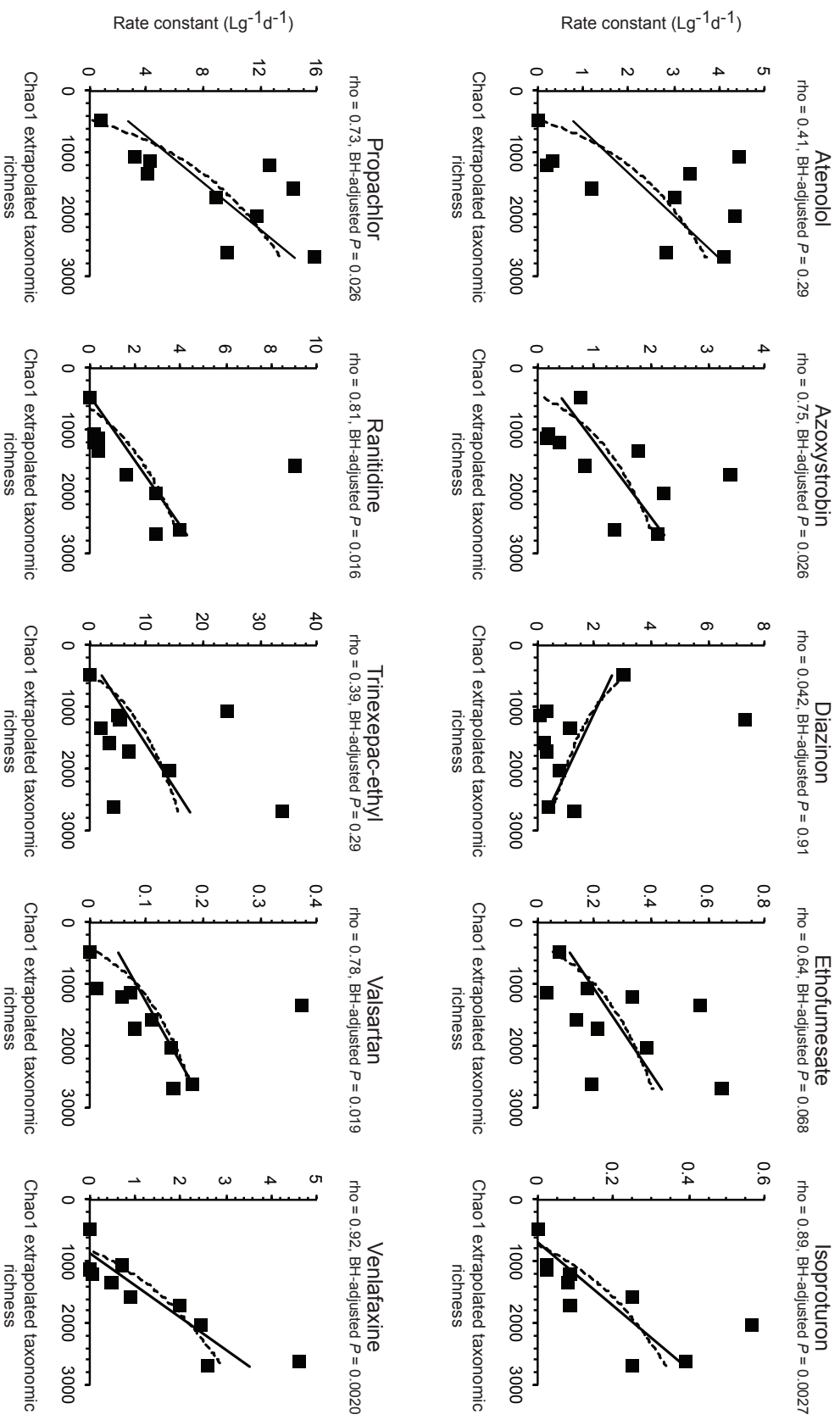
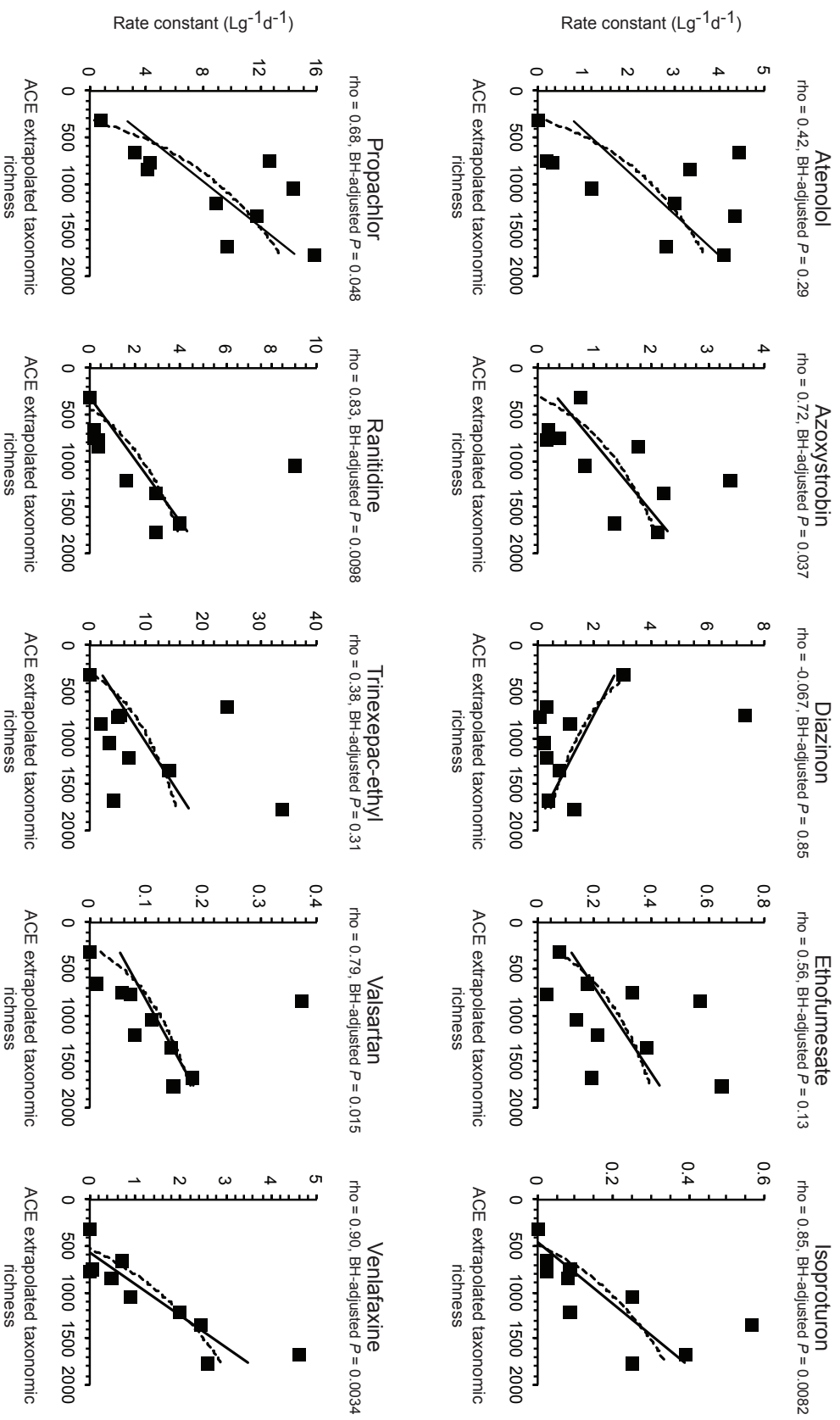


