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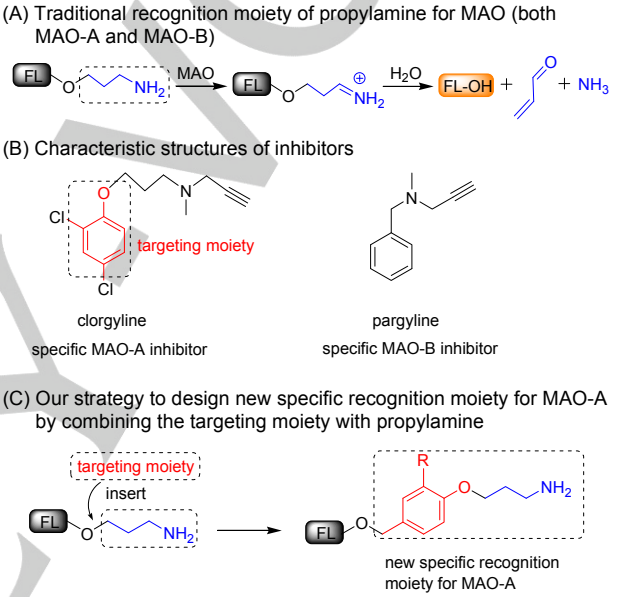
A Strategy for Specific Fluorescence Imaging of Monoamine Oxidase A in Living Cells

Xiaofeng Wu,[a,b] Wen Shi,[a] Xiaohua Li[a] and Huimin Ma*[a,b]

Abstract: Monoamine oxidase (MAO) has two isoforms, MAO-A and MAO-B, which show different functions and thus selective fluorescence imaging of which is important for biological studies. Currently, however, specific detection of MAO-A remains a great challenge. Herein, we report a new strategy for specific imaging of MAO-A via designing fluorescent probes by combining the characteristic structure of the enzymatic inhibitor with propylamine as a recognition moiety. The high specificity of our representative probe is demonstrated by imaging MAO-A in different live cells such as SH-SY5Y (high level of MAO-A) and HepG2 (high level of MAO-B), as further validated by both control probe and western blot analyses. The superior specificity of the probe may benefit the accurate detection of MAO-A in complex biosystems. Importantly, in this work the use of the characteristic structure of an inhibitor may serve as a general strategy to design a specific recognition moiety of fluorescent probes for an enzyme.

Monoamine oxidase (MAO), a flavoenzyme that can oxidize an amine to the corresponding imine followed by hydrolysis to an aldehyde, is localized in the outer membrane of mitochondria in various cells.[1] In human, MAO exists in two isoforms, MAO-A and MAO-B, which have 70% identical sequence of gene but play different functions in the metabolic process.[1,2] MAO-A preferentially breaks down serotonin, norepinephrine and epinephrine,[2a] whereas MAO-B mainly oxidizes phenethylamine and methylhistamine.[2b] The two enzymes can be distinguished by their corresponding specific inhibitors of clorgyline for MAO-A and pargyline for MAO-B.[3] Moreover, MAO-A is considered as the primary cause of neuropsychiatric and depressive disorders, and MAO-B is thought to be tightly associated with several neurodegenerative diseases.[1,4] Thus, the assay, and in particular, specific detection of MAO are of great significance to better elucidate its functions in complicated biosystems.

Due to the high sensitivity and unrivaled spatiotemporal resolution,[5] fluorescence probes combined with confocal imaging techniques have now gained increasing interest in monitoring MAO in living biosystems.[6] However, current fluorescence probes are mainly designed for the two isomers of MAO[6] or MAO-B[7], and only two probes for MAO-A to the best of our knowledge.[8] Moreover, one of the MAO-A probes is the naphthalimide-based skeleton, which in fact is not very suitable for bioimaging due to its relatively short excitation wavelength; the other is the tetraphenylethylene-based probe, which exhibits even shorter excitation wavelength of 360 nm and rather poor sensitivity (detection limit, μg/mL level). Most importantly, the existing design of the two MAO-A probes can not serve as a general strategy that is used to develop a superior MAO-A probe for fluorescence bioimaging of MAO-A. In this study, we present such a strategy by combining the characteristic structure of the enzymatic inhibitor with propylamine as a recognition moiety.



