

Structural binding interaction of polybrominated diphenyl ethers (PBDEs) with thyroxine binding globulin: Insights into thyroid signaling disruption

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Polybrominated diphenyl ethers (PBDEs) represent an important class of halogenated flame retardants incorporated into a variety of consumer products to slowdown the spread of fire and mitigate the damage to property and human life. They have widespread environmental presence attributed to their leach out from consumer products and persistent nature making them resistant to degradation. Multiple studies have highlighted the structural resemblance between PBDEs and thyroid hormones, allowing them to mimic thyroid hormone activity and potentially disrupt its function. Therefore, it becomes pertinent to investigate and gather more data on PBDE induced thyroid dysregulation and associated toxicological effects in humans. Thyroxine-binding globulin (TBG) regulates thyroid hormone metabolism and its distribution in body making it vital for controlling thyroid hormone homeostasis. The objective of this study was to investigate the molecular interactions of commonly detected PBDEs, BDE-100 and BDE-209 with in the TBG ligand binding pocket. These ligands underwent Schrodinger's induced fit docking (IFD) along with structural binding analysis, which included molecular interaction evaluation and binding energy calculation. The analysis demonstrated that all the ligands were strongly bound within the TBG pocket, with a high degree of similarity in the TBG interacting residues between the specified PBDE ligands and the native TBG ligand, thyroxine. The calculated binding energy values for BDE-209 were higher than that of TBG native ligand, while BDE-100 values were somewhat lower but not significantly so. In conclusion, the results indicated that BDE-209 is more effective than BDE-100 in inhibiting the binding of thyroid hormones to TBG, though both PBDEs possess this ability. As a result, this could disrupt the circulatory transport of thyroid hormones and their availability at target sites, potentially causing thyroid dysregulation.

Keywords: Endocrine disruption, Polybrominated diphenyl ethers, Thyroid dysregulation, Structural characterisation

Fire poses a major threat to property and human life, and significantly increases public costs^{1,2}. To mitigate these risks, flame retardants are incorporated into various materials, providing an essential safety measure that guarantees adherence to fire safety regulations and assists in delaying the progression of flames^{3,4}. They minimize the damage on property and save human lives by offering extra escape time to the vulnerable section of population including senior citizens, children, and low-income population. According to a recent report, the global flame-retardant market reached US\$ 9.2 billion in 2022 with projection of US\$ 13.5 billion by the year 2028⁵. Polybrominated diphenyl ethers (PBDEs) are synthetic flame retardants historically used in electronics, textiles, and furniture^{6,7}. The PBDEs exposure is associated with cancer, neurotoxicity, and other metabolic dysfunction, primarily through

endocrine disruption and interference with hormonal signaling⁸. Generally, the majority of the PBDEs are resistant to degradation⁹ and their breakdown potential diminishes with an increase in halogenation levels^{10,11}. Their widespread presence in the environment can be attributed to their propensity to leach from consumer products. Additionally, their persistent and bioaccumulative characteristics further enhance their extensive environmental distribution. Numerous studies have confirmed the presence of these substances in various environmental settings, with particularly higher concentrations observed in industrialised and urban areas¹². They can enter the human body through multiple pathways, including dermal contact, inhalation of contaminated dust or soil, and ingestion of polluted food or water. However, PBDEs have garnered considerable attention because of their potential to cause negative health impacts in both humans and wildlife^{13,14}.

The three commonly used commercial PBDE mixtures containing penta, octa and deca-BDE were

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listed among persistent organic pollutants (POPs) in the last two decades under Stockholm Convention in 2009 and 2017 due to their inherent high persistence, bioaccumulation, long-range transport, and toxic nature¹⁵⁻¹⁷. While PBDEs have been restricted, banned, or phased out in countries like the United States, Japan, India, and those within the European Union^{18,19}, but they are still reported from indoor environments in high concentrations due to leach out from the buildings and furnishing products^{20,21}, resulting in continuous human exposure and bioaccumulation²². Moreover, their gradual migration from consumer products into the environment probably will continue for numerous years in future too²³. In China, the use and production of penta and octa-BDE commercial mixtures were banned in year 2014 which reduced the lower brominated PBDE contamination levels in food and human milk samples²⁴⁻²⁶, however, the industrial synthesis and application of deca-BDE is still permitted with an annual output of nearly 24,000 metric tons^{17,27,28}. Also the exposure from indoor contamination is more concerning as majority of the people spend more than 90% of their life in indoor environment^{29,30}. Specifically, children usually are at increased risk of exposure to PBDEs due to an increased hand-to-mouth activity, different breathing zone, faster metabolism, and increased inhalation rate³¹⁻³³. Additionally, toddlers are exposed to PBDEs through dust via hand-to-mouth contact at levels nine times higher than adults, with median daily exposure estimates of 1380 ng for toddlers compared to 154 ng for adults³⁴. Furthermore, daily exposure to PBDEs from all sources for children aged 1–5 years was estimated at 13.3 ng/kg-bw/day, with approximately 77% of this exposure coming from dust³⁵. Among the various PBDEs, BDE-209 is among the most prevalent in environmental compartments³⁶, with median concentrations in dust samples in the USA of 4.5 µg/g in homes and 4.2 µg/g in offices³⁷. High levels of BDE-209, especially in homes, schools, and cars, indicate a growing trend of contamination³⁸. BDE-209's unique physicochemical properties include its high stability, hydrophobicity, and ability to persist in the environment. These characteristics allow it to accumulate in various environmental compartments and resist degradation, contributing to its widespread presence and potential toxicity³⁹. Likewise, BDE-100 is another PBDE compound produced on a large scale, but toxicological data remain scarce, raising

scientific concern. As key regulators of cellular energy and function, mitochondria were used to assess the effects of BDE-100 at concentrations ranging from 0.1 to 50 µM, with high concentrations inducing notable mitochondrial alterations⁴⁰.

The PBDEs have widespread environmental presence sharing their structural similarity with thyroid hormones⁴¹. Therefore, it becomes pertinent to investigate and gather more data on thyroid dysregulation and associated toxicological effects in humans. Thyroxine-binding globulin (TBG) is vital for controlling thyroid hormone homeostasis. The regulation of thyroid hormone metabolism and distribution in the body primarily relies on TBG. TBG binds a substantial portion of thyroid hormones, thereby regulating their distribution and availability to target tissues, which makes it highly important for controlling the availability of free, physiologically active thyroid hormones. The levels of free thyroid hormones provide a more accurate reflection of the relevant physiological status than total hormone levels, which can be influenced by variations in binding protein levels. In conclusion, TBG is an essential component of the intricate regulatory system that controls thyroid hormone balance. Its dynamic interactions with thyroid hormones, along with its role in various physiological and pathological processes, underscore the importance of understanding its contribution to overall thyroid health⁴²⁻⁴⁵. This study is aimed to characterise the structural binding of the commonly found PBDEs, BDE-100 and BDE-209 to the ligand binding pocket of the thyroxine transport protein, TBG, using molecular docking simulations. The objectives were to describe the structural interactions between indicated PBDEs and TBG, and to investigate the potential disruption of thyroid hormone transport by these frequently identified compounds. While previous research has highlighted the possibility of thyroid dysfunction due to various PBDE congeners, studies examining their impact on thyroid hormone transport, particularly concerning these two PBDEs, BDE-100 and BDE-209 are limited. Moreover, despite previous studies on other congeners, it is essential to prioritise further research on BDE-209 and BDE-100 due to their widespread use and potential risks. BDE-209, commonly produced in deca-formulation products, remains a significant environmental and health concern because of its stability and persistence. Similarly, BDE-100, though less studied, shares similar properties and is also produced at large scale. Given their enduring presence in the environment and their possible long-term impacts, studying these two compounds is

crucial to fully understanding their effects, even in light of prior research on other congeners. Furthermore, no structural studies have been published on the interactions of these two PBDE ligands with the TBG ligand binding pocket. Thus, this study fills this gap by focusing on the structural interactions of BDE-100 and BDE-209 with TBG.

Materials and Methods

For this study, two frequently detected PBDE ligands, BDE-100 and BDE-209 were used. The PubChem compound database (<https://pubchem.ncbi.nlm.nih.gov/>) was used to retrieve their three-dimensional structural coordinates. Additionally, the Schrodinger 2017 suite was used to perform the structural binding study of these PBDE ligands, with Maestro 11.4 acting as the graphical user interface (Schrodinger, LLC, New York, NY, 2017). The specific methodology is explained in our earlier research^{46,47}.

Protein preparation

The Protein Data Bank (PDB; <http://www.rcsb.org/>) was used to obtain the three-dimensional structural coordinates for the TBG crystal structure in complex with the natural ligand, thyroxine (T4), solved at 1.55 Å resolution (PDB code: 4X30). Processing came next, in which the protein complex was ready for subsequent stages using Schrodinger Glide's protein preparation wizard methodology for molecular simulation investigations (Schrodinger suite 2017-4; Schrodinger, LLC) as described previously^{46,47}. The TBG crystal complex was initially imported into the Glide docking program as part of the protein preparation process. Moreover, water molecules were eliminated, and hydrogen atoms and charges were added. Finally, energy minimisation was carried out after the hydrogen bond networks were optimised.

Ligand preparation

The structures of PBDEs (BDE-100 and BDE-209) were obtained from the PubChem database, with chemical IDs 154083 and 14410, respectively. Their two-dimensional structures are shown in Fig. 1. For simulation investigations, the indicated ligands were prepared using Schrodinger's LigPrep module (Schrodinger 2017: LigPrep, Schrodinger, LLC) as described in our earlier research^{46,47}.

Induced Fit Docking

Both PBDE ligands, BDE-100 and BDE-209, as well as T4, were docked into the TBG ligand binding

pocket utilizing Schrodinger's Induced Fit Docking (IFD) module, as previously outlined in our studies^{46,47}. Unlike conventional rigid docking, IFD allows for flexibility in both the protein's ligand binding site as well as ligand. To develop and validate protocols for accurately predicting the poses of receptor-ligand interactions and the corresponding alterations in the ligand binding pocket of the protein receptor, we utilised Schrodinger's Glide and Refinement module in Prime. In summary, the initial phase of the IFD process involved generating a grid at the binding site of the native ligand, T4, within TBG. The protein preparation phase utilised an RMSD cutoff of 0.18 Å to conduct constrained minimisation of the protein receptor. Subsequently, initial Glide docking was executed with a softened potential and optional removal of side chains for both the PBDE ligands, resulting in the retention of twenty docking poses by default. Following this, side chain predictions were made for amino acids within a 5 Å radius of each receptor-ligand complex for any given pose, and minimisation was carried out. Additionally,

