

Supplementary Material

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SUPPLEMENTARY VIDEO 1 | Digital video showing the sponge-dominated benthic community at the Arctic Schulz Bank seamount as recorded by the AEGIR 6000 ROV during a dive aimed to deploy the incubation chambers. Note the abundance of *Schaudinnia rosea*, which are the white tubular sponges.

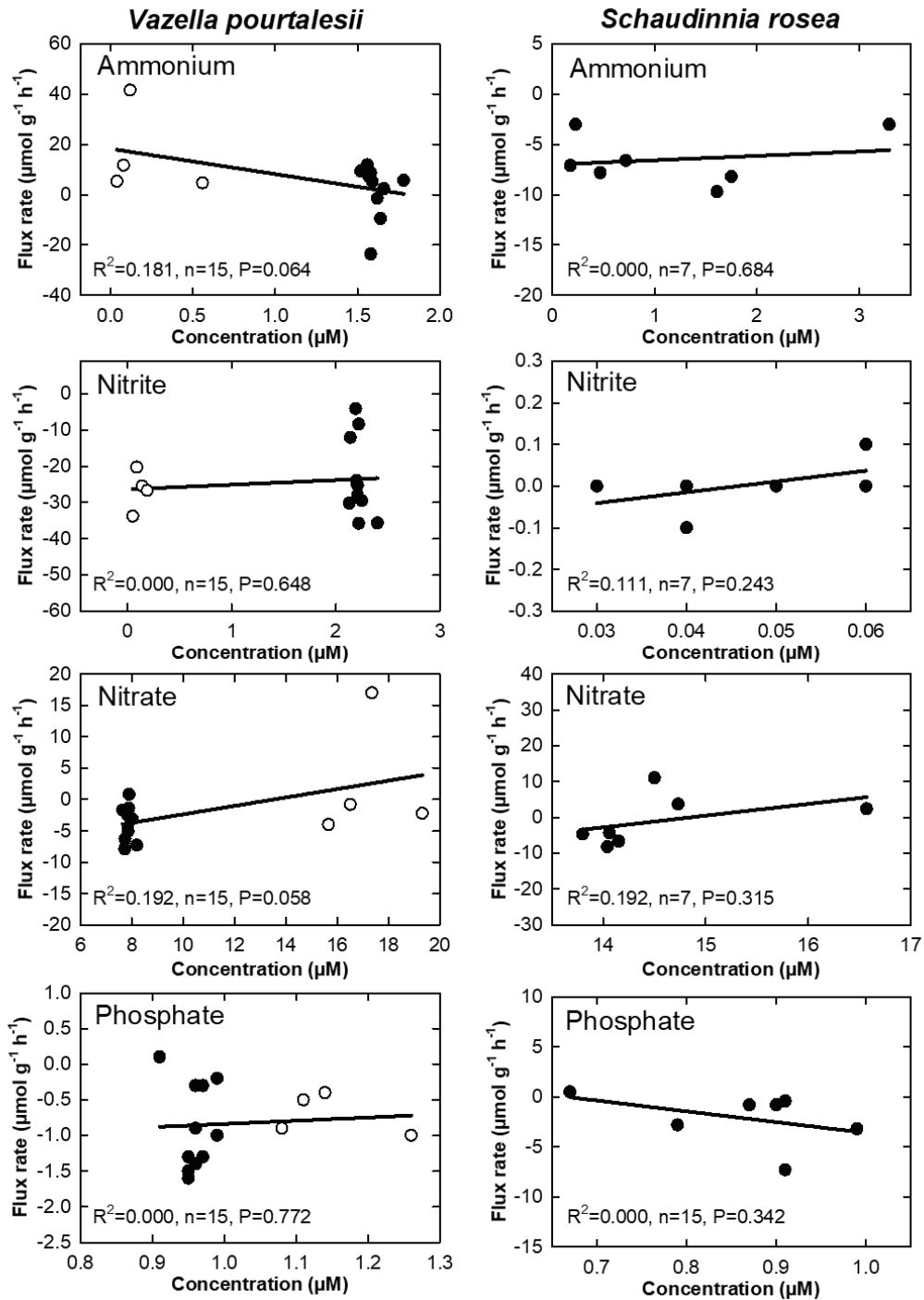
SUPPLEMENTARY VIDEO 2 | Digital video showing the monospecific aggregation of *Vazella pourtalesii* at Sambro Bank Sponge Conservation Area on the Nova Scotia Shelf, Canada, as recorded by the ROPOS ROV.