Scheme 1. (A) Traditional recognition moiety of propylamine reacting with both MAO-A and MAO-B. (B) Characteristic structures of specific MAO-A and MAO-B inhibitors. (C) Our strategy for new specific recognition moiety of MAO-A.

As is known, the great challenge in the design of fluorescence probes for a given analyte is how to effectively find or construct a specific recognition moiety.[5] For MAO, propylamine is usually used as a reactive recognition moiety of fluorescent probes, but such probes react with not only MAO-A but also MAO-B in some cases (Scheme 1A).[6c] This indicates that propylamine itself is not very selective for MAO-A. To design a new recognition moiety specific for MAO-A, we notice that clorgyline is a specific inhibitor of MAO-A, whereas pargyline with a similar structure is a specific inhibitor of MAO-B; on this basis, we believe that the characteristic structure of the MAO-A inhibitor (i.e., substituted phenol of clorgyline) may be employed as a targeting moiety that can selectively bind to MAO-A rather than MAO-B (Scheme 1B). In other words, a new specific recognition moiety of MAO-A may be constructed by combining the targeting moiety with propylamine to further enhance specificity (Scheme 1C). With this in mind, probes **1-6** were synthesized by incorporating the new recognition moiety into an excellent fluorochrome of resorufin, bearing different substituents such as hydrogen, fluoro, chloro, bromo, methoxyl and nitro groups (Scheme 2A). The detection mechanism of the

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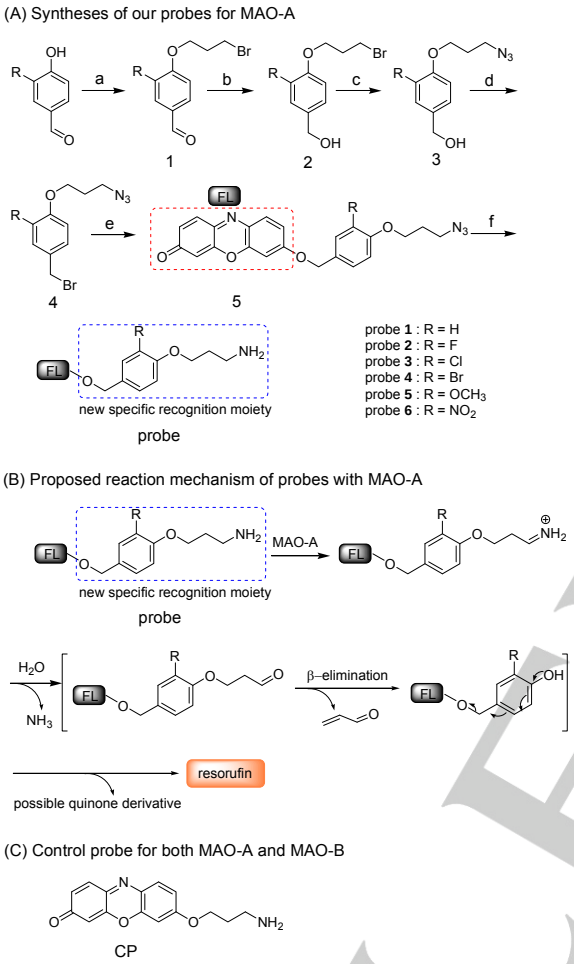
probes was based on oxidative deamination, then β-elimination and finally 1,6-rearrangement elimination to release resorufin (Scheme 2B). In addition, a control probe (**CP**) without the targeting moiety was also prepared for comparison following the procedure by Chang's group (Scheme 2C).[6c] The detailed syntheses, characterization and photophysical data (Table S1) of all the compounds were given in the Supporting Information.



Scheme 2. (A) Syntheses of probes **1**-**6** for MAO-A. Reagents and conditions: (a) 1,3-dibromopropane, K_2CO_3, DMF, 50 °C, 12 h; (b) $NaBH_4$, MeOH, 30 °C, 8 h; (c) NaN_3, K_2CO_3, DMF, 50 °C, 10 h; (d) PBr_3, CH_2Cl_2, rt, 6 h; (e) resorufin sodium salt, K_2CO_3, DMF, 100 °C, 12 h; (f) PPh_3, THF/H_2O (5/1, v/v), rt, 24 h. (B) Proposed reaction mechanism of the probes. (C) Structure of control probe.

