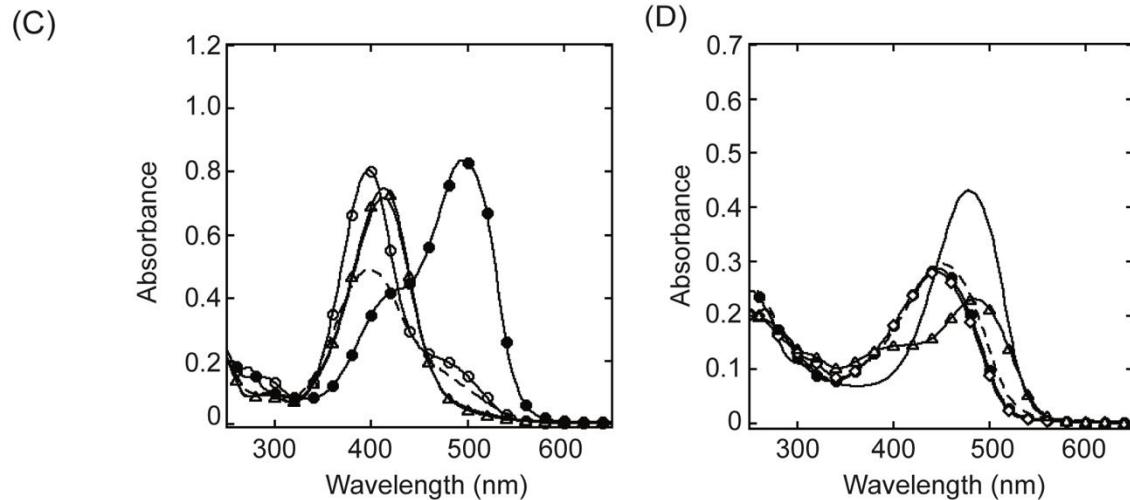
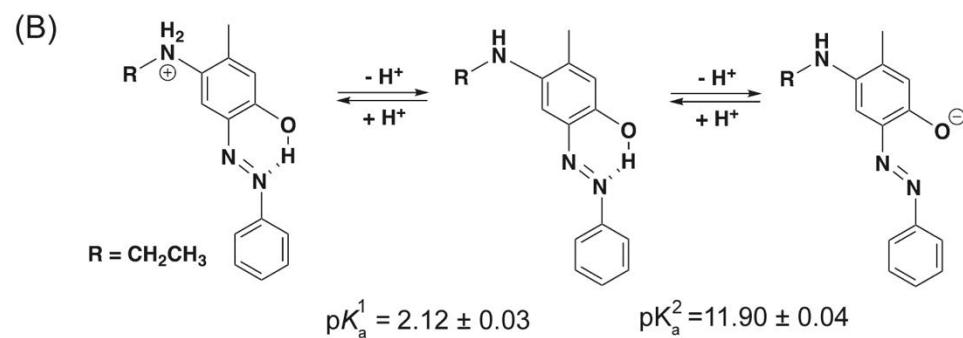
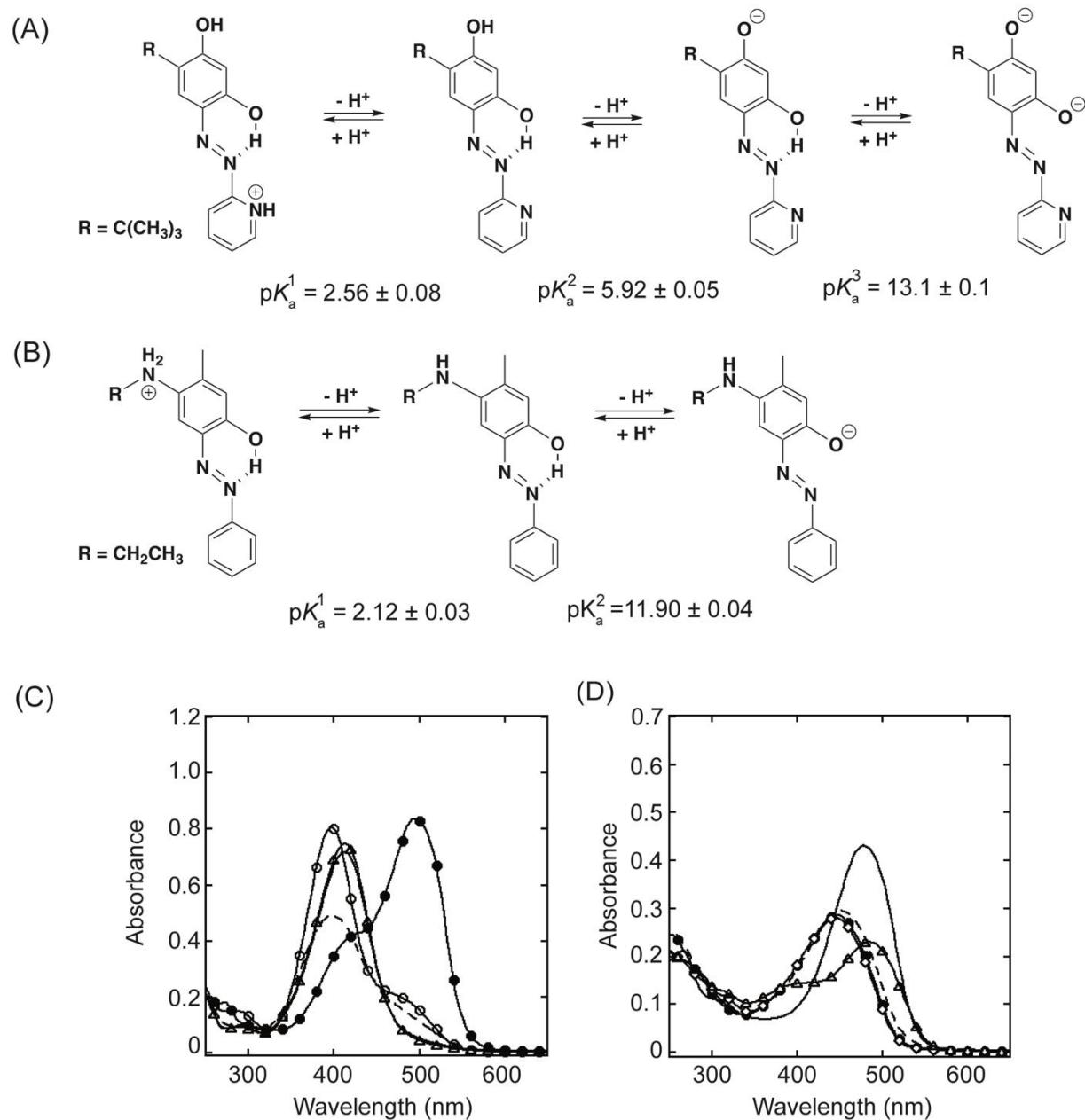
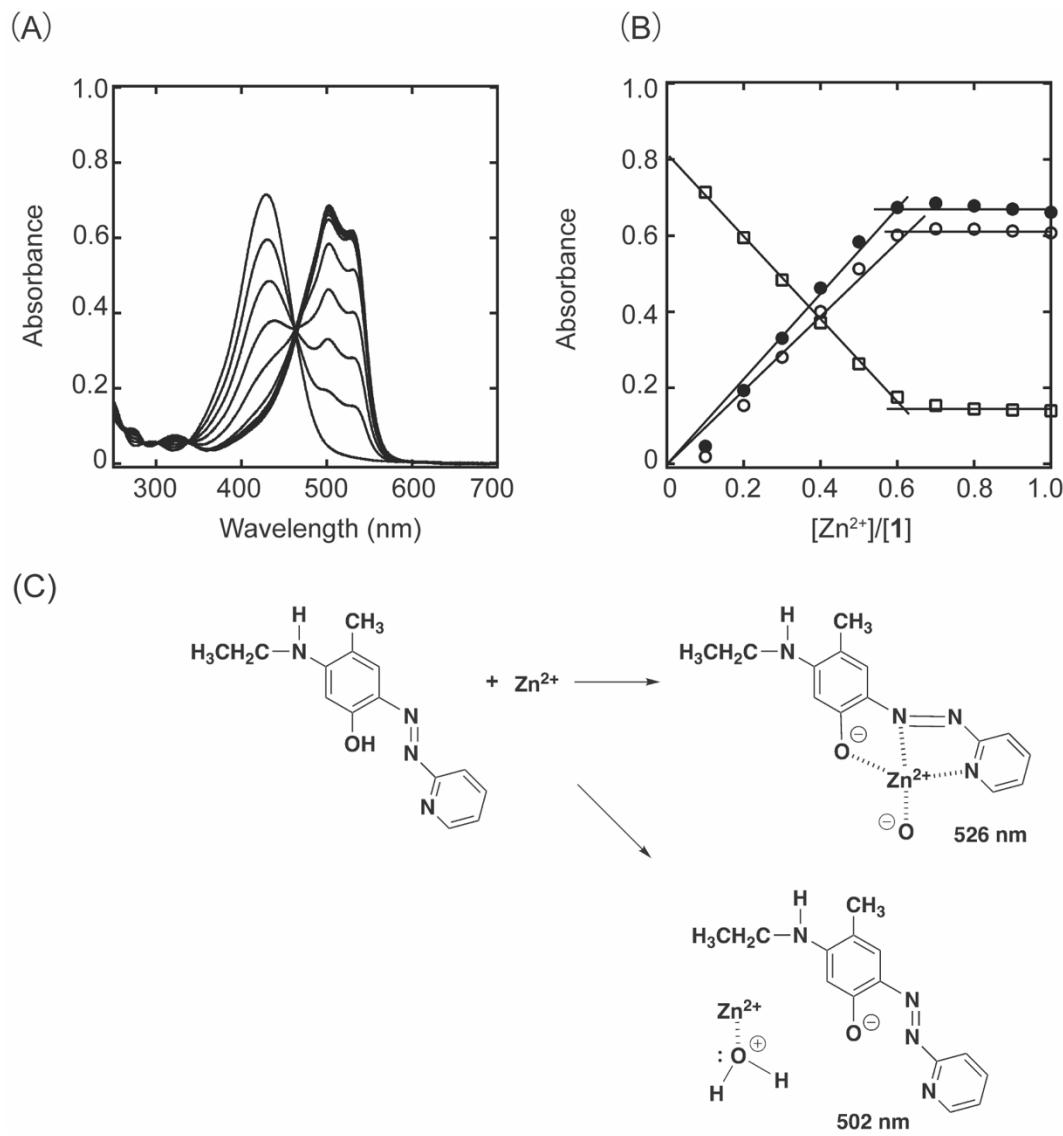