SUPPLEMENTARY VIDEO 3 | Video showing the incubation of an individual of *Schaudinnid rosea* at the Arctic Schulz Bank seamount as recorded by the AEGIR 6000 ROV.

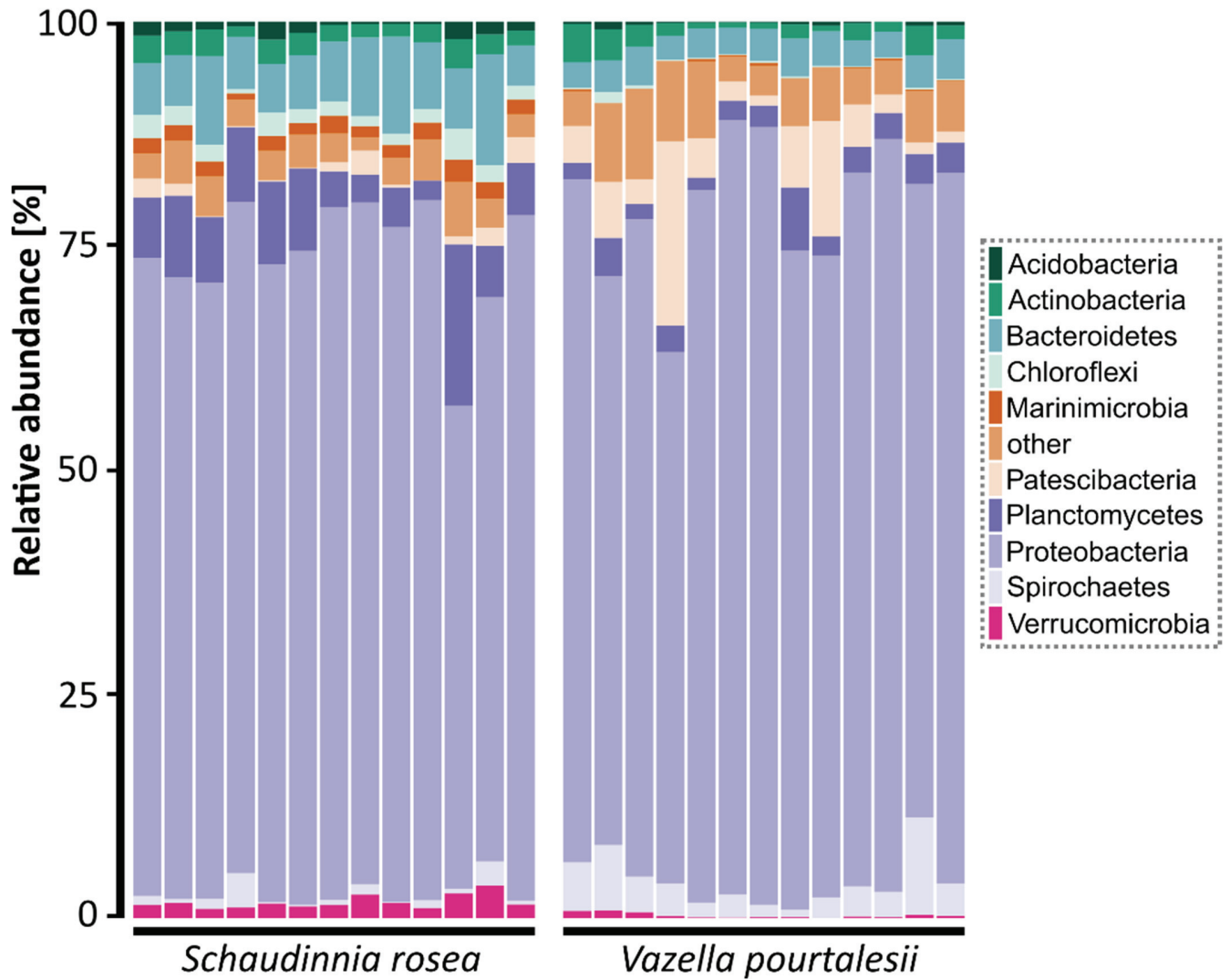
SUPPLEMENTARY VIDEO 4 | Video showing the incubation of an individual of *Vazella pourtalesii* at Sambro Bank Sponge Conservation Area on the Nova Scotia Shelf, Canada, as recorded by the ROPOS ROV.

