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The mechanism of chlorogenic acid inhibits lipid oxidation: An investigation using multi-spectroscopic methods and molecular docking

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17 **Abstract:** Endogenous lipase and lipoxygenase play important roles in accelerating lipid oxidation.  
18 Polyphenols are a series of commonly used chemicals for preserving fish and seafood products, due to their  
19 positive inhibitory effects on lipid oxidation. However, the mechanism involved is still unknown. The  
20 inhibitory effects of chlorogenic acid (CGA) on lipase and lipoxygenase were investigated and explored  
21 with multi- spectroscopic and molecular docking approaches. Results showed that CGA could inhibit the  
22 activities of lipase and lipoxygenase with concentration increased in a highly dose-dependent manner. CGA  
23 quenched intrinsic fluorescence intensities of enzymes by static quenching and binding with CGA which  
24 led to changes in 3D structures of enzymes. Results of the molecular docking confirmed binding modes,  
25 binding sites and major interaction forces between CGA and enzymes, which reduced the corresponding  
26 activity. Thus, this study could provide basic mechanisms of the inhibitory effects of polyphenols on lipid  
27 oxidation during food preservation.

28

29 **Keywords:** Chlorogenic acid; Lipase; Lipoxygenase; Spectroscopy analysis; Molecular docking;

## 30 **1 Introduction**

31 Lipase (triacylglycerol acylhydrolases, EC 3.1.1.3) belongs to carboxylesterases and widely exists in  
32 animals and plants. It catalyzes the hydrolysis of triglycerides, which contain long-chain fatty acids at sn-2  
33 and sn-1 positions, to free fatty acid and glycerol at the lipid-water interface (Cherif & Gargouri, 2009).  
34 Hydrolysis products can further be oxidized by lipoxygenase and free radicals. Lipoxygenase (LOX, EC  
35 1.13.11.12), a class of protein which contains non-heme iron, specifically catalyzes polyunsaturated fatty  
36 acids and fatty acid esters with a 1,4-*cis, cis* pentadiene structure into hydroperoxide (Andreou, et al., 2010).  
37 The catalytic site of LOX is composed of metal ion and amino acid residues. LOX oxidizes unsaturated  
38 fatty acids and esters into hydro peroxide derivatives (Nikpour, et al., 2013). Previous studies showed that  
39 lipase and LOX affect important physiological reactions which are involved in the pathogenesis of various  
40 diseases in humans (Schreiber, et al., 2019).

41 Enzymatic reactions are not only closely related to human diseases, but are also associated with lipid  
42 oxidation of fish and fish products during transportation, processing and storage. Oxidizing reaction in the  
43 muscle tissue leads to undesirable changes and quality deterioration, such as production of off-odor, rancid  
44 flavors, and changes in color and texture (Chauhan, et al., 2018). The increasing content of carbonyl  
45 compounds and free fatty acid, which are the main products of enzymatic reactions, influence the flavor of  
46 meat (Huang & Ahn, 2019). When the concentration of compounds like hexanal, pentanal, 2, 6-nonadienal  
47 and 1-octen-3-one, plus 2, 3-octanedione is high enough, it will produce unpleasant odor. Furthermore, when  
48 oxidative products of lipid accelerate protein oxidation, some functions for instance, water holding capacity  
49 and protein extractability decline with the oxidation proceeding. These lead to the deterioration of protein  
50 functional properties during food processing and preservation, for example, loss of moisture, decrease in  
51 hardness and emulsion capacity (Utrera, et al., 2015). Therefore, the inhibition of endogenous enzyme-  
52 induced lipid oxidation has become more and more important to fish and fish products.

53 Polyphenols, as one of the representative natural antioxidants, have been shown to perform well in  
54 inhibiting lipid oxidation during fish processing and preservation. For instance, the combination of tea  
55 polyphenols and vacuum packaging treatment used in weever (*Micropterus salmoides*) storage, presented  
56 better quality enhancement effects and good quality control which extended the corresponding shelf life at  
57 0 °C and 4 °C (Ju, et al., 2018). Glazing treatment with rosemary (*Rosmarinus officinalis*) extract displayed  
58 the best performance in controlling protein and lipid changes of mud shrimp (*Solenocera melantho*) stored  
59 at -20 °C (Shi, et al., 2019). Furthermore, phenolic compounds such as caffeic acid, coumaric acid, capsaicin,  
60 quercetin, epigallocatechingallate (EGCG) showed inhibitory effects on pancreatic lipase *in vitro* (Martinez-  
61 Gonzalez, et al., 2017). Chlorogenic acid (CGA), the ester of caffeic acid and quinic acid, is a type of  
62 polyphenol widely present in natural plants. CGA exhibits various biological properties which include  
63 antioxidant, antibacterial, anti- inflammation (Karar, et al., 2016) and anti-glycation (Gugliucci, et al., 2009).  
64 Therefore, the absorption of CGA might induce biological effects in the whole body system, such as  
65 protection against cardiovascular disease; and the inhibition of the formation of mutagenic and carcinogenic  
66 N-nitroso compounds (Olthof, et al., 2001). Besides the healthy and various biological effects, it has been  
67 demonstrated that it is effective in food preservation, for example peach storage (Jiao, et al., 2019) and raw  
68 refrigerated chicken (Sun, et al., 2020). In recent years, research on CGA has focused on the preservation  
69 of aquatic products. For example, CGA-gelatin combined with partial freezing effectively delayed the decay  
70 of sword prawn (*Parapenaeopsis hardwickii*) (Ge, et al., 2020). However, there are very few studies that  
71 have demonstrated the application of grass carp preservation in the field. Recently, we found that CGA  
72 showed good efficiency in inhibiting lipid oxidation of grass carp muscle during chilled storage (Cao, et al.,  
73 2019). However, the mechanism of action of CGA and mode of inhibition of lipid oxidation during fish  
74 preservation is still not yet clear. Thus, the interactions between CGA and lipase/lipoxygenase are important

75 for understanding the mechanism of the application of CGA on grass carp preservation.

76 In this study, the interactions of CGA with endogenous enzymes extracted from grass carp muscle were  
77 investigated using enzyme activity inhibition assay, intrinsic fluorescence quenching measurement,  
78 secondary structure determination and Fourier transform- infrared spectroscopy (FT-IR) measurement.  
79 Moreover, the information of binding modes and binding sites of CGA on lipase and LOX were separately  
80 explored utilizing the molecular docking method. We aimed to explain or give some insights into the  
81 inhibitory mechanism of CGA on lipid oxidation during fish preservation.

82

## 83 **2 Materials and methods**

### 84 **2.1 Materials**

85 CGA was purchased from Melonepharma (Dalian, Liaoning, China) while 4-nitrophenyl butyrate (4-  
86 NPB) was obtained from Sigma–Aldrich Chemical Co (St. Louis, MO, USA) and linoleic acid from Aladdin  
87 (Shanghai, China). Protein loading buffer (5×) was purchased from Kerui (Wuhan, Hubei, China). All  
88 reagents and chemicals used were of analytical grade.