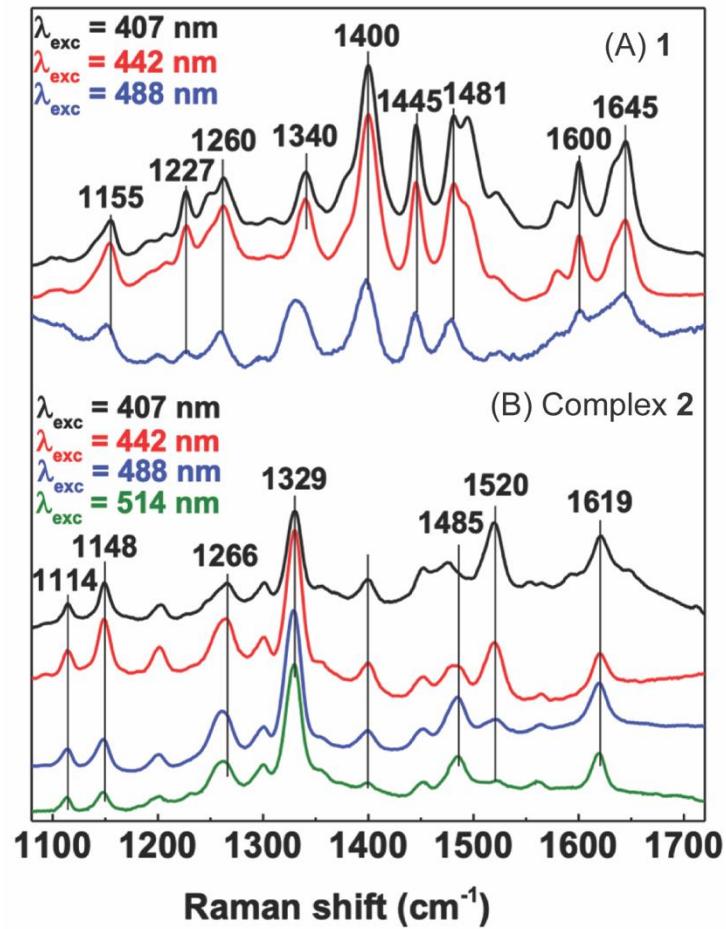
## Supporting Information



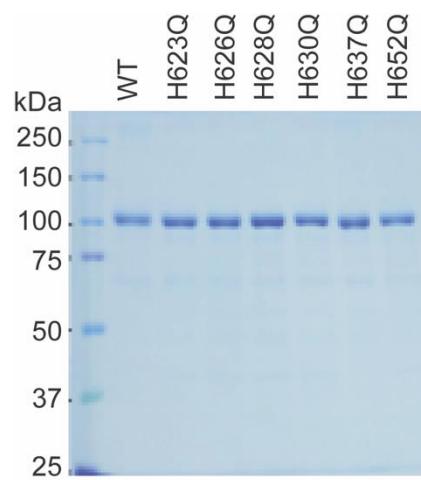
**Figure S1.**  $pK_a$ s of TPQ-2HP (A) and LTQ-PH (B) determined by spectroscopic pH titration. C) UV-vis spectra of TPQ-2HP at pH -0.33 ( $-○-$ ), pH 4.38 (----), pH 7.10 (—), pH 10.16 ( $-△-$ ) and pH 13.18 ( $-●-$ ) [1]. D) UV-vis spectra of LTQ-PH at pH 0.23 ( $-○-$ ), pH 3.11 (----), pH 7.01 (—), pH 10.00 ( $-△-$ ) and pH 13.43 ( $-●-$ ) [2].



**Figure S2.** UV-vis spectroscopic titration of **1** with  $\text{Zn}^{2+}$  at pH 8.0. (A) UV-vis spectral changes observed during titration of **1** with  $\text{Zn}^{2+}$ . (B) Plot of absorbance changes at 430 (—□—), 502 (—●—), 526 nm (—○—) versus the molar ratio of  $[\text{Zn}^{2+}]/[\mathbf{1}]$ . (C) Proposed mechanism for the formation of 502 and 526 nm species.



**Figure S3.** Room temperature RR spectra of **1** (A), Complex **2** (B) with varying excitation wavelength.



**Figure S4.** An SDS-PAGE analysis demonstrating that all mutants (H623Q, H626Q, H628Q, H630Q, H637Q, and H652Q) are secreted as WT-LOXL2.

**Table S1.** A set of primers used for site-directed mutagenesis.

Mutant	Primer	Sequence
H623Q	forward	CACCGCTGGATCTGG <u>CAGG</u> ACTGTCACAGGCAC
	reverse	GTGCCTGTGACAGT <u>CTGCC</u> AGATCCACGCGTG
H626Q	forward	GATCTGGCAC <u>GA</u> CTGTC <u>CAGA</u> GGCACTACCACAGCATG
	reverse	CATGCTGTGGTAGTGC <u>CTG</u> ACAGTCGTGCCAGATC
H628Q	forward	GCACGA <u>CTG</u> T <u>CACAGG</u> <u>CAGT</u> ACCACAGCATGGAGGTG