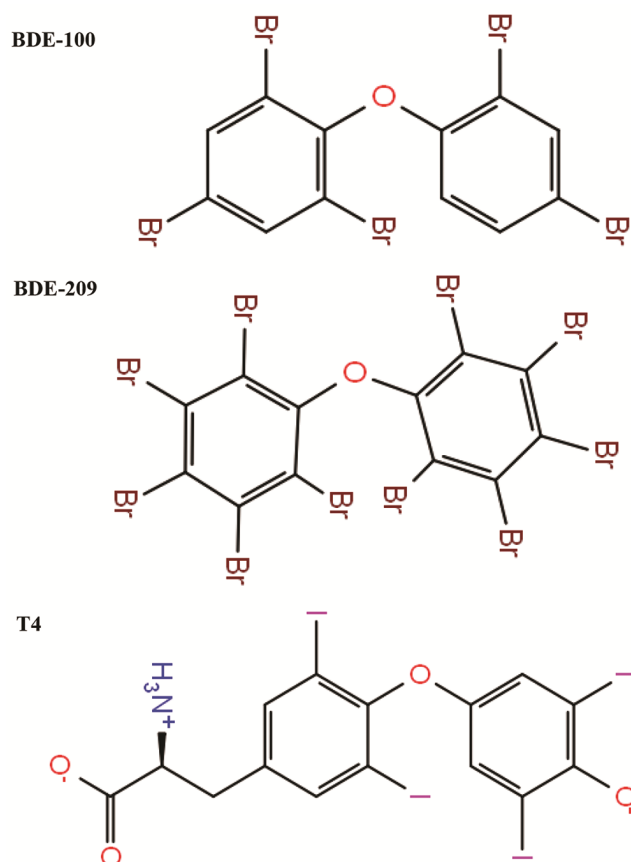


Fig.1 — Two-dimensional structure of BDE-100, BDE-209 and TBG native ligand, T4.

ligand minimisation was conducted for each receptor-ligand complex pose. We also performed Glide redocking and estimated the IFD score. An extended sampling protocol was implemented as well. Furthermore, IFD was conducted for the native ligand of TBG, T4 too.

Binding energy estimation

The binding affinity of both the PBDE ligands, BDE-100 and BDE-209 for the TBG binding pocket was calculated using the molecular mechanics generalised born surface area (MMGB-SA) function from the Prime module of Schrodinger 2017, as detailed in our previous studies^{46,47}.

Results

The two frequently detected PBDEs congeners, BDE-100, and BDE-209, successfully docked in the TBG ligand binding pocket. The stability of the indicated PBDE ligands in the TBG ligand binding pocket was suggested by the tight placement of each ligand in the ligand binding pocket utilising the IFD technique. Only the top-ranking pose was ultimately selected and proceeded with for structural binding investigation and characterisation, even though several display poses were generated for every protein-ligand docking complex. Similarly, TBG native ligand T4 docked successfully and was firmly positioned in the ligand binding pocket after IFD. Again, the top-ranking display pose was chosen and proceeded with for additional examination. The Fig. 2 displays the top ranked docking display poses that reveal interactions between the TBG amino acid residue and each of the indicated PBDE ligands.

Moreover, Fig. 3 shows the optimal docking pose that displays interactions between TBG amino acid residues and its native ligand, T4. The indicated PBDE ligands, BDE-100 and BDE-209 interacted with 15 and 17 respectively amino acid residues in the TBG ligand binding pocket (Fig. 2A & 2B).

IFD of BDE-100 ligand with TBG

The IFD docking display complex TBG-BDE100 demonstrated an array of interactions with a multitude of amino acid residues of TBG. In total, 15 amino acid residues were identified, each engaging in a variety of molecular interactions such as hydrophobic interactions, hydrogen bonding, and van der Waals forces with BDE-100. The amino acid residues within the TBG ligand binding pocket that participated in various interactions included Ser-24, Ala-27, Gln-238, Leu-246, Leu-248, Ser-266, Leu-269, Lys-270, Trp-272, Asn-273, Leu-276, Leu-376, Arg-378, Arg-381, and Ile-383 (Fig. 2A). Additionally, one hydrogen bonding interaction between BDE-100 and Arg-381 was also observed.

Likewise, the native ligand docking display complex, TBG-T4, displayed several molecular contacts with many TBG amino acid residues (Fig. 3). Fifteen amino acid residues in total were shown to exhibit various molecular interactions with T4, such as hydrophobic, hydrogen bonding, van der Waals, salt bridge, etc. The amino acids in question were Ser-23, Ala-27, Gln-238, Leu-246, Leu-248, Leu-269, Lys-270, Trp-272, Asn-273, Leu-276, Leu-376, Arg-378, Arg-381, Ser-382 and Ile-383. Additionally, T4 demonstrated two interactions with Asn-273 through