### 89 **2.2 Fish sample preparation**

90 All procedures were approved by the Animal Care and Use Committee of Huazhong Agricultural  
91 University and performed in accordance with the Guidelines for Care and Use of Laboratory Animals of  
92 Huazhong Agricultural University. Fresh grass carp ( $3.5\pm 0.5$  kg,  $n=10$ ) were purchased from a local fish  
93 market (Wuhan, Hubei, China). The sampled fish were anaesthetized using MS - 222 (100 mg/L, 3-  
94 Aminobenzoic acid ethyl ester methanesulfonate, Shanghai yuanye Bio-Technology Co., Ltd, Shanghai, P.R.  
95 China) and were unconscious before slaughter. Then the fish were immediately decapitated and gutted, and  
96 the red muscle under the skin was removed, and the white muscle collected, weighed and mixed for further  
97 study.

### 98 **2.3 Extraction of endogenous enzymes**

99 The extraction of lipase was carried out following the Smichi method (Smichi, et al., 2013). The fish  
100 muscle sample was homogenized in ten times volume (1:10, *w/v*) 25mM Tris-HCl buffer (pH=8.0, 4 °C,  
101 150 mM NaCl, 2 mM benzamidine) with a blender (Y-QSJ1, Oidire, German) for 3×10 s (4000 rpm). Then  
102 the mixture was stirred with a magnetic bar (Thermo, Massachusetts, USA) for 45 min (4 °C), and  
103 centrifuged for 20min (4 °C, 10000×g). The supernatant was collected and ammonium sulphate added (40%  
104 of the supernatant weight). The mixture was stirred for 45 min at 4 °C, and centrifuged at 10000×g for 15  
105 min. The supernatant was collected and ammonium sulphate added to 60% saturation. Lastly, the solution  
106 was stirred and centrifuged using the same procedure, and the sediment (lipase) was collected into a dialysis  
107 bag for desalting with former Tris-HCl buffer for 24h, and the buffer was changed every 6h.

108 The lipoxygenase (LOX) was extracted according to a former method (Gata, et al., 1996). Generally,  
109 the fish muscle sample was homogenized in five times volume (*v/m*: 5:1) phosphate buffer (pH=7.4, 50mM,  
110 1mM Dithiothreitol, 1 mM Ethylenediaminetetraacetic acid (EDTA)) with a blender (4000 rpm, 4×10s).  
111 The mixture was stirred with a magnetic bar at 4 °C for 30min, and further centrifuged (4 °C, 10000×g) for  
112 20min. The supernatant was collected and filtrated through a gauze to obtain a crude enzyme solution. To  
113 the crude solution was added ammonium sulphate to 20% saturation, stirred for 45min (4 °C) and then  
114 centrifuged for 15 min (4 °C, 10000×g). The supernatant was collected and ammonium sulphate added to  
115 40% saturation, stirred and centrifuged with former parameters. Finally, the sediment (LOX) was collected  
116 and dialyzed following the same extraction procedure of lipase.

### 117 **2.4 SDS-PAGE (Sodium dodecyl sulfate - polyacrylamide gel electrophoresis)**

118 The protein content in a sample was determined with the Lowry method (Lowry, et al., 1951), and the  
119 molecular weight of the endogenous enzyme was determined using SDS-PAGE analysis (n=4). The detailed

120 procedure of the SDS-PAGE was describe in our previous study (Huo, et al., 2016) with slight modification  
121 of the solution. The best concentration of separating gel was set to 10%. After electrophoresis, the gel was  
122 stained with ~0.1% (w/v, 0.29g in 250 ml) Coomassie blue R-250, dissolved with the solution (250 ml) of  
123 8% (v/v) acetic acid and 25% (v/v) ethanol (95%); and destained overnight in 8% (v/v) acetic acid and 25%  
124 (v/v) ethanol (95%). The markers of proteins (10 to 250 kDa) were also run in parallel on the same gel to  
125 determine the molecular weights of the protein.

## 126 **2.5 Enzyme inhibition assay**

127 Lipase activity was determined using the 4-NPB method (n=3) (Kuepethkaew, et al., 2017). The  
128 substrate solution was prepared by dissolving 4-NPB in isopropanol. The reaction was carried out by mixing  
129 800  $\mu$ L diluted lipase, 800  $\mu$ L CGA solution, and 2.0 mL 50 mM Tris-HCl buffer (pH=8.0, containing 0.5 %  
130 Tritox X 100, 25mM NaCl). The reaction was initialized with the addition of 400  $\mu$ L substrate solution, and  
131 the mixture reacted at 37  $^{\circ}$ C for 15 min. The absorbance was measured with ultraviolet-visible  
132 spectrophotometer at 410 nm and one unit of enzyme activity was defined as the enzyme liberated per  $\mu$ mol  
133 of p-nitrophenol in 1 minute. There were three types of inhibition experiments performed with different  
134 concentrations of solution. For the inhibition ratio, the concentrations of lipase and 4-NPB solution were  
135 0.1mg/mL and 3mM, respectively. For the inhibition type experiments, the following concentrations were  
136 used: lipase: 0.025, 0.05, 0.1, 0.2, 0.3 mg/mL; CGA: 0, 0.1, 0.2, 0.3 mg/mL; 4-NPB: 3mM. For the inhibition  
137 kinetics experiments, the following concentrations were investigated: lipid: 0.1mg/mL; CGA: 0, 0.1, 0.2,  
138 0.3 mg/mL; 4-NPB: 1, 2, 3, 4, 5 mmol/L.

139 LOX's activity was measured according to a former method (n=3) (Gata, et al., 1996). The substrate  
140 solution of LOX was prepared by dissolving linoleic acid in distilled water (10 mL, 180 $\mu$ L Tween 20) and  
141 the pH value was adjusted to 9.0 with 2 M NaOH. Subsequently, 200 $\mu$ L diluted LOX solution was mixed

142 with 200 $\mu$ L CGA solution and 50 mM citric acid buffer (pH=5.5, 2.4mL), and the mixed solution was  
143 incubated for 10 min (25  $^{\circ}$ C). Then, 200 $\mu$ L substrate solution was added to initialize the reaction. One  
144 minute after the reaction, the absorbance at 234 nm was recorded. One unit of LOX's activity was defined  
145 as an increase of absorbance at 234 nm of 0.001 per min under assay condition (Gata, et al., 1996). For the  
146 inhibition ratio, the concentrations of LOX and linoleic acid were 0.1 mg/mL and 20 mM, respectively. For  
147 the inhibition type experiments, the following concentrations were used: LOX: 0.05, 0.1, 0.2, 0.3, 0.4  
148 mg/mL; CGA: 0, 0.05, 0.1, 0.2 mg/mL; linoleic acid: 15 mM. For the inhibition kinetics experiments, the  
149 following concentrations were investigated: LOX: 0.1 mg/mL; CGA: 0, 0.05, 0.1, 0.2 mg/mL; linoleic acid:  
150 5, 10, 15, 20, 25 mmol/L.

