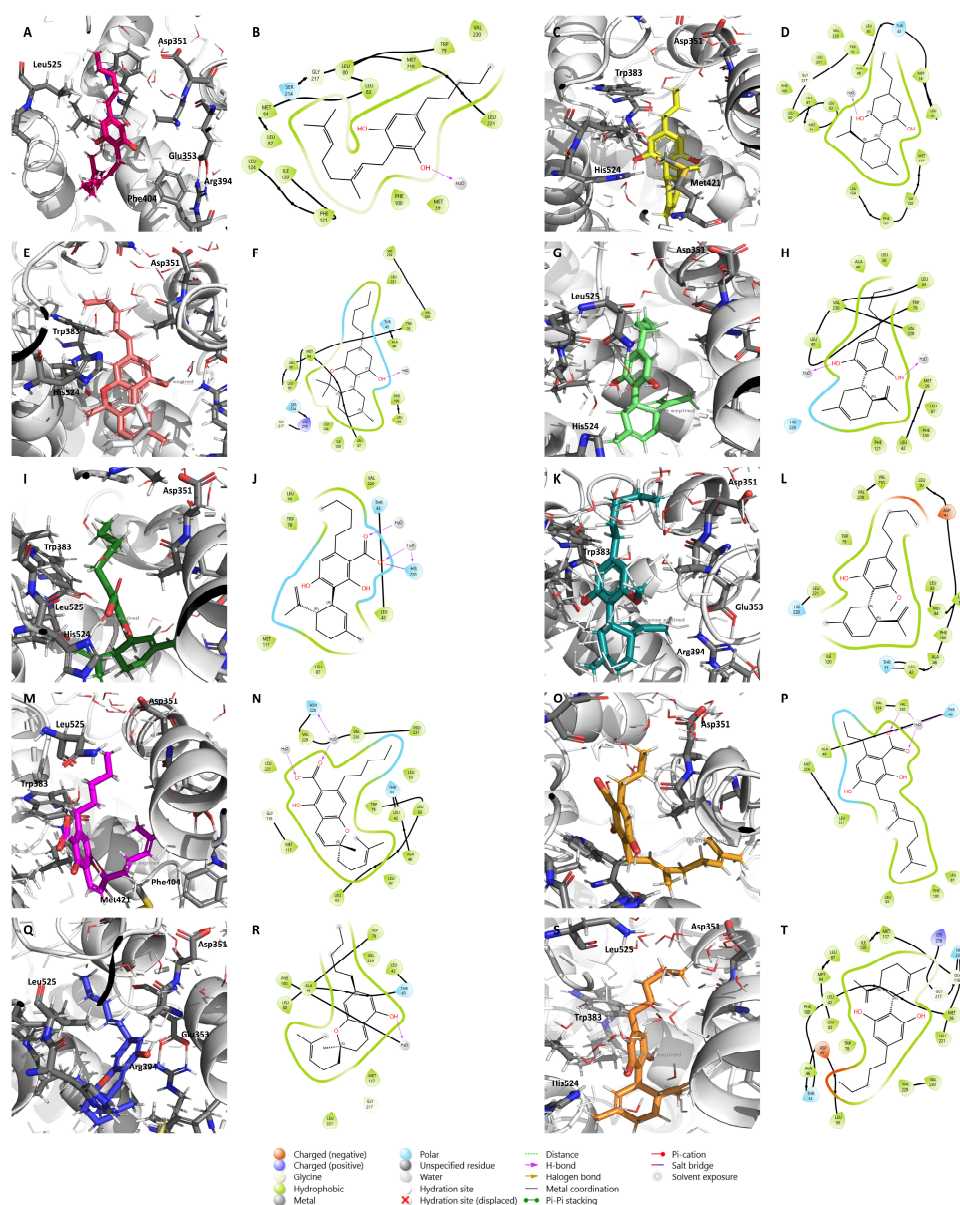


Figure 5. Molecular dynamics simulation on ER α for the nine minor cannabinoids, **CBG** (A,B), **CBDV** (C,D), **CBN** (E,F), **CBDB** (G,H), **CBDA** (I,J), **CBDM** (K,L), **CBCA** (M,N), **CBGVA** (O,P), and **CBD** (Q,R), as well as **CBD** (S,T). A molecular dynamics simulation was performed around the conformation of the small molecules obtained from the docking analysis on ER α . The main amino acid residues of the target are shown as gray sticks, while the cannabinoids are shown as colorful sticks.

The results showed that, with the exception of **CBDM** (Figure 5F), for all the other cannabinoids the complex ER α /cannabinoid acquires a position in which the cannabinoid slightly moves away from Asp351, a residue that is essential for the antagonistic activity, and gets buried in the bottom of the ER α binding site, suggesting that these compounds may not antagonize the receptor (Figure 5). However, considering the 2D maps, **CBDM** (Figure 5L) and **CBD** (Figure 5T) are complexed in the vicinity of Asp351 (referred to as Asp47 in the 2D maps), suggesting that these cannabinoids might influence the antagonistic conformation of the receptor. In fact, *in vitro* studies have already demonstrated that **CBD** displays antagonistic activity on ER [44]. Nevertheless, the cannabinoids were still able to establish some important interactions for their stability, namely with Phe404 and Trp383.

AR has been receiving a lot of attention for its role in ER $^+$ breast cancer development and, consequently, as a potential therapeutic target for this disease [24,86]. According to the

function played by this steroid receptor in sensitive ER⁺ tumors, the compounds studied should, for therapeutic purposes, act as AR agonists [87]. Therefore, we docked the nine selected cannabinoids on an agonistic structure of this receptor and the results showed that the AR binding site appears to be small to properly accommodate these cannabinoids. Nevertheless, they established interactions, mainly hydrophobic, with several residues, including Met745, Trp741, Leu704, Met895, Met342, and Thr877 (Figure 6). Furthermore, they were stabilized by hydrogen bonds with Thr877, Leu704, and Met742. Thr877 has been known to be important for the agonist's stabilization [88–90]. In fact, CBD docking in AR showed the lack of ability of this compound to interact with Thr877 (Figure 6J) and our previous in vitro studies have demonstrated that CBD acts as an AR antagonist with inverse agonist properties [44]. Following this, we postulate that CBDA, CBCA, and CBGVA, by establishing this bond with Thr877, may act as AR agonists, while the others may act as AR antagonists.