	reverse	CACCTCCATGCTGTGG <u>TA</u> <u>CTGCC</u> GTGACAGTCGTGC
H630Q	forward	CTGTCACAGGC <u>ACTAC</u> <u>CCAGA</u> GCATGGAGGTGTTACC
	reverse	GGTGAACACCTCCATG <u>CTGG</u> TAGTGCCTGTGACAG
H637Q	forward	ATGGAGGTGTT <u>ACCC</u> <u>AGT</u> ATGACCTGCTGAAC
	reverse	GTCAGCAGGT <u>CATA</u> <u>CTGG</u> TAACACCTCCAT
H652Q	forward	AAGGTGGCAGAGGCC <u>CAGA</u> AGGCCAGCTCTGC
	reverse	GCAGAAC <u>CTGGC</u> CT <u>CTGG</u> CC <u>CTG</u> CCACCTT

**Table S2.** Acquisition parameters for EPR spectroscopy

Compound		Power (mW)	Power Attenuation (dB)	Field Center (G)	Sweep Width (G)
Complex 3	solid state	2	20	3100	1000.1
Complex 4	solid state	2	20	3100	1000.1
Complex 3	in DMSO	2	20	2200	1800
Complex 4	in DMSO	2	20	2200	1800

**Table S3.** g strain values in DMSO

Compound	g strain
Complex 3	0.092
Complex 4	0.080

## References

1. Mure, M.; Brown, D. E.; Saysell, C.; Rogers, M. S.; Wilmot, C. M.; Kurtis, C. R.; McPherson, M. J.; Phillips, S. E.; Knowles, P. F.; Dooley, D. M., Role of the interactions between the active site base and the substrate Schiff base in amine oxidase catalysis. Evidence from structural and spectroscopic studies of the 2-hydrazinopyridine adduct of Escherichia coli amine oxidase. *Biochemistry* **2005**, *44*, (5), 1568-82.
2. Mure, M.; Wang, S. X.; Klinman, J. P., Synthesis and characterization of model compounds of the lysine tyrosyl quinone cofactor of lysyl oxidase. *J Am Chem Soc* **2003**, *125*, (20), 6113-25.