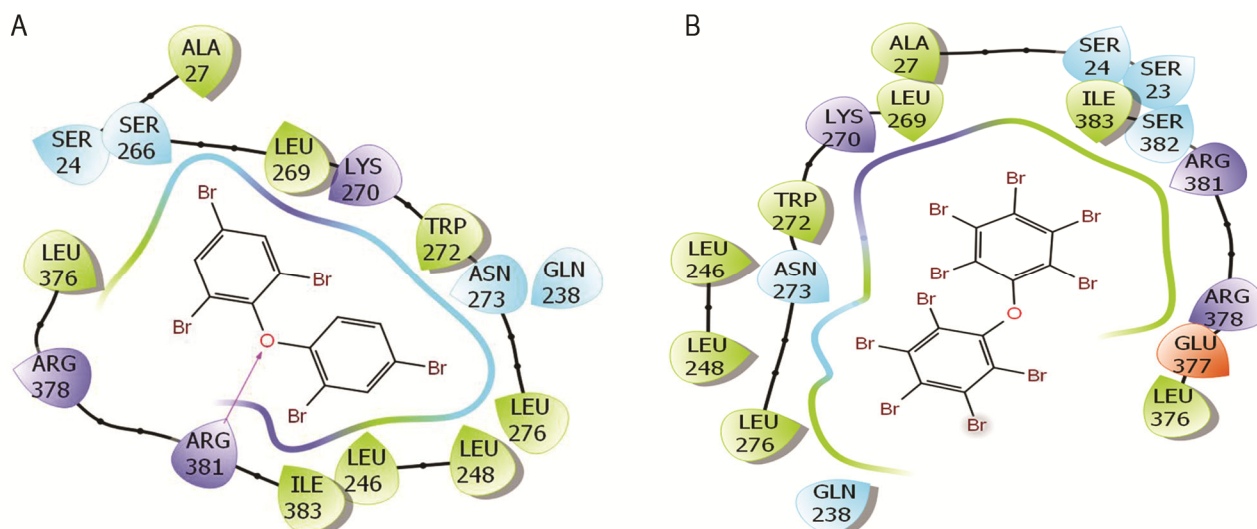


Fig. 2— Molecular interactions of PBDEs (A) BDE-100, (B) BDE-209 with amino acid residues lining TBG ligand binding pocket.

hydrogen bonds. Furthermore, T4 established two additional hydrogen bonding interactions with Arg-381 and Arg-378, respectively. Additionally, two salt bridge interactions with Lys-270 and Arg-381 were also observed (Fig. 3). Moreover, Table 1 lists additional crucial structural binding characterization parameters for BDE-100 and the TBG native ligand, T4, such as IFD, Dock score, Glide score, binding energy, etc. Furthermore, it was calculated that BDE-100 and T4 shared about 87% of their TBG-interacting amino acid residues. Besides, two additional amino acid residues Ser-24 and Ser-266 were also observed interacting with BDE-100. In contrast to TBG native ligand T4, the calculated binding energy for BDE-100 was low, which is crucial for structural binding characterisation.

IFD of BDE-209 ligand with TBG

The congener BDE-209 showed a variety of molecular interactions with TBG amino acid residues. Seventeen amino acid residues were seen in the docking display pose of BDE-209 interacting with TBG in different molecular ways (Fig. 2B). The amino acid residues within the TBG ligand binding pocket that participated in various interactions

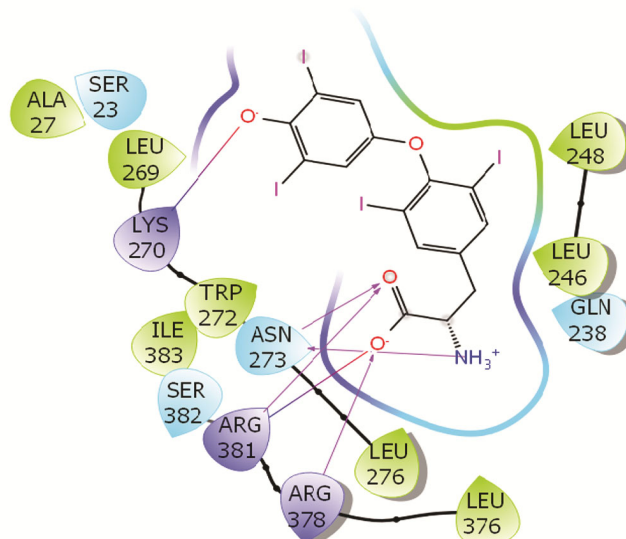


Fig. 3— Molecular interactions of a TBG native ligand, T4 with amino acid residues lining TBG ligand binding pocket.

included Ser-23, Ser-24, Ala-27, Gln-238, Leu-246, Leu-248, Leu-269, Lys-270, Trp-272, Asn-273, Leu-276, Leu-376, Glu-377, Arg-378, Arg-381, Ser-382 and Ile-383. Additionally, a 100% match in amino acid interactions was found when the docking poses of the native ligands T4 and BDE-209 were compared. However, because of extra amino acid residues, such as Ser-24 and Glu-377, other molecular interactions were also seen in the TBG-BDE209 complex (Fig. 2B).

Discussion

The objective of this study was to gain structural understanding of the possible interruption of circulatory thyroid hormone transport by PBDEs, BDE-100, and BDE-209, as well as to predict the resulting implications in thyroid dysregulation. Our analysis of the structural binding data showed that both PBDE ligands, BDE-100 and BDE-209, successfully bound within the ligand-binding pocket of TBG. The results also indicated that the docked complexes, TBG-BDE100 and TBG-BDE209 were stable. This stability and the overall quality of the TBG-PBDE complexes were further confirmed by the calculated binding energy values and various structural binding parameters, such as the Dock score, IFD score, and glide score. Numerous molecular interactions, including salt bridges, hydrophobic interactions, van der Waals forces and hydrogen bonding observed in the docked complexes of TBG and PBDEs, significantly contributed to the stability of these complexes. A comparative analysis of the selected docking displays of TBG-PBDE complexes in relation to the native ligand configuration of the TBG-T4 complex, showed 87–100% similarity in the interactions of amino acid residues within the ligand binding pocket of TBG. The binding energy values determined for BDE-100 were less than that estimated for the native ligand of TBG, T4, while the values calculated for BDE-209 exceeded those estimated for T4. Therefore, our findings indicate that the PBDE ligands, BDE-100, and BDE-209, may interfere with the transport of thyroid hormones by TBG. This disruption could lead to thyroid dysfunction,

Table 1 — Structural binding indices of plasticizers (BDE-100, BDE-209) and a TBG native ligand, T4

Ligand	Number of interacting residues	Percentage of interacting residues common with native ligand (%)	IFD score	Docking score (Kcal/mol)	Glide score (Kcal/mol)	MMGB-SA (Kcal/mol)
BDE-100	15	86.6%	-828.74	-6.91	-6.91	-108.52
BDE-209	17	100%	-831.12	-8.16	-8.16	-146.14
T4	15	100%	-833.29	-8.37	-8.37	-124.31

potentially resulting in several health problems including developmental issues. The binding energy estimation results indicate that the TBG-BDE209 complex exhibits greater stability compared to the TBG-BDE100 complex, suggesting that BDE-209 has a higher binding affinity for the TBG binding pocket than BDE-100. The enhanced stability of the TBG-BDE209 complex indicates a stronger association, which may lead to a more significant disruption of TBG's physiological functions compared to the TBG-BDE100 complex. This observed difference is likely to have a substantial effect on their thyroid dysfunction activities.

