Predicting Antioxidant Synergism via Artificial Intelligence and Benchtop Data

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ABSTRACT

Lipid oxidation is a major issue affecting products containing unsaturated fatty acids as ingredients or components, leading to the formation of low molecular weight species with diverse functional groups that impart off-odors and off-flavors. Aiming to control this process, antioxidants are commonly added to these products, often deployed as combinations of two or more compounds, a strategy that allows for lowering the amount used while boosting the total antioxidant capacity of the formulation. While this approach allows for minimizing the potential organoleptic and toxic effects of these compounds, predicting how these mixtures of antioxidants will behave has traditionally been one of the most challenging tasks, often leading to simple additive, antagonistic, or synergistic effects. Approaches to understanding these interactions have been predominantly empirically driven, but thus far inefficient and unable to account for the complexity and multifaceted nature of antioxidant responses. To address this current gap in knowledge, we describe the use of an artificial intelligence model based on deep learning architecture to predict the type of interaction (synergistic, additive, and antagonistic) of antioxidant combinations. Here, each mixture was associated with a combination index value (CI) and used as input for our mode, which was challenged against a test (n=140) dataset. Despite the encouraging preliminary results, this algorithm failed to provide accurate predictions of oxidation experiments performed in-house, using binary mixtures of phenolic antioxidants and a lard sample. To overcome this problem, the AI algorithm was then enhanced with various amounts of experimental data (antioxidant power data assessed by the TBARS assay), demonstrating the importance of having chemically-relevant experimental data to enhance the model's performance and provide suitable predictions with statistical relevance. We believe the proposed method could be used as an auxiliary tool in benchmark analysis routines, offering a novel strategy to enable broader and more rational predictions related to the behavior of antioxidant mixtures.

KEYWORDS

Lipid oxidation, antioxidant, synergism, machine learning

1. INTRODUCTION

Lipid oxidation is a major issue affecting products containing unsaturated fatty acids as ingredients or components. These include, for instance, cosmetics [1, 2], vegetable oils[3-7], seafood[8-10], processed meat[11-14], and animal feed[15-18]. The oxidative deterioration of these samples can occur via chemical, thermal, enzymatic, and/or photocatalytic mechanisms. Among these, auto-oxidation (spontaneously initiated in the presence of atmospheric oxygen) is the least selective and probably the most difficult to control. Among other targets, the oxidation of lipids leads to the formation of low molecular-weight species with diverse functional groups (carboxylic acids, aldehydes, and ketones) that impart off-odors[19] and off-flavors[20]. This process is also known as rancidity and can not only impart an unpleasant taste but also diminish the nutritional value[21, 22] and the overall quality of the sample, which ultimately impacts the health of the end consumer[23]. Moreover, the oxidation of lipid-based foods also contributes to the shorter shelf-life of these products [23-26], resulting in considerable economic losses in all segments of the supply chain[27, 28].

Therefore, it is critical to develop strategies to mitigate or prevent lipid oxidation in foods. For this purpose, the use of antioxidants has proven to be one of the most effective and frequently adopted methods,[29-34] a strategy that has been also extended to pharmaceuticals[35, 36] as well as nutraceutical products[36, 37]. Although these antioxidants are derived from natural[38-41] (e.g, tocopherols, phenolic acids, polyphenols, and ascorbic acid) or synthetic sources[42-45], they offer different mechanisms of action[46-52] and allow targeting the reaction at different stages, from scavenging free radicals [53], to quenching triplet oxygen [54], to chelating metal cations[55]. Regardless of the mechanism of action, antioxidants are normally deployed as combinations of two or more compounds, a strategy that allows lowering the amount used while boosting the total antioxidant capacity of the formulation. While this approach allows minimizing the potential organoleptic and toxic effects of these compounds, predicting how these mixtures of antioxidants will behave has traditionally been one of the most challenging tasks[56-58], often leading to simple additive[59] (even antagonistic[60]) effects, instead of the desired synergistic response[61-63]. Although the interaction between some classes of antioxidants is well known [64], there is a current need for a strategy that could enable broader and more rational predictions related to the antioxidant capacity of mixtures. Approaches to understanding these interactions have been predominantly empirically driven, where the total antioxidant

effectiveness is assessed by using assays such as total oxidation index (TOTOX) [65], thiobarbituric acid reactive substances (TBARS) [66], peroxide value (PV)[67], p-anisidine test [68], ferric reducing antioxidant power (FRAP) [69], or DPPH scavenging [70]. The gathered experimental data can be then analyzed as a function of the composition of the antioxidant mixture through the use of standard methods such as isobole diagrams [71], response curves or interaction index parameters[72]. Albeit effective for simple experimental designs, these one-dimensional methods often hinder the evaluation of non-linear interactions[73-75] due to the complexity and multifaceted nature of antioxidant responses, which are often affected by several factors such as their mechanism of action, structural properties, and matrix effects. On the contrary, machine learning approaches are particularly well suited to address these complex problems and have been recently applied to make predictions related to taste[76-79] and fermentation[80] of foods, screen for Nrf2-agonists [81], identify flours infested by insects [82], and even discover green insecticides[83].

In this scenario, we describe the first use of an artificial intelligence model based on deep learning architecture[84] to predict the type of interaction (synergistic, additive, and antagonistic) of antioxidant combinations. The proposed strategy uses the Simplified Molecular Input Line Entry System (SMILES) notation[85] to represent the antioxidants combinations as text representations. Each mixture is then associated with a combination index value (CI)[86], an established metric often used to assess the magnitude of these interactions. The proposed method also utilizes a self-data augmentation method to overcome overfitting due to the limited amount of data for the training step. This strategy was implemented by representing the stoichiometric ratio as a repetition of the same antioxidant compound instead of numerical representations (*vide infra*, Figure 1), allowing the rearrangement of the SMILES strings to all possible non-repeated positions in the final mixture. In this sense, the use of chemical descriptors (density, functional groups, polarity, etc) can be avoided, reducing the complexity of the AI model and easily allowing its implementation in benchmark routines. The performance capability of our model was first assessed by predicting CI values using a database developed from literature reports (n=700), showing a relatively good agreement (R^2_{test}= 0.92 and R^2_{train}=0.95) between the predicted output and the actual value for both the training (n=560) and test (n=140) datasets. Despite these encouraging results, this algorithm failed to provide accurate predictions of oxidation experiments performed in-house, using binary mixtures of

phenolic antioxidants and a lard sample. To overcome this problem, the AI algorithm was then enhanced with various amounts of experimental data (antioxidant power data assessed by the TBARS assay) collected using lard samples. This approach allowed the model to learn from the experimental chemical space targeted by our research, which was not specifically described in the surveyed literature. Our results showed that significant improvements in the model's performance were obtained as the amount of fine-tuning data increased, increasing the correlation between the predicted and experimental results from R^2=0.01 (no correlation) to an R^2 value of 0.90. These results not only demonstrate the predictive power of the proposed algorithm but also the importance of having chemically-relevant experimental data to enhance the model's performance and provide suitable predictions with statistical relevance.

2. MATERIALS AND METHODS

2.1 Hardware configuration. All the computational work presented in this manuscript was carried out in the Palmetto Cluster at Clemson University. The node was set to 32 cores (ncpus) and the allocated memory was set to 372Gb. As a graphical processing unit (GPU), a NVIDIA Tesla V100 was used to train the foundational chemistry model as well as to fine-tune the generated model into the regressors. It is important to state that while access to the cluster was critical to speed up the initial training of the foundational chemistry model, the trained algorithm can be then executed on a standard computer. As a gauge of the resources applied, the foundational model training and subsequent fine-tuning were completed in approximately 14 hours (12 hours for training + 2 hours of fine-tuning). Notably, the same computational process could require up to a week on an average computer equipped with an NVIDIA GTX 1050.

2.2 uACL antioxidant database. The proprietary antioxidant database (referred as uACL DB) was developed by manually retrieving data from the literature and includes various antioxidant molecules, solvents, samples, and experimental conditions for their evaluation. In all cases, the antioxidant combinations were represented in SMILES notation along with their molar ratio and respective metric to measure the degree of interaction such as the combination index (CI), the difference in FRAP[87], % of the synergistic or antagonistic effect[88] as well as Trolox equivalent antioxidant capacity (TEAC)[89]. The resulting

database displayed approximately 1100 entries and the gathered data was analyzed by a python algorithm to avoid duplicates.

2.3 Data splitting and augmentation. The uACL DB was randomly split into training (85%) and test dataset (15%). The decision to allocate 85% the data for training and 15% for testing was based on the balance required to ensure our model had access to enough data to learn the patterns from the chemical space, while also having a representative number of unseen entries to evaluate the model's performance. Aiming to avoid data leaking between the datasets, all the files were compared by an *ad-hoc* Python algorithm. An additional manual check of each entry was also implemented as a safeguard to prevent overoptimistic performance measures.

Then, each dataset was duplicated and assigned either a textual or numerical representation, giving a total of 4 databases (numerical_train, numerical_test, textual_train, textual_test). For the pair assigned as numerical, the stoichiometric ratio of all combinations was represented as a number in between a non-SMILES special character (e.g., 2A 2B). On the other hand, for the pair assigned as textual, the stoichiometric ratio was represented as repetitions of the antioxidants (*e.g.* AABB). Then, a Python algorithm was used to augment the textual datasets by permuting the antioxidant smiles to all possible non-repeated positions in the final mixture. These processes are presented in Figure 1.

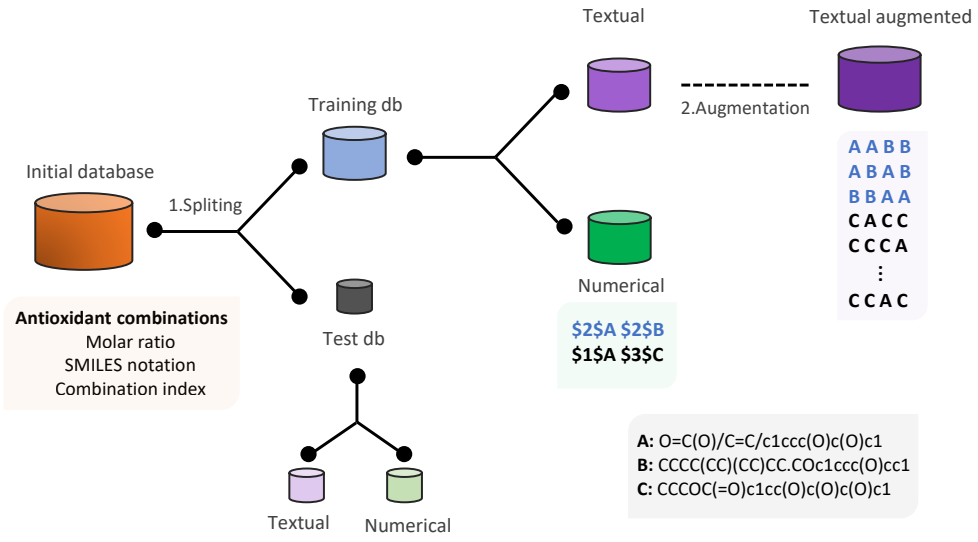

Figure 1: Schematic representation for the proposed data splitting and augmentation.

2.4 Foundational chemistry model. The foundational general chemistry model was developed by following the same strategy described in a previous publication of our group[90]. Briefly, Transformer-type architectures[91] are now commonly used in Natural Language Processing and are pre-trained using Self-Supervised Learning on large amounts of text data to create Foundation Models for different human languages. This pre-training is expensive (in terms of computational resources) but gives the model a broad understanding of the language(s), allowing it to adapt to specific downstream tasks quickly and efficiently. Transformers introduce the concept of an attention mechanism, which allows models to assign different weights of importance to certain words within a sentence during prediction generation.[92] Uniquely, these models process all words in the text simultaneously, thereby offering a significant boost in computational speed and efficiency. The central component of the Transformer is the self-attention mechanism, which evaluates the influence of each word on others within the same text fragment. This functionality enhances the model's contextual understanding and performance on tasks like translation, summarization, and sentiment analysis. In this manuscript, a general chemistry model was pre-trained on a large corpus of chemical reaction information, which was then fine-tuned for a specific task. The ELECTRA deep learning model used in this manuscript had 4 hidden layers for the generator and 16 for the discriminator, with a vocabulary size of 30,000 and 40 training epochs. The output model containing all trained parameters was stored in a directory called the foundational general chemistry model. The molecular Transformer USPTO_MIT Mixed Augmented database[91, 93] was used to train as well as to evaluate the proposed chemistry model.

2.5 Fine-tuning method. Both the numerical and the textual databases were used to fine-tune the last layer of general chemistry foundational model into a regressor. The appropriate test dataset for each stoichiometric representation type (text or numerical) was used to investigate the performance of the generated regressor by assessing unseen antioxidant mixtures by the algorithm. Regarding the neural network architecture, the parameters “max_seq_lenght”, “train_batch_size”, and “learning_rate” were adjusted to 128, 32, and $4E^{-5}$, respectively.

2.6 Spectrophotometric Methodology. The oxidative process of a commercial sample of organic pork lard (Fatworksx, Premium Cooking Oil, EST.M-8757) under heating conditions (85ºC for 4 h) was evaluated after adding the corresponding antioxidants. The antioxidants were either individual components or binary mixtures of 10 different phenolic antioxidants, at different ratios. Standard solutions of each antioxidant (propyl gallate, PG; 2,4,5-trihydroxybutirophenone, TBHP; *tert*-butylhydroquinone, TBHQ; nordihydroguaiaretic acid, NDGA; *tert*-butyl-4-hydroxyanisole, BHA; 2,6 di-tert-butyl-4hidroxymethylphenol, PHENOL; 3,5 di-*tert*-butyl-4-hydroxytoluene, BHT; lauryl gallate, LG; octyl gallate, OG; ethoxyquin; ETOX) were obtained by dissolving a known amount of the pure standard in ethanol. The abbreviation of each antioxidant compound can be found in. Then, each antioxidant was incorporated into different aliquots of the commercial lard. Accordingly, 15 g of pre-melted commercial lard were mixed with 200 µL of the antioxidant standard solution to acquire a final concentration of 1 $mmol.kg^{-1}$ of antioxidant. To prepare 1 mL of the antioxidant´s binary combinations, proper volumes of lard containing the antioxidants were combined to get antioxidant ratios of 1/4:3/4, 2/4:2/4, and 3/4:1/4, respectively. Under those selected experimental conditions, 145 samples of lard containing antioxidants were evaluated. The oxidative effect of prepared lard samples was evaluated by the TBARS assay. The analytical procedure was carried out by adding 100 µL of lard to a glass vial containing 2 mL reagent solution (Thiobarbituric acid/trichloroacetic acid/ hydrochloric acid mixture). Then, the reaction mixture was heated up in a hot bath set at 100 ºC for 15 min. Consequently, the colorless starting solution turned to a pink-colored solution which developed an absorption band centered at 533 nm. Before spectrophotometric measurements, the resulting pink solution was centrifuged at 14500 rpm for 5 min. It is important to point out that lard and olive oil are commonly samples used as a lipid substrate to study rancidity [94-96]. While these samples share certain characteristics, they also offer are crucial differences that might influence the outcomes of our investigation. For example, organic pork lard does not contain any synthetic antioxidants while olive oil (particularly commercially available), typically contain multiple antioxidants. These compounds can interfere with the natural oxidation process, making lard a more suitable substrate to investigate the effect of the selected mixtures of phenolic antioxidants, as proposed in our studies.

2.7. TBARS assay. Fat-containing foods are highly susceptible to lipid oxidation, especially those containing polyunsaturated fatty acids. After the oxidative process, the generated hydroperoxides decompose into secondary oxidized products which are mainly aldehydes like malondialdehyde (MDA).[97] Besides peroxide determination to evaluate rancidity, MDA determination is often used in the assessment of lipid oxidation.[98] Thus, an spectrophotometric method based on the reaction of 2-thiobarbituric acid (TBA) with MDA (described in the Experimental Section) was selected. In this method, TBA is mixed and heated with the sample in acidic media to form a pink compound (maximum absorbance at 532-535nm), a product of the reaction with MDA and other lipid peroxidation products. It is also important to point out that the TBA assay not only allows quantifying MDA (mainly produced) but also other secondary oxidized products generated such as hexanal, and 4-hydroxynonenal (HNE) among others. For that reason, the expression thiobarbituric acid reactive substances (TBARS) assay is more widely accepted than the TBA method**.**

2.8 Combination Index (CI) Δ_{TBARS}. The CI is crucial to the development and evaluation of our artificial intelligence approach to predict the type and magnitude of interaction in antioxidant combinations. In this sense, it is worth understanding the basics underlying CI and how this metric, although not intended to be directly related to Δ_{TBARS}, can be used to assess the same phenomenon (antioxidant interaction). The combination index (CI) is a common metric used in isobologram analysis, typically deployed to quantitively measure the interaction between two or more drugs at specific concentrations. Interpreting CI values is straightforward. When the CI is greater than 1 (CL >1), it points to antagonistic interactions, suggesting that the combined effect of the active compound is less than what one would anticipate from their separate effects. If CI is equal to 1 (CI =1), additive interactions are expected. This implies that the response level for the combined active compounds is the same as the individual components. Finally, a CI less than 1 (CI <1) indicates synergistic interactions. In this scenario, the combinations of the active compounds surpass what one would predict from their individual effects. More information regarding the calculation of CI can be found elsewhere.[86]

As it will be further explained, the magnitude of antioxidant interaction can be assessed by using the TBARS assay. Briefly, the discrepancy between the readings obtained with samples infused with antioxidants and

their individual controls is noted as (Δ_{TBARS}). Therefore, synergistic interactions would result in a Δ_{TBARS} value greater than 0, whereas antagonistic interactions would yield a Δ_{TBARS} value less than 0. Then, mixtures leading to Δ_{TBARS} values that showed negligible variances compared to the baseline were considered to exhibit an additive antioxidant behavior. In this context, Δ_{TBARS} values display an inverse relationship with the CI value, which was chosen as a metric for the model. Therefore, a heightened level of synergistic antioxidant interactions leads to a reduction in the CI and a corresponding elevation in Δ_{TBARS}.