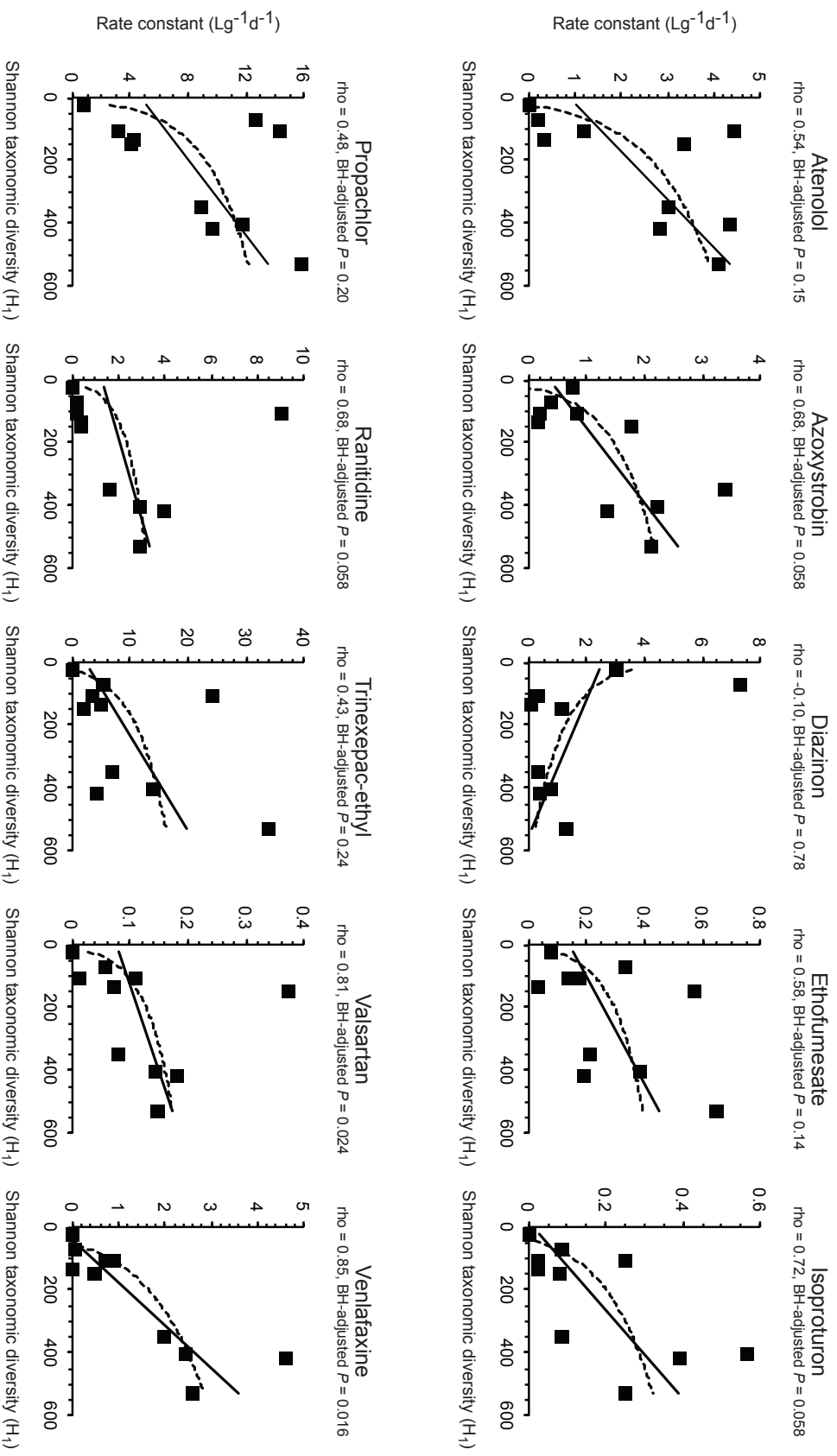
**Figure S1.** Associations between the observed taxonomic richness measurements and the active biomass-normalized first-order rate constants for each individual micropollutant biotransformation. Each square symbol indicates the measurements for one independent WWTP community. The solid lines are the best-fit linear models and the dashed lines are the best-fit logarithmic models. Definitions:  $\rho$ , Spearman rank correlation coefficient; BH-adjusted  $P$ , Benjamini-Hochberg-adjusted two-sided  $P$ .