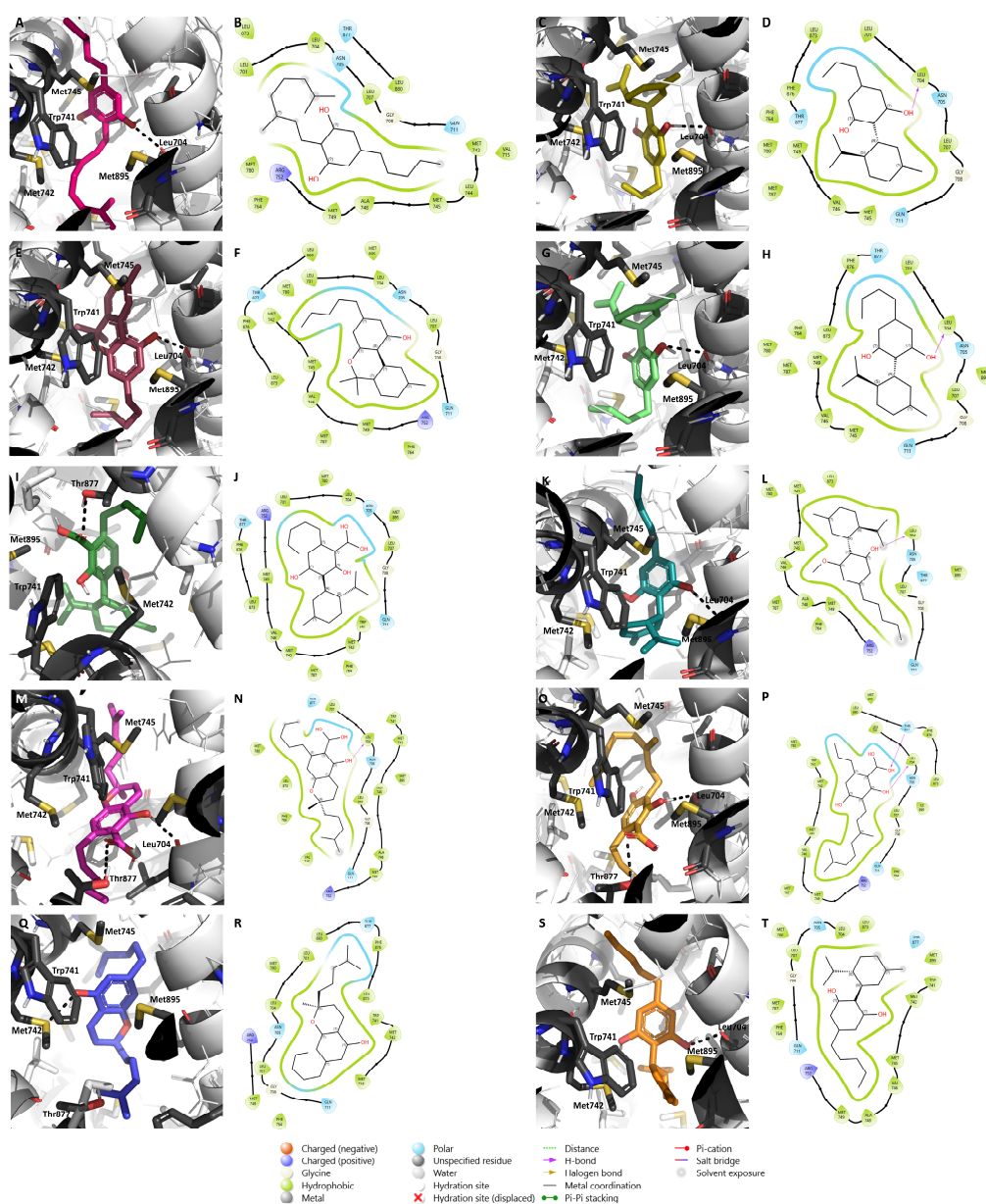


Figure 6. Molecular docking of the nine minor cannabinoids, CBG (A,B), CBDV (C,D), CBN (E,F), CBDB (G,H), CBDA (I,J), CBDM (K,L), CBCA (M,N), CBGVA (O,P), and CBD (Q,R), as well as CBD (S,T), in AR. The images represent both 2D and 3D AR/cannabinoid interactions. AR structure

has the PDB code 2AMA and is represented in as cartoon. The main amino acid residues of the target, including Met745, Leu704, Trp741, Met895, Met742, and Thr877, are shown as gray sticks, while the cannabinoids are shown as different colorful sticks. Hydrogen bonds are represented as black dashed lines in the 3D representations and as purple arrows in the 2D maps.

2.2. Effects of the Cannabinoids in Aromatase

Since our docking analysis suggested that the seven minor cannabinoids selected had the potential to inhibit aromatase, a radiometric assay was performed to confirm these assumptions, using human placental microsomes, an aromatase enriched matrix [26]. The anti-aromatase activity of the compounds **CBG** and **CBN**, as well as **CBD**, was also evaluated in this assay. The reference AIs used in a clinic, Ana, Let, and Exe, were used as positive controls. Our results showed that none of the minor cannabinoids significantly inhibited aromatase, 12% (**CBDV**) being the highest anti-aromatase activity value determined (Table 4). As expected, **CBD**, at 10 μM , presented an anti-aromatase activity of 83.23% (Table 4). In accordance with our previous studies [25,26,91–93], the reference AIs induced a high anti-aromatase activity (>98%) (Table 4).

Table 4. Percentages of anti-aromatase activity obtained for the cannabinoids under study.

Cannabinoid	Aromatase Inhibition (%) \pm SEM	Binding Affinity—Aromatase (kcal/mol)
CBC	8.9 \pm 1.7	−6.0
CBCA	3.0 \pm 0.9	−6.4
CBD	83.2 \pm 0.6	−8.7
CBDA	3.4 \pm 1.3	−5.7
CBDB	6.4 \pm 3.6	−6.9
CBDM	4.5 \pm 2.8	−7.3
CBDV	12.0 \pm 2.5	−7.6
CBG	3.6 \pm 2.3	−6.1
CBGVA	7.8 \pm 0.9	−5.8
CBN	3.8 \pm 0.5	−5.9
Ana	98.8 \pm 0.2	−8.2
Let	99.4 \pm 0.2	−7.3
Exe	98.4 \pm 0.3	−8.2

Microsomes (20 μg) were incubated with NADPH (15 mM), each cannabinoid (10 μM), and [1β - ^3H]-androstenedione (40 nM), during 15 min at 37 $^\circ\text{C}$. Results are presented as a percentage of tritiated water released, in relation to the control, and are represented as the mean \pm SEM of three independent experiments carried out in triplicate. The reference AIs, Ana and Let, at 1 μM , were used as positive controls.

2.3. Effects of Cannabinoids in Estrogen Receptor (ER)

For the evaluation of the effects of cannabinoids on ER activity, the VM7Luc4E2 cell line was treated for 24 h with each phytocannabinoid (1–10 μM) in the presence (ER antagonism) or absence (ER agonism) of E_2 (91.8 pM) or T (1 nM). Our results (Figure 7) demonstrated that, in the absence of E_2 or T, **CBN** ($p < 0.05$, $p < 0.01$, $p < 0.001$; Figure 7C), **CBDA** ($p < 0.01$; Figure 7E), **CBCA** ($p < 0.05$; $p < 0.01$; $p < 0.001$; Figure 7G), and **CBC** ($p < 0.05$; $p < 0.01$; Figure 7I) presented a negative effect for agonism, whereas **CBDV** ($p < 0.001$; Figure 7B), **CBDB** ($p < 0.001$; Figure 7D), and **CBDM** ($p < 0.001$; Figure 7F) presented a positive effect and thus exhibited ER agonist activity. Of note, **CBG** (Figure 7A) and **CBGVA** (Figure 7H) did not exert any significant effect on the activity of this receptor. A reduction in VM7Luc4E2 cell viability for these conditions was observed for **CBDV** ($p < 0.01$; Supplementary Figure S5B), **CBN** ($p < 0.001$; Supplementary Figure S5C), **CBDB** ($p < 0.01$; $p < 0.001$; Supplementary Figure S5D), and **CBDM** ($p < 0.05$; $p < 0.01$; Supplementary Figure S5F). In the presence of E_2 , for ER antagonism evaluation, a signifi-

cant decrease in relation to the control value was only observed for 5 and 10 μM of **CBN** ($p < 0.001$; Figure 7C), and for **CBDB** ($p < 0.001$; Figure 7D), and **CBC** ($p < 0.05$; Figure 7I), both at 10 μM , suggesting that these compounds act as ER antagonists. For the remaining cannabinoids under study, no significant differences were observed (Figure 7). However, it is important to consider that at these conditions, contrary to **CBG** and **CBGVA**, a significant reduction ($p < 0.05$; $p < 0.01$; $p < 0.001$; Supplementary Figure S5) in cell viability was detected, which may influence the transactivation results. When the antagonism was addressed in the presence of T instead of E_2 , different behaviors were observed. Regarding **CBDV** ($p < 0.01$; $p < 0.001$; Figure 7B), **CBDB** ($p < 0.001$; Figure 7D), and **CBDM** ($p < 0.05$; $p < 0.01$; $p < 0.001$; Figure 7F), no effects were noted for the antagonism over T. On the other hand, **CBN** at 10 μM ($p < 0.001$; Figure 7C), **CBDA** at 1 and 10 μM ($p < 0.05$; $p < 0.001$; Figure 7E), and **CBC** at 10 μM ($p < 0.05$; Figure 7I) acted as ER antagonists under these conditions. No significant effects were detected for **CBG** (Figure 7A), **CBCA** (Figure 7G), and **CBGVA** (Figure 7H). Nevertheless, **CBDV** ($p < 0.05$; $p < 0.001$; Supplementary Figure S5B), **CBN** ($p < 0.001$; Supplementary Figure S5C), **CBDB** ($p < 0.01$; $p < 0.001$; Supplementary Figure S5D), **CBDM** ($p < 0.05$; $p < 0.01$; $p < 0.001$; Supplementary Figure S5F), and **CBC** ($p < 0.05$; $p < 0.001$; Supplementary Figure S5I) reduced cell viability under these conditions. As previously reported by our group, **CBD** acts as an ER antagonist, with inverse agonist properties [44].

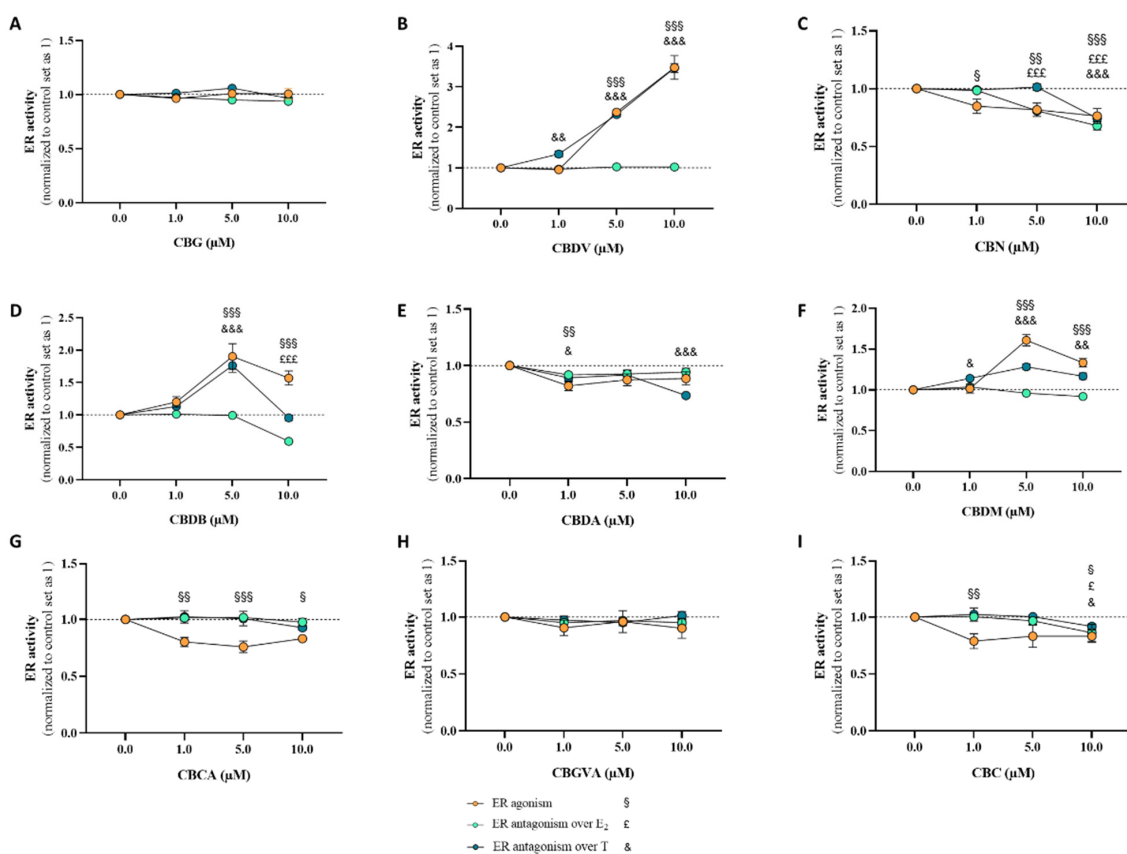


Figure 7. Transactivation assays for the determination of ER α agonist/antagonist activity induced by the nine minor cannabinoids, **CBG** (A), **CBDV** (B), **CBN** (C), **CBDB** (D), **CBDA** (E), **CBDM** (F), **CBCA** (G), **CBGVA** (H), and **CBC** (I). VM7Luc4E2 cells were treated with the cannabinoids (1, 5, and 10 μM) in the absence (ER α agonism) or presence (ER α antagonism) of testosterone (T; 1 nM) or estradiol (E₂; 91.8 pM) for 24 h. Results are presented as the mean \pm SEM of at least three independent experiments performed in triplicate. Statistically significant differences between the control (cells not exposed to cannabinoids), set as 1, and cells not treated with T or E₂ are expressed as § ($p < 0.05$), §§ ($p < 0.01$), and §§§ ($p < 0.001$), while the differences between the control and cells

treated with cannabinoids in the presence of E₂ are expressed as £ ($p < 0.05$) and £££ ($p < 0.001$), and the differences between cells treated with cannabinoids in the presence of T are expressed as & ($p < 0.05$), && ($p < 0.01$), and &&& ($p < 0.001$).