3. RESULTS AND DISCUSSION

The following paragraphs aim to describe the rational development and implementation of an AI model to predict the antioxidant capacity power of antioxidant mixtures. Beforehand, it is important to point out that the algorithm was initially trained using the MIT Mixed Augmented database[93] to generate a foundational general chemistry model. Then, this model was improved by the following three steps: I) Data splitting and augmentation; II) Model fine-tuning and testing, and III) Model enhancement by fine-tuning with chemically-relevant experimental data. First, the original database (developed from literature reports) was randomly divided into a training (85% of the database) and a test dataset (15% of the database). For both cases, the stoichiometric ratio of the mixture of antioxidants was represented either by repetitions of the same antioxidant in the SMILES notations or by numbers, as described in the experimental section of this manuscript. Second, both versions of the training dataset (numerical or textual) were used to fine-tune the foundational general chemistry model into a unique AI regressor to predict CI values. Then, the performance of all the generated antioxidant regressors was assessed by using the corresponding test dataset (textual or numerical) to measure key metrics such as root-mean-square error (RMSE), mean absolute percentage error (MAPE), as well as R^2. Finally, the regressor with the best predictive capability was enhanced by incorporating different amounts of benchtop data (antioxidant capacity of binary mixtures of phenolic antioxidants). An overview of these steps is represented in Figure 2.

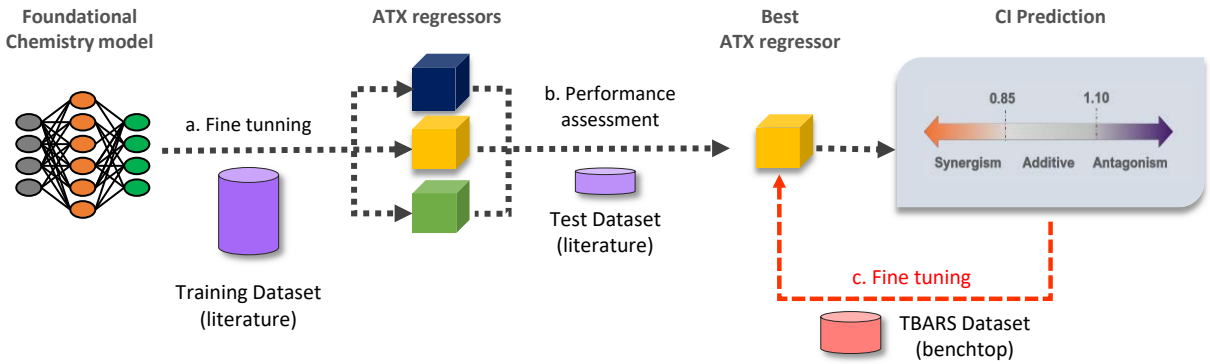

Figure 2: General overview of the process to fine-tune the foundational general chemistry model into several antioxidant regressors (a) followed by their respective performance assessments (b). The best antioxidant regressor was then fine-tuned with benchtop data (c) to enhance the CI prediction capability of the model with respect to mixtures of phenolic antioxidants. The relationship between CI values and the antioxidant behavior is described in the Experimental section.

Foundational Chemistry Model. As demonstrated in previous publications[90, 93, 99], the general chemistry model was pre-trained from scratch by using the well-known USPTO_MIT mixed augmented database that contains approximately one million unlabeled organic chemical reactions. Briefly, this step was included to increase the model's vocabulary (~5000 unique tokens) by providing sufficient chemical information in the form of text notation. Moreover, the parameters such as weights and bias were continuously adjusted during the training session (training dataset) to improve the model's performance using unseen chemical data (test dataset). This task was accomplished by monitoring the output of the loss function (e.g. "the loss") versus the number of epochs, leading to a loss of 4.00 at epoch number 32, which was considered acceptable. On the other hand, the loss for the training dataset at the same epoch number was 3.87, suggesting that a convergence point was reached by using both datasets and thus suggesting that more training was unlikely to further improve the model. The generated foundational chemistry model was then fine-tuned into several antioxidant regressors under different data representation scenarios.

3.1 Fine-tuning the foundational model into several regressors. A database developed and curated by our research group (ATX_uACL db) was developed from previous literature reports and used to fine-tune the last layer of the foundational general chemistry into several regressors. Our database contains approximately 1100 combinations (binary and tertiary) in the SMILES notation along with quantitative metrics regarding their antioxidant power such as combination index (CI), the difference in FRAP[87], % of

the synergistic or antagonistic effect[88] as well as Trolox equivalent antioxidant capacity (TEAC)[89]. Among those, mixtures with their respective combination indexes are the most common entry in our database (approximately 700) and, given their abundance, were selected to fine-tune the general chemistry model into the regressors. It is important to point out that only those combinations that aligned with both these quantitative metrics and established assay methodology described in the literature were incorporated into our database. For comparison purposes, our database displays 297 entries describing synergistic or antagonistic effects in terms of percentage, 161 for TEAC, and 85 for the differences in FRAP. Therefore, the use of CI was considered most appropriate for the proposed task since a higher number of antioxidant combinations leads to a more representative chemical space and to a more robust and accurate regressor. Aiming to further increase the total number of antioxidant mixtures, the stoichiometric number of each combination was represented as repetitions of the smiles strings rather than the numerical value itself (*vide infra*, Figure 1). In this sense, a mixture that contains two components (A and B) in the molar ratio 2:3 would render 10 unique combinations (permutations of B A B A B, for example). The proposed strategy was then implemented and compared to the use of numerical representation for the molar ratio (e.g., 2A 3B) during the model's fine-tuning into regressors as summarized in Table 1.

Table 1: summarized results for fine-tuning the general chemistry model into regressor with numerical and textual representations. RMSE: root mean square deviation; MAPE: mean absolute percentage error. all the equations used for the calculations in this table can be found in the Supporting Information.

		Test dataset		**Train dataset**	
Model	**epoch**	**RMSE**	**MAPE (%)**	**RMSE**	**MAPE (%)**
Numerical	001	3.77×10^{-2}	17.5	1.33×10^{-1}	20.0
	005	4.59×10^{-2}	16.2	1.00×10^{-1}	17.0
	010	2.90×10^{-2}	12.9	6.20×10^{-2}	12.3
	025	1.82×10^{-2}	10.1	3.90×10^{-2}	12.0
	100	1.21×10^{-2}	8.73	2.10×10^{-2}	7.34
	250	1.24×10^{-2}	8.65	6.30×10^{-3}	5.50
	350	**1.07×10^{-2}**	**7.76**	1.20×10^{-2}	5.24
	500	1.19×10^{-2}	8.11	1.10×10^{-2}	4.97
	750	1.37×10^{-2}	9.21	1.00×10^{-2}	4.82

	001	3.90×10^{-2}	13.9	6.10×10^{-2}	16.4
	005	2.90×10^{-2}	8.81	3.00×10^{-2}	11.5
	010	2.73×10^{-2}	11.3	2.90×10^{-2}	5.60
	025	1.95×10^{-2}	9.49	2.50×10^{-2}	5.27
Textual	100	1.24×10^{-2}	7.94	9.70×10^{-3}	6.21
	250	1.13×10^{-2}	7.02	9.30×10^{-3}	4.92
	350	1.04×10^{-2}	7.01	8.60×10^{-3}	4.60
	500	**1.01×10^{-2}**	**6.64**	5.26×10^{-3}	3.72
	750	1.17×10^{-2}	6.97	5.10×10^{-3}	3.76

Regarding the models fine-tuned with numerical representations, it can be observed that a minimum value of root mean square deviation (RMSE = 1.07×10^{-2}) and mean absolute percentage error (MAPE = 7.76) was achieved at epoch 350 (~20 minutes) for the test dataset. In other words, the combination index (CI) predicted by the model differs (on average) by 7.76% from the ground truth value. Any additional increase in training negatively impacted the performance of the algorithm assessing new data, indicating that the neural network was overfitted. This idea was also supported by the fact that the RMSE and MAPE are continuously decreasing while assessing the training dataset. On the other hand, the models fine-tuned with text representations performed better (RMSE = 1.01×10^{-2} and MAPE = 6.64) at epoch 500, suggesting that the textual model requires more training (~30 minutes) to achieve its best performance. To further investigate the prediction capability of both model types at their respective best epoch, the predicted CI was evaluated as a function of the target CI (value extracted from literature), results that are summarized in Figure 3.