## 151 **2.6 Fluorescence spectra measurements**

152 The detected enzyme solution (0.1mg/mL) contains relative buffer and different concentrations  
153 of CGA (0 M to 40.0 $\times 10^{-6}$  M, stepped by 5 $\times 10^{-6}$  M). The fluorescence spectra of the sample (n=3  
154 for every group) were recorded on F-4500 fluorescence spectrometer (Hitachi, Japan) after standing  
155 for 30 min to equilibrate, and the fluorescence measurement was performed at three different  
156 temperatures (298K, 303K and 310K). The fluorescence intensity was corrected using the following  
157 equation:

$$158 \quad F_{corr} = F_{obs} \times e^{(A_{ex}+A_{em})/2} \quad (1)$$

159 where  $F_{cor}$  and  $F_{obs}$  refer to the corrected and observed fluorescence intensities, respectively.  $A_{ex}$  and  $A_{em}$   
160 represented the absorption of the ligand at excitation and emission wavelengths, respectively.

161 For the fluorescence quenching measurement, the following parameters were set: excitation wavelength:  
162 280 nm; emission slits: 5 nm; voltage: 400V; scanning rate: 1200 nm/min; and emission spectra: 290 to 450  
163 nm. For synchronous fluorescence spectra, several parameters were changed: the intervals between emission

164 and excitation wavelength ( $\Delta\lambda$ ): 15 nm and 60 nm; emission spectra: 240 to 310 nm.

## 165 **2.7 Ultraviolet-visible (UV-VIS) absorption spectra measurements**

166 The detected enzyme solution (0.1 mg/mL) containing relative buffer and different concentrations of  
167 CGA (0 to  $40 \times 10^{-6}$  M, stepped by  $10 \times 10^{-6}$  M) were detected with UV-2600 spectrophotometer (UNIC,  
168 China) and performed in the range of 230 - 450 nm at room temperature (n=3 for every group) .

## 169 **2.8 Circular dichroism (CD) spectra measurements**

170 The changes in secondary structures of endogenous enzymes before and after adding CGA were  
171 recorded by a Jasco-1500 spectrophotometer (JASCO, Japan) 2.0 mm path length cell at room temperature  
172 (n=3 for every group). The constant concentration of enzymes was 0.05mg/mL, CGA concentrations in the  
173 complexes were 0, 20.0 and  $40.0 \times 10^{-6}$  M. The CD spectra were recorded from 190 to 250 nm with a scan  
174 rate of 200 nm /min, the response time was 2 s. The spectra data were converted to mean ellipticity in deg  
175  $\text{cm}^2 \text{dmol}^{-1}$  to calculate the secondary structure of enzymes.

## 176 **2.9 Fourier transform infrared (FT-IR) spectroscopy measurements**

177 The FT-IR spectra were recorded by a Nicolet470 FT-IR spectrometer (Nicolet, USA) (n=3 for every  
178 group). The detected enzyme solutions (0.1 mg/mL) containing various CGA (0.0, 20.0 and  $40.0 \times 10^{-6}$   
179 mol/L) were lyophilized for measurement, and the KBr disc was prepared and measured by adding KBr  
180 with or without samples. The spectra were scanned in the range of 500-4000  $\text{cm}^{-1}$  with 64 scans and 4  $\text{cm}^{-1}$   
181 resolutions. Background spectrum was recorded before each sample measurement.

## 182 **2.10 Dynamic light scattering (DLS)**

183 The enzyme solution (0.01 mg/mL) containing relative buffer and different concentrations of CGA (0  
184 to  $4 \times 10^{-6}$  M, stepped by  $1 \times 10^{-6}$  M) was detected by light scattering determined with Zetasizer Nano ZS90  
185 (Malvern, UK). Each measurement was performed with 11 scans and each sample (n=3 for every group)

186 replicated three times.

## 187 **2.11 Molecular docking**

188 The interaction between CGA and lipase or LOX were simulated using the molecular docking method  
189 performed with CDOCKER module available in Discovery Studio 2016 (BIOVIA, USA). The structures of  
190 CGA were collected from PubChem (<http://pubchem.ncbi.nlm.nih.gov/>), and the crystal structures of lipase  
191 (Protein Data Bank (PDB) ID: 1ETH) and LOX (PDB ID: 2P0M) were downloaded from PDB  
192 (<http://www.rcsb.org/>).

193 To prepare protein structures, several steps were initially completed in the software, such as the removal  
194 of water molecules and addition of hydrogen atoms. The structure of CGA was optimized due to minimized  
195 energy. The docking between CGA and proteins was based on CHARMM force field. The top hit value was  
196 set to 10, pose cluster radius was set to 0.5, other docking parameters were default if not mentioned. The  
197 lipase-CGA and LOX-CGA interactions are illustrated in 3D and 2D diagrams using Discovery Studio (Xu,  
198 et al., 2019).

## 199 **2.12 Statistical analysis**

200 Statistical analysis was performed with SPSS 22.0 (IBM, New York, USA) using one-way ANOVA.  
201 Duncan(D) adjustment was used to determine the significant difference between different groups.  
202 Significant differences were declared at  $p < 0.05$ . The results were expressed as means  $\pm$  SD (standard  
203 deviation).

204

## 205 **3 Results and discussion**

### 206 **3.1 SDS-PAGE analysis of endogenous enzymes in fish flesh**

207 The purity of enzymes was confirmed by SDS-PAGE, and the results are shown in Fig. 1a. The  
208 molecular weights of lipase and LOX were about 36 kDa and 97 kDa, and the results are illustrated in Fig.  
209 1a-sample 5 and 1a-sample 3. The molecular weight of LOX is similar to that reported in mackerel (*Scomber*

210 *scombrus*) and ham (Banerjee, 2006), and the molecular weight of lipase was also found in grey mullet and  
211 whiteleg shrimp (Smichi, et al., 2013).

### 212 **3.2 Inhibitory activities and inhibition kinetics for endogenous enzymes**

213 The inhibitory activities of endogenous lipase and LOX in fish flesh were investigated and the results  
214 are illustrated in Fig. 1b-1d. For the inhibitory ratio, the inhibition curves under different concentrations of  
215 CGA on the activities of endogenous enzymes were constructed (Fig.1b1 and 1b2). Results show that  
216 inhibitory ratios of CGA against enzyme activities were increased with the addition of CGA. The IC<sub>50</sub> values  
217 of CGA on lipase and LOX were 0.58 and 0.32 mg/mL, respectively. Results indicate that CGA was an  
218 efficient inhibitor for both lipase and LOX and had significantly stronger inhibitory activity for LOX  
219 compared with lipase. The kinetic plots of CGA inhibiting lipase and LOX under the same conditions were  
220 explored to elucidate the effects (Fig. 1c). As shown in Fig. 1c1 and 1c2, a group of straight lines passed  
221 through the origin point, thus both the inhibition processes of CGA on lipase and LOX were reversible (Yu,  
222 et al., 2019).

