

Table S4. PICRUSt-predicted biotin synthesis gene abundance from wastewater microbial community

Gene ID ¹	KEGG orthology	Full gene name	<i>A. protothecoides</i> ⁴			<i>C. sorokiniana</i>		
			Original MC ²	Adapted MC ³	Adapted MC + algae	Original MC	Adapted MC	Adapted MC + algae
bioC	K02169	malonyl-CoA O-methyltransferase	749 a ⁵	848 a	294 b	433 ab	539 a	125 b
bioF	K00652	8-amino-7-oxononanoate synthase	2155 a	2440 a	1069 a	1380 a	2307 a	1789 a
bioA	K00833	SAM-8-amino-7-oxononanoate aminotransferase	1990 a	1609 a	893 a	1335 a	1489 a	1235 a
bioD	K01935	dethiobiotin synthetase	1879 a	1607 a	894 a	1275 a	1486 a	1231 a
bioB	K01012	biotin synthase	3538 a	2346 ab	1246 b	2462 a	2061 a	1453 a
bisC	K08351	biotin/methionine sulfoxide reductase	28 a	14 b	14 b	20 a	13 ab	7 b
bioW	K01906	6-carboxyhexanoate--CoA ligase	264 a	9 b	3 b	192 a	7 b	3 b
bioH	K02170	biotin biosynthesis protein	191 a	292 a	161 a	102 ab	183 a	26 b
Total			10793 a	9165 ab	4573 b	7199 a	8085 a	5871 a

¹Gene IDs are based on the KEGG orthology and match those shown in Figure S2

²Original community refers to microorganisms present in the wastewater prior to cultivation in aerated bioreactors.

³Adapted community refers to microorganisms present after 4-5 days of culture in aerated bioreactors without algae.

⁴The algae strain was only added to one set of bioreactors but all bioreactors under this heading were part of the same batch.

⁵Within an algae species, values with the same letter in the same row are not statistically different at the 0.05 level based on n=3 replicates