Then, we investigated the specificity of probes **1**-**6** as well as **CP** for MAO-A over MAO-B. Because of the rather close molecular weight of MAO-A (60 kDa) and MAO-B (59 kDa),[7b] the ratio ($\Delta F_A/\Delta F_B$) of fluorescence intensity of a probe reacting with MAO-A and MAO-B at the same mass concentration may be used as an indicator of specificity coefficient. As shown in Figure S1 and Figure 1, the fluorescence of **CP** reacting with MAO-A and MAO-B is almost the same, clearly indicating that **CP** (the control probe) without the targeting moiety (substituted phenol of clorgyline) shows no specificity for MAO-A over MAO-B. Compared to **CP**, however, probes **1**-**6** all exhibit larger fluorescence ratios (Figure 1A), among which probes **3** and **4** produce a fluorescence ratio of as high as 42 and 41, respectively, demonstrating that these two probes have the highest specificity for MAO-A. Docking studies (Figure S2) are also roughly consistent with the observations (Figure 1A). All the results confirm that the introduction of the characteristic structure of the enzymatic inhibitor into the recognition moiety is rational. As mentioned above, there exists difference in the specificity among the probes. The reason for this may be rather complicated, but a possible explanation is due to that the steric hindrance of the different substituents may play a role in interacting with the active center of the enzyme.[9]

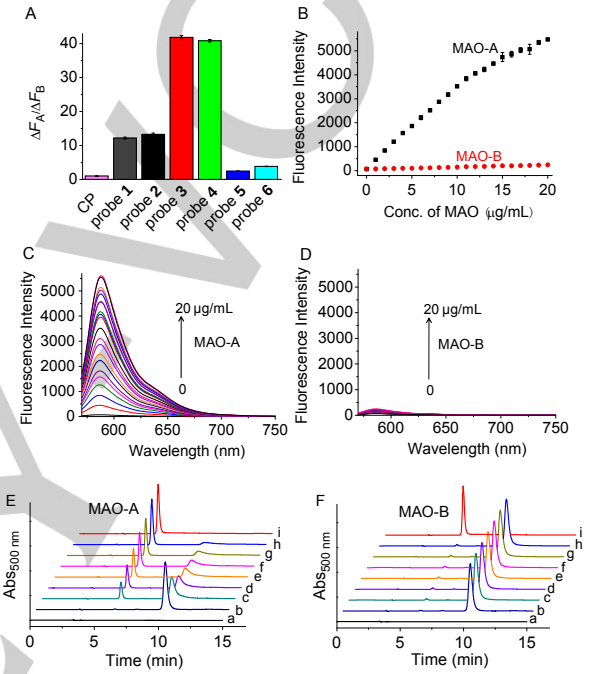


Figure 1. (A) Ratio ($\Delta F_A/\Delta F_B$) of fluorescence intensity of 5 μM of probes **1**-**6** and **CP** reacting with MAO-A and MAO-B (each 10 μg/mL). ΔF is the fluorescence intensity difference after and before reaction. The reaction was performed in pH 7.4 PBS at 37 °C for 3 h. (B) Fluorescence intensity of probe **3** reacting with MAO-A and MAO-B (0 – 20 μg/mL). (C), (D) Fluorescence responses of probe **3** (5 μM) to MAO-A and MAO-B at varied concentrations, respectively. $\lambda_{ex/em}$ = 550/586 nm. (E), (F) HPLC kinetic profiles of probe **3** (100 μM) reacting with 100 μg/mL of MAO-A and MAO-B, respectively. (a) Blank; (b) probe **3** (t_R = 9.94 min); (c-h) the reaction solutions of probe **3** with MAO-A or MAO-B for 10, 30, 60, 90, 120 and 180 min, respectively; (i) 100 μM resorufin (t_R = 6.06 min). Absorbance detection at 500 nm with methanol (flow rate, 0.55 mL/min) and water (flow rate, 0.45 mL/min) as eluents.

