Supplementary Information

An atypical phosphodiesterase capable of degrading haloalkyl phosphate diesters from *Sphingobium* sp. strain TCM1

Katsumasa Abe[1], Naoko Mukai[1], Yuka Morooka[1], Takeshi Makino[1], Kenji Oshima[2], Shouji Takahashi[1], Yoshio Kera[1,*]

[1]Department of Bioengineering, Nagaoka University of Technology, Nagaoka, Niigata, Japan

[2]Department of Biological and Chemical Systems Engineering, National Institute of Technology, Kumamoto College, Yatsushiro, Kumamoto, Japan

*Address correspondence to Yoshio Kera, yoshkera@vos.nagaokaut.ac.jp

Table S1 PDE and PME activities during purification step

Step	Total activity (μmol•min^{-1})		B*p*NPP/*p*NPP
	B*p*NPP	*p*NPP	
Cell-free extract	463	1253	0.4
Ammonium sulfate fractionation	366	1007	0.4
Phenyl Sepharose HP	251	79.0	3.2
Q Sepharose HP	94.9	29.7	3.2
Superdex 200 pg	68.4	17.4	3.9

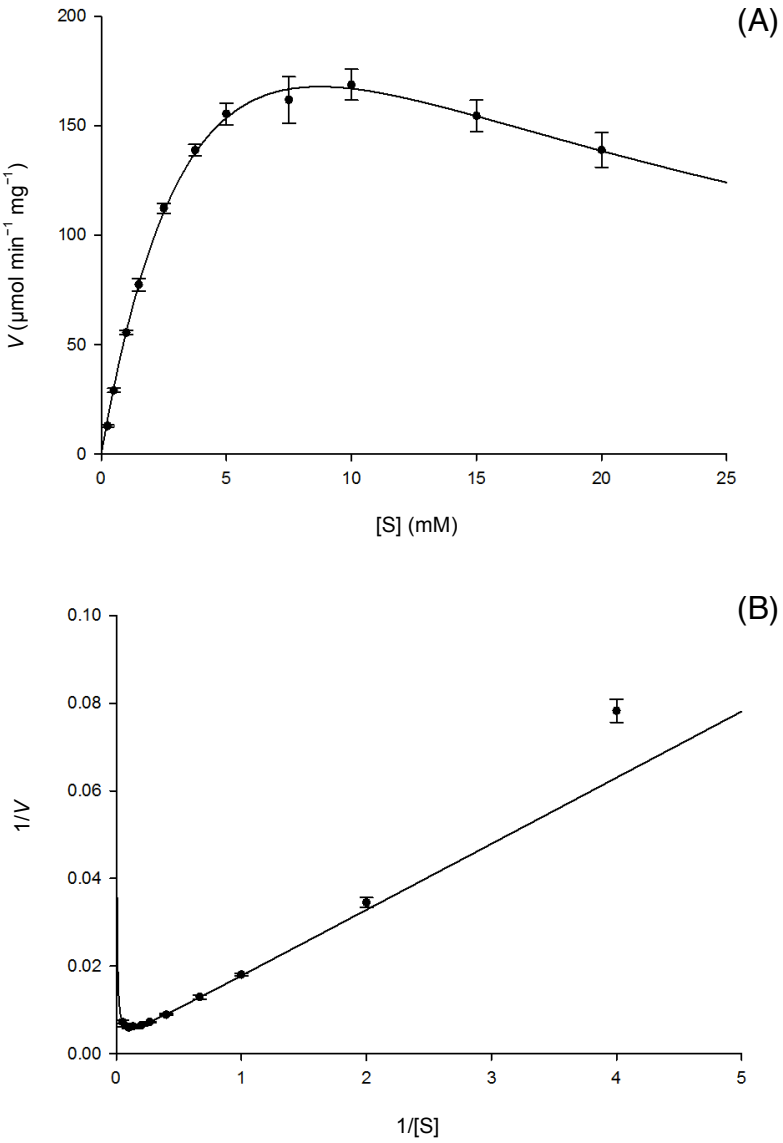

Figure S1 Effect of substrate concentration on the PDE activity (A) and Lineweaver-Burk plot (B) of PDE activity. *V* and [S] indicate velocity and substrate concentration, respectively. The data are means ± standard error (SE) from three independent experiments