2.4. Effects of Cannabinoids in Androgen Receptor (AR)

The activity of the nine minor cannabinoids towards AR was assessed through the AR-EcoScreen™ assay. The cells were treated with the cannabinoids (1–10 µM) for 24 h in the presence (antagonism) or absence (agonism) of R1881 (0.1 nM). The results demonstrated that all the studied cannabinoids caused no AR agonism ($p < 0.05$; $p < 0.01$; $p < 0.001$; Figure 8). On the contrary, all the nine cannabinoids exerted AR antagonistic activity, suggesting that they act as AR antagonists ($p < 0.01$; $p < 0.001$; Figure 8). **CBG** ($p < 0.001$; Figure 8A), **CBN** ($p < 0.001$; Figure 8C), **CBDB** ($p < 0.001$; Figure 8D), and **CBC** ($p < 0.01$; $p < 0.001$; Figure 8I) antagonistic activities were verified for all the concentrations studied, while for **CBDV** ($p < 0.001$; Figure 8B), **CBDA** ($p < 0.001$; Figure 8E), **CBDM** ($p < 0.001$; Figure 8F), and **CBCA** ($p < 0.001$; Figure 8G), the AR antagonistic activity was only observed at 5 and 10 µM and for **CBGVA** ($p < 0.001$; Figure 8H), only at 10 µM. In addition, contrary to **CBGVA** for which an increase in the luciferase activity signal was verified at 10 µM ($p < 0.01$; $p < 0.001$), which might be due to cell proliferation, all the other treatments slightly reduced cell viability ($p < 0.05$; $p < 0.001$), mainly at 10 µM (Supplementary Figure S6). As previously reported by our group, **CBD** acts as an AR antagonist, with inverse agonist properties [44].

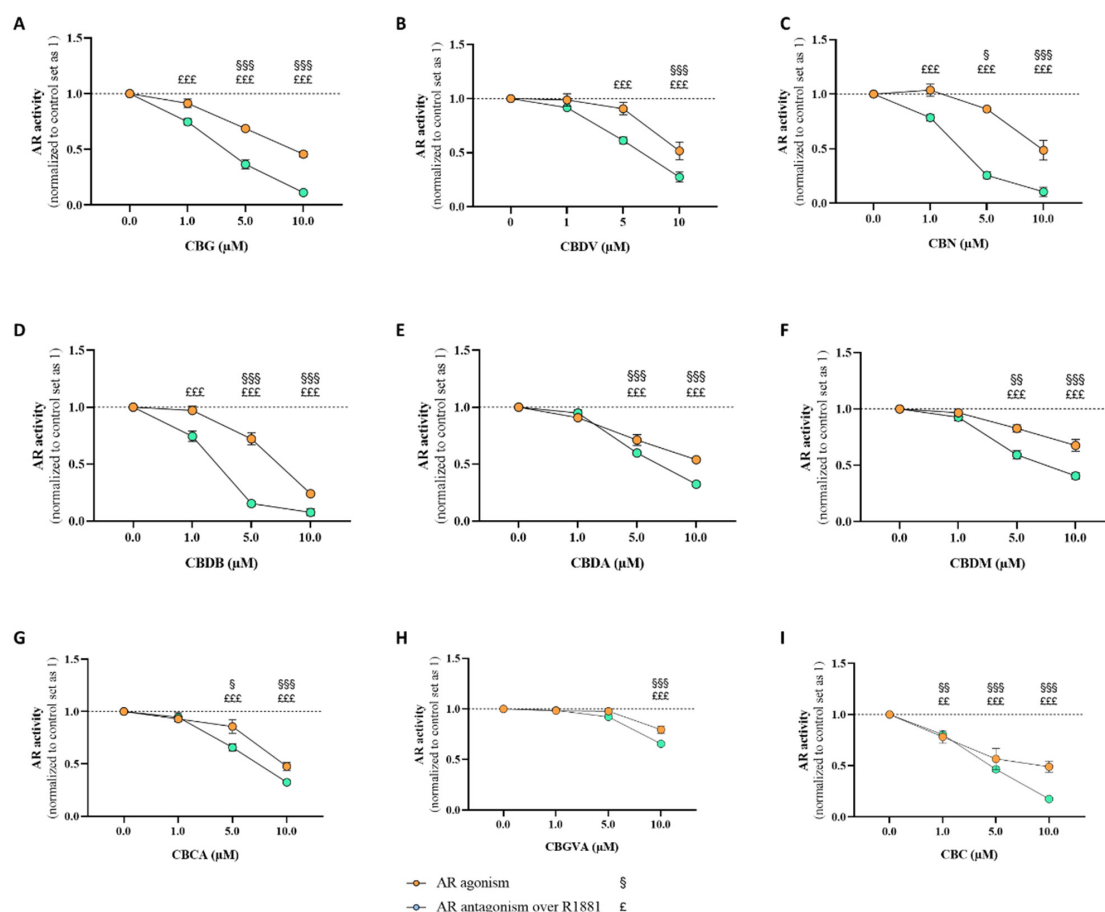


Figure 8. Transactivation assays for the determination of AR agonist/antagonist activity induced by the nine minor cannabinoids, **CBG** (A), **CBDV** (B), **CBN** (C), **CBDB** (D), **CBDA** (E), **CBDM** (F), **CBCA** (G), **CBGVA** (H), and **CBC** (I). CHO-K1 cells were treated with the cannabinoids (1, 5, and 10 µM) in the absence (AR agonism) or presence (AR antagonism) of R1881 (0.1 nM) for 24 h. Results are presented as the mean ± SEM of at least three independent experiments performed in triplicate.

Statistically significant differences between the control (cells not exposed to cannabinoids), set as 1, and cells not treated with R1881 are expressed as § ($p < 0.05$), §§ ($p < 0.01$), and §§§ ($p < 0.001$), while the differences between the control and cells treated with cannabinoids in the presence of R1881 are expressed as ££ ($p < 0.01$) and £££ ($p < 0.001$).

2.5. Scores and Ranking of the Cannabinoids Using ToxPi

The data regarding the scores of the docking in aromatase, ER, and AR, as well as aromatase inhibition and ER and AR agonistic/antagonistic activities of the nine studied cannabinoids and CBD were added to ToxPi and used to score and rank the compounds overall. As expected, **CBD** obtained the best ToxPi score (0.7121) mainly due to its aromatase inhibition results, score of the docking in aromatase, ER antagonistic activity over T, and AR inverse agonistic and antagonistic activities. Regarding the minor phytocannabinoids, **CBDB** scored the best (0.5248) because of the high values determined for ER antagonistic activity over E₂ and AR docking score, as well as AR inverse agonistic and antagonistic activities. **CBN** ranks in third place with a ToxPi score of 0.4864 for which ER and AR docking scores, ER antagonism over E₂ and T, and AR antagonistic activity contributed the most. The scores for the remaining minor cannabinoids were mainly determined by AR modulation, except for **CBDA**, in which ER modulation contributed significantly, and for **CBDM**, where the aromatase binding score was also relevant. The cannabinoid with the worst ToxPi score was **CBGVA** (0.1219). The overall rank and ToxPi scores are presented in Figure 9.

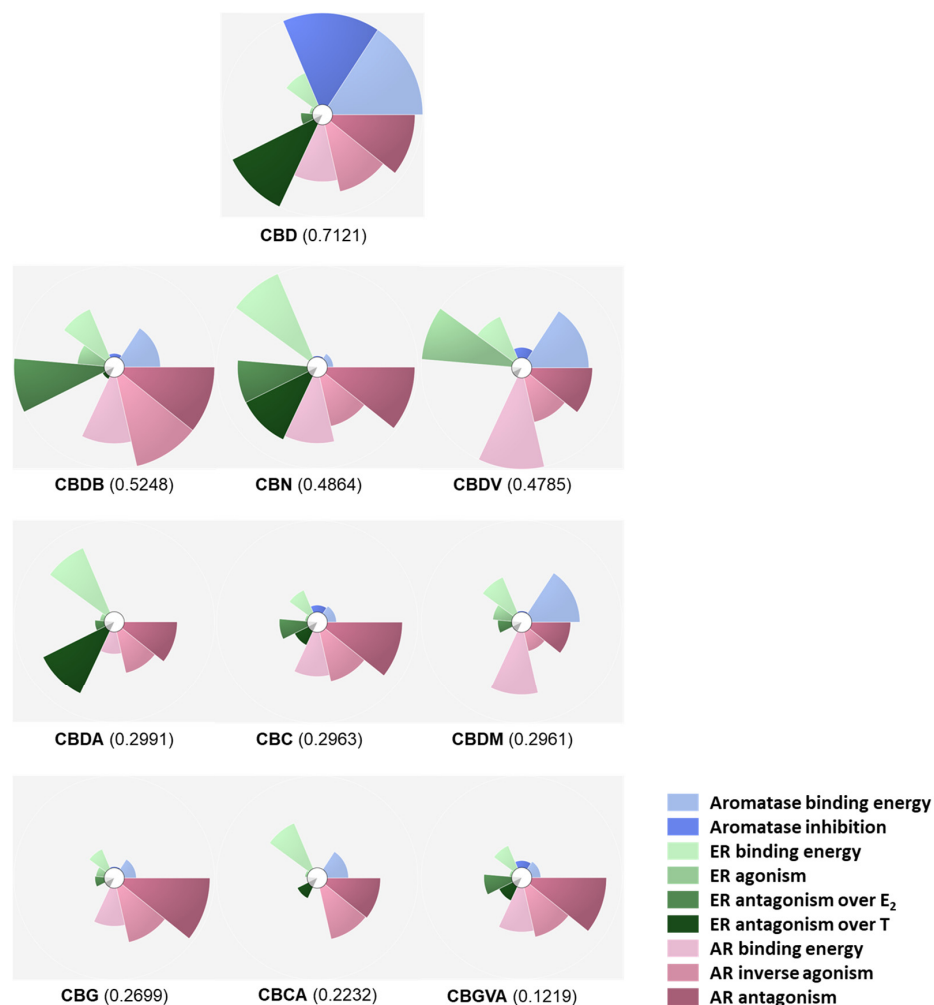


Figure 9. ToxPi scores and ranks. The information regarding the docking analysis in aromatase, ER, and AR, as well as the information about aromatase inhibition and ER and AR agonistic/antagonistic

activities for the nine selected cannabinoids and **CBD**, was inserted in different slices in ToxPi and used to rank the compounds.

3. Discussion

The use of endocrine therapies, such as AIs and anti-estrogens, for ER⁺ breast cancer treatment has been facing concerns and limitations mainly due to endocrine resistance development, which has led to a search for their combination with other innovative therapies. However, these therapies also cause resistance [13,94–96], which is the reason why the discovery and development of novel therapeutic approaches are necessary. Various studies on the anti-tumor effects of cannabinoids in different cancer forms have been performed, showing promising results. Indeed, our group has demonstrated that **THC** and **CBD** decrease aromatase and ER α protein levels in ER⁺ breast cancer cells and that **CBD** can also inhibit aromatase [42] and presents ER and AR antagonistic, as well as inverse agonist, properties, in both receptors [44]. Other studies reported that **THC** presents anti-proliferative effects in ER⁺ breast cancer cells independent of ER and AR [63], although having the ability to impair ER α signaling by up-regulating ER β [55]. Moreover, it was already described that **THC** and **CBD** exert no ER agonistic activity [62]. Considering all this, the ability of the known 129 phytocannabinoids to modulate key targets associated with ER⁺ breast cancer progression was investigated in this study.

Due to its fundamental role in local estrogen production and tumor development, aromatase was the first target studied. Our *in silico* studies predicted that 45 out of the 129 phytocannabinoids may act as AIs. Besides the binding affinity score, one of the reasons for their selection was the interactions that they, in theory, manage to establish with this enzyme, such as a hydrogen bond with the Asp309 residue, considered fundamental for the aromatization reaction [84,85]. In fact, the AIs used in the clinic do bind to this key residue, thereby presenting high anti-aromatase activity [83,97,98]. ER α , a key target that through estrogen binding promotes the signal transduction necessary for tumor growth and survival, was also explored. In this case, 85 cannabinoids out of the 129 showed important binding features that led us to consider them as potential ER α antagonists. One of the most important features taken into consideration was their ability to be localized in the vicinity of helix 12, a flexible helix of ER α that, upon antagonist binding, prevents the binding of coactivators, compromising receptor activation [99]. On the other hand, their possible proximity and establishment of hydrogen bonds with Asp351, a residue close to helix 12 and to which antagonists typically bind, were also taken into account [6]. Considering these results, it is possible to suggest that, theoretically, cannabinoids have a higher potential to bind and act as ER α antagonists than as AIs. Furthermore, 36 compounds out of the 45 potential AIs and of the 85 potential ER antagonists were simultaneously considered as both promising AIs as well as ER α antagonists, suggesting that they may act as multi-target compounds in ER⁺ breast cancer. In fact, the importance of multi-target compounds has been pointed out by several authors [6,13,91,100–104], since by having the ability to simultaneously modulate different targets, they may exhibit fewer side effects. Additionally, our group has previously verified that aromatase, ER α , and ER β binding sites present some similarities, reinforcing the possible application of multi-target compounds in this disease [6].

However, for *in vitro* studies, we focused our attention on only 7 out of the 36 cannabinoids, **CBDV**, **CBDB**, **CBDM**, **CBDA**, **CBCA**, **CBGVA**, and **CBC**, as the remaining were not commercially available. Additionally, despite the absence of *in silico* evidence of a relevant modulation of aromatase and ER α , **CBG** and **CBN** were included in our study, as some studies in different tumors, including triple-negative breast cancer, have pointed out their therapeutic potential as anti-cancer compounds [75,76]. Regarding aromatase activity, we confirmed that **CBG** and **CBN** do not inhibit this enzyme. However, none of the other seven cannabinoids were able to greatly inhibit aromatase (only up to 12% inhibition). **CBD**, as expected and corroborating our previous work [65], presented high anti-aromatase activity. In fact, our previous molecular docking studies suggested the binding

of **CBD** to key aromatase residues [65] and herein, **CBD** displayed the best docking score (-8.7 kcal/mol), followed by **CBDV** (-7.6 kcal/mol), which was found to inhibit aromatase by 12% at 10 μ M. For aromatase inhibition, among the investigated cannabinoids, the presence of a carboxylic acid seems detrimental for activity (comparing, for example, **CBG** with **CBGVA**) and slight modifications in the hydrophobic tail of the cannabidiol type of metabolites influence the affinity for the enzyme, as evidenced when comparing **CBDV** (C_3) with its homologues **CBDB** (C_4) and **CBDM** (C_5).

In relation to ER α , different results were obtained for the nine studied phytocannabinoids. According to our transactivation results, cannabidiol derivatives **CBDV**, **CBDB**, and **CBDM** are ER α agonists, with **CBDV** and **CBDB** presenting full agonist activity properties (i.e., 75-fold increase over basal response [105]). The ER agonist activity verified for these cannabinoids is not in line with previous studies that, based on **THC** and **CBD** activities, indicated that cannabinoids do not exhibit ER agonist activity [62]. Although this agonist activity is not attractive for ER $^+$ breast cancer cases, it may be clinically relevant in other pathological conditions, such as neurodegenerative disorders, liver injuries, or cardiovascular diseases, where a beneficial action should not be ruled out [106,107]. On the other hand, **CBN**, **CBDA**, **CBCA**, and **CBC** may potentially act as ER inverse agonists, which may be beneficial for ER $^+$ breast cancer cases since, by presenting opposite actions to ER agonists, they prevent the tumorigenic effects of ER α . These results correlate with *in silico* studies in which **CBDA** (-8.3 kcal/mol) presented the highest affinity for the ER. For ER inverse agonism, cyclization, particularly chromene formation, was important for activity, as in the case of cannabichromene derivatives **CBC** and **CBCA**, and for chromane **CBN**. Moreover, except for the linear **CBGVA**, the carboxylic acid derivatives investigated (**CBCA**, **CBDA**) were active against this receptor.

Nevertheless, the behavior exhibited by the phytocannabinoids changes under hormone influence. Contrary to **CBDV** that loses ER agonistic activity, **CBDB** and **CBDM** become ER antagonists in the presence of E_2 . In the presence of T, **CBDA** maintains ER α antagonist activity, while in the presence of E_2 , this activity is abolished. These different behaviors can be explained by the binding affinities to ER α in the presence of the different hormones. Moreover, the fixed E_2 concentration (91.8 pM) used for the assessment of antagonistic activity induces the maximum activation of the receptor, which might be too high to detect activity of weaker antagonistic compounds. On the other hand, antagonistic activities in the presence of T (1 nM) might be more notable due to the concentration of T used, which is not associated with maximum effects. Curiously, **CBDB** fails as an ER antagonist in the presence of T. In both conditions, **CBN** and **CBC** act as ER α antagonists with inverse agonist properties, though this effect was only observed at the highest concentration for the latter compound. As previously reported, this behavior was similar to that of **CBD** [44]. This represents a therapeutic advantage for ER $^+$ breast cancer and other clinical conditions that may be treated with ER α antagonists [108]. Of all the studied cannabinoids, only the two representatives of the cannabigerol type, the biosynthetic precursor **CBGVA** and **CBG**, showed no effect on ER activity, highlighting the importance of cyclization features for ER activity.

As previously mentioned, AR is gaining significant therapeutic attention in breast cancer, with some AR-target therapies being studied in different models. In fact, AR activation can modulate other receptors, such as ER and HER2 [109]. Regarding ER $^+$ breast cancer and considering the beneficial effect of AR in those cases, the use of AR agonists would benefit the treatment of this disease, in a non-resistant scenario [20,87]. Unfortunately, our results, both *in silico* and *in vitro*, revealed that the nine cannabinoids studied acted as AR antagonists with inverse agonist properties, a behavior similar to the one observed for **CBD** [44]. This result is in accordance with some other studies that have pointed out that drugs of abuse, such as marijuana, by preventing the binding of dihydrotestosterone to AR, present AR antagonist activity [110,111]. Furthermore, due to the nature of this steroid receptor, almost only steroid hormones can act as AR agonists. Nevertheless, and despite the apparently disadvantageous effects of these compounds on

AR, when ER is not overexpressed or activated in tumors, AR displays pro-survival and tumorigenic roles, contributing to tumor development [24,112]. This scenario is frequently found in resistant stages, which makes the use of AR antagonists an attractive approach. Thus, our data suggest that cannabinoids, by acting as AR antagonists with inverse agonist properties, might be a beneficial therapy in resistant scenarios, or might even impair the AR oncogenic role known for ER⁺ breast cancer cells treated with Exe [24]. In fact, there are some ongoing clinical trials with AR antagonists and AIs or anti-estrogens for breast cancer treatment [113,114]. Furthermore, by acting as AR antagonists, the studied cannabinoids may also be attractive for other pathological conditions where AR antagonists could be clinically applied, such as prostate cancer and benign prostatic hyperplasia [115,116]. Moreover, some triple-negative breast tumors show dependence on AR signaling for growth and survival [117]. In fact, two AR antagonists, Bicalutamide and Enzalutamide, were already evaluated in clinical trials (NCT00468715, NCT01889238) [118–120]. Therefore, the use of the minor phytocannabinoids evaluated in this study may also be beneficial for the management of this breast cancer subtype.

By using ToxPi metrics, we confirmed the previous assumption that **CBD** is the best cannabinoid when the simultaneous action towards aromatase, ER, and AR is considered, which highlights its therapeutic potential for ER⁺ breast cancer. The best minor phytocannabinoid is **CBDB**, a **CBD** derivative, mainly due to its great ER antagonistic activity over E₂ and its AR inverse agonistic and antagonistic activities. Similarly, the second best minor phytocannabinoid is **CBN**, whose score is also a result of its good scores on ER and AR molecular docking, but also on ER and AR antagonistic activities. Thus, considering that the effects exhibited by **CBD** on aromatase and ER surpass the ones induced on AR, which was not verified for the other cannabinoids, we can conclude that the scores attributed to the minor cannabinoids are mainly determined by the modulation of AR. Moreover, as formerly mentioned, ER antagonism is a crucial therapeutic action to be considered for ER⁺ breast cancer treatment, reason why we postulate that **CBDB** and **CBN** might be the most promising minor phytocannabinoids for hormone-dependent breast cancer treatment, along with the major phytocannabinoid **CBD**. Carboxylic acid derivatives, such as **CBGVA** and **CBCA**, occupy the last positions, indicating that this structural function is not beneficial overall. In the future, the study of these compounds in different breast cancer and non-cancer models will be of paramount importance to fully address the therapeutic potential of cannabinoids in breast cancer and guide their eventual application in the clinic.

4. Materials and Methods

4.1. Molecular Docking

A molecular docking analysis was performed to investigate the binding of 129 phytocannabinoids to aromatase, ER α , and AR. Considering mainly their resolution value, length, and absence of mutations, and the complexed ligand, the PDB structures 3S79 and 2AMA were chosen for aromatase [121] and AR [122] studies, respectively. In addition, a molecular docking was performed for each target using the ligands already reported for them, as inhibitors, antagonists, and natural substrates, as well as the respective decoys in order to validate the docking program (data not presented in the manuscript). In relation to aromatase structure and considering different studies suggesting that the Asp309 residue, crucial for the aromatization reaction, should be protonated [84,123], this residue, as well as Asp371, were considered neutral, as previously described [91]. Regarding ER α structure, the model used was generated using different and complementary structures, as previously described [91]. The structures of the compounds were either collected from ChEMBL [124] or designed using Marvin (ChemAxon, Budapest, Hungary). Their charges and configurations were further corrected using AutodockTools [125] and the molecular docking was performed using PyRx 0.8 software [126]. For each molecular target, a grid box with no more than 30 × 30 × 30 (x, y, z) dimensions was placed in the ligand binding site, covering all the important residues and considering the position of the original ligand. A maximum of nine poses for each compound was generated and the chosen ones were

selected taking into account the score value and the interaction between the compounds and the targets. Additionally, 2D and 3D maps representing the interactions between the targets and the cannabinoids were generated in Maestro 5.9 (Schrödinger Release 2024-3: Maestro, Schrödinger, LLC, New York, NY, USA, 2024) and PyMol 2.5.7 (Schrödinger, LLC, New York, NY, USA, 2020), respectively.

4.2. Molecular Dynamics Simulation

For molecular dynamics (MD) simulation, a 5 Å spherical droplet containing 100 water molecules was placed surrounding the conformation of the small molecules obtained from the docking study on ER α ; the complexes were energy-minimized using the MMFF94x force field until an RMS gradient < 0.1 kcal/Å/mol. The ligand/macromolecule complexes were then subjected to MD simulation using MOE-dynamic implemented in MOE 2014.09 (Chemical Computing Groups, Montreal, QC, Canada). MD simulation was performed by choosing the MMFF94x force field and NVT (N, total atom; V, volume; T, temperature) ensemble and Nosé–Poincaré–Andersen (NPA) algorithm, with a 0.002 ps time step and sampling every 0.5 ps. The system was heated from 0 K to 300 K in 100 ps (heat stage), followed by 10,000 ps of a production stage at 300 K; the system was then cooled back to 0 K in 100 ps (cooling stage). The potential energy of the system and the root mean square deviation (RMSD) of the ligand were used to keep track of the system's behavior during the simulation. Simulation observation was performed by examining the ligand/macromolecule complex interaction between ligand atoms and target atoms at the end of the simulation. This analysis was carried out for the nine cannabinoids selected, as well as for **CBD**.

4.3. Anti-Aromatase Activity

Considering the molecular docking results, the anti-aromatase activity of the nine selected minor cannabinoids, cannabigerol (**CBG**), cannabidivarin (**CBDV**), cannabinol (**CBN**), cannabidiol-C4 (**CBDB**), cannabidiolic acid (**CBDA**), cannabidiol monomethyl ether (**CBDM**), cannabichromenic acid (**CBCA**), cannabigerovarinic acid (**CBGVA**), and cannabichromene (**CBC**; Figure 2), was assessed through a radiometric assay by measuring the tritiated water released from [1 β -³H]-androstenedione (PerkinElmer Life Sciences, Boston, MA, USA), using human placental microsomes, according to Thompson and Siteri [127] and Heidrich et al. [128] modified methods [26]. This radiometric assay is the one recommended by OCSPP Guideline 890.1200 for aromatase activity assessment [129]. Despite the previously reported anti-aromatase activity of **CBD** [65], it was also assessed here at the same concentration used for the minor cannabinoids for comparison purposes. Each compound was diluted in a 67 mM potassium phosphate buffer (pH 7.4) and the aromatization reaction was performed using 20 μ g of microsomal protein, 15 μ M of NADPH, 40 nM of [1 β -³H]-androstenedione, and 10 μ M of each phytocannabinoid in a final reaction volume of 500 μ L at 37 °C, during 15 min, as previously described [26]. Then, the samples were transferred to scintillation tubes containing a liquid scintillation cocktail (ICN Radiochemicals, Irvine, CA, USA), and scintillations were then counted in a liquid scintillation counter (LKB Wallac 1209 Rackbeta, LKB Wallac, Turku, Finland). The tritiated water released from [1 β -³H]-androstenedione was used as an index of estrogen formation [26].

Stock solutions of each cannabinoid were prepared in 100% DMSO and stored at –20 °C. All the experiments were performed in triplicate in at least three independent experiments. Ana, Let, and Exe at 1 μ M were used as reference AIs.

4.4. ER and AR Transactivation Assays

Considering the molecular docking results, the activity of the nine selected cannabinoids towards human ER and AR was assessed as previously described [44,100], and according to the guidelines from The Organization for Economic Cooperation and Development (OECD) for Testing of Chemicals, Tests No. 455 and 458, respectively. These bioassays are based on stably transfected mammalian cell lines and validated for a reliable

detection of human ER and AR agonists and antagonists. Regarding the ER assay, we used the VM7Luc4E2 cells, which were kindly provided by Michael Denison (University of California, USA). These cells express both human ER α and ER β isoforms and were cultured in DMEM without phenol red, supplemented with 4.5% CFBS, 1% penicillin/streptomycin, 2% L-glutamine, and 110 mg/mL sodium pyruvate for 3 days before the beginning of the experiments, and then plated at a 4×10^5 cells/mL cell density in white 96-well plates. After adhesion, cells were treated with the cannabinoids (1–10 μ M) for 24 h, in the absence (ER agonism) or presence of 91.8 pM 17 β -estradiol (E₂; ER antagonism) or 1 nM testosterone (T; ER antagonism). The agonistic and antagonistic activities were measured using the Steady-Glo[®] Luciferase Assay System (Promega Corporation, Madison, WI, USA) in a multimode plate reader (EnSpire[®], Perkin Elmer, Inc., Waltham, MA, USA). Cell viability was assessed with the CellTiter-Glo[®] Luminescent Cell Viability Assay (Promega Corporation, Madison, WI, USA).

For AR activity assessment, the AR-EcoScreen[™] cell line (#JCRB1328, from Japanese Collection of Research Bioresources Cell Bank, Tokyo, Japan) applied was based on Chinese hamster ovary (CHO-K1) cells expressing the human AR with a firefly luciferase reporter construct inserted and a renilla luciferase gene for the simultaneous evaluation of viability. Cells were seeded at a density of 9×10^4 cells/mL in a DMEM/F12 medium without phenol red, containing 5% CFBS and 1% penicillin/streptomycin, in white 96-well plates. After adhesion, cells were exposed to the cannabinoids (1–10 μ M) for 24 h, in the absence (AR agonism) or presence of 0.1 nM methyltrienolone (R1881; AbMole BioScience, Houston, TX, USA) for investigating AR antagonism. Both AR activity and cell viability were assessed using the Dual-Glo[®] Luciferase Assay System (Promega Corporation, Madison, WI, USA) in a multimode plate reader (EnSpire[®], Perkin Elmer, Inc., Waltham, MA, USA).

At least three independent experiments were conducted in triplicate and the results are presented as fold change compared to a control (cells not exposed to cannabinoids), which was set as 1.

As experimental controls, T (781.2 pM–25.6 μ M) and E₂ (180 fM–367 nM) were tested as positive controls for ER agonism, while Raloxifene (12.0 pM–24.5 nM; Biosynth Ltd., Berkshire, UK) was used as a positive control for ER antagonism. Regarding AR assays, R1881 (7.8 pM–1 nM) and hydroxyflutamide (OHF; 4.1 nM–9 μ M; Sigma Aldrich Co., St. Louis, MO, USA) were used as positive controls for AR agonism and antagonism, respectively. Stock solutions of all the cannabinoids, as well as T, E₂, Raloxifen, R1881, and OHF, were prepared in 100% DMSO and stored at -20 °C. Before each experiment, fresh dilutions were prepared in a medium and the final concentration of DMSO in an exposure medium was 0.06%.

4.5. ToxPi Construction

Data from the nine selected cannabinoids, as well as **CBD**, on aromatase, ER, and AR were used in ToxPi packages to predict the most promising molecules. ToxPi scores and rankings were achieved through the analysis previously published [130]. Here, each slice of the ToxPi is composed of one assay with the respective results, namely, molecular docking in aromatase, aromatase inhibition, molecular docking in ER, ER agonism, ER antagonism over E₂, ER antagonism over T, molecular docking in AR, AR agonism, and AR antagonism. Scores and rankings were generated considering the score values obtained through a molecular docking analysis and through the in vitro studies performed for the three targets.