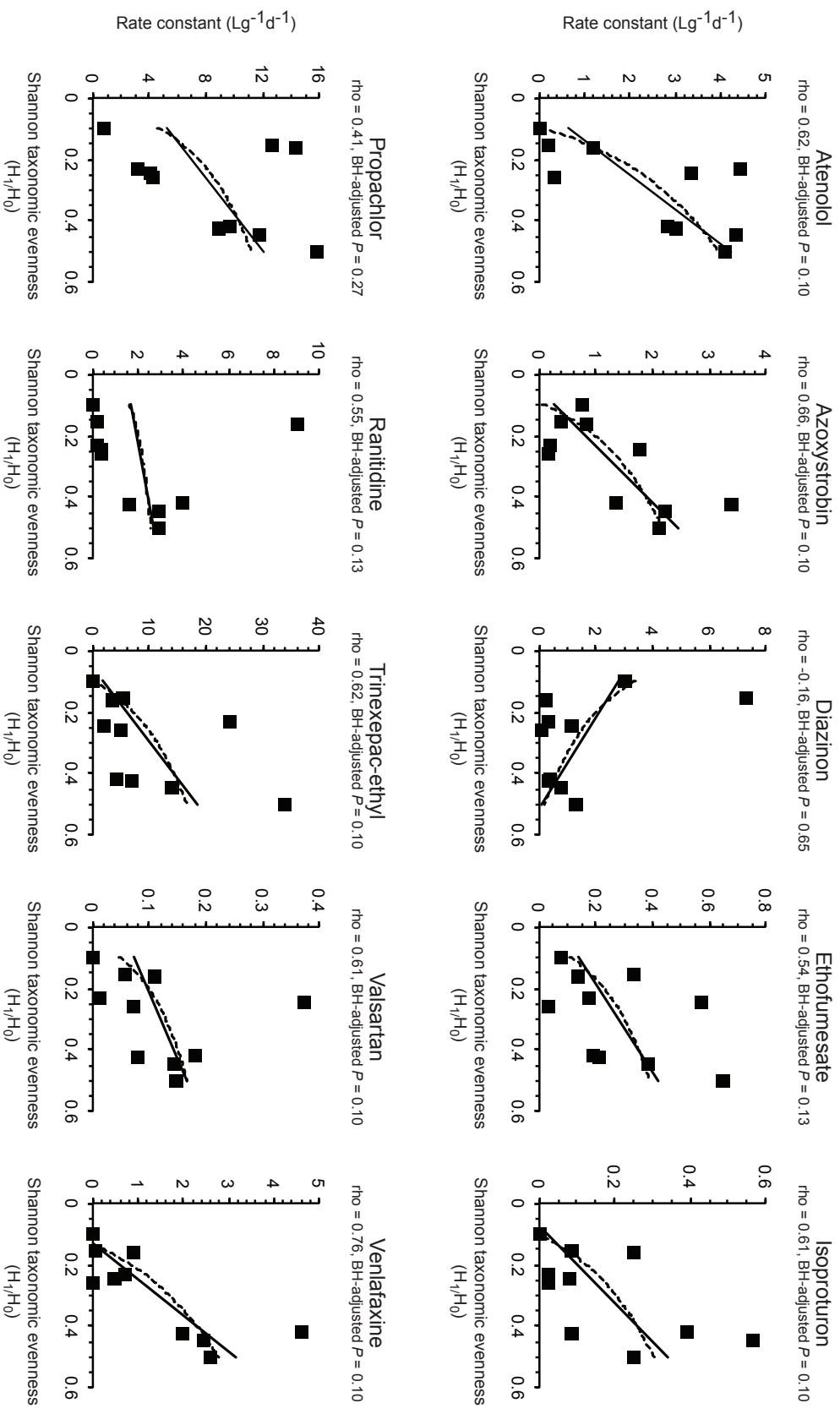
**Figure S2.** Associations between the Chao1 extrapolated taxonomic richness measurements and the active biomass-normalized first-order rate constants for each individual micropollutant biotransformation. Each square symbol indicates the measurements for one independent WWTP community. The solid lines are the best-fit linear models and the dashed lines are the best-fit logarithmic models. Definitions:  $\rho$ , Spearman rank correlation coefficient; BH-adjusted  $P$ , Benjamini-Hochberg-adjusted two-sided  $P$ .