SUPPLEMENTARY DATA FILE 1 | Excel file containing the triangular matrix of Weighted UniFrac distances between pairs of samples, including tissue of *Schaudinnia rosea* and *Vazella pourtalesii*, and seawater from their respective habitats. Distances resulted from the taxonomic classification of Amplicon Sequence Variants (ASVs) performed using a Bayes classifier and were calculated based on a phylogeny produced with FastTree2. Distances were then submitted to the non-metric multidimensional scaling to produce the ordination space of [Figure 5](#).

SUPPLEMENTARY DATA FILE 2 | Excel data file containing the calculations of the annual net nutrient flux across the aggregations of *Vazella pourtalesii*.



SUPPLEMENTARY FIGURE 1 | Linear regression analysis examining nutrient flux rates as a function of ambient nutrient concentration for the two assayed sponge species. In *Vazella pourtalesii*, in-situ incubations (open circles) were combined with 1st day laboratory incubations (solid circles) for the analyses. Note that the relationship lacks statistical significance in all cases ($P > 0.05$) and that the strength of the association between the two variables is consistently very low (adjusted $R^2 < 0.2$).



SUPPLEMENTARY FIGURE 2 | Summary of relative abundances in the composition of the microbiomes (at the phylum level) of *Schaudinnia rosea* and *Vazella pourtalesii*. The ten most abundant phyla are displayed, while the remaining, low-abundance phyla are combined under the category “other”. Additional information on the microbiomes of these sponge species can be found somewhere else (Bayer et al., 2020; Busch et al., 2020b, 2020a).

SUPPLEMENTARY TABLE 1 | Summary of tests examining differences in the flux rate of nutrients (ammonium, nitrite, nitrate, phosphate) in *Vazella pourtalesii* as function of rates having been through an *in-situ* incubation or a laboratory incubation. Note that ammonium, nitrite and phosphate results made normal and homoscedastic data sets suitable for the parametric *t*-test. The non-normal and heteroscedastic data of nitrate were analyzed through the non-parametric Mann-Whitney *U* test. In no case, there were statistically significant differences between incubation modes. Therefore, result from both incubation modes were pooled together to extract global average values. “N”, “Mean” and “SD” indicate, respectively, the number of replicates per incubation mode, along with its average value and standard deviation. “*p*” indicates the statistical significance of each pairwise comparison test.

Nutrient	N	Mean	SD	Statistic type	Statistic value	<i>p</i>
Ammonium						
in situ	4	15.8	17.4	<i>t</i> -test	-1.858	0.086
ex situ	11	2.3	10.5			
Nitrite						
in situ	4	-26.6	5.6	<i>t</i> -test	0.554	0.589
ex situ	11	-23.4	10.7			
Nitrate *						
in situ	4	2.5	9.7	<i>U</i> -test	10.000	0.133
ex situ	11	-3.8	2.7			
Phosphate						
in situ	4	-0.7	0.3	<i>t</i> -test	-0.551	0.591
ex situ	11	-0.9	0.6			

SUPPLEMENTARY TABLE 2 | Summary of net fluxes of NH_4^+ over the seven consecutive laboratory incubations of eleven *Vazella pourtalesii* individuals (Ind. codes #5 to #15). The ambient ammonium concentration (μM) at the beginning of each incubation is given on the left-hand section of the table and the measured net flux rate ($10^{-3} \mu\text{mol}$ of ammonium per sponge mL and hour) in the right-hand section. Note that individuals 1-4 are missing from the table, because they were incubated *in situ* but not in the laboratory. The mean (AVG) value of each incubation step and its associated standard deviation (SD) are given at the two bottom rows of the table.