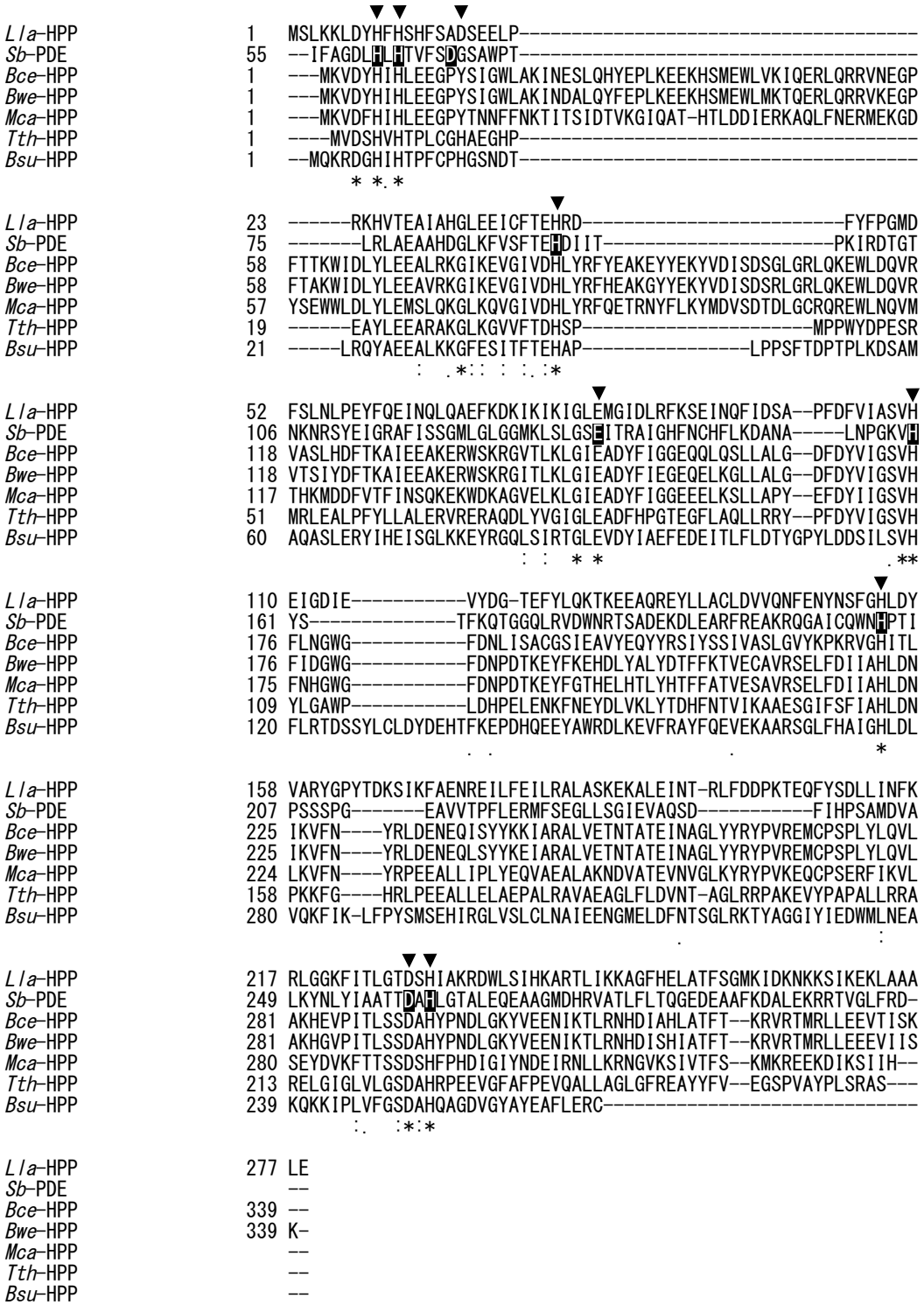

Figure S2 Amino acid sequence alignment of PHP domain of *Sb*-PDE (Ile55-Asp307) with L-histidinol phosphate phosphatase (HPP) from various organisms. *Lla*,

Lactococcus lactis subsp. *lactis* Il1403 (accession no. NP_267372); *Bce*, *Bacillus cereus* (WP_000861821); *Bwe*, *B. weihenstephanensis* (WP_078175627); *Mca*, *Macrococcus caseolyticus* (WP_012656252); *Tth*, *T. thermophilus* (WP_011227864); and *Bsu, B. subtilis* (WP_021480315). Identical residues and amino acid substitutions with low and high similarities are indicated by asterisks, and dots and double dots, respectively. Histidine, glutamate and aspartate residues which are metal coordination residues of L-histidinol phosphate phosphatase from *Lactococcus lactis* subsp. *lactis* Il1403 are indicated by triangles. Putative metal coordination residues of *Sb*-PDE are shown in reverse letters.