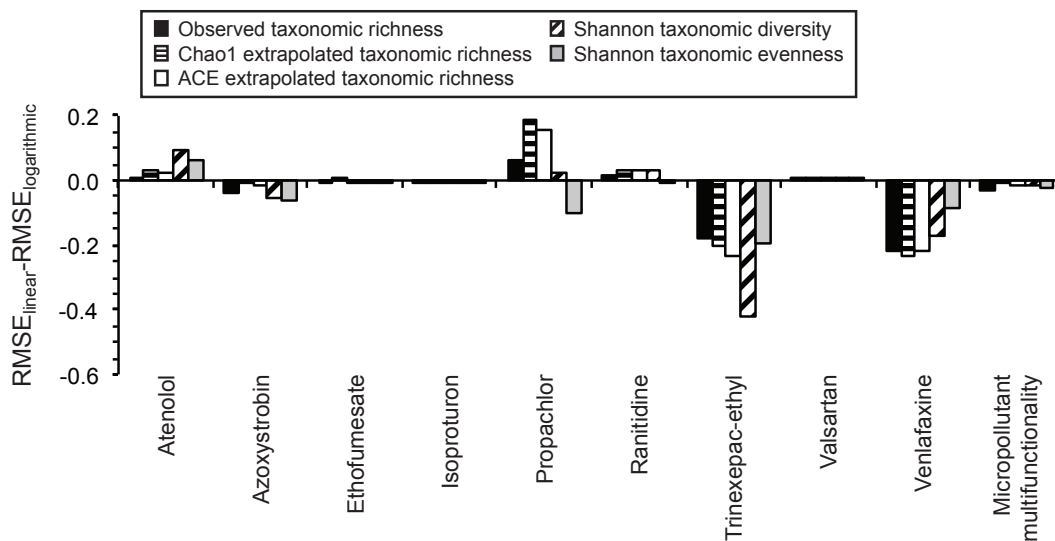
**Figure S3.** Associations between the ACE extrapolated taxonomic richness measurements and the active biomass-normalized first-order rate constants for each individual micropollutant biotransformation. Each square symbol indicates the measurements for one independent WWTP community. The solid lines are the best-fit linear models and the dashed lines are the best-fit logarithmic models. Definitions:  $\rho$ , Spearman rank correlation coefficient; BH-adjusted  $P$ , Benjamini-Hochberg-adjusted two-sided  $P$ .



**Figure S4.** Associations between the Shannon taxonomic diversity measurements and the active biomass-normalized first-order rate constants for each individual micropollutant biotransformation. Each square symbol indicates the measurements for one independent WWTP community. Shannon taxonomic diversity is reported in terms of the Hill number  $H_1$ . The solid lines indicate the best-fit linear models and the dashed lines are the best-fit logarithmic models. Definitions:  $\rho$ , Spearman rank correlation coefficient; BH-adjusted  $P$ , Benjamini-Hochberg-adjusted two-sided  $P$ .



**Figure S5.** Associations between the Shannon taxonomic evenness measurements and the active biomass-normalized first-order rate constants for each individual micropollutant biotransformation. Each square symbol indicates the measurements for one independent WWTP community. Shannon taxonomic evenness is reported in terms of the Hill numbers  $H_1$  and  $H_0$ . The solid lines are the best-fit linear models and the dashed lines are the best-fit logarithmic models. Definitions:  $\rho$ , Spearman rank correlation coefficient; BH-adjusted  $P$ , Benjamin-Hochberg-adjusted two-sided  $P$ .



**Figure S6.** The difference between the root mean squared errors for the best-fit linear and best-fit logarithmic models ( $RMSE_{linear} - RMSE_{logarithmic}$ ) between biodiversity (independent variable  $x$ ) and the rates of individual micropollutant biotransformations or micropollutant multifunctionality (dependent variable  $y$ ).

**Table S1.** <sup>a,b</sup>Active biomass-normalized first-order rate constants ( $Lg^{-1}d^{-1}$ ) for each micropollutant biotransformation.

Micropollutant	Name of full-scale wastewater treatment plant									
	DOM1	DOM2	DOM3	DOM4	DOM5	IND1	IND2	IND3	IND4	IND5
atenolol	4.33	3.00	4.10	0.355	2.85	4.41	3.36	1.20	0.187	0.00322
azoxystrobin	2.24	3.39	2.11	0.166	1.37	0.199	1.78	0.818	0.398	0.747
diazinon	0.741	0.313	1.29	0.114	0.384	0.310	1.15	0.212	7.28	3.02
ethofumesate	0.388	0.209	0.647	0.0286	0.187	0.175	0.570	0.137	0.334	0.0756
isoproturon	0.564	0.0850	0.251	0.0226	0.389	0.0216	0.0803	0.251	0.0864	0.00342
propachlor	11.8	8.85	15.8	4.23	9.65	3.18	4.09	14.4	12.7	0.722
ranitidine	2.94	1.61	2.90	0.362	3.99	0.205	0.357	9.04	0.237	0.0235
trinexpac-ethyl	13.8	6.84	34.0	5.06	4.06	24.0	1.99	3.26	5.28	0.226
valsartan	0.145	0.0786	0.149	0.0746	0.182	0.0141	0.372	0.112	0.0566	0.00212
venlafaxine	2.44	2.00	2.60	0.0296	4.64	0.707	0.471	0.896	0.0772	0.00890

<sup>a</sup>Active biomass was estimated using the method described by Majewsky and colleagues (1). <sup>b</sup>The observed first-order rate constants were previously reported by Helbing and colleagues (2).

**Table S2.** Measured operational and environmental metrics for each full-scale wastewater treatment plant.

Operational or environmental metric	Name of full-scale wastewater treatment plant									
	DOM1	DOM2	DOM3	DOM4	DOM5	IND1	IND2	IND3	IND4	IND5
temperature, [°C]	9	12	17	11	8	25	29	35	24	41
pH	7.6	7.6	7.5	8.1	8.1	7	7.3	6.2	7	8.1
dissolved oxygen, [mg/L]	1.7	1.7	0.8	6.2	2.4	2.8	1.5	4.8	3.4	1
total suspended solids, [g/L]	3	3	12.4	2.3	2.2	6.8	4.7	6.9	6	9.6
total daily flow rate, [m <sup>3</sup> ]	1622	17358	962	16375	10314	9119	8113	21360	5720	5800
hydraulic retention time, [hour]	4	2.8	24	5.9	20	14	17	21.3	35.7	20
solids retention time, [day]	5.1	5.4	9.8	2.6	20.5	9.5	12	6.1	99.6	5
influent ammonia-nitrogen, [mg/L]	18.6	3.3	24.9	10	26.2	23	86	n.a.	86.2	100
influent ammonia-nitrogen, [mg/L]	0.1	0.2	0	5	0.1	0.9	2	n.a.	57.2	62
influent total phosphorous, [mg/L]	5	2	9	3	5	3	6	n.a.	n.a.	22
influent total phosphorous, [mg/L]	1.3	0.1	0.4	0.1	0.1	n.a.	1.6	n.a.	n.a.	17.6
influent BOD <sub>5</sub> , [mg/L]	203	54	320	160	n.a.	500	n.a.	1892	650	3000
effluent BOD <sub>5</sub> , [mg/L]	8	3	1	10	n.a.	n.a.	n.a.	25	8	159
influent <sup>d</sup> COD, [mg/L]	310	96	n.a.	332	n.a.	846	820	1873	1565	n.a.
effluent COD, [mg/L]	34	42	n.a.	19	n.a.	165	n.a.	219	208	n.a.

<sup>a</sup>All operational and environmental metrics were previously reported by Helbling and colleagues (2). <sup>b</sup>n.a., data was not available from the wastewater treatment plant. <sup>c</sup>BOD<sub>5</sub>, 5-day biological oxygen demand. <sup>d</sup>COD, chemical oxygen demand.



**Table S3.** Experimentally observed biotransformation types and biotransformation products for each micropollutant.

Micropollutant	Predominant use	<sup>a</sup> Experimentally observed biotransformation types	
		Experimentally observed biotransformation products	Experimentally observed biotransformation products
atenolol	pharmaceutical	amide hydrolysis	atenolol acid
azoxystrobin	pesticide	carboxylic acid ester hydrolysis	azoxystrobin acid
diazinon	pesticide	aromatic thiophosphate hydrolysis	pyrimidinol
ethofumesate	pesticide	ether dealkylation	2-keto-ethofumesate
isoproturon	pesticide	urea dealkylation and urea di-dealkylation	N-demethyl isoproturon and N-didemethyl isoproturon
propachlor	pesticide	glutathione coupling and hydrolysis oxidation	propachlor-ESA and propachlor-OXA
ranitidine	pharmaceutical	S-oxidation and N-oxidation	ranitidine-S-oxide and ranitidine-N-oxide
trinexepac-ethyl	pesticide	carboxylic acid ester hydrolysis	trinexepac-acid
valsartan	pharmaceutical	amide dealkylation	valsartan acid
venlafaxine	pharmaceutical	amine dealkylation and ether dealkylation	N-demethyl venlafaxine and O-demethyl venlafaxine

<sup>a</sup>All experimentally observed biotransformation types and biotransformation products were previously reported by Helbing and colleagues (2).

**Table S4.** Micropollutant multifunctionality measurements for each full-scale wastewater treatment plant community.

Measurement	Name of full-scale wastewater treatment plant									
	DOM1	DOM2	DOM3	DOM4	DOM5	IND1	IND2	IND3	IND4	IND5
<sup>a</sup> micropollutant multifunctionality	0.649	0.0590	0.879	-0.809	0.362	-0.364	0.132	0.060	-0.144	-0.823

<sup>a</sup>Micropollutant multifunctionality was measured using the active biomass-normalized first-order rate constants for each micropollutant biotransformation and the method described by Zavaleta and colleagues (3).

**Table S5.** Linear and logarithmic models for describing the observed positive associations between biodiversity (independent variable  $x$ ) and the rates of individual or the collective rates of multiple micropollutant biotransformations (dependent variable  $y$ ).