223 For the inhibitory kinetics study, the double reciprocal plot or Lineweaver-Burk plot was employed to  
224 analyze the kinetics parameters, Michaelis-Menten constant ( $K_m$ ) and the maximum velocity ( $V_m$ ), in the  
225 presence of CGA and 4-npb/ linoleic acid (Fig.1d1 and 1d2). For lipase, the addition of CGA increased the  
226  $K_m$  value (from 0.93 mg/mL to 2.06 mg/mL), but the  $V_m$  (0.01/min) was constant, which indicates that CGA  
227 competitively inhibited lipase activity due to binding to the catalytic site of enzymes. The free enzyme  
228 inhibition constant ( $K_i$ ) was 0.23 mg/mL for the lipase inhibition measurement. The competitive inhibition  
229 of pancreatic lipase was also reported for compounds extracted from plants such as Ligupurpuroside B and  
230 tea saponin (Ying, et al., 2018). For LOX, the increasing value of  $K_m$  (from 4.16 mg/mL to 5.03 mg/mL)  
231 and decreasing value of  $V_m$  (from 0.22/min to 0.16/min) indicates that there is mixed type inhibition. Results

232 imply that CGA might bind to LOX and linoleic acid-LOX complex simultaneously (Yu, et al., 2019).  
233 Similar results were also reported in the inhibition of mackerel (*Scomber scombrus*) muscle lipoxygenase  
234 by green tea polyphenols (Sreeparna, 2006). Finally, the  $K_i$  and the bound enzyme inhibition constant ( $K_{is}$ )  
235 were found to be 0.32 mg/mL and 0.57 mg/mL.

### 236 3.3 Fluorescence quenching

237 The effect of CGA on tertiary structures of enzymes could be evaluated by the intrinsic fluorescence,  
238 which indicates the interactions of CGA and amino acids in aromatic ring structures in proteins including  
239 tryptophan (Trp), tyrosine (Tyr) and phenylalanine (Phe) (Cysewski, 2008). The fluorescence emission  
240 spectra of lipase and LOX in the presence of different concentrations of CGA at 298K were studied (Fig.  
241 2a1 and 2a2). The fluorescence intensities of enzymes were decreased following an increase in CGA and  
242 were decreased 44.35% and 60.20% for lipase and LOX respectively. The quenching effects of intrinsic  
243 fluorescence indicate the existence of interactions between enzymes and CGA. The intrinsic fluorescence  
244 of LOX is easily quenched with CGA, which means there are more opportunities for interaction between  
245 CGA and LOX. The results could explain the stronger inhibition of LOX with CGA than with lipase. As  
246 shown in Fig. 2a2, the slight redshift in maximum emission wavelength of LOX suggest the increasing  
247 hydrophilic microenvironment around fluorophore and amino acid residues after binding with CGA (Xiong,  
248 et al., 2016). Furthermore, similar variation tendency was obtained for the fluorescence spectra of lipase  
249 and LOX in the presence of different concentrations of CGA at 304K and 310K (Data not shown).

#### 250 3.3.1 Mechanism of fluorescence quenching

251 The quenching mechanism by small molecule quenchers can be classified as static quenching and  
252 dynamic quenching, which can be analyzed using the Stern-Volmer equation (Lakowicz, Joseph, 2006):

$$253 \quad \frac{F_0}{F} = 1 + K_{SV}[Q] = 1 + K_q\tau_0[Q] \quad (2)$$

254 where  $F_0$  and  $F$  are the fluorescence intensities of the complex without and with CGA, respectively;  $K_{sv}$  is  
255 the quenching constant;  $K_q$  is the quenching rate constant of the biomolecule;  $[Q]$  is the concentration of  
256 CGA and  $\tau_0$  is the average life time of molecules in the absence of the quencher (the value is  
257 approximately  $10^{-8} \text{ s}^{-1}$ ).

258 As shown in Fig. 2b1 and Fig. 2b2, the Stern-Volmer curves show good liner relationships. The  $K_{sv}$  and  
259  $K_q$  for the interactions between CGA and enzymes at different temperatures were collected in Table 1. The  
260  $K_q$  of lipase and LOX were  $2.11 \times 10^{12} \text{ L/mol}\cdot\text{s}$  and  $3.94 \times 10^{12} \text{ L/mol}\cdot\text{s}$  at 298K respectively, which were  
261 much higher than the maximum dispersion collision quenching constant ( $2.00 \times 10^{10} \text{ L/mol}\cdot\text{s}$ ). The results  
262 suggest that the formation of complexes between CGA and endogenous enzymes and the quenching types  
263 of lipase and LOX caused by CGA belong to static quenching. Besides, the  $K_{sv}$  values of both interaction  
264 systems decreased with increasing temperature, which also presented the characteristics of fluorescence  
265 static quenching.

266 The binding constant ( $K_a$ ) and the number of binding sites ( $n$ ) of the static quenching process were  
267 further evaluated by the following equation (Lakowicz, Joseph R, 2000):

$$268 \quad \log \frac{F_0 - F}{F} = \log K_a + n \log [Q] \quad (3)$$

269 where  $F_0$  and  $F$  are fluorescence intensities of the complex without and with CGA,  $[Q]$  is the concentration  
270 of CGA. As listed in Table 1, the  $K_a$  values of lipase-CGA complexes were lower than those of LOX-CGA  
271 complexes at different temperatures. The decreased trend of  $K_a$  values of the temperature also show that the  
272 CGA which induced the quenching mechanism of two types of enzymes was static quenching. The values  
273 of  $n$  were approximately equal to 1, which demonstrate that there was only one class of binding site for  
274 CGA on two types of enzymes and the formation of complexes in intermolecular interactions at a molar  
275 ratio of 1:1. The values of  $K_a$  and  $n$  decreased with increasing temperature, which might have been caused

276 by the decomposition of enzyme-CGA complex.

### 277 3.3.2 Thermodynamic parameters

278 The Van't Hoff equation (Function 4) and Gibbs equation (Function 5) were used to calculate the  
279 thermodynamic parameters of interactions between small molecules and proteins (Ross & Subramanian,  
280 1981):

$$281 \ln K_a = -\frac{\Delta H}{RT} + \frac{\Delta S}{R} \quad (4)$$

$$282 \Delta G = \Delta H - T\Delta S \quad (5)$$

283 where  $K_a$  is the binding constant at different temperature  $T$  (298K, 304K, 310K);  $\Delta H$ ,  $\Delta S$  and  $\Delta G$  are the  
284 changes of enthalpy, entropy and free energy, respectively;  $R$  is the gas constant (8.314 J/mol·K).

285 The values of  $\Delta H$ ,  $\Delta S$  and  $\Delta G$  are presented in Table 1, the negative values of  $\Delta H$  and  $\Delta S$  show that  
286 the hydrogen bond and Van der Waals force interactions might play a major role during the binding process  
287 of both lipase-CGA and LOX-CGA systems (Ross & Subramanian, 1981). The negative values of  $\Delta G$   
288 suggest that the interactions between endogenous enzymes of fish flesh and CGA were spontaneous.

### 289 3.4 Synchronous fluorescence spectra analysis

290 The synchronous fluorescence spectroscopy is often used to analyze microenvironment changes  
291 surrounding amino acid fluorophore residues and study protein conformation changes. The  $\Delta\lambda$  between  
292 emission wavelength and excitation wavelength established at 15 nm and 60 nm reflect the spectra features  
293 of Tyr and Trp, respectively.