Ind. code	Ambient NH_4^+ (μM)							NH_4^+ flux rate ($10^{-3} \mu\text{mol mL}^{-1} \text{h}^{-1}$)						
	Incubation step							Incubation step						
	1	2	3	4	5	6	7	1	2	3	4	5	6	7
5	1.5	2.1	1.6	0.3	0.6	0.3	1.5	9.4	8.5	3.1	3.4	-1.2	-1.3	2.5
6	1.6	2.0	1.6	0.5	0.7	0.5	1.6	7.2	7.0	0.1	-6.4	-2.2	-5.5	-5.3
7	1.6	2.3	1.7	0.3	0.7	0.5	1.5	-1.4	5.8	1.6	-4.0	-1.2	-5.6	-3.0
8	1.6	1.6	1.6	0.0	0.6	0.5	1.4	9.4	11.4	2.4	0.6	3.0	4.0	7.5
9	1.6	2.0	1.7	0.3	0.7	0.5	1.5	-9.5	-16.0	-6.1	-6.1	-7.6	-14.7	-6.2
10	1.8	2.0	1.5	0.3	0.6	0.4	1.4	5.7	13.8	9.0	4.1	-1.0	-5.5	3.0
11	1.6	2.0	1.5	0.4	0.6	0.5	1.5	11.9	17.4	2.5	-5.9	-2.9	-2.7	-3.4
12	1.6	2.0	1.5	0.4	0.5	0.5	1.5	8.7	12.1	-4.7	-6.1	-8.0	-12.3	-11.8
13	1.6	2.2	1.6	0.4	0.6	0.4	1.4	-23.6	-20.0	-24.5	-18.3	-19.4	-24.4	-18.7
14	1.7	2.0	1.6	0.4	0.6	0.4	1.4	2.4	-5.9	-0.3	-6.0	-6.5	-7.7	-7.5
15	1.6	2.1	1.7	0.5	0.6	0.4	1.4	5.2	0.2	-6.4	-5.5	-10.9	-13.0	-6.7
AVRG	1.6	2.0	1.6	0.3	0.6	0.5	1.5	2.3	3.1	-2.1	-4.6	-5.2	-8.1	-4.5
SD	0.1	0.2	0.1	0.1	0.0	0.1	0.1	10.5	12.3	8.7	6.1	6.2	7.7	7.2

SUPPLEMENTARY TABLE 3 | Summary of PERMANOVA tests showing the statistical significance of the groups of samples identified by a nMDS analysis (**Figure 5**) based on between-sample UniFrac distances obtained for the amplicon data.

Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value
<i>Schaudinnia rosea</i>	<i>Vazella pourtalesii</i>	26	999	40.9	0.001
<i>Schaudinnia rosea</i>	seawater <i>Schaudinnia rosea</i>	19	999	16.3	0.001
<i>Vazella pourtalesii</i>	seawater <i>Vazella pourtalesii</i>	16	999	30.2	0.002

SUPPLEMENTARY TABLE 4 | Genes encoding for enzymes involved in microbial nitrogen (A) cycle and phosphonate catabolism (B) detected in the microbiome of the sponge *Vazella pourtalesii*. The metagenome assembled genomes (MAGs) and their respective phylogenetic affiliations are given, following Bayer et al. (2020). Bold writing indicates MAGs that were enriched in the sponge over seawater. Enzymes missing in the MAGs are indicated by a dash (-) and enzymes found in the unbinned data are indicated by an asterisk (*).