Micropollutant	Biodiversity measurement	Best-fit			Best-fit		
		linear model	$R^2_{\text{linear}}$	$b_{\text{RMSE}_{\text{linear}}}$	logarithmic model	$R^2_{\text{logarithmic}}$	$\text{RMSE}_{\text{logarithmic}}$
atenofool	observed taxonomic richness	$y=0.0041x-0.42$	0.381	1.48	$y=2.4\ln(x)-13$	0.387	1.48
	Chao1 extrapolated taxonomic richness	$y=0.0014x+0.078$	0.328	1.54	$y=2.1\ln(x)-13$	0.358	1.51
	ACE extrapolated taxonomic richness	$y=0.0022x+0.075$	0.323	1.55	$y=2.1\ln(x)-12$	0.341	1.53
	Shannon taxonomic diversity	$y=0.0066x+0.87$	0.426	1.43	$y=1.3\ln(x)-4.1$	0.497	1.34
	Shannon taxonomic evenness	$y=8.9x-0.23$	0.506	1.32	$y=2.4\ln(x)+5.7$	0.549	1.26
azoxystrobin	observed taxonomic richness	$y=0.0024x-0.40$	0.409	0.859	$y=1.4\ln(x)-7.4$	0.351	0.900
	Chao1 extrapolated taxonomic richness	$y=0.00082x+0.027$	0.295	0.938	$y=1.1\ln(x)-6.8$	0.285	0.945
	ACE extrapolated taxonomic richness	$y=0.0013x-0.086$	0.343	0.906	$y=1.2\ln(x)-6.8$	0.321	0.921
	Shannon taxonomic diversity	$y=0.0042x+0.36$	0.495	0.794	$y=0.71\ln(x)-2.3$	0.428	0.846
	Shannon taxonomic evenness	$y=5.4x-0.27$	0.536	0.761	$y=1.3\ln(x)+3.1$	0.455	0.825
diazinon	observed taxonomic richness	$y=-0.0034x+3.8$	0.164	2.15	$y=-2.0\ln(x)+14$	0.175	2.13
	Chao1 extrapolated taxonomic richness	$y=-0.0010x+3.1$	0.107	2.22	$y=-1.5\ln(x)+13$	0.120	2.20
	ACE extrapolated taxonomic richness	$y=-0.0017x+3.3$	0.123	2.20	$y=-1.6\ln(x)+13$	0.136	2.18
	Shannon taxonomic diversity	$y=-0.0046x+2.5$	0.136	2.18	$y=-1.1\ln(x)+6.9$	0.218	2.08
	Shannon taxonomic evenness	$y=-6.8x+3.5$	0.188	2.12	$y=-2.0\ln(x)-1.2$	0.236	2.05
ethofumesate	observed taxonomic richness	$y=0.00037x+0.025$	0.227	0.192	$y=0.21\ln(x)-1.1$	0.219	0.193
	Chao1 extrapolated taxonomic richness	$y=0.00015x+0.043$	0.247	0.190	$y=0.20\ln(x)-1.2$	0.249	0.190
	ACE extrapolated taxonomic richness	$y=0.00020x+0.050$	0.229	0.192	$y=0.20\ln(x)-1.1$	0.226	0.193
	Shannon taxonomic diversity	$y=0.00057x+0.14$	0.253	0.189	$y=0.10\ln(x)-0.24$	0.227	0.192
	Shannon taxonomic evenness	$y=0.70x+0.071$	0.230	0.192	$y=0.18\ln(x)+0.51$	0.213	0.194
isoprotruron	observed taxonomic richness	$y=0.00052x-0.18$	0.559	0.131	$y=0.28\ln(x)-1.6$	0.487	0.141
	Chao1 extrapolated taxonomic richness	$y=0.00019x-0.13$	0.538	0.134	$y=0.26\ln(x)-1.7$	0.496	0.140
	ACE extrapolated taxonomic richness	$y=0.00030x-0.14$	0.540	0.133	$y=0.26\ln(x)-1.6$	0.498	0.140
	Shannon taxonomic diversity	$y=0.00071x+0.012$	0.460	0.145	$y=0.12\ln(x)-4.5$	0.415	0.150
	Shannon taxonomic evenness	$y=0.80x-0.058$	0.369	0.156	$y=0.19\ln(x)+0.44$	0.323	0.162
propachlor	observed taxonomic richness	$y=0.014x-0.74$	0.487	3.96	$y=8.0\ln(x)-43$	0.502	3.90
	Chao1 extrapolated taxonomic richness	$y=0.00553x+0.12$	0.510	3.87	$y=7.7\ln(x)-48$	0.557	3.68
	ACE extrapolated taxonomic richness	$y=0.0082x-0.029$	0.519	3.84	$y=7.8\ln(x)-45$	0.558	3.68
	Shannon taxonomic diversity	$y=0.017x+4.7$	0.318	4.57	$y=3.0\ln(x)-6.9$	0.325	4.54

ranitidine	Shannon taxonomic evenness	$y=17x+3.6$	0.213	4.91	$y=4.1\ln(x)+0.14$	0.181	5.01
	observed taxonomic richness	$y=0.0049x-1.2$	0.220	2.63	$y=2.9\ln(x)-17$	0.229	2.61
	Chao1 extrapolated taxonomic richness	$y=0.0019x-0.85$	0.227	2.62	$y=2.7\ln(x)-18$	0.243	2.59
	ACE extrapolated taxonomic richness	$y=0.0030x-0.93$	0.233	2.61	$y=2.8\ln(x)-17$	0.251	2.57
	Shannon taxonomic diversity	$y=0.0039x+1.3$	0.060	2.88	$y=0.83\ln(x)-2.0$	0.082	2.85
trinexepac-ethyl	Shannon taxonomic evenness	$y=2.5x+1.4$	0.016	2.95	$y=0.58\ln(x)+3.0$	0.013	2.95
	observed taxonomic richness	$y=0.018x-2.2$	0.186	10.5	$y=9.5\ln(x)-51$	0.158	10.7
	Chao1 extrapolated taxonomic richness	$y=0.0070x-1.3$	0.203	10.4	$y=9.0\ln(x)-56$	0.171	10.6
	ACE extrapolated taxonomic richness	$y=0.011x-1.1$	0.195	10.4	$y=8.7\ln(x)-50$	0.159	10.7
	Shannon taxonomic diversity	$y=0.033x+2.3$	0.284	9.84	$y=5.3\ln(x)-17$	0.221	10.3
valsartan	Shannon taxonomic evenness	$y=42x-2.3$	0.288	9.81	$y=10\ln(x)+2.4$	0.260	10.0
	observed taxonomic richness	$y=0.00016x+0.0083$	0.165	0.103	$y=0.11\ln(x)-0.56$	0.207	0.101
	Chao1 extrapolated taxonomic richness	$y=0.000061x+0.021$	0.164	0.103	$y=0.097\ln(x)-0.59$	0.211	0.100
	ACE extrapolated taxonomic richness	$y=0.000090x+0.025$	0.148	0.104	$y=0.094\ln(x)-0.52$	0.195	0.101
	Shannon taxonomic diversity	$y=0.00018x+0.077$	0.092	0.108	$y=0.0046\ln(x)-0.12$	0.179	0.102
venlafaxine	Shannon taxonomic evenness	$y=0.23x+0.051$	0.095	0.107	$y=0.074\ln(x)+0.22$	0.141	0.105
	observed taxonomic richness	$y=0.0050x-2.0$	0.765	0.776	$y=2.6\ln(x)-15$	0.614	0.995
	Chao1 extrapolated taxonomic richness	$y=0.0019x-1.7$	0.794	0.727	$y=2.4\ln(x)-16$	0.641	0.960
	ACE extrapolated taxonomic richness	$y=0.0029x-1.7$	0.786	0.741	$y=2.4\ln(x)-15$	0.640	0.961
	Shannon taxonomic diversity	$y=0.0074x-0.030$	0.742	0.814	$y=1.2\ln(x)-4.8$	0.624	0.982
multifunctionality	Shannon taxonomic evenness	$y=8.5x-1.1$	0.639	0.962	$y=2.1\ln(x)+4.2$	0.574	1.05
	observed taxonomic richness	$y=0.0019x-1.3$	0.779	0.280	$y=1.0\ln(x)-6.7$	0.726	0.311
	Chao1 extrapolated taxonomic richness	$y=0.00071x-1.1$	0.780	0.279	$y=0.97\ln(x)-7.1$	0.763	0.290
	ACE extrapolated taxonomic richness	$y=0.0011x-1.1$	0.772	0.284	$y=0.97\ln(x)-6.6$	0.747	0.300
	Shannon taxonomic diversity	$y=0.0026x-0.61$	0.694	0.329	$y=0.47\ln(x)-2.4$	0.658	0.348
Shannon taxonomic evenness	$y=3.06x-0.90$	0.595	0.379	$y=0.76\ln(x)+1.0$	0.544	0.402	