294 As shown in Figs. 2c1, c2 and Figs. 2d1, d2, the synchronous fluorescence intensities of Tyr and Trp  
295 were both decreased following an increase in CGA. For  $\Delta\lambda=15$  nm, a weak blue shift trend of maximum  
296 emission wavelength was observed with the gradual addition of CGA into the lipase solution (Fig. 2c1), but  
297 there was no shift observed for LOX (Fig. 2c2), which indicates that the interaction between lipase and

298 CGA slightly increased the hydrophobicity of microenvironment around Tyr residues (Peng, et al., 2016).  
299 For  $\Delta\lambda=60$  nm, there was no obvious shift found in lipase (Fig. 2d1), a small red shift of maximum emission  
300 wavelength in LOX (Fig. 2d2) suggests that the addition of CGA slightly improved the polarity of the Trp  
301 residue microenvironment (Zhu, et al., 2017). The results imply that CGA may be closer to the Trp residue  
302 than Try residue in the LOX-CGA interaction, but it might not bind closer to neither Tyr nor Trp in lipase.  
303 According to the above results, there was no significant change in the enzymatic amino acid  
304 microenvironment. The changes in maximum emission wavelength with synchronous fluorescence are  
305 basically consistent with the results of former fluorescence quenching analysis.

### 306 **3.5 UV-VIS spectroscopy analysis**

307 UV-VIS absorption spectroscopy is a simple and useful method for investigating protein structural  
308 changes. The interactions of lipase/LOX, and CGA at different concentrations were studied using UV-VIS  
309 spectroscopy. As shown in Fig. 3a1 and Fig. 3a2, with the continuous increase in CGA concentration, the  
310 absorption peaks around 220 nm were gradually increased with a small blue shift indicating that CGA  
311 influenced the skeleton structures of these two types of endogenous enzymes (Farhadian, et al., 2019). The  
312 increased absorption intensity and red shift of peaks around 275 nm suggest the formation of complexes  
313 between enzymes and CGA. The absorbance of lipase-CGA and LOX-CGA complexes was significantly  
314 elevated with increasing concentrations between 250 nm and 350 nm. This implies that CGA could lead to  
315 the modification of polarity and hydrophilicity of microenvironment around aromatic amino acid residues  
316 of endogenous enzymes, which are responsible for changes of lipase and LOX conformation (Menezes, et  
317 al., 2019). Moreover, the shift of maximum emission wavelength and differences in UV spectra reconfirmed  
318 the fluorescence quenching of interactions between lipase/LOX and CGA was static quenching instead of  
319 dynamic quenching, which is similar former results presented in fluorescence quenching spectra (Zhu, et

320 al., 2017).

### 321 **3.6 CD spectra analysis**

322 The CD spectroscopy has been widely used to determine the changes in protein conformation. Different  
323 secondary structures of protein have different characteristic absorption bands in CD spectra. The fractions  
324 of  $\alpha$ -helix,  $\beta$ -sheet,  $\beta$ -turn and random coil in lipase and LOX without or with CGA are presented in Table  
325 2. Following an increase in CGA concentration, lipase's  $\alpha$ -helix content decreased, while the contents of  $\beta$ -  
326 sheet and  $\beta$ -turn increased, and there was no apparent change observed in random coil content. Results  
327 support the notion that the binding of CGA and lipase might destroy the hydrogen and van der Waals' bonds  
328 in the secondary structure of lipase, which could lead to the extension of the spiral structure (Zhu, et al.,  
329 2018). The  $\alpha$ -helix around the catalytic site of lipase stabilizes the enzyme, thus the loss of helical content  
330 might result in the destabilization of the structure of spatial protein (Su, et al., 2016).

331 On the other hand, the fractions of  $\alpha$ -helix and  $\beta$ -sheet in the secondary structure of LOX increased,  
332 instead of decreasing in  $\beta$ -turn and random coil, which suggests that the secondary structure of LOX might  
333 be more firming after binding with CGA. The electrostatic interactions might have led to the increase in  $\alpha$ -  
334 helix content (Shen, et al., 2019). The results described above indicate that the interactions with CGA  
335 affected the secondary structure of enzymes, and may have further hampered enzymatic catalytic sites and  
336 active centers, affecting the activity of enzymes (Peng, et al., 2016). The results are in accordance with the  
337 conclusion obtained from inhibitory effects of CGA on enzymatic activities in this study.

### 338 **3.7 FT-IR spectra studies**

339 The conformational changes of enzymes affected by CGA could also be investigated through FT-IR  
340 spectra. As shown in Fig. 3b1 and Fig. 3b2, the FT-IR spectra of free enzymes and enzyme-CGA complexes  
341 in the region of 4000-400  $\text{cm}^{-1}$  were investigated. In spectroscopy of lipase-CGA complex (Fig. 3b1), the

342 peak ( $3229\text{ cm}^{-1}$ ) might be associated with the N-H stretching vibration and the peak ( $2989\text{ cm}^{-1}$ ) with  
343 asymmetrical stretch of C-H (He, et al., 2018). The amide I ( $1700\text{-}1600\text{ cm}^{-1}$ ) peak with the wavenumber at  
344  $1632\text{ cm}^{-1}$  originated from C=O stretching vibration. The amide II ( $1600\text{-}1500\text{ cm}^{-1}$ ) peaks which appeared  
345 around  $1550\text{ cm}^{-1}$  resulted from C-N stretching and N-H bending vibrations (Zhu, et al., 2019). The  
346 intensities of these peaks increased compared to those in free lipase.

347 In spectroscopy of the LOX-CGA complex (Fig. 3b2), there was a slight deviation and shift of the  
348 amide A peak at  $3446\text{ cm}^{-1}$ , which originated mainly from the O-H stretching vibration and the N-H  
349 stretching vibration, compared to LOX. The broader band at  $2450\text{ cm}^{-1}$  and the shift at  $1138\text{ cm}^{-1}$  might be  
350 associated with intermolecular interactions. The intensities of peaks were slightly changed during the  
351 interaction. The results confirm that interactions exist between CGA and enzymes, and hydrogen bonds are  
352 the important force in complexes. The changes of spectra in amide I and amide II infrared absorption bands  
353 suggest that CGA not only interacted with lipase and LOX, but also altered the secondary structures of  
354 enzymes, which is consistent with results of CD spectra analysis.

### 355 **3.8 Particle size analysis**

356 The average particle sizes of enzyme-CGA complexes were investigated. Following the elevation of  
357 CGA concentration, the average diameters of lipase increased from  $1083\pm 14\text{ nm}$  to  $1314\pm 18\text{ nm}$  (Fig. 3c1),  
358 which confirm that the formation of lipase-CGA complex and CGA could cause the aggregation of lipase.  
359 However, the average particle size of LOX only slightly increased from  $149\pm 1\text{ nm}$  to  $155\pm 1\text{ nm}$  (Fig.  
360 3c2), which suggests that the complex might be formed between LOX and CGA, but the aggregation of the  
361 enzyme was not obvious. The difference might be attributed to the different structures of lipase and LOX.  
362 These phenomena are similar to those reported between wine polyphenols and yeast protein extract,  
363 mannoproteins (Neguela, et al., 2016). The particle size distribution of enzyme-CGA complexes in Fig. 3d1

364 and Fig.3 d2 illustrates that lipase has a wider particle size distribution than LOX following the increase in  
365 CGA concentration, which is consistent with former results (Zhu, et al., 2017).