To better understand the binding of the probes to MAO-A and MAO-B, the kinetic parameters were determined according to the Michaelis-Menten equation. As shown in Table S2 and Figure S3, all the probes display higher affinity and kinetic efficiency for MAO-A [K_m = (2.9 ~ 31.6) μM; k_{cat}/K_m = (0.4 ~ 6.6) × 10^6 s^{-1} M^{-1}] than for MAO-B [K_m = (58.7 ~ 146.0) μM; k_{cat}/K_m = (4.8 ~ 7.3) × 10^4 s^{-1} M^{-1}]. Among the probes, probe **3** exhibited the strongest affinity (K_m = 2.9 μM) and the best kinetic efficiency (k_{cat}/K_m = 6.6 × 10^6 s^{-1} M^{-1}) for MAO-A, whereas probe **3** showed the lowest affinity and rather poor kinetic efficiency for MAO-B (K_m = 146.0 μM; k_{cat}/K_m = 5.7 × 10^4 s^{-1} M^{-1}). Similar to probe **3**, probe **4** also shows high affinity and kinetic efficiency for MAO-A. These kinetic measurements are roughly consistent

with the fluorescence responses of the probes toward MAO-A and MAO-B (Figure 1 and Figure S1). The above observations also support the design strategy of our probes. In addition, it is noted that, upon reaction with MAO-A, the fluorescence enhancement of probe **3** is larger than that of probe **4** (Figure 1B-1C and Figure S1). Considering the highest specificity and fluorescence enhancement for MAO-A, therefore, probe **3** will be employed for the following examination.

Probe **3** itself exhibits an absorption at 470 nm (Figure S4) and almost no emission ($\Phi \approx 0.04$, Table S1), but its reaction with MAO-A produces a strong absorption at about 571 nm, concomitant with a dramatic color change from nearly colorless to pink (Figure S4) and a large fluorescence enhancement at 586 nm (Figure 1C). These spectral characteristics of the reaction solution rather resemble those of resorufin, suggesting the release of the fluorochrome. However, probe **3** scarcely generates such spectroscopic responses to MAO-B (Figure 1D and Figure S4). This distinct spectroscopic difference indicates the specific response of probe **3** to MAO-A rather than MAO-B. Then, the reaction conditions of probe **3** with MAO-A were optimized, revealing that the reaction can be well performed under the physiological conditions (pH 7.4 and 37 °C) for 3 h (Figures S5 and S6). Under the optimized conditions, a good linear equation of $\Delta F = 312 \times C$ (μg/mL) + 192 (R = 0.993) was obtained in the MAO-A range of 0.01-15 μg/mL (Figure S7), with a detection limit of 2.7 ng/mL (k = 3).

The selectivity of probe **3** for MAO-A over various potential interfering species was investigated in detail, including inorganic salts, gluocose, vitamin C, vitamin B_6, glutathione, creatinine, urea, reactive oxygen species, and some commonly coexisting amino acids and oxidative enzymes. As shown in Figure S8, probe **3** also exhibits high selectivity for MAO-A over the other species examined, which may be ascribed to the specific oxidation of the substrate by MAO-A.

The reaction mechanism of probe **3** with both MAO-A and MAO-B was further explored by HPLC and mass spectral analyses. Figures 1E and 1F show the kinetic process of the probe reacting with MAO-A and MAO-B, respectively, monitored by HPLC. Upon reaction with MAO-A (Figure 1E), the peak at 9.94 min representing probe **3** (curve b) decreases gradually with time, accompanied by the appearance of a new peak at 6.06 min indicative of the released resorufin (curve i), as verified by mass spectral analysis (m/z = 212.05 $[M]^-$, Figure S9). This suggests that the reaction of probe **3** may proceed following the route shown in Scheme 2B. Besides, the reaction was nearly completed within 3 h, which accords with the observation by fluorescence (Figure S6). Under the same conditions, however, the formation of resorufin is not detected in the case of MAO-B, as depicted in Figure 1F and Figure S9. These results indicate again that probe **3** is highly specific for MAO-A but not MAO-B.

Moreover, inhibitor experiments of clorgyline for MAO-A and pargyline for MAO-B[3] were conducted, which also prove that the fluorescence change of probe **3** as well as **CP** results from the enzymatic action (Figure S10). In addition, probe **3** and **CP** display good biocompatibility (Figure S11).