<sup>a</sup>R<sup>2</sup>, coefficient of determination. <sup>b</sup>RMSF; root mean squared error.

**Table S6.** Bacterial enzymes that are predicted to catalyze each of the experimentally observed micropollutant biotransformations.

Micropollutant	<sup>a</sup> Experimentally observed		<sup>b</sup> Predicted bacterial enzymes	<sup>b</sup> EC number
	biotransformations			
atenolol	amide hydrolysis		amidase atenolol amidohydrolase bromoxynil nitrilase	EC 3.5.1.4 EC 3.5.1.1- EC 3.5.5.6
			<i>cis</i> -aconitamide amidase	EC 3.5.1.1-
azoxystrobin	carboxylic acid ester hydrolysis		1-hydroxy-2-oxolinonene 1,2-monoxygenase	EC 1.14.13.1-
			1-oxa-2-oxocycloheptane lactonase	EC 3.1.1.1-
			2-hydroxy-6-oxo-6-(2-hydroxyphenoxy)hexa-2,4-dienoate esterase	EC 3.1.1.1-
			2-pyrone-4,6-dicarboxylate hydrolase	EC 3.1.1.57
			4-hydroxyphenyl 4-hydroxybenzoate hydrolase	EC 3.1.1.1-
			4-pyridoxolactonase	EC 3.1.1.27
			4-sulfophenol acetate esterase	EC 3.1.1.1-
			5-pyridoxolactonase	EC 3.1.1.6
			acetylsterase	EC 3.1.1.2
			arylesterase	EC 3.1.1.1-
			butyrolactone hydrolase	EC 3.1.1.1
			carboxylesterase	EC 3.1.1.1-
			CHMOD hydrolase	EC 3.1.1.84
			cocaine esterase	EC 3.1.1.1-
			diethylsuccinate esterase	EC 3.1.1.1-
			dihydrocoumarin hydrolase	EC 3.1.1.1-
			dimethyl isophthalate esterase	EC 3.1.1.1-
			eggonine methyl esterase	EC 3.1.1.1-
			endosulfan lactone lactonase	EC 3.1.1.1-
	ethylsuccinate esterase	EC 3.1.1.1-		
	isopropyl salicylate esterase	EC 3.1.1.1-		
	malathion esterase	EC 3.1.1.1-		
	malathion monocarboxylate esterase	EC 3.1.1.1-		
	monomethyl isophthalate esterase	EC 3.1.1.1-		
	pyrethroid hydrolase	EC 3.1.1.88		

		tropinesterase	EC 3.1.1.10
diazinon	aromatic thiophosphate hydrolysis	aryldialkylphosphatase isocarbophos phosphodiesterase triazophos phosphodiesterase	EC 3.1.8.1 EC 3.1.4.- EC 3.1.4.-
cethofumesate	ether dealkylation	2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase 2,4,5-trichlorophenoxyacetic acid oxygenase 3-methylgallate O-demethylase 4-chlorophenoxyacetate monooxygenase 4-methoxybenzoate monooxygenase tetrahydrofolate-dependent O-demethylase vanillate monooxygenase vanillate O-demethylase	EC 1.14.11.- EC 1.14.13.- EC 2.1.1.- EC 1.14.- EC 1.14.99.15 EC 2.1.1.- EC 1.14.13.82 EC 2.1.1.-
isoproturon	urea dealkylation and urea di-dealkylation	2-hydroxy-2',6'-diethyl-N-acetanilide hydrolase alachlor hydrolase caffeine demethylase heteroxanthine demethylase hydroxymonomethylisoproturon dimethylaminohydrogenase isoproturon dimethylaminohydrogenase monodemethylisoproturon dimethylaminohydrogenase N-isopropylacetaniline monooxygenase paraxanthine demethylase theobromine demethylase	EC 3.3.2.- EC 3.3.2.- EC 1.13.12.- EC 1.14.13.128 EC 1.5.99.- EC 1.5.99.- EC 1.5.99.- EC 1.14.- EC 1.13.12.- EC 1.13.12.-
propachlor	glutathione coupling, dehalogenation and halosubstitution	1,1-dichloroethane reductive dehalogenase 1,1,1-trichloroethane reductive dehalogenase 1,2-dichloroethene reductive dehalogenase 1,2,4-trichlorobenzene reductive dehalogenase 1,4-dichlorobenzene reductive dehalogenase 2-chloro-N-isopropylacetanilide reductive dehalogenase 2-chlorobenzoate reductive dehalogenase 2,4-dichloroaniline reductive dehalogenase 2,4-dichlorobenzoyl-CoA reductase 2,4-dichlorophenoxyacetate reductive dehalogenase 2,5-dichlorohydroquinone reductive dechlorinase 2,6-dichlorobenzamide reductive dehalogenase 2,6-dichlorobenzoate reductive dehalogenase	EC 1.97.1- EC 1.97.1- EC 1.97.1- EC 1.97.1- EC 1.97.1- EC 1.97.1- EC 1.97.1- EC 1.97.1- EC 1.3.1.63 EC 1.97.1- EC 1.97.1- EC 1.97.1- EC 1.97.1-