### 366 **3.9 Molecular docking analysis**

367 Molecular docking is an effective and reliable computational technique for predicting possible binding  
368 modes and studying ligand binding mechanisms of small molecules and protein. In this study, for the sake  
369 of exploring deeper insight into the nature of the interactions between lipase/LOX and CGA theoretically,  
370 the molecular docking method was used to analyze the binding process based on the CDOCKER protocol.

371 The docking interaction plots at the best active sites of enzymes are illustrated in Fig. 4a and Fig. 4b,  
372 and the interaction details between the amino acid residues and CGA in different conditions from 3D  
373 docking mode and 2D schematic diagram are demonstrated in Fig. 4c-d. It can clearly be seen that CGA  
374 formed hydrogen bonds with lipase (Fig. 4c1), including conventional hydrogen bond with aspartic (Asp)  
375 80 (Bond length-2.33 Å), carbon hydrogen bonds with catalytic residue serine (Ser) 153 (3.07 Å) and  
376 arginine (Arg) 257 (2.86 Å),  $\pi$ -donor hydrogen bond with histidine (His) 264 (3.16 Å). Besides, hydrophobic  
377 interactions between the benzene ring and Trp 253 (5.32 Å) near the acyl-binding pocket, weak interactions  
378 such as Van Der Waals' force with surrounding amino acid residues are also presented in the interaction.  
379 The results suggest that CGA was located close to Ser153 and His264 (Fig. 4d1), which were reported to be  
380 amino acid residues near an enzyme active site (Martinez-Gonzalez, et al., 2017), and explained the  
381 inhibitory effect of CGA on lipase activities. The result is in good agreement with the competitive type of  
382 inhibition obtained from former lipase-CGA inhibition assay.

383 For the LOX-CGA complex, CGA formed more hydrogen bonds (Fig. 4c2 and 4d2), including  
384 conventional hydrogen bonds with glutamic (Glu) 357 (Bond length-2.87 Å, 2.03 Å) and Arg 403 (2.87 Å,  
385 2.47 Å), carbon hydrogen bond with Glu 357 (3.04 Å), Arg 403 (2.35 Å) and phenylalanine (Phe) 175 (2.48

386 Å). Hydrophobic interactions also exist between the benzene ring of CGA and Arg 403 (4.47 Å), isoleucine  
387 (Ile) 400 (5.35 Å) and Ile 173 (5.37 Å). Miscellaneous interactions like metal-acceptor (3.09 Å) formed  
388 between Fe and CGA. It can be deduced that hydrogen bonds, hydrophobic interactions and the Van Der  
389 Waals' force are the dominant interactive forces that promote the binding of LOX and CGA, which further  
390 validate or reconfirm the results of fluorescence spectra analysis.

391

#### 392 **4 Conclusions**

393 The experimental results showed the inhibitory effect of CGA on endogenous lipase and LOX in grass carp  
394 muscle, and the inhibition types were competitive inhibition and mixed inhibition respectively. In the study,  
395 the interaction mechanisms between CGA and enzymes were also investigated using multi-spectroscopy  
396 methods combined with molecular docking studies. These results indicated the formation of enzyme-CGA  
397 complexes and changes in enzymatic conformation during binding reactions. The intrinsic fluorescence  
398 intensities in two types of enzymes were significantly quenched with CGA mainly through static quenching.  
399 The hydrophilic microenvironment and polar environment surrounding aromatic amino acid residues in  
400 enzymes resulting from CGA were reflected in the shifts in fluorescence spectra and UV-Vis spectra. The  
401 changes in the CD spectra and FT-IR spectra showed that CGA had different effects on secondary structures  
402 of lipase and LOX. The addition of CGA resulted in the aggregation of lipase as demonstrated from the  
403 results of particle size analysis. Molecular docking analysis suggested that CGA may bind close to the active  
404 site of lipase. Hydrogen bonds, hydrophobic interactions and the Van Der Waals' force were the main  
405 interactions. The interactions between CGA and enzymes may provide a better understanding of the  
406 inhibitory mechanism of CGA during the period of preservation, and in favor of its application in aquatic  
407 products. This study could provide basic mechanisms of the inhibitory effects of polyphenols on lipid

408 oxidation during food preservation.

409

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413

#### 414 **Authorship contribution statement**

415 **Qiongju Cao**: Methodology, Formal analysis, Writing - original draft. **Yuan Huang**: Methodology, Formal  
416 analysis. **Quan-Fei Zhu**: Formal analysis; **Mingwei Song**: Conceptualization, Funding acquisition.  
417 **Shanbai Xiong**: Academic instructor, Project administration. **Anne Manyande**: Writing - review & editing.  
418 **Hongying Du**: Supervision, Conceptualization, Formal analysis, Funding acquisition, Writing - review &  
419 editing.

420

421 **Conflict of interest**: The authors report no conflict of interest.

422

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534  
535

536 **Table 1.** Quenching constants ( $K_{SV}$ ), binding constants ( $K_a$ ) and thermodynamic parameters of enzymes-  
 537 CGA under different temperatures

	T (K)	$K_{sv}$ ( $10^4$ L/mol)	$K_q$ ( $10^{12}$ L/mol·s)	$R_a^2$	$K_a$ ( $10^5$ L/mol)	n	$R^2$	$\Delta H$ (KJ/mol)	$\Delta S$ (J/mol·K)	$\Delta G$ (KJ/mol)
Lipase	298	2.11	2.11	0.990	0.33	1.05	0.998			-25.68
	304	1.67	1.67	0.997	0.16	0.99	0.996	-97.57	-241.23	-24.48
	310	1.55	1.55	0.995	0.07	0.92	0.995			-22.78
LOX	298	3.94	3.94	0.996	2.06	1.17	0.999			-30.56
	304	3.75	3.75	0.994	1.75	1.15	0.998	-63.76	-111.42	-30.00
	310	3.04	3.04	0.993	0.78	1.10	0.998			-29.22

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541 **Table 2** Conformation changes in secondary structures of enzymes under difference treatments of CGA.

	Concentration of CGA ( $10^{-6}$ mol·L <sup>-1</sup> )	Secondary structure (%)			
		$\alpha$ -Helix	$\beta$ -Sheet	$\beta$ -Turn	Random coil
lipase	0	43.17	25.17	5.93	25.67
	20	41.05	27.40	6.50	25.00
	40	38.53	26.15	8.73	26.53
LOX	0	43.70	20.00	12.00	24.30
	20	44.03	23.73	9.03	23.17
	40	46.40	23.97	7.80	23.30

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545 **Figures/Tables Legends**

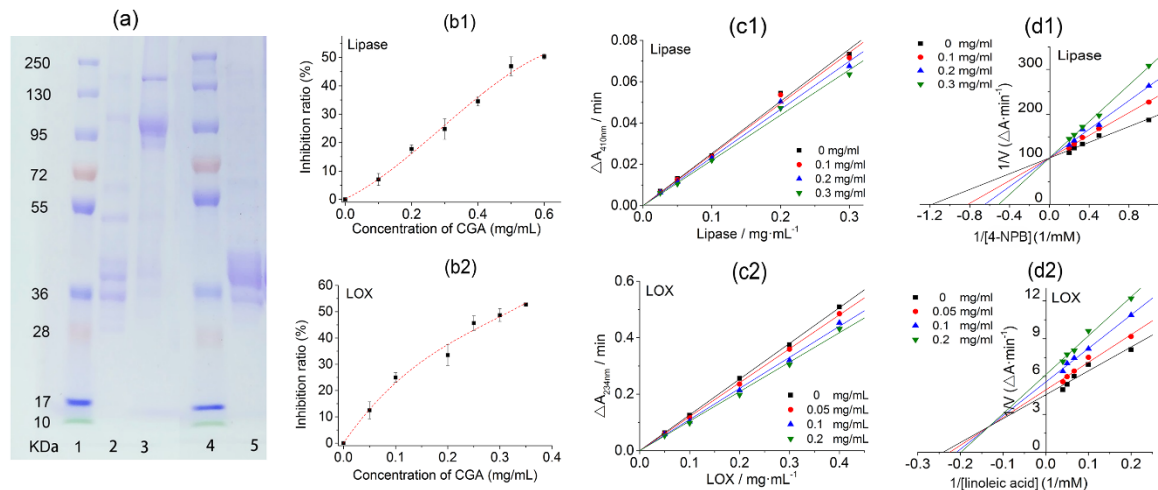
546 **Fig. 1** Results of purity of enzymes (SDS-PAGE) and inhibitory activities of lipase and LOX. *Note: a) 1*  
547 *and 4-Markers; 2-Crude enzyme sample; 3-LOX; 5-Lipase; b) Inhibitory ratios of lipase (b1:  $c_{lipase}=0.1$*   
548 *mg/mL;  $c_{4-npb}=3.0$  mM) and LOX (b2:  $c_{LOX}=0.1$  mg/mL;  $c_{linoleic\ acid}=20.0$  mM); c) Inhibitory types of lipase*  
549 *(c1:  $c_{4-npb}=3.0$  mM;  $c_{CGA}=0.0-0.3$  mg/mL) and LOX (c2:  $c_{linoleic\ acid}=15.0$  mM;  $c_{CGA}=0.0-0.2$  mg/mL).*  
550 *d) Inhibitory kinetics of lipase (d1:  $c_{lipase}=0.1$  mg/mL;  $c_{4-npb}=1.0-5.0$  mM;  $c_{CGA}=0.0-0.3$  mg/mL) and*  
551 *LOX (d2:  $c_{LOX}=0.1$  mg/mL;  $c_{linoleic\ acid}=5.0-25.0$  mM;  $c_{CGA}=0.0-0.2$  mg/mL)*

552 **Fig. 2.** Fluorescence spectra analysis of the interaction between CGA and lipase (a1-d1) or LOX (a2-d2).  
553 *Note: Figure legends:  $c_{CGA}=0.0, 5.0, 10.0, 15.0, 20.0, 25.0, 30.0, 35.0, 40.0 \times 10^{-6}$  mol/L; a) Fluorescence*  
554 *spectra ( $T=298K$ ); b) Stern-Volmer plots for fluorescence quenching; c and d) Synchronous fluorescence*  
555 *spectrum of lipase and LOX,  $c-\Delta\lambda=15$  nm,  $d-\Delta\lambda=60$  nm.*

556 **Fig. 3.** UV-VIS/FT-IR spectra and particle size analysis of lipase (a1-d1) or LOX (a2-d2) after the interaction  
557 of CGA. *Note: Figure legends:  $c_{CGA} \times 10^{-6}$  mol/L; a) UV-VIS absorption; b) FT-IR spectra; c)*  
558 *Distribution of average particle size; d) Intensity of particle size distribution.*

559 **Fig. 4.** Molecular docking analysis of the interaction of CGA and lipase (a1-d1) or LDX (a2-d2). *Note: a)*  
560 *and b): Docking ligand in the binding site; c) Results of 3D molecular docking modeling; d) Results of*  
561 *2D molecular docking modeling.*

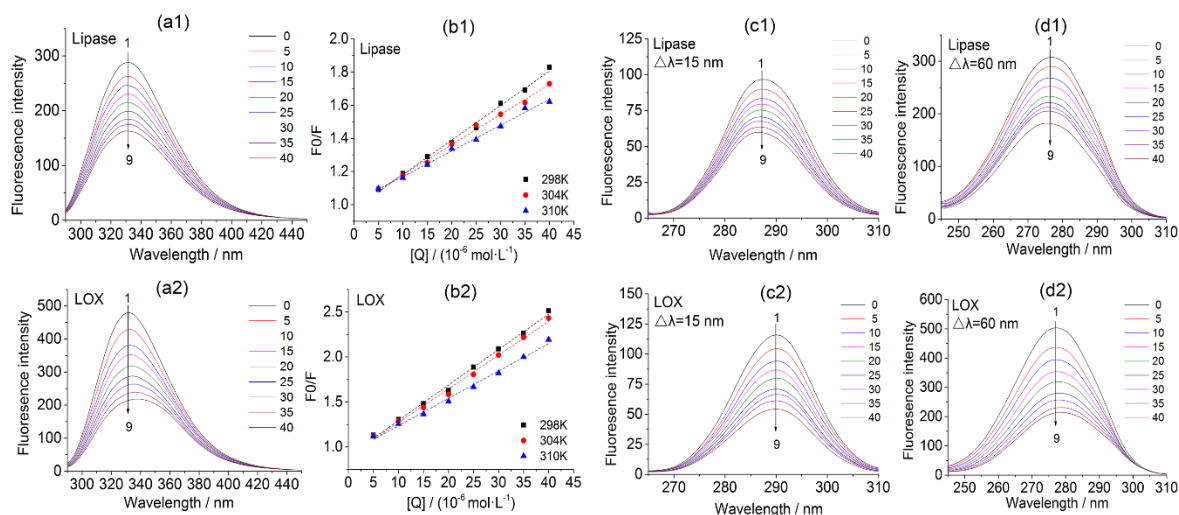
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564 **Fig. 1** Results of purity of enzymes (SDS-PAGE) and inhibitory activities of lipase and LOX. *Note: a) 1*  
 565 *and 4-Markers; 2-Crude enzyme sample; 3-LOX; 5-Lipase; b) Inhibitory ratios of lipase (b1:  $c_{lipase}=0.1$*   
 566 *mg/mL;  $c_{4-npb}=3.0$  mM) and LOX (b2:  $c_{LOX}=0.1$  mg/mL;  $c_{linoleic\ acid}=20.0$  mM); c) Inhibitory types of lipase*  
 567 *(c1:  $c_{4-npb}= 3.0$  mM;  $c_{CGA}= 0.0-0.3$  mg/mL) and LOX (c2:  $c_{linoleic\ acid}= 15.0$  mM;  $c_{CGA}= 0.0-0.2$  mg/mL).*  
 568 *d) Inhibitory kinetics of lipase (d1:  $c_{lipase} = 0.1$  mg/mL;  $c_{4-npb} = 1.0-5.0$  mM;  $c_{CGA} = 0.0-0.3$  mg/mL) and*  
 569 *LOX (d2:  $c_{LOX} = 0.1$  mg/mL;  $c_{linoleic\ acid}= 5.0-25.0$  mM;  $c_{CGA}= 0.0-0.2$  mg/mL)*

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**Fig. 2.** Fluorescence spectra analysis of the interaction between CGA and lipase (a1-d1) or LOX (a2-d2).