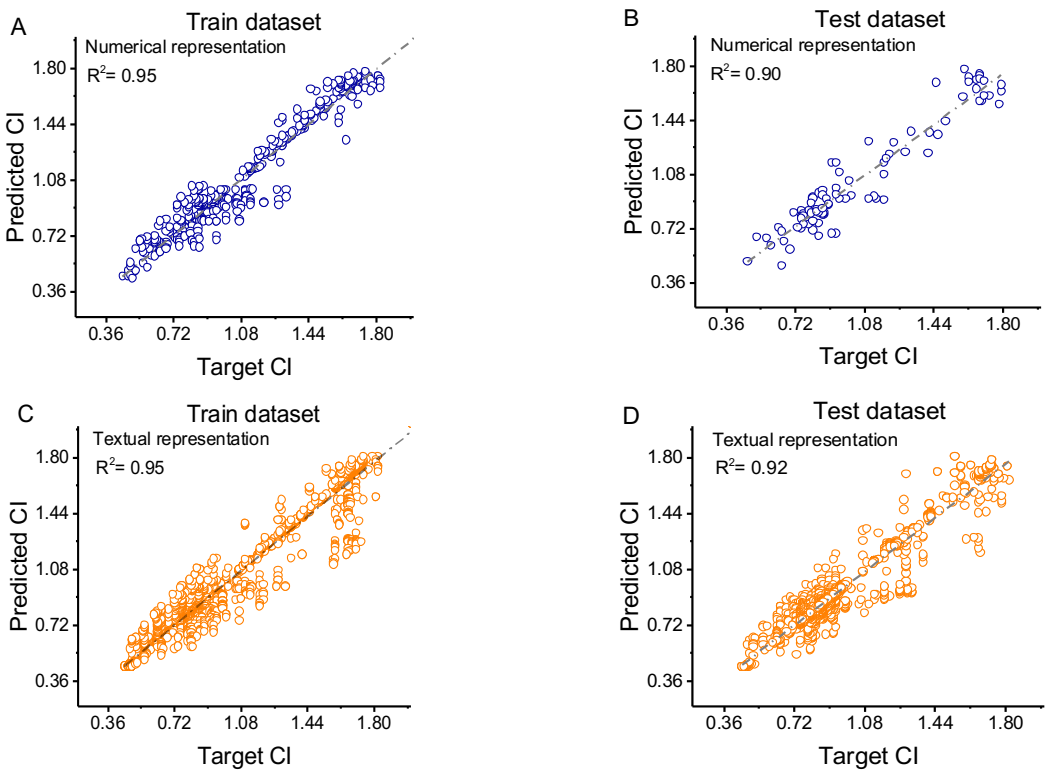

Figure 3: Predicted CI as a function of the target CI for both textual and numerical representation models and using the train and test datasets.

The textual and numerical models displayed a good agreement (R^2= 0.92 and R^2= 0.90, respectively) with respect to the target CI in the test dataset, demonstrating a satisfactory prediction capability at their best epochs. For both models, an R^2 of 0.95 was achieved by assessing the training dataset (Figure 3A and Figure 3C), which indicates that the neural network (for the textual model, R^2 = 0.92) is slightly better than the numerical model (R^2 = 0.90) at predicting unseen data (Figure 3B and Figure 3D). Although only a slight difference between the two models was observed, the use of textual representations could benefit the neural network's performance in cases where a limited amount of training data is available. In this scenario, a few experimental points (or data from the literature) could be augmented and then used to train the algorithm. In essence, while there are multiple ways to represent the same combination, the selection does not alter the overall count of unique antioxidant combinations. Although not relevant from a human point of view, this strategy is extremely powerful in the context of transformers-based architectures. The learning process of this deep learning algorithm (Electra in our case) is dependent on the sequence of the input, where subtle rearrangements of the SMILES string are perceived as distinct sequences by the model.

Consequently, this approach expands the model's exposure to the variety of possible input during training, contributing to a more robust and flexible understanding of individual antioxidant components in different contexts (combinations). Moreover, it is important to point out that some parts of the input are randomly 'masked' or hidden during the training phase. Then, the model is subsequently tasked with inferring these hidden sections, relying on the contextual environment offered by the unmasked components (antioxidants). In other words, the proposed permutations ultimately enhance the model's predictive performance and adaptability, allowing it to better handle the intricacies and complexities of antioxidant mixtures in different combinations.

For demonstration purposes, decreasing the size of the training dataset by half still allowed the textual model to display an acceptable performance (R^2 = 0.86); while cutting the numerical set by half rendered significantly poorer performances (R^2 = 0.61) when assessing the antioxidant combinations present in the test dataset (data not shown). Aiming to get further insights regarding the performance of both models, the cumulative distribution function (CDF)[100] was plotted versus the combination index for the target and predicted values (test dataset), as shown in Figure 4.

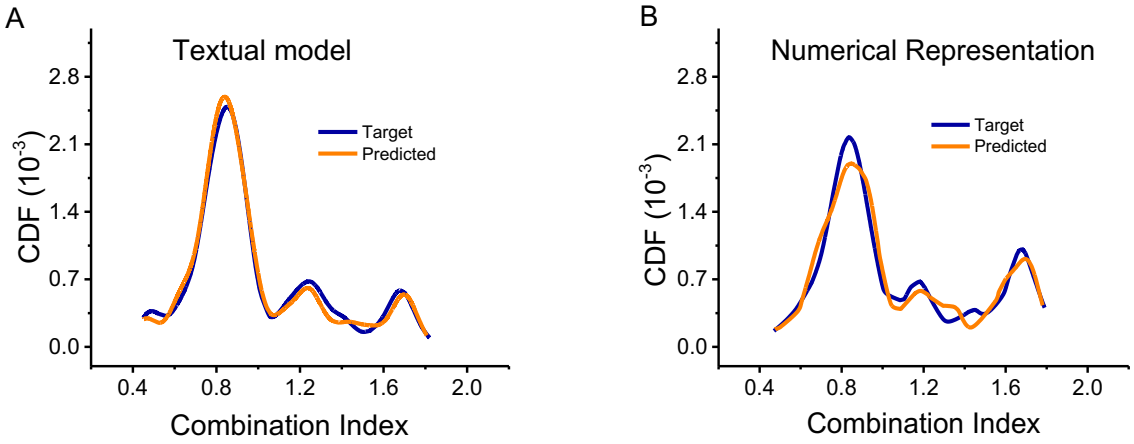

Figure 4: Cumulative distribution function versus the combination index for the textual (A) and numerical model (B).

This analysis showed that the cumulative distribution of the true combination index (blue line) falls in three main regions, displaying a higher CDF at a CI value of around 0.85. In other words, there is a higher probability of finding combination indexes with values equal to or lower than 0.85 (synergistic interactions)

in the test dataset, s finding that is aligned with the structure of our dataset. This characteristic was also observed in the training dataset (data not shown), indicating that the data splitting of the original database into the two subsets (train and test) was unbiased and representative. Moreover, there is a good agreement between the CDF for the predicted values for the textual model (Figure 4A, orange line) and the true output (Figure 4A, blue line) in all three regions. On the other hand, the predicted CDF for the numerical model (Figure 4B, orange line) is slightly off in all three regions, especially the one with CI > 1.10. These findings support the use of the textual model rather than the numerical one to investigate synergistic antioxidant interactions, occurence of great interest when developing novel antioxidant mixtures.Therefore, the textual model was selected and then applied to predict the behavior of antioxidant mixtures.

3.2 Experimental screnning. The antioxidant power of binary combinations of common phenolic compounds was investigated by using the thiobarbituric acid reactive substances (TBARS) assay[97, 101] and lard as a lipidic substrate. Briefly, thiobarbituric acid undergoes a complexation reaction with malondialdehyde (MDA), a well-known marker for oxidative stress in samples containing lipids, rendering a pink chromogen compound that can be quantitatively assessed via spectrophotometry.[97] Thus, the magnitude of the oxidative stress can be easily related to absorbance changes, allowing for an assessment of the rancidity in food samples in the presence or absence of antioxidants. In this scenario, lard samples were prepared with binary combinations of 10 phenolic antioxidants, incubated in a convection oven, and the resulting absorbance was compared to the absorbance generated in samples containing the individual components. The data analysis was accomplished through the use of a graphical method similar to an isobologram (see Supporting Information) allowing for the calculation of the difference (Δ_{TBARS}) between the absorbance obtained with samples containing antioxidants and the individual controls. Thus, synergistic combinations would render $\Delta_{TBARS} > 0$, while antagonistic interactions would generate $\Delta_{TBARS} < 0$. Following the same rationale, mixtures leading to Δ_{TBARS} values that showed only small differences with respect to the baseline were considered to feature an additive antioxidant behavior. Also in line with this analysis, Δ_{TBARS} values will be inversely proportional to the CI value, selected as an outcome for the model. Thus, a higher degree of synergistic antioxidant interactions results in a lower CI and in an increase in Δ_{TBARS}.

Figure 5 shows representative examples of the experimental Δ_{TBARS} obtained from binary combinations of phenolic antioxidants at either 1:3 or 3:1 molar ratios. Graphical representations of all other combinations are provided as Supporting Information.