The high specificity of probe **3** makes it possible to accurately detect the MAO-A activity in living cells. To demonstrate this potential, SH-SY5Y and HepG2 cells that overexpress MAO-A[10a] and MAO-B[10b], respectively, as also evidenced in Figure S12 by Western blot analysis, were used as model cells. The concentration- and time-dependent experiments of probe **3** in cells revealed that 5 μM probe **3** and 3-h incubating time are appropriate (Figures S13 and S14). As shown in Figure 2, whether HepG2 cells themselves (image a) or probe **3**-loaded HepG2 cells (image b) display extremely low fluorescence, and the relative pixel intensities from these two images are nearly equal (Figure 2C), which illustrates that probe **3** indeed does not react with intracellular MAO-B. However, SH-SY5Y cells treated with probe **3** generate strong fluorescence (image d), though the cells themselves hardly show fluorescence (image c). Furthermore, the strong fluorescence in the SH-SY5Y cells treated with probe **3** can be largely suppressed by 75% (image e in Figure 2B and 2C) using clorgyline (specific MAO-A inhibitor). The above results strongly support that probe **3** can selectively image MAO-A but not MAO-B in living cells. On the other hand, when HepG2 and SH-SY5Y cells were treated with **CP** (control probe), both of the two kinds of the cells produced strong fluorescence, and these strong fluorescence signals can be largely decreased by pargyline and clorgyline (Figure S15), respectively, suggesting that **CP** without the targeting moiety can not distinguish the two isomers of MAO. These results also support that probe **3** is a superior MAO-A probe, which can effectively image MAO-A in cells.

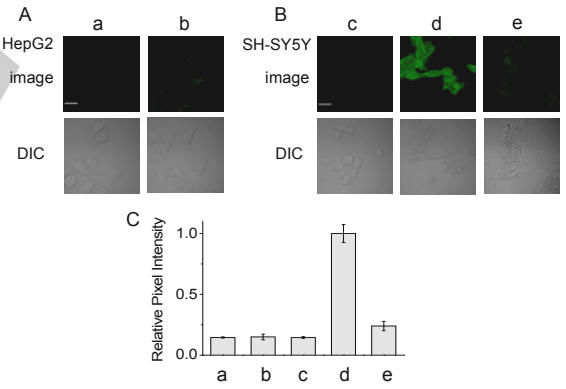


Figure 2. Confocal fluorescence images of (A) HepG2 and (B) SH-SY5Y cells. (a) and (c): cells only (control); (b) and (d): the cells incubated with probe **3** (5 μM) for 3 h; (e): the cells pretreated with clorgyline (50 μM) for 1 h, and then incubated with probe **3** (5 μM) for 3 h. The differential interference contrast (DIC) images of the corresponding samples are shown in the second row. Scale bar, 20 μm. (C) Relative pixel intensity (n = 3) from the images a-e in panels A and B (the pixel intensity from image d is defined as 1.0).

To further prove that probe **3** indeed reacts with MAO-A rather than MAO-B in the cells, a MAO-A plasmid-transfected experiment was made, together with a vector control.[7b] As shown in Figure 3, neither the probe **3**-loaded HepG2 cells themselves nor the HepG2 cells transfected with the vector control and then loaded with probe **3** exhibit obvious fluorescence (images a and b) due to the rather low level of

MAO-A. Nevertheless, when the MAO-A plasmid-transfected HepG2 cells were incubated with probe **3**, a great fluorescence enhancement (image c) was observed, and the enhanced fluorescence can be diminished by about 85% (image d and Figure 3B) by clorgyline (specific MAO-A inhibitor). This indicates that the plasmid-transfected HepG2 cells did produce a high level of MAO-A, as confirmed by western blot analysis (Figure 3C), and probe **3** reacts with intracellular MAO-A only.

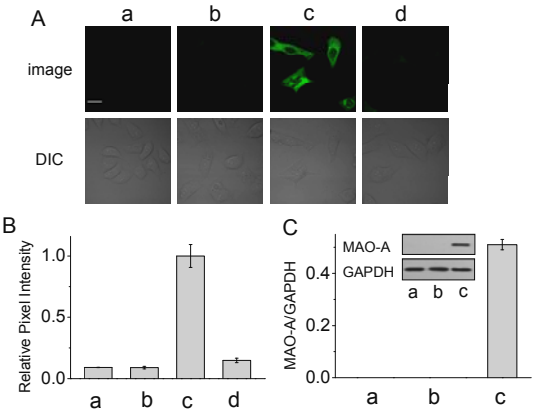


Figure 3. (A) Confocal fluorescence images of HepG2 cells incubated with probe **3** (5 μM) for 3 h. (a) Unpretreated cells; (b) cells were pre-transfected with a vector control; (c) cells were pre-transfected with MAO-A plasmid; (d) cells were pre-transfected with MAO-A plasmid and then pre-treated with clorgyline (50 μM) for 1 h. The DIC images of the corresponding samples are shown in the second row. Scale bar, 20 μm. (B) Relative pixel intensity measurements (n = 3) from the images a-d in panel A (the pixel intensity from image c is defined as 1.0). (C) Western blot analyses of MAO-A in HepG2 cells from images a-c (glyceraldehyde-3-phosphate dehydrogenase, GAPDH, was used as a protein standard). The results are the mean ± SD (n =3).