(A) Pathway	Enzymes	EC	K term	Reaction	MAGs	Phylogenetic affiliation
Nitrification	ammonia monooxygenase (<i>amoABC</i>)	1.14.99.39	K10944, K10945, K10946	$\text{NH}_3^+ \rightarrow \text{NH}_2\text{OH}$	74, 90, 143 131	Crenarchaeota Crenarchaeota
	hydroxylamine dehydrogenase (<i>hao</i>)	1.7.2.6	K10535	$\text{NH}_2\text{OH} \rightarrow \text{NO}_2^-$	46	Gammaproteobacteria
	nitrite oxidoreductase (<i>nxrA</i>)	1.7.99.-	K00370	$\text{NO}_2^- \rightarrow \text{NO}_3^{2-}$		*
	nitrate reductase (<i>narG</i> , <i>narH</i> , <i>narJ</i>)	1.7.5.1	K00370, K00371, K00374	$\text{NO}_3^{2-} \rightarrow \text{NO}_2^-$		-
Denitrification	nitrate reductase (cytochrome) (<i>napA</i> , <i>napB</i>)	1.9.6.1	K02567, K02568	$\text{NO}_3^{2-} \rightarrow \text{NO}_2^-$	70 64	Alphaproteobacteria Actinobacteriota
	nitrite reductase (NO-forming) (<i>nirK</i> , <i>nirS</i>)	1.7.2.1	K00368, K15864	$\text{NO}_2^- \rightarrow \text{NO}$	90, 143 36, 101, 131	Crenarchaeota Crenarchaeota
	nitric oxide reductase (<i>norB</i> , <i>norC</i>)	1.7.2.5	K04561, K02305	$\text{NO} \rightarrow \text{N}_2\text{O}$	86	Acidobacteriota
	nitrous-oxide reductase (<i>nosZ</i>)	1.7.2.4	K00376	$\text{N}_2\text{O} \rightarrow \text{N}_2$		-
Dissimilatory nitrate reduction	nitrate reductase (<i>narG</i> , <i>narH</i> , <i>narJ</i>)	1.7.5.1	K00370, K00371, K00374	$\text{NO}_3^{2-} \rightarrow \text{NO}_2^-$	70 64	Alphaproteobacteria Actinobacteriota
	nitrate reductase (cytochrome) (<i>napA</i> , <i>napB</i>)	1.9.6.1	K02567, K02568	$\text{NO}_3^{2-} \rightarrow \text{NO}_2^-$	52	Planctomycetota
	nitrite reductase (cytochrome c-552) (<i>nrfA</i> , <i>nrfH</i>)	1.7.2.2	K03385, K15876	$\text{NO}_2^- \rightarrow \text{NH}_3^+$	*	*

	nitrite reductase (NADH) (<i>nirB</i> , <i>nirD</i>)	1.7.1.15	K00362, K00363	$\text{NO}_2^- \rightarrow \text{NH}_3^+$	52, 99 64 89	Planctomycetota Actinobacteriota Gammaproteobacteria
Nitrogen fixation	nitrogenase molybdenum-iron protein (<i>nifD</i> , <i>nifK</i> , <i>nifH</i> , <i>anfG</i>)	1.18.6.1	K02586, K02591, K02588, K00531	$\text{N}_2 \rightarrow \text{NH}_3^+$	88 91 77, 127 24 135	Firmicutes Planctomycetota Firmicutes Bacteroidota Alphaproteobacteria
other	hydroxylamine reductase (<i>hcp</i>)	1.7.99.1	K05601	$\text{NH}_2\text{OH} \rightarrow \text{NH}_3^+$	119 127	Planctomycetota Firmicutes
Assimilation	glutamate dehydrogease (<i>gudB</i> , <i>rocG</i>)	1.4.1.2	K00260, K15371	$\text{NH}_3^+ + \text{C}_5\text{H}_6\text{O}_5 \rightarrow \text{C}_5\text{H}_9\text{NO}_4$	27, 50, 58, 65, 70, 96, 104, 109, 114, 118 10, 34, 51, 108, 137 56 74, 90, 143 75, 94, 132 8, 126, 140 64 105 141 63, 89 67, 110 13	Alphaproteobacteria Gammaproteobacteria Spirochaetota Crenarchaeota Planctomycetota SAR324 Actinobacteriota Verrucomicrobiota Alphaproteobacteria Gammaproteobacteria Planctomycetota Myxococcota