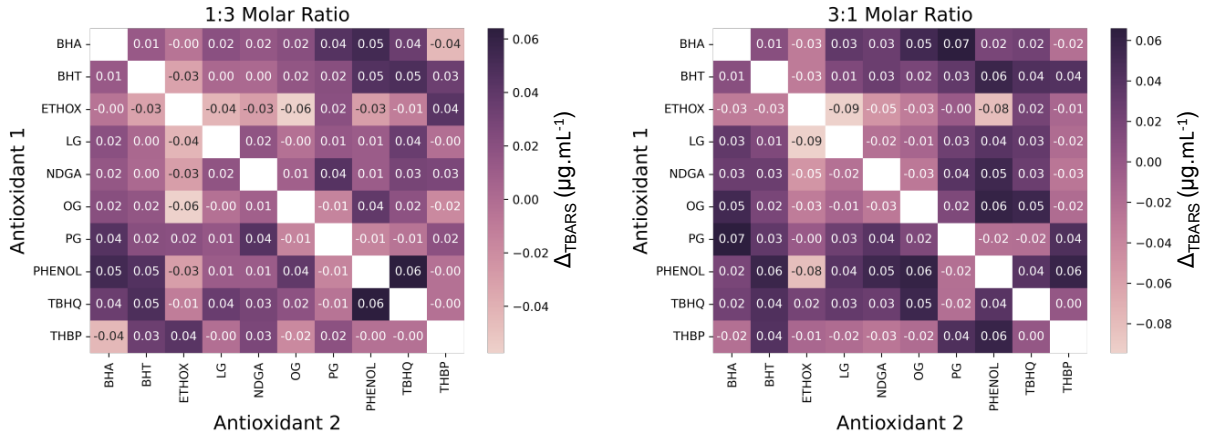

Figure 5: Experimental Δ_{TBARS} for phenolic antioxidant combinations at different molar ratios.

In line with scarce literature reports,[102] it is interesting to note that mixtures containing ETHOX mostly rendered antagonistic interactions (light pink color). On another hand, the vast majority of the synergistic interactions (dark purple) included mixtures containing either BHA or BHT, a finding that is also in good agreement with previous publications[64, 103-105] This phenomenon can be attributed to the potent free radical scavenging capabilities of BHA and BHT, which effectively delays the oxidative deterioration of food products. The synergistic effect emerges from their ability to intervene at varying stages of the oxidation process, neutralizing free radicals through the donation of hydrogen atoms.[34] It is worth mentioning that, at the molar ratio of 3:1, propyl gallate (PG) and BHA rendered a notable synergistic effect, displaying a Δ_{TBARS} of approximately +0.07. This elevated synergistic effect observed occurs due to the complementary mechanism of these two antioxidants, regenerating each other and stabilizing free radicals as reported by several groups.[64, 106, 107] It is also important to note that Δ_{TBARS} values in the ±0.1 were obtained, defining reasonable limits for our model[108] and allowing us to focus on mixtures featuring $-0.05 < \Delta_{TBARS} > +0.06$.

3.3 Challenging the model against benchtop data. It is worth mentioning that up until this point, our results provided strong evidence about the predictive power of the regressor trained and tested with textual representations of ~1100 antioxidants mixtures from the literature (R^2=0.92). Therefore, it was reasonable

to expect that our approach would provide accurate predictions of the CI values of the binary mixtures of phenolic antioxidants (see Supporting Information). Towards this goal, the antioxidant combinations used to obtain the data shown in Figure 5 were translated into SMILES format and used as input for the textual model with the best performance (epoch 500). This strategy relies on the fact that only the textual notation of those mixtures would be necessary to correctly predict their type of interaction rather than the use of chemical descriptors. It's important to emphasize that the SMILES notation is only capable of encoding 2.5D information regarding the antioxidant chemical structure. In this sense, the lack of 3D structural information may hinder critical molecular interactions relevant to understand antioxidant synergism. The predicted combination index for those mixtures versus its ground normalized experimental value (Δ_{TBARS}), is presented in Figure 6. In this initial assessment of the predictive power of the model, there was no evident correlation between the predicted CI value and the experimentally- obtained Δ_{TBARS} values.

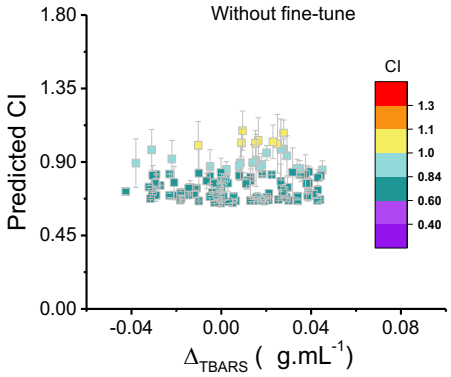

Figure 6: Predicted CI versus Δ_{TBARS} before model fine-tuning for the phenolic antioxidant combinations

Although these results were far from ideal, this outcome was somewhat expected since none of the compounds used in the benchtop experiments had been presented to the algorithm during the training session. In addition, the use of the proposed Δ_{TBARS} as a metric to quantify antioxidant interaction does not directly translate into CI values. These aspects are relevant because they suggest that despite the diversity of the mixtures in the training set, the model could not identify the chemical features of the selected phenolic antioxidants. These findings were somewhat expected, as approaches (based on a natural language processing) present limitations when presented with new structures (not present in the database), often leading to inaccurate predictions.

To address this shortcoming and enhance the predictive capabilities of the algorithm, a second fine-tuning step was implemented (c, in Figure 2), where increasing amounts of experimental data (SMILES notation and Δ_{TBARS} represented in terms of CI) were presented to the model. A summary of the results of the analysis is shown in Figure 7, where the correspondence between the two parameters was evaluated as a function of the amount (% of the experimental dataset, ~225 entries) used for the fine-tuning step.

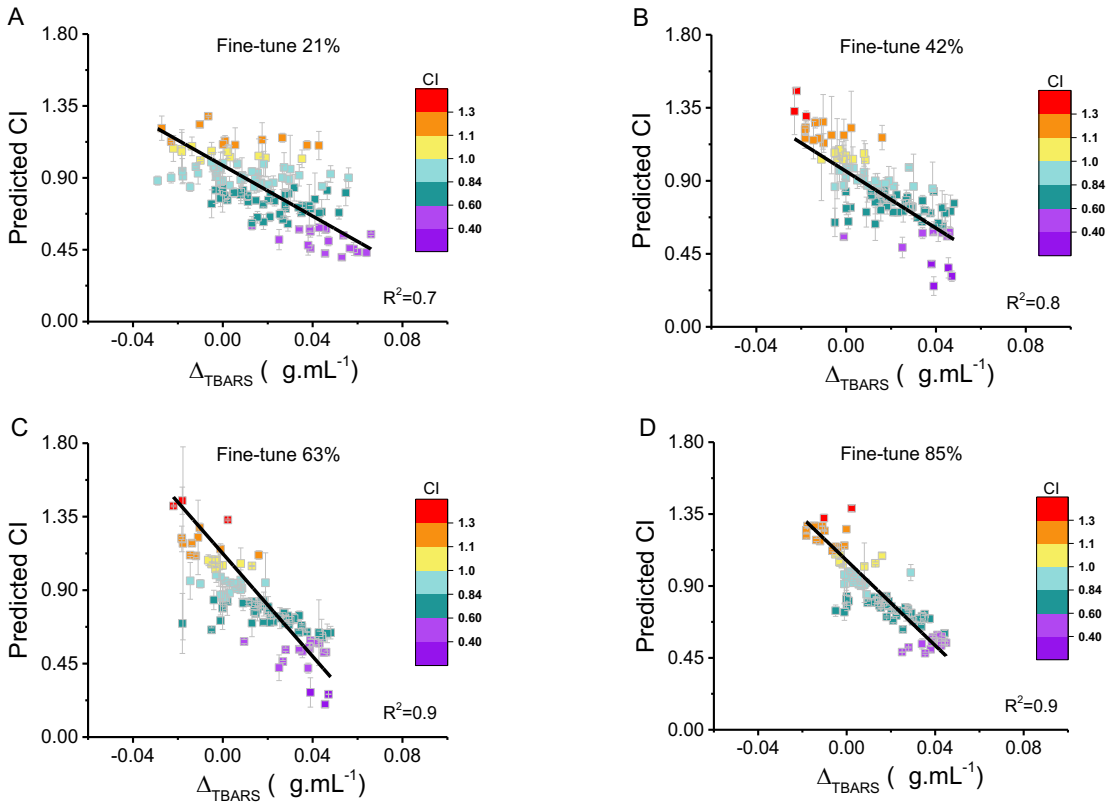

Figure 7: Relationship between the predicted CI and the experimental Δ_{TBARS} at 21%, 42%, 63%, and 85% fine-tune conditions.

As shown in Figure 7A, a fine-tuning step with just 21% of the experimental data (47 randomly selected data points) allowed the model to capture enough chemical patterns to render a positive correlation between the two variables. Despite this improvement, it is important to mention that the correlation within each group of data was rather poor. This trend is evident, for example, for CI values in the 1.1 – 1.3 range (antagonistic behavior), that expand horizontally covering a Δ_{TBARS} range from -0.03 g.ml^{-1} (antagonistic) all the way to +0.04 g.ml^{-1} (synergistic). This outcome aligns with our initial expectations, as exposing the model to a modest fraction of the experimental chemical space is only sufficient to elucidate a basic grasp of the

prevent trend between CI and delta Δ_{TBARS}. Fortunately, as more experimental data was presented, the model was able to identify the chemical patterns within each group, leading to more accurate predictions of the CI values. When the model was fine-tuned with 63% of the experimental data (142 randomly selected data points), a substantially better agreement (R^2= 0.90) between the CI and Δ_{TBARS} was obtained, showing only a few predicted values erroneously classified. For example, points of the same color should be clustered at a specific region of Δ_{TBARS} and not shift horizontally. In practical terms, this behavior is not critical as long as the predicted points fall in their true interaction category (synergistic: CI < 0.85, additive: 0.85 < CI > 1.10, or antagonistic interaction: CI > 1.10). On the other hand, when the model was fine-tuned with 85% of the experimental data (191 randomly selected datapoints), a full agreement and lower dispersion of the data was obtained, indicating the possibility of using this model for predicting the behavior of the selected antioxidant mixtures.