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*Note: Figure legends:  $c_{CGA} = 0.0, 5.0, 10.0, 15.0, 20.0, 25.0, 30.0, 35.0, 40.0 \times 10^{-6} \text{ mol/L}$ ; a) Fluorescence*

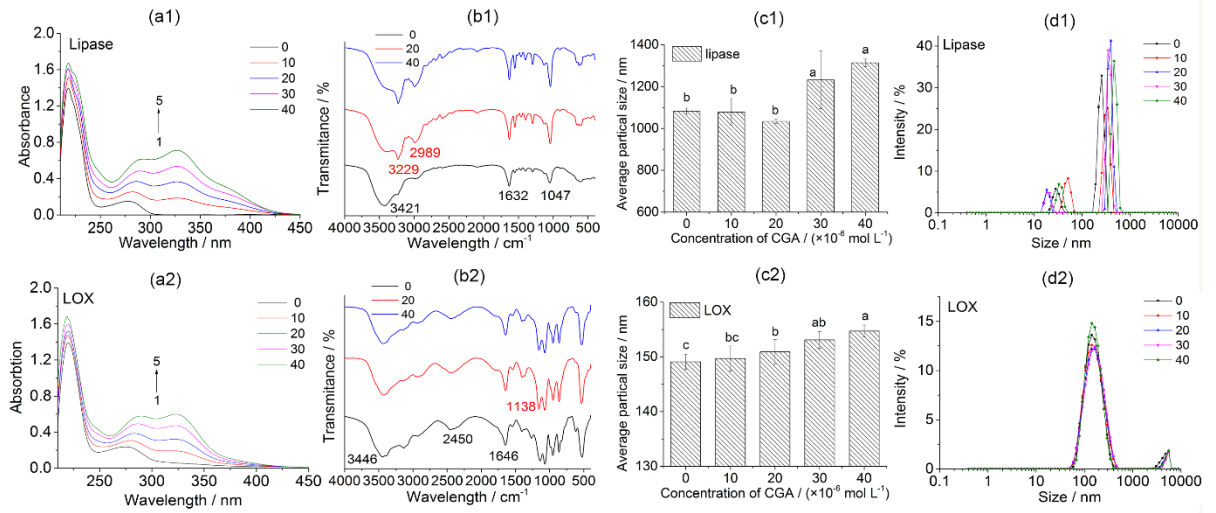
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*spectra ( $T=298\text{K}$ ); b) Stern-Volmer plots for fluorescence quenching; c and d) Synchronous fluorescence*

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*spectrum of lipase and LOX, c- $\Delta\lambda=15 \text{ nm}$ , d- $\Delta\lambda=60 \text{ nm}$ .*

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**Fig. 3.** UV-VIS/FT-IR spectra and particle size analysis of lipase (a1-d1) or LOX (a2-d2) after the

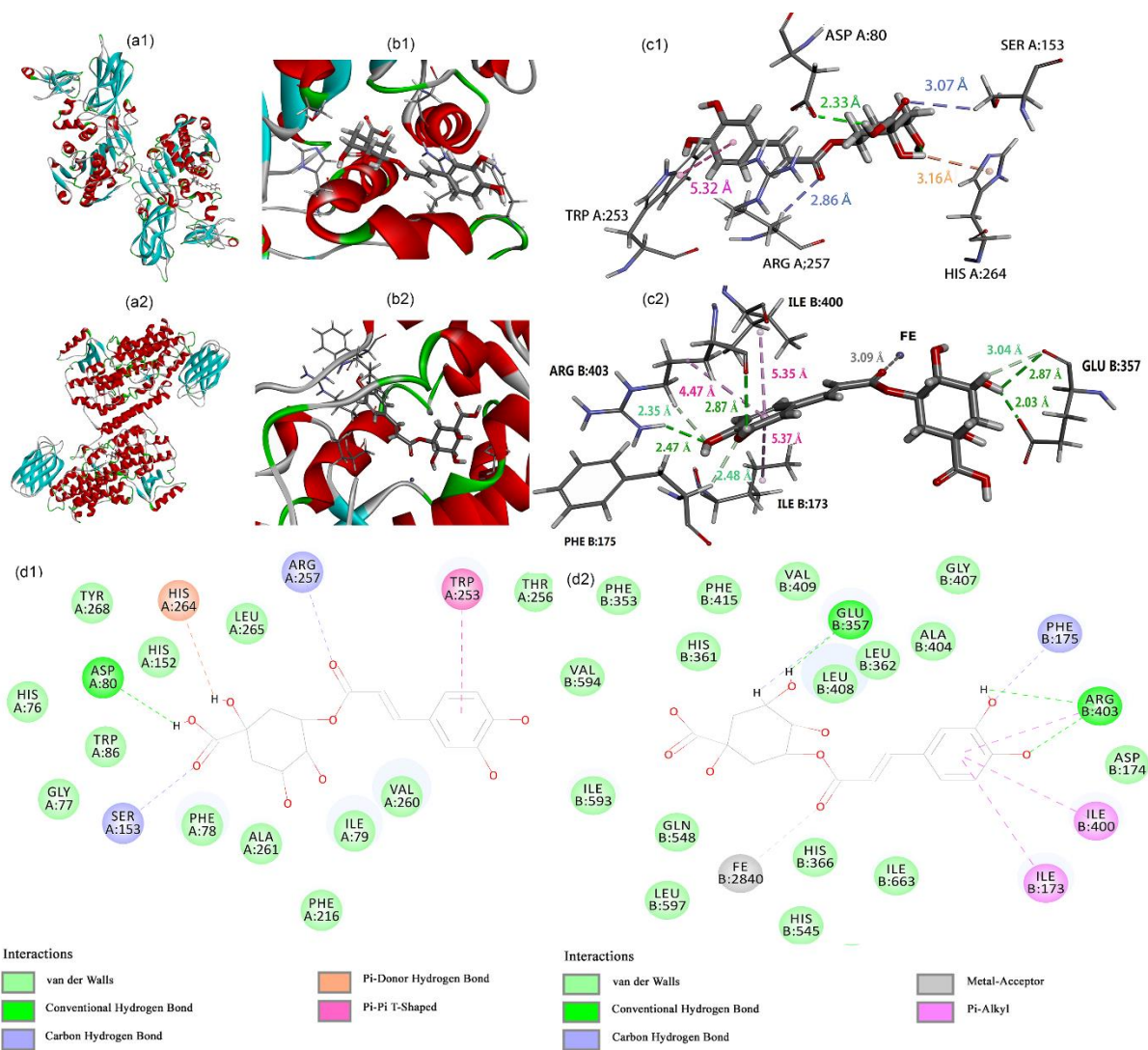
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interaction of CGA. Note: Figure legends:  $c_{CGA} = \times 10^{-6}$  mol/L; a) UV-VIS absorption; b) FT-IR spectra;

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c) Distribution of average particle size; d) Intensity of particle size distribution.

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**Fig. 4.** Molecular docking analysis of the interaction of CGA and ligase (a1-d1) or LDX (a2-d2). *Note:*

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*a) and b): Docking ligand in the binding site; c) Results of 3D molecular docking modeling; d) Results*

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*of 2D molecular docking modeling.*

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