# Electronic Supplementary Information

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Text. S1

The optimized structures of enrofloxacin and its degradation products were obtained by using density functional theory (DFT) calculation with the B3LYP function, the 6-31+G(d,p) basis set, and the IEFPCM solvent correction (Frisch et al., 2017). The docking simulation was performed in AutoDock Vina software with the grid box of 30Å × 40Å × 30Å for completely encompassing the binding region (Trott and Olson, 2010). The cleavage complex with 5CDQ code was downloaded from Protein Data Bank, showing the structural basis of DNA gyrase inhibition by moxifloxacin (a fluoroquinolone antibiotics).

Frisch, M. J.; et al., Gaussian 09, revision B.01; Gaussian Inc.: Wallingford, CT, 2010.

Trott, O., Olson, A. J. (2010) AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization and multithreading, Journal of Computational Chemistry, 31, 455-461

Fig. S1. The changed amount of enrofloxacin (initially 5.0 mg $L^{-1}$) under the same culture condition without inoculation of *Spirulina platensis*.

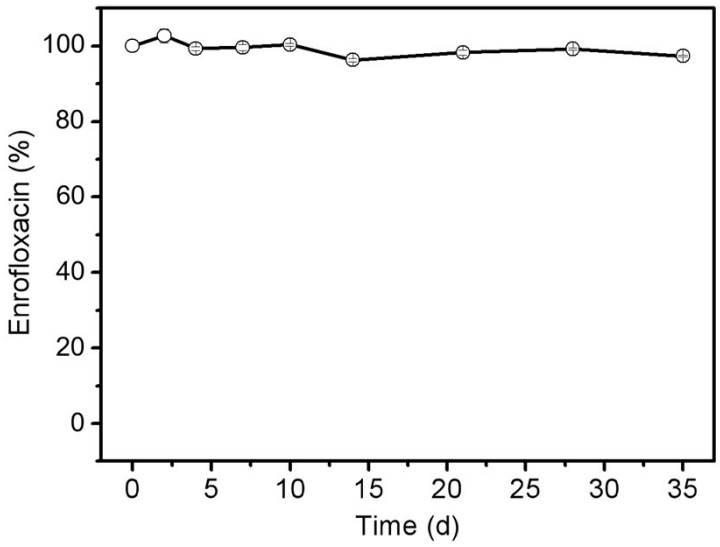

Fig. S2. The representative HPLC-MS chromatogram of enrofloxacin and its degradation products after 10 days cultivation of *Spirulina platensis*.

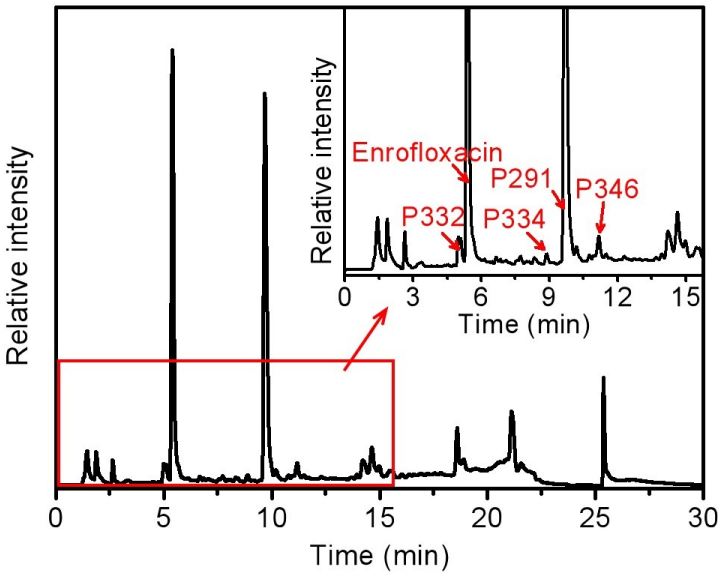

Fig. S3. The mass spectra and corresponding structural interpretation for enrofloxacin.

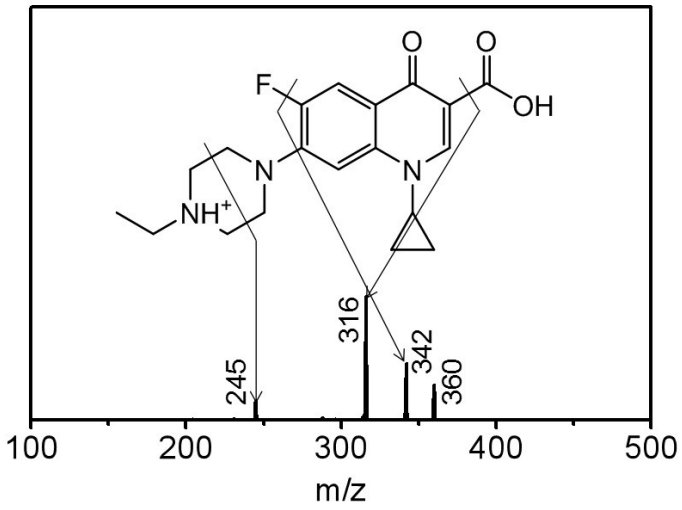

Fig. S4. The proposed degradation pathways of enrofloxacin after 10 days cultivation of *Spirulina platensis*.

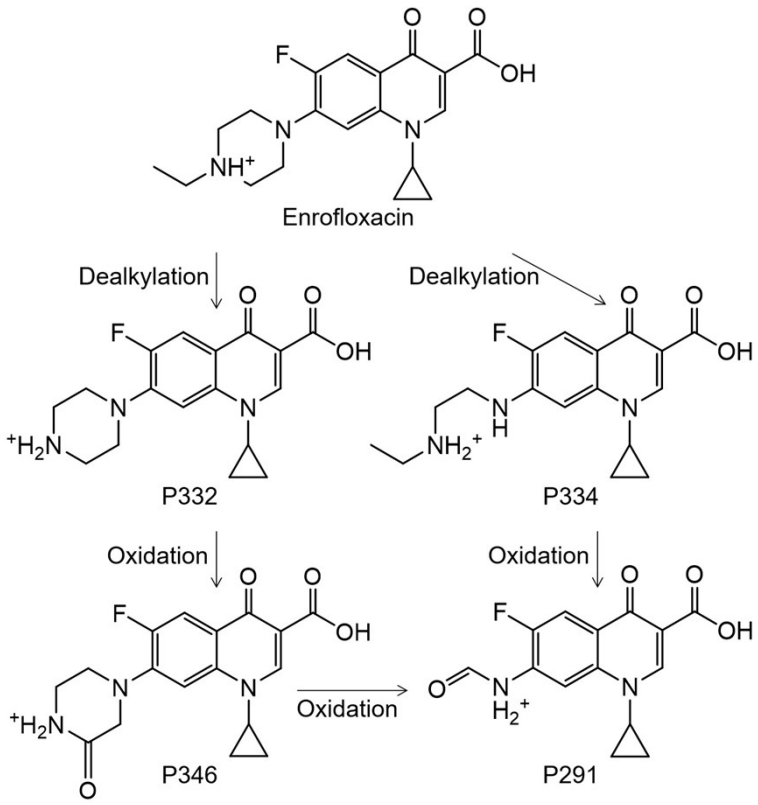

Fig. S5. The critical interactions of (a) P332, (b) P346, (c) P291, and (d) P334 with DNA gyrase.