In summary, we have proposed a general design strategy for a fluorescent probe specific for an enzyme by using the characteristic structure of the enzymatic inhibitor, and this is successfully demonstrated with MAO-A. By combining the substituted phenol of clorgyline with propylamine as a new recognition moiety for MAO-A, resorufin-based probes **1**-**6** were prepared. The substituted phenol of clorgyline may serve as a targeting moiety, whose introduction into the recognition moiety strengthens the specificity of the probes for MAO-A. As a result, all of the six probes show higher selectivity for MAO-A than the control probe without the targeting moiety, among which probe **3** displays the highest specificity. The superior analytical performance of probe **3** has been demonstrated by imaging SH-SY5Y and HepG2 cells with different levels of MAO-A, and further confirmed by the control probe under the same conditions. Moreover, cell transfection experiments also validated that probe **3** is capable of distinguishing MAO-A from MAO-B. Using the proposed strategy, more new MAO-A probes with different spectroscopic properties may be developed, which would promote the understanding of MAO-A biofunctions. In addition, our strategy may be suitable to design specific probes for other enzymes.

Acknowledgements

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Keywords: analytical methods • fluorescent probes • new specific recognition moiety • monoamine oxidase A

[1] a) M. D. Berry, A. D. Juorio, I. A. Paterson, *Prog. Neurobiol.* **1994**, *42*, 375-391; b) M. B. H. Youdim, J. J. Beccafusco, *J. Neural. Transm.* **2005**, *112*, 519-537; c) M. B. H. Youdim, D. Edmondson, K. F. Tipton, *Nat. Rev. Neurosci.* **2006,** *7*, 295-309.

[2] a) C. C. Wang, E. Billett, A. Borchert, H. Kuhn, C. Ufer, *Cell. Mol. Life. Sci.* **2013**, *70*, 599-630; b) J. Saura, Z. Bleuel, J. Ulrich, A. Mendelowitsch, K. Chen, J. C. Shih, P. Malherbe, M. D. Prada, J. G. Richards, *Neuroscience* **1996**, *70*, 755-774.

[3] a) D. L. Murphy, S. Lipper, S. Slater, D. S. Ling, *Psychopharmacology* **1979**, *62*, 129-132; b) R. M. Geha, I. Rebrin, K. Chen, J. C. Shih, *J. Biol. Chem*. **2001**, *276*, 9877-9882; c) D. E. Edmondson, C. Binda, J. Wang, A. K. Upadhyay, A. Mattevi, *Biochemistry* **2009**, *48*, 4220-4230; d) A. Holt, M. D. Berry, A. A. Boulton, *Neurotoxicology* **2004**, *25*, 251-266.

[4] a) R. Mcdermott, D. Tingley, J. Cowden, G. Frazzetto, D. D. P. Johnson, *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 2118-2123; b) K. Yamaguchi, R. Ueki, H. Nonaka, F. Sugihara, F. Matsuda, S. Sando, *J. Am. Chem. Soc.* **2011**, *133*, 14208-14211; c) S. C. Godar, M. Bortolato, M. P. Castelli, A. Casti, A. Casu, K. Chen, M. G. Ennas, S. Tambaro, J. C. Shih, *J. Psychiatr. Res.* **2014**, *56*, 1-9.