As per a literature review, few studies are documented on structural binding characterisation of PBDEs ligands with proteins including TBG⁴⁸⁻⁵⁰. However, there are no known structural investigations reported on molecular interactions of BDE-100 and BDE-209 with TBG. Nevertheless, we recently published the structural characterisation and molecular interactions of TBG with BDE-28, BDE-85, BDE-154 and BDE-183⁵¹. In another study, we performed structural binding characterisation of BDE-153 against TBG ligand binding pocket⁵². Additionally, we reported the binding of both hydroxy and methoxy metabolites of PBDE's to TBG⁵³. Furthermore, *in vitro* binding experiments utilising fluorescent probes have demonstrated that several hydroxylated PBDEs effectively bind to TBG with some of the analogues exhibiting greater binding compared to T4⁵⁴. Findings from a fluorescence displacement assay indicated that hydroxylated PBDEs could potentially displace thyroid hormones from their binding sites on TBG⁵⁵. Additionally, a Surface Plasmon Resonance investigation revealed that certain hydroxylated metabolites of PBDEs exhibited strong binding affinity to TBG⁵⁶. Several contemporary investigations have revealed that PBDE sulphate metabolites bind with TBG, which may indicate a disruption in normal thyroid function⁵⁷.

Numerous epidemiological studies have explored the relationship between circulating thyroid hormone (TH) levels and exposure to polybrominated diphenyl ethers (PBDEs) in human tissues. However, the findings remain indecisive, and no conclusive outcomes have been established. The relationship between PBDE exposure and serum T4 levels has been the subject of conflicting research. Some investigations have reported positive correlations⁵⁸⁻⁶⁰, while others have observed negative relationships⁶¹⁻⁶³, and certain

studies have found no significant associations in both pregnant women and adult men^{64,65}. The observed positive correlations between PBDEs and total thyroxine (TT4) and free thyroxine (FT4) contrast with the typical outcomes of animal research conducted in laboratories. These discrepancies may arise from several factors, including elevated exposure levels and the younger developmental stages of the animals at the time of exposure, variations between acute and chronic exposure, and the distinct impacts of different congeners⁵⁵. A study highlighted that prenatal exposure to polybrominated diphenyl ethers (PBDEs) may increase thyroid-stimulating hormone (TSH) levels in the umbilical cord blood of infants delivered vaginally⁶⁶. Another study revealed negative correlation between serum TSH levels and PBDE exposure at median concentrations below 30 ng/g lipid. In contrast, a positive association was observed when median levels exceeded 100 ng/g lipid, with no significant correlation found in the 30-100 ng/g lipid range⁶⁷. A similar trend was seen in the relationship between PBDE exposure and TT4 serum levels⁶⁸.

Likewise, laboratory animal studies have similarly demonstrated changes in thyroid hormone concentrations due to exposure to PBDEs⁶⁹. Specifically, variations in T4 levels have been observed in rodents, felines, and avian species subjected to PBDEs exposure⁷⁰⁻⁷². Numerous studies involving rodents have indicated that exposure to PBDEs is associated with decreased serum levels of T4, ultimately resulting in hypothyroidism. Studies on rats have shown that TBG binding with PBDEs⁷³, is inversely correlated with thyroid hormone levels and PBDE exposure⁷⁴. A study on rodents found a notable reduction in T4 levels on exposure to PBDEs both before and after birth⁷⁵⁻⁷⁶. Reduced T4 levels were observed in rat offspring exposed to PBDEs during pregnancy⁷⁷. A zebrafish study investigating the transgenerational effects of BDE-209 exposure revealed lower T4 levels and decreased expression of the thyroid hormone receptor gene in F1 individuals⁷⁸.

Conclusion

The findings from our research indicated that the two PBDE ligands, BDE-100 and BDE-209 showed considerable overlap in the amino acid residues interacting within the TBG ligand binding pocket, akin to those of the native ligand T4. Importantly, the binding energy of BDE-209 exceeded that of T4, while BDE-100 displayed lower values without significant difference. As a result, our initial findings

suggest that BDE-209, along with BDE-100 to a lesser extent, may engage in competitive binding with TBG, potentially displacing the native ligand T4. This competitive interaction could interfere with the transport of thyroid hormones in the bloodstream, potentially leading to thyroid hormone dysfunction and related health issues.

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Conflict of interest

The authors acknowledge that there is no conflict to declare.

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