		3-monobromobisphenol A reductive dehalogenase	EC 1.97.1-
		3,3'-dibromobisphenol A reductive dehalogenase	EC 1.97.1-
		3,3',5'-tribromobisphenol A reductive dehalogenase	EC 1.97.1-
		3,3',5',5'-tetrabromobisphenol A reductive dehalogenase	EC 1.97.1-
		carbon tetrachloride reductive dehalogenase	EC 1.97.1-
		chloroform reductive dehalogenase	EC 1.97.1-
		DDE reductive dehalogenase	EC 1.97.1-
		DDT reductive dehalogenase	EC 1.97.1-
		dichloromethane reductive dehalogenase	EC 1.97.1-
		maleylacetate reductase	EC 1.3.1.32
		methyl chloride reductive dehalogenase	EC 1.97.1-
		tetrachloroethene reductive dehalogenase	EC 1.97.1.8
		tetrachlorohydroquinone reductive dehalogenase	EC 1.8.99.-
		vinyl chloride reductive dehalogenase	EC 1.97.1-
		2-haloacid dehalogenase	EC 3.8.1.2
		DDMS dehalogenase	EC 3.8.1.-
		dichloroacetate halidohydrolase	EC 3.8.1.-
		haloacetate dehalogenase	EC 3.8.1.3
		haloalkane dehalogenase	EC 3.8.1.5
ranitidine	S-oxidation and N-oxidation	2-(methylthio)benzothiazole monooxygenase	EC 1.14.-
		benzothioephene monooxygenase	EC 1.14.13.-
		DBT monooxygenase	EC 1.14.13.-
		phorate monooxygenase	EC 1.10.3.2
trimezepac-ethyl	carboxylic acid ester hydrolysis	1-hydroxy-2-oxolinonene 1,2-monooxygenase	EC 1.14.13.-
		1-oxa-2-oxocycloheptane lactonase	EC 3.1.1.-
		2-hydroxy-6-oxo-6-(2-hydroxyphenoxy)hexa-2,4-dienoate esterase	EC 3.1.1.-
		2-pyrone-4,6-dicarboxylate hydrolase	EC 3.1.1.57
		4-hydroxyphenyl 4-hydroxybenzoate hydrolase	EC 3.1.1.-
		4-pyridoxolactonase	EC 3.1.1.27
		4-sulfophenol acetate esterase	EC 3.1.1.-
		5-pyridoxolactonase	EC 3.1.1.-
		acetylesterase	EC 3.1.1.6
		arylesterase	EC 3.1.1.2
		butyrolactone hydrolase	EC 3.1.1.-
		carboxylesterase	EC 3.1.1.1

		CHMOD hydrolase	EC 3.1.1.-
		cocaine esterase	EC 3.1.1.84
		diethylsuccinate esterase	EC 3.1.1.-
		dihydrocoumarin hydrolase	EC 3.1.1.-
		dimethyl isophthalate esterase	EC 3.1.1.-
		ecgonine methyl esterase	EC 3.1.1.-
		endosulfan lactone lactonase	EC 3.1.1.-
		ethylsuccinate esterase	EC 3.1.1.-
		isopropyl salicylate esterase	EC 3.1.1.-
		malathion esterase	EC 3.1.1.-
		malathion monocarboxylate esterase	EC 3.1.1.-
		monomethyl isophthalate esterase	EC 3.1.1.-
		pyrethroid hydrolase	EC 3.1.1.88
		tropinesterase	EC 3.1.1.10
valsartan	amide	2-hydroxy-2',6'-diethyl-N-acetanilide hydrolase	EC 3.3.2.-
	dealkylation	alachlor hydrolase	EC 3.3.2.-
		caffeine demethylase	EC 1.13.12.-
		heteroxanthine demethylase	EC 1.14.13.128
		hydroxymonomethylisoprotruron dimethylaminohydrogenase	EC 1.5.99.-
		isoprotruron dimethylaminohydrogenase	EC 1.5.99.-
		monodemethylisoprotruron dimethylaminohydrogenase	EC 1.5.99.-
		N-isopropylacetaniline monoxygenase	EC 1.14.-
		paraxanthine demethylase	EC 1.13.12.-
		theobromine demethylase	EC 1.13.12.-
venlafaxine	amine	4-methylaminobutanate oxidase	EC 1.5.3.19
	dealkylation and ether	caffeine demethylase	EC 1.13.12.-
	dealkylation	cyclohexylamine oxidase	EC 1.4.3.12
		dimethylamine dehydrogenase	EC 1.5.8.1
		heteroxanthine demethylase	EC 1.14.13.128
		N-methylaurine dehydrogenase	EC 1.4.99.2
		trimethylamine dehydrogenase	EC 1.5.8.2

<sup>a</sup>The experimentally observed biotransformation types and biotransformation products were previously reported by Helbling and colleagues (2). <sup>b</sup>The predicted bacterial enzymes and EC numbers for each observed biotransformation were obtained from the University of Minnesota Biocatalysis/Biodegradation Database (4). <sup>c</sup>Ammonia monoxygenase was excluded from the predicted bacterial enzymes for ethofumesate because we experimentally demonstrated that ammonia monoxygenase does not catalyze this biotransformation (2).



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