SUPPORTING INFORMATION

Structural Analysis of Aliphatic vs. Aromatic Substrate Specificity in a Copper Amine Oxidase from *Hansenula polymorpha*

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| structure | space group | unit cell lengths (Å) | β angle (°) |
|--------------------|-------------|---|-------------|
| native HPAO-1 | $P2_1$ | a = 104.15, b = 223.08, c = 104.25 | 95.77 |
| ethylamine-HPAO-1 | $P2_1$ | a = 104.41, b = 232.83, c = 105.12 | 96.66 |
| benzylamine-HPAO-1 | $P2_1$ | <i>a</i> = 104.24, <i>b</i> = 233.71, <i>c</i> = 105.05 | 96.57 |

Table S1: Unit cell parameters for native-HPAO-1 and substrate-HPAO-1 complexes.

Table S2: Species in the substrate-HPAO-1 active sites. A = axial copper ligand, E = equatorial copper ligand, * = evidence of second overlapping binding site. Occupancies are listed in parentheses.

| Substrate | Chain | Electronic form of cofactor | Chain | Copper ligands | Chain | Species bound in active site |
|-------------|-------|-----------------------------|-------|-------------------|-------|------------------------------|
| ethylamine | all | aminoquinol (1) | А | $A = H_2O_2$ | А | ethylamine (1)* |
| | | • • • • | В | $A = H_2O_2$ | В | ethylamine (1) |
| | | | С | $A = H_2O$ | С | ethylamine (1)* |
| | | | | $E = H_2O$ | | |
| | | | D | $A = H_2O$ | D | ethylamine (1)* |
| | | | Е | $A = H_2O_2$ | Е | ethylamine (1) |
| | | | | $E = H_2O$ | | |
| | | | F | $A = H_2O_2$ | F | ethylamine (1)* |
| benzylamine | all | aminoquinol (1) | А | $A = H_2O_2$ | all | benzylamine (1) |
| | | | В | $A = H_2O_2$ | | |
| | | | С | $A = H_2O$ | | |
| | | | | $E = H_2O$ | | |
| | | | D | $A = H_2O$ | | |
| | | | Е | $A = H_2O_2$ | | |
| | | | F | $A = H_2O_2$ | | |

| Active site constituent | Average B-value ($Å^2$) | | | |
|--|---------------------------|---------------------|--|--|
| | ethylamine complex | benzylamine complex | | |
| Copper ions | 23.3 | 30.8 | | |
| H ₂ O copper ligands | 41.3 | 29.4 | | |
| H ₂ O ₂ copper ligands | 22.0 | 30.2 | | |
| ethylamine | 35.2 | | | |
| benzylamine | | 38.0 | | |

Table S3: Average B-values for active site constituents.

Figure S1: Domain organization in HPAO-1. One monomer is drawn in cartoon and colored by domain (D2, purple; D3, green; D4, blue; connecting loops, yellow; β -hairpin arms, red). The second monomer is drawn as a semi-transparent surface rendering. TPQ atoms are drawn as space-filling spheres and colored by atom type (carbon, white), and copper ions are drawn as gold spheres.



Figure S2: Electron density suggesting an alternate ethylamine conformer. Peaks in the F_o - F_c map near the site of ethylamine binding in all polypeptide chains in the EtAm-HPAO-1 structure are superimposed onto one active site and shown as green mesh contoured to 3.5 σ .