[5] a) X. Li, X. Gao, W. Shi, H. Ma, *Chem. Rev*. **2014**, *114*, 590-659; b) X. Wu, X. Li, W. Shi, Q. Gong, H. Ma, *Angew. Chem. Int. Ed.* **2016**, *55,* 14728-14732; *Angew. Chem.* **2016**, *128*, 14948-14952; c) L. H. Qian, L. Li, S. Q. Yao, *Acc. Chem. Res.* **2016**, *49*, 626-634; d) H. W. Liu, K. Li, X. X. Hu, L. M. Zhu, Q. M. Rong, Y. C. Liu, X. B. Zhang, J. Hasserodt, F. L. Qu, W. H. Tan, *Angew. Chem. Int. Ed.* **2017**, *56*, 11788-11792; *Angew. Chem.* **2017***, 129,* 11950-11954; e) L. Wang, L.Yuan, X. Zeng, J. J. Peng, Y.Ni, J. C. Er, W. Xu, B. K. Agrawalla, D. D. Su, B. Kim, Y. T. Chang, *Angew. Chem. Int. Ed.* **2016**, *55*, 1773-1776; *Angew. Chem.* **2016**, *128*, 1805-1808; f) Z. X. Liu, X. Zhou, Y. Miao, Y. Hu, N. Kwon, X. Wu, J. Yoon, *Angew. Chem. Int. Ed.* **2017**, *56*, 5812-5816; *Angew. Chem*. **2017**, *129*, 5906-5910.

[6] a) G. Chen, D. J. Yee, N. G. Gubernator, D. Sames, *J. Am. Chem. Soc.* **2005**, *127*, 4544-4545; b) W. H. Zhou, M. P. Valley, J. Shultz, E. M. Hawkins, L. Bernad, T. Good, D. Good, L. T. Riss, D. H. Klaubert, K. V. Wood, *J. Am. Chem. Soc.* **2006**, *128*, 3122-3123; c) A. E. Albers, K. A. Rawls, C. J. Chang, *Chem. Commun*. **2007**, 4647-4649; d) D. Kim, S. Sambasivan, H. Nam, K. H. Kim, J. Y. Kim, T. Joo, K. H. Lee, K. T. Kim, K. H. Ahn, *Chem. Commun*. **2012**, *48*, 6833-6835.

[7] a) S. Long, L. Chen, Y. Xiang, M. Song, Y. Zheng, Q. Zhu, *Chem. Commun*. **2012**, *48*, 7164-7166; b) L. Li, C. W. Zhang, C. Y. J. Chen, B. W. Zhu, C . Chai, Q. H. Xu, E. K. Tan, Q. Zhu, K. L. Lim, S. Q. Yao, *Nat. Commun.* **2014**, *5*, 3176; c) L. Li, C. W. Zhang, J. Y. Ge, L. H. Qian, B. H. Chai, Q. Zhu, J. S. Lee, K. L. Lim, S. Q. Yao, *Angew. Chem. Int. Ed.* **2015**, *54,* 10821-10825; *Angew. Chem.* **2015**, *127*, 10971-10975.

[8] a) X. Wu, L. Li, W. Shi, Q. Gong, X. Li, H. Ma, *Anal*. *Chem*. **2016**, *88*, 1440-1446 ; b) W. Shen, J. Yu, J. Ge, R. Zhang, F. Cheng, X. Li, Y. Fan, S. Yu, B. Liu, Q. Zhu, *ACS Appl. Mater. Interfaces* **2016**, *7*, 928-935.

[9] J. C. Ma, M. Yoshimura, E. Yamashita, A. Nakagawa, A. Ito, T. Tsukihara, *J. Mol. Biol.* **2004**, *338*, 103-114.

[10] a) M. Naoi, W. Maruyama, Y. Akao, H. Yi, Y. Yamaoka, *J. Neural. Trans. Suppl.* **2006**, *71*, 67-77; b) J. C. Shih, K. Chen, *Curr. Med. Chem.* **2004**, *11*, 1995-2005.

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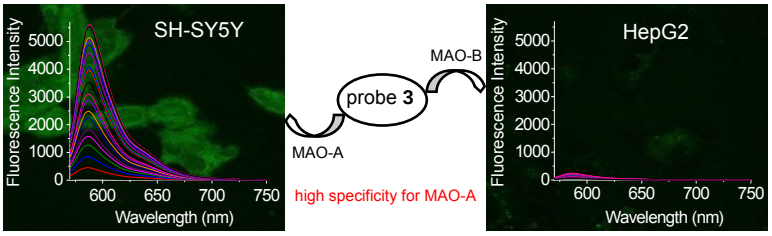

We have proposed a general design strategy for a fluorescent probe specific for an enzyme by using the characteristic structure of the enzymatic inhibitor, and this is successfully demonstrated with MAO-A. The superior analytical performance of such a probe **3** has been verified by imaging SH-SY5Y and HepG2 cells with different levels of MAO-A, as further confirmed by the control probe. Probe **3** may be useful for better understanding of MAO-A biofunctions.

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