4. CONCLUSIONS

This work describes the first example of using Artificial Intelligence based on deep learning architecture; to predict antioxidant interactions (synergism, additive, and antagonism) by using SMILES notation to predict combination indexes. The best-generated algorithm (R^2_{test}= 0.92 and R^2_{train}=0.95; assessing our proprietary database) was achieved through a new data augmentation strategy where the stoichiometric ratio in the antioxidant mixture was replaced by repetitions of the corresponding antioxidant in SMILES format. This proposed augmentation approach leads to a more representative chemical space during the model training, which addresses common overfitting problems due to the use of relatively small datasets. Then, the predictive capability of the algorithm was challenged against experimental benchtop data collected through TBARS assay. As a result, an expected inverse correlation between the predicted CI and Δ_{TBARS} increases (R^2= 0.7 to 0.9) as the amount of fine-tuning data increases (21% to 85%), suggesting that the model successfully recognized chemical patterns from the antioxidant compounds used in the experimental analysis. We believe that the proposed method could be used as an auxiliary tool in benchmark analysis routines, offering a novel strategy to enable broader and more rational predictions related to the antioxidant mixtures behavior, information that can't be obtained by using only experimental or computational approaches alone.

5. COMPETING INTERESTS

The authors declare no competing interest

6. SUPPORTING INFORMATION

Dependence of the loss with respect to the epoch number (foundational chemistry model training), Equations to calculate root mean square error and mean absolute percentage error equations, Experimental Δ_{TBARS} for all binary phenolic antioxidants mixtures, and SMILES notation of all binary phenolic antioxidant combinations.

7. ACKNOWLEDGMENTS

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8. DATA AVAILABILITY

The datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

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For Table of Contents Only

Supporting Information for

Predicting Antioxidant Synergism via Artificial Intelligence and Benchtop Data

Lucas Ayres, Tomás Benavidez, Armelle Varillas, Jeb Linton, Daniel C. Whitehead, and Carlos D. Garcia

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1. Foundational chemistry model training.

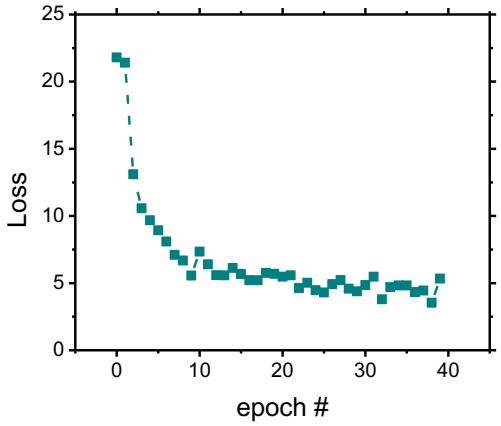


Figure S1: Training loss versus the number of epochs for the foundational general chemistry model

2. Root mean square error and Mean absolute percentage error equations.

Root mean square error

$$RMSE = \sqrt{\sum_{i=1}^{n} \frac{(\hat{y}_i - y_i)^2}{n}}$$

Predicted True

Mean absolute percentage error

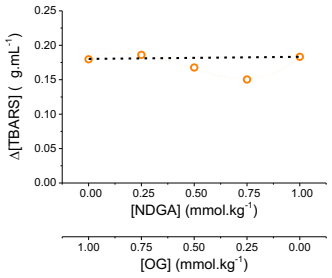
$$\mathrm{M} = \frac{1}{n} \sum_{t=1}^{n} \left| \frac{A_t - F_t}{A_t} \right|$$

True Predicted

True

Figure S2: Equations used for calculating root mean square error (RMSE) and mean absolute percentage error (M).

3. Experimental Δ_{TBARS} for all binary phenolic antioxidant mixtures.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0.20
0.15
0.10
0.05
0.00
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[NDGA] (mmol.kg-1)
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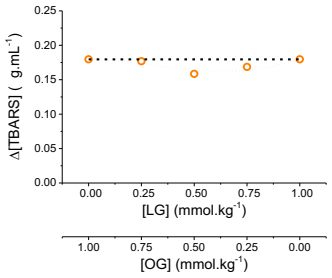
[OG] (mmol.kg-1)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0.20
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0.00
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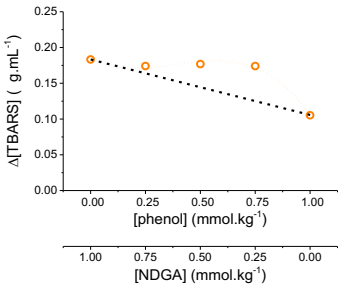
[OG] (mmol.kg-1)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0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
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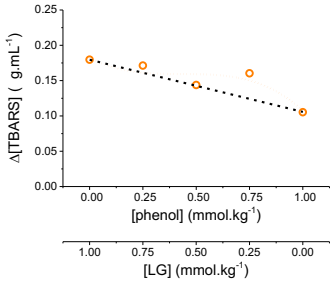
[NDGA] (mmol.kg-1)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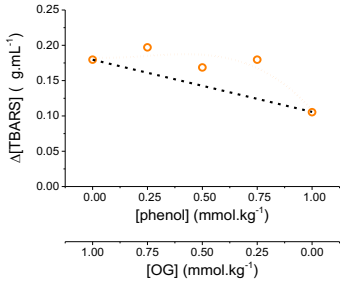
[LG] (mmol.kg-1)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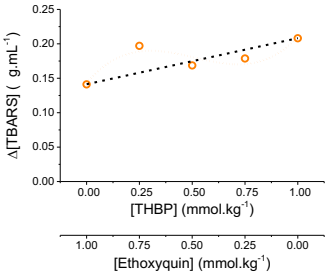
[OG] (mmol.kg-1)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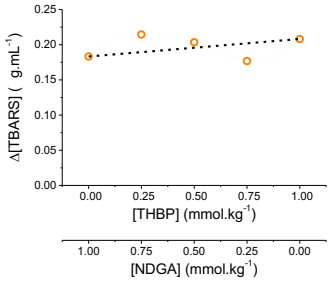
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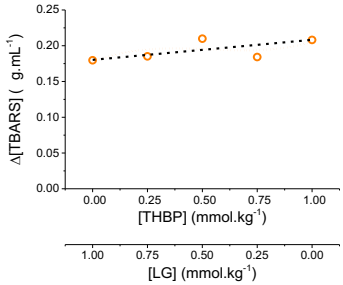
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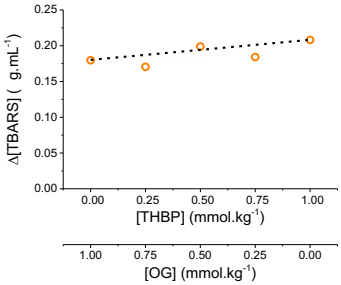
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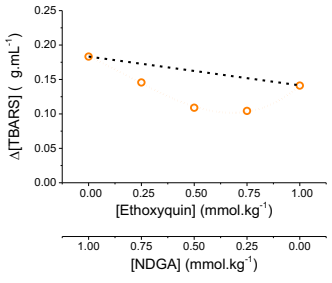
[OG] (mmol.kg-1)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0.10
0.05
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[Ethoxyquin] (mmol.kg-1)
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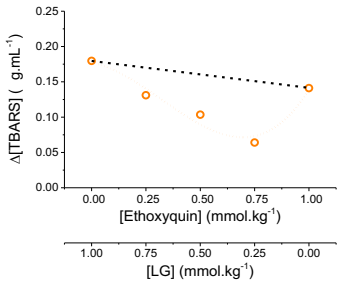
[NDGA] (mmol.kg-1)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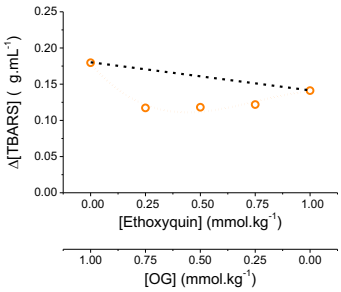
[LG] (mmol.kg-1)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0.05
0.00
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[Ethoxyquin] (mmol.kg-1)
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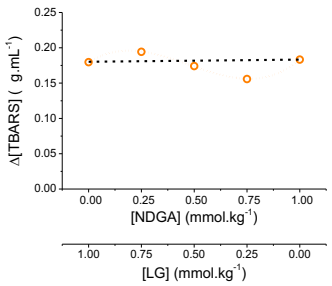
[OG] (mmol.kg-1)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0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[NDGA] (mmol.kg-1)
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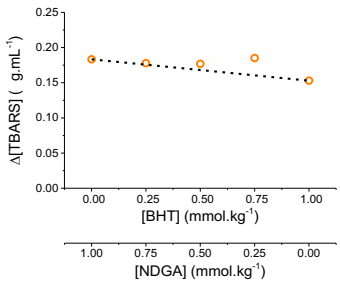
[LG] (mmol.kg-1)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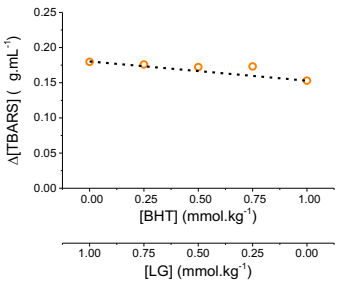
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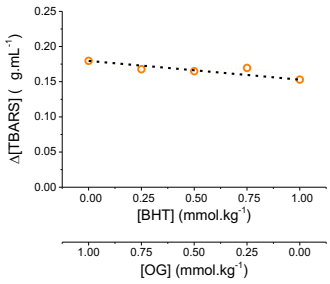
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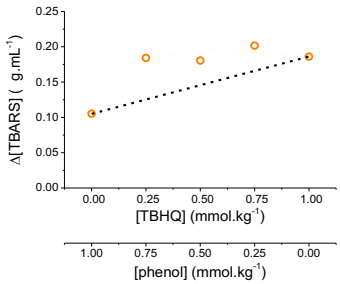
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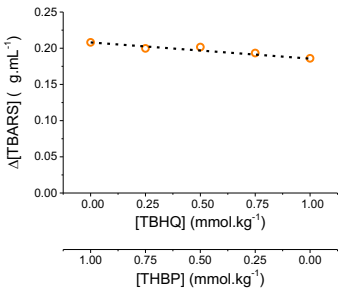
[phenol] (mmol.kg-1)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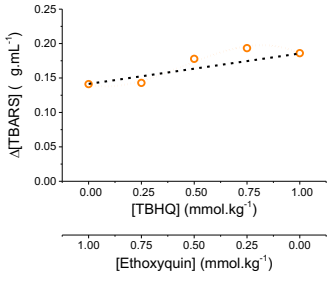
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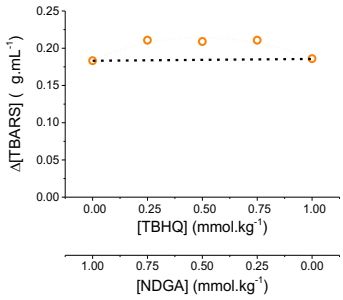
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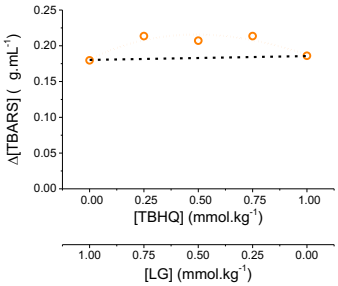
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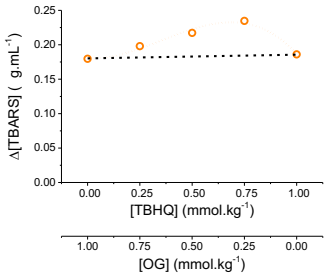
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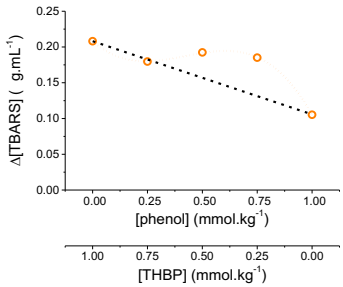
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0.00
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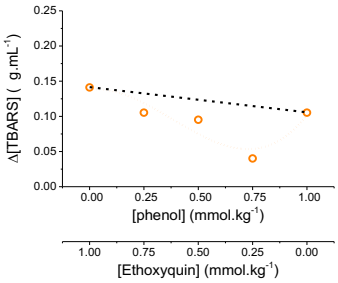
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0.05
0.00
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[phenol] (mmol.kg-1)
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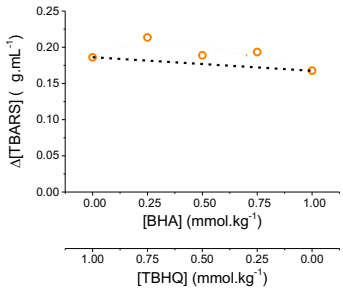
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0.00
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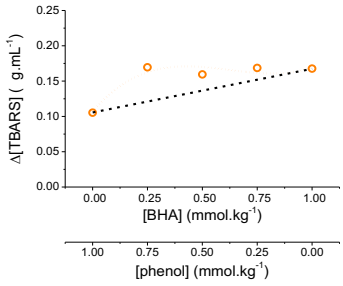
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[TBHQ] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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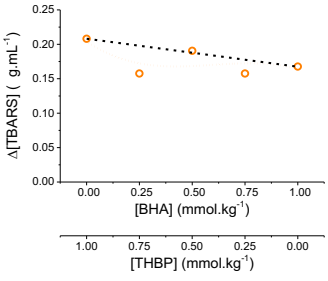
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[phenol] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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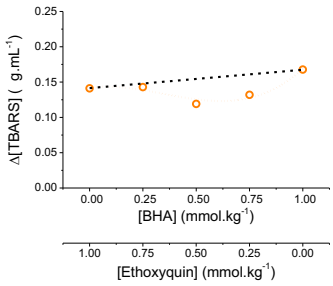
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[THBP] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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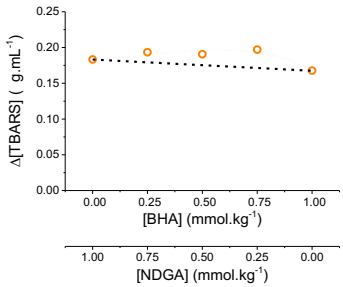
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[Ethoxyquin] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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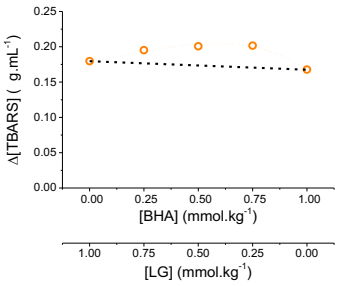
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[NDGA] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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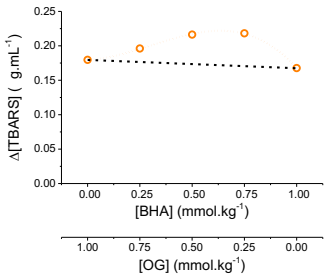
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[LG] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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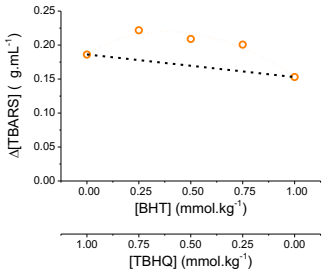
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[OG] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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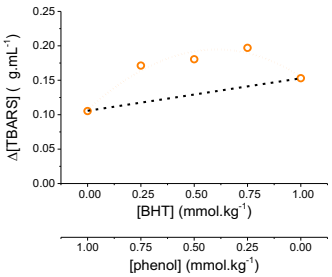
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHT] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[TBHQ] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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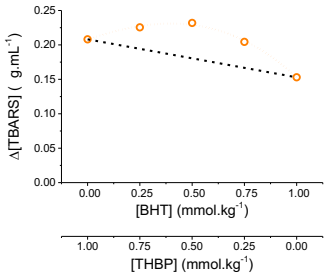
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHT] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[phenol] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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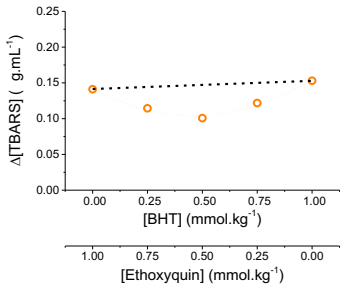
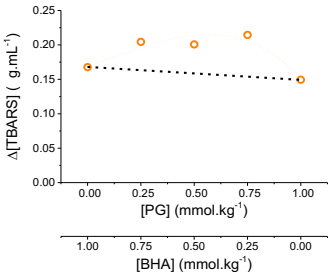
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHT] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[THBP] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
0.25
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHT] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[Ethoxyquin] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
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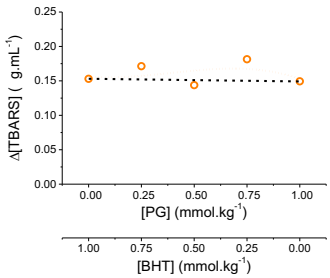
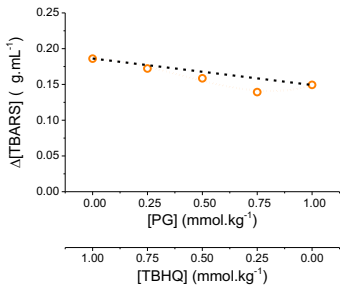
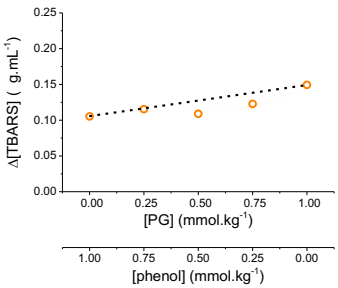
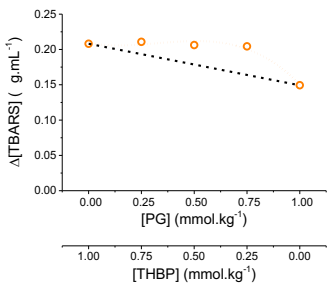
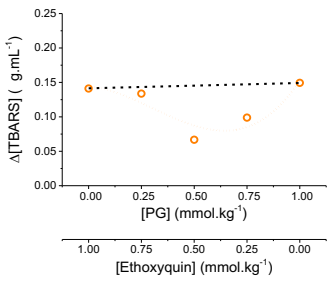
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[PG] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[BHA] (mmol.kg-1)

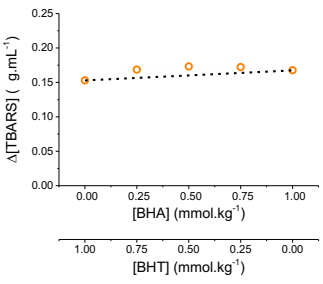

Δ[TBARS] (g.mL-1)
0.25
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[PG] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[BHT] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
0.25
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[PG] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[TBHQ] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
0.25
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[PG] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[phenol] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
0.25
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[PG] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[THBP] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
0.25
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[PG] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[Ethoxyquin] (mmol.kg-1)


Δ[TBARS] (g.mL-1)
0.25
0.20
0.15
0.10
0.05
0.00
0.00 0.25 0.50 0.75 1.00
[BHA] (mmol.kg-1)
1.00 0.75 0.50 0.25 0.00
[BHT] (mmol.kg-1)

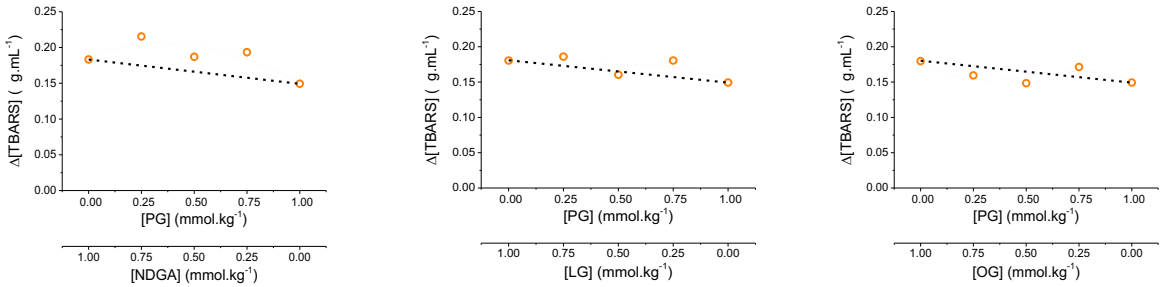


Figure S3: Graphical representation displaying the antioxidant effect for all the phenolic compounds.

4. Smiles notation of all binary phenolic antioxidant combinations.

Table S 1: SMILES notation for all the binary phenolic antioxidant combination.

Combination	Molar ratio	Canonical SMILES
PG BHA	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1
PG BHA	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCC(CC)(CC)CC.COc1ccc(O)cc1
PG BHA	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCC(CC)(CC)CC.COc1ccc(O)cc1
PG BHT	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1
PG BHT	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1
PG BHT	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1
PG TBHQ	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O
PG TBHQ	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(C)(C)c1cc(O)ccc1O
PG TBHQ	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(C)(C)c1cc(O)ccc1O
PG Phenol	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
PG Phenol	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
PG Phenol	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
PG THBP	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O
PG THBP	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCC(=O)c1cc(O)c(O)cc1O

PG THBP	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCC(=O)c1cc(O)c(O)cc1O
PG ETHO	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
PG ETHO	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
PG ETHO	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
PG NDGA	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
PG NDGA	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
PG NDGA	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
PG LG	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
PG OG	1:3	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
PG OG	1:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
PG OG	3:1	CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHA BHT	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1
BHA BHT	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1
BHA BHT	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1
BHA TBHQ	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O
BHA TBHQ	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(C)(C)c1cc(O)ccc1O
BHA TBHQ	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(C)(C)c1cc(O)ccc1O
BHA Phenol	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
BHA Phenol	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
BHA Phenol	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
BHA THBP	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O
BHA THBP	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(=O)c1cc(O)c(O)cc1O
BHA THBP	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(=O)c1cc(O)c(O)cc1O

BHA ETHO	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
BHA ETHO	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
BHA ETHO	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
BHA NDGA	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
BHA NDGA	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
BHA NDGA	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
BHA LG	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHA LG	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHA LG	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHA OG	1:3	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHA OG	1:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHA OG	3:1	CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCC(CC)(CC)CC.COc1ccc(O)cc1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHT TBHQ	1:3	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O
BHT TBHQ	1:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(C)(C)c1cc(O)ccc1O
BHT TBHQ	3:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(C)(C)c1cc(O)ccc1O
BHT Phenol	1:3	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
BHT Phenol	1:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
BHT Phenol	3:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
BHT THBP	1:3	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O
BHT THBP	1:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCC(=O)c1cc(O)c(O)cc1O
BHT THBP	3:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCC(=O)c1cc(O)c(O)cc1O
BHT ETHO	1:3	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
BHT ETHO	1:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2

BHT ETHO	3:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
BHT NDGA	1:3	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
BHT NDGA	1:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
BHT NDGA	3:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
BHT LG	1:3	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHT LG	1:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHT LG	3:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHT OG	1:3	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHT OG	1:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
BHT OG	3:1	Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 Cc1cc(C(C)(C)C)c(O)c(C(C)(C)C)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
TBHQ Phenol	1:3	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
TBHQ Phenol	1:1	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
TBHQ Phenol	3:1	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O
TBHQ THBP	1:3	CC(C)(C)c1cc(O)ccc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O
TBHQ THBP	1:1	CC(C)(C)c1cc(O)ccc1O CCCC(=O)c1cc(O)c(O)cc1O
TBHQ THBP	3:1	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CCCC(=O)c1cc(O)c(O)cc1O
TBHQ ETHO	1:3	CC(C)(C)c1cc(O)ccc1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
TBHQ ETHO	1:1	CC(C)(C)c1cc(O)ccc1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
TBHQ ETHO	3:1	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
TBHQ NDGA	1:3	CC(C)(C)c1cc(O)ccc1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
TBHQ NDGA	1:1	CC(C)(C)c1cc(O)ccc1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
TBHQ NDGA	3:1	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
TBHQ LG	1:3	CC(C)(C)c1cc(O)ccc1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1

TBHQ LG	1:1	CC(C)(C)c1cc(O)ccc1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
TBHQ LG	3:1	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
TBHQ OG	1:3	CC(C)(C)c1cc(O)ccc1O CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
TBHQ OG	1:1	CC(C)(C)c1cc(O)ccc1O CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
TBHQ OG	3:1	CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CC(C)(C)c1cc(O)ccc1O CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
Phenol THBP	1:3	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O
Phenol THBP	1:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCC(=O)c1cc(O)c(O)cc1O
Phenol THBP	3:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCC(=O)c1cc(O)c(O)cc1O
Phenol ETHO	1:3	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
Phenol ETHO	1:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
Phenol ETHO	3:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
Phenol NDGA	1:3	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
Phenol NDGA	1:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
Phenol NDGA	3:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
Phenol LG	1:3	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
Phenol LG	1:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
Phenol LG	3:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
Phenol OG	1:3	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
Phenol OG	1:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
Phenol OG	3:1	CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CC(C)(C)c1cc(CO)cc(C(C)(C)C)c1O CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
THBP ETHO	1:3	CCCC(=O)c1cc(O)c(O)cc1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
THBP ETHO	1:1	CCCC(=O)c1cc(O)c(O)cc1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2
THBP THO	3:1	CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCOc1ccc2c(c1)C(C)=CC(C)(C)N2

THBP NDGA	1:3	CCCC(=O)c1cc(O)c(O)cc1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
THBP NDGA	1:1	CCCC(=O)c1cc(O)c(O)cc1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
THBP NDGA	3:1	CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
THBP LG	1:3	CCCC(=O)c1cc(O)c(O)cc1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1
THBP LG	1:1	CCCC(=O)c1cc(O)c(O)cc1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
THBP LG	3:1	CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1
THBP OG	1:3	CCCC(=O)c1cc(O)c(O)cc1O CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1
THBP OG	1:1	CCCC(=O)c1cc(O)c(O)cc1O CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
THBP OG	3:1	CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCC(=O)c1cc(O)c(O)cc1O CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1
ETHO NDGA	1:3	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
ETHO NDGA	1:1	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
ETHO NDGA	3:1	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1
ETHO LG	1:3	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1
ETHO LG	1:1	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
ETHO LG	3:1	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
ETHO OG	1:3	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
ETHO OG	1:1	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
ETHO OG	3:1	CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCOc1ccc2c(c1)C(C)=CC(C)(C)N2 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
NDGA LG	1:3	CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1
NDGA LG	1:1	CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
NDGA LG	3:1	CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CCCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
NDGA OG	1:3	CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c(O)c1
NDGA OG	1:1	CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1

NDGA OG	3:1	CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CC(Cc1ccc(O)c(O)c1)C(C)Cc1ccc(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
LG OG	1:3	CCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
LG OG	1:1	CCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1
LG OG	3:1	CCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1 CCCCCCCCOC(=O)c1cc(O)c(O)c(O)c1