4.6. Statistical Analysis

The statistical analysis was performed with GraphPad Prism 8.0.1[®] software (GraphPad Software, Inc., San Diego, CA, USA) and by an analysis of variance (ANOVA), followed by Bonferroni and Tukey post hoc tests for multiple comparisons (two-way ANOVA and one-way ANOVA, respectively). Values of $p < 0.05$ were considered statistically significant. All the data were expressed as the mean \pm standard error of the mean (SEM).

5. Conclusions

Through *in silico* and *in vitro* assays, this study presents a comprehensive analysis of the potential therapeutic effects of the cannabinoids, described so far, for the treatment of hormone-dependent breast tumors. These compounds showed ability to modulate key targets responsible for tumor development, such as aromatase, ER, and AR, and the integrated activities implemented on them may together represent an advantage for treatment at different stages of the disease. In fact, the nine minor cannabinoids studied showed, *in vitro*, potential to act either as ER antagonists with inverse agonist properties, or as ER agonists. Moreover, despite the lack of significant aromatase inhibition, all cannabinoids may act as AR antagonists with inverse agonist action. Regarding their chemical characters, key features for ER antagonism like the chromene ring or detrimental substituents for aromatase inhibition, such as the carboxylic acid, were identified and can guide the selection of further investigations on minor cannabinoids. Moreover, by elucidating their molecular targets and mechanisms of action, this study opens up a prospective application of these compounds in other cancers and clinical conditions. From the best of our knowledge, this is the first study exploring the molecular targets of minor cannabinoids and, together with previous studies, it reinforces the importance and therapeutic potential of cannabinoids in breast cancer, paving the way for novel and alternative therapeutic approaches and highlighting the medicinal potential of *Cannabis*.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/ph17091245/s1>, Figure S1. Chemical structures of the cannabinoids described in Table 1. Figure S2. Chemical structures of the cannabinoids described in Table 2. Figure S3. Chemical structures of the cannabinoids described in Table 3. Figure S4. Molecular dynamics (MD) of ER α complexed with CBC (A), CBCA (B), CBD (C), CBDA (D), CBDB (E), CBDM (F), CBDV (G), CBG (H), CBGVA (I), and CBN (J). Results at the beginning ($t = 0$ ps, green) and at the end ($t = 10,200$ ps, blue) of the simulation (left), RMSD plot (center) and Potential Energy plot (right) during the time of simulation. Figure S5. Effects of the nine minor cannabinoids, CBG (A), CBDV (B), CBN (C), CBDB (D), CBDA (E), CBDM (F), CBCA (G), CBGVA (H) and CBC (I), on VM7LucE2 cell viability. Cells were treated with the cannabinoids (1, 5 and 10 μ M) in the absence (ER α agonism) or presence (ER α antagonism) of testosterone (T; 1 nM) or estradiol (E2; 91.8 pM) for 24h. Results are presented as mean \pm SEM of at least three independent experiments performed in triplicate. Statistically significant differences between control (cells not exposed to cannabinoids), set as 1, and cells not treated with T or E2 are expressed as * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$), while the differences between control and cells treated with cannabinoids in the presence of E2 are expressed as \$ ($p < 0.05$), \$\$ ($p < 0.01$) and \$\$\$ ($p < 0.001$), and the differences between control cells and cells treated with cannabinoids in the presence of T are expressed as # ($p < 0.05$), ## ($p < 0.01$) and ### ($p < 0.001$). Figure S6. Effects of the nine minor cannabinoids, CBG (A), CBDV (B), CBN (C), CBDB (D), CBDA (E), CBDM (F), CBCA (G), CBGVA (H) and CBC (I), on CHO-K1 cells viability. Cells were treated with the cannabinoids (1, 5 and 10 μ M) in the absence (AR agonism) or presence (AR antagonism) of R1881 (0.1 nM) for 24h. Results are presented as mean \pm SEM of at least three independent experiments performed in triplicate. Statistically significant differences between control (cells not exposed to cannabinoids), set as 1, and cells not treated with R1881 are expressed as * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$), while the differences between control and cells treated with cannabinoids in the presence of R1881 are expressed as \$\$\$ ($p < 0.001$).

Author Contributions: C.F.A.: Writing—original draft, Investigation, Formal analysis, Validation, Methodology, Funding acquisition, Conceptualization. A.P.: Writing—review and editing, Formal analysis. M.J.V.: Writing—review and editing, Formal analysis, Resources. G.C.-d.-S.: Writing—review and editing, Supervision, Funding acquisition, Resources, Conceptualization. A.M.V.: Writing—review and editing, Resources. M.E.S.: Writing—review and editing, Resources. N.T.: Writing—review and editing, Supervision, Validation, Funding acquisition, Resources, Conceptualization. C.A.: Writing—review and editing, Formal analysis, Validation, Funding acquisition, Resources, Conceptualization, Supervision, Project administration. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by national funds from FCT—Fundação para a Ciência e a Tecnologia, in the scope of the project UIDP/04378/2020 and UIDB/04378/2020 of the Research Unit on Applied Molecular Biosciences—UCIBIO and the project LA/P/0140/2020 of the Associate Laboratory Institute for Health and Bioeconomy—i4HB.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The original contributions presented in the study are included in the article/Supplementary Material, further inquiries can be directed to the corresponding author.

Acknowledgments: The authors give thanks to Fundação para a Ciência e Tecnologia (FCT) for the Cristina Almeida PhD grant (UI/BD/151314/2021) and Cristina Amaral contract, by REQUIMTE, under the funding program (DL 57/2016—Norma Transitória), and through the grant SFRH/BPD/98304/2013. The authors also thank Paula Serrão (Radioactivity Laboratory, Faculty of Medicine, University of Porto, Porto, Portugal) for helping with liquid scintillation counter.

Conflicts of Interest: The authors have no conflicts of interest to declare.

Abbreviations

Δ^9 -THCA: Δ^9 -tetrahydrocannabinolic acid; Δ^9 -THCV: Δ^9 -tetrahydrocannabivarin; Δ^9 -THCVA: Δ^9 -tetrahydrocannabivarinic acid; 17β -estradiol: E₂; AIs: aromatase inhibitors; Ana: anastrozole; AR: androgen receptor; CBC: cannabichromene; CBCA: cannabichromenic acid; CBD: cannabidiol; CBDA: cannabidiolic acid; CBDB: cannabidiol-C4; CBDM: cannabidiol monomethyl ether; CBDV: cannabidivarin; CBDVA: cannabidivarinic acid; CBG: cannabigerol; CBGA: cannabigerolic acid; CBGVA: cannabigerovarinic acid; CBN: cannabinol; CBV: cannabivarin; ER: estrogen receptor; ER⁺: estrogen receptor-positive; Exe: exemestane; GPP: geranyl diphosphate; HER2⁺: human epidermal growth factor receptor 2-positive; Let: letrozole; MD: molecular dynamics; T: testosterone; THC: Δ^9 -tetrahydrocannabinol.

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