	glutamine synthetase (<i>glnA</i> , <i>GLUL</i>)	6.3.1.2	K01915	$\text{NH}_3^+ + \text{C}_5\text{H}_9\text{NO}_4 \rightarrow \text{C}_5\text{H}_{10}\text{N}_2\text{O}_3$	<p>19, 21, 27, 50, 58, 65, 70, 96, 104, 109, 118</p> <p>4, 9, 10, 34, 40, 51, 58, 139</p> <p>56, 91, 93, 94, 125</p> <p>32, 52, 61, 75, 91, 113, 116, 119, 121, 132, 134</p> <p>8, 126, 140</p> <p>64, 80, 111</p> <p>6, 22</p> <p>74, 143</p> <p>3, 28</p> <p>42, 71, 115, 124, 135, 141</p> <p>47, 53, 94, 97, 100, 123</p> <p>26, 66, 111</p> <p>44, 55, 87, 92, 124, 142</p> <p>1, 2, 7, 24, 49, 54, 60, 87</p> <p>35, 45, 46, 63, 69, 89</p> <p>72</p> <p>59, 67, 110, 121</p> <p>11, 15, 18, 107, 133</p> <p>36, 101, 131</p> <p>14, 37, 68</p> <p>23, 84, 85, 112</p> <p>Alphaproteobacteria</p> <p>Gammaproteobacteria</p> <p>Spirochaetota</p> <p>Planctomycetota</p> <p>SAR324</p> <p>Actinobacteriota</p> <p>Myxococcota</p> <p>Crenarchaeota</p> <p>Bacteroidota</p> <p>Alphaproteobacteria</p> <p>Chloroflexota</p> <p>Actinobacteriota</p> <p>Firmicutes</p> <p>Bacteroidota</p> <p>Gammaproteobacteria</p> <p>Acidobacteriota</p> <p>Planctomycetota</p> <p>Thermoplasmatota</p> <p>Crenarchaeota</p> <p>Marinisomatota</p> <p>Verrucomicrobiota</p>
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(B) Pathway	Enzymes	EC	K term	Reaction	MAG(s)	Phylogenetic affiliation
C-P lyase pathway	ABC transporter (<i>phnCDE</i>)	7.3.2.2 TC: 3.A.1.9	K02041, K02044, K02042	uptake	22 74, 143 15, 83, 107, 117, 130 112 36, 101 17, 111 17, 49 124 100	Myxococcota Crenarchaeota Thermoplasmatota Verrucomicrobiota Crenarchaeota Actinobacteriota Bacteroidota Alphaproteobacteria Chloroflexota
	C-P lyase (<i>phnGHIJKLM</i>)	4.7.1.1	K06163	C-P bond cleavage	124	Alphaproteobacteria *
	related to C-P lyase: DUF1045				124, 135	Alphaproteobacteria
	2-aminoethylphosphonate-pyruvate transaminase, pyruvate aminotransferase (<i>phnW</i>)	2.6.1.37	K03430	2AEP + Pyruvate => Phosphonoacetaldehyde + L-Alanine	52, 94, 116, 119 74, 90, 143 75 10 124, 135, 141 47, 53 123, 131 9, 35, 63, 89 59 44 15, 83 86 23, 84, 112 37, 82 24	Planctomycetota Crenarchaeota Alphaproteobacteria Gammaproteobacteria Alphaproteobacteria Chloroflexota Crenarchaeota Gammaproteobacteria Myxococcota Firmicutes Thermoplasmatota Acidobacteriota Verrucomicrobiota Marinisomatota Bacteroidota

	phosphonoacetaldehyde hydrolase, phosphonotase (<i>phnX</i>)	3.11.1.1	K05306	Phosphonoacetaldehyde <=> Acetaldehyde + Pi	52, 119	Planctomycetota
other	phosphonoacetate hydrolase (<i>phnA</i>)	3.11.1.2	K19670	Phosphonoacetate + H ₂ O <=> Acetate + Orthophosphate	121 59 124, 135 75 63 23, 85, 112	Planctomycetota Myxococcota Alphaproteobacteria Planctomycetota Gammaproteobacteria Verrucomicrobiota

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