

## Supplementary Information

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

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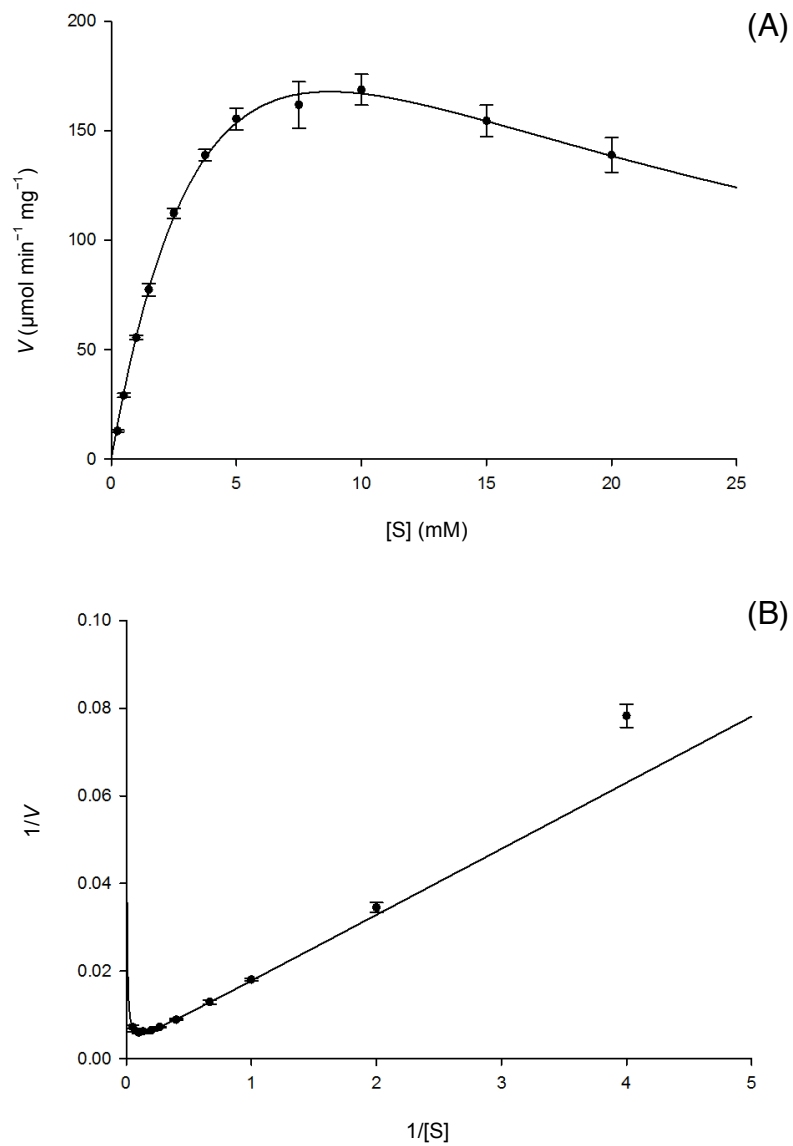
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**Table S1** PDE and PME activities during purification step

Step	Total activity		B <i>p</i> NPP/ <i>p</i> NPP
	( $\mu\text{mol}\cdot\text{min}^{-1}$ )		
	B <i>p</i> NPP	<i>p</i> 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  $\pm$  standard error (SE) from three independent experiments

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<i>Lla</i> -HPP	1	MSLKKLDYHFHSHFSADSEELP-----	
<i>Sb</i> -PDE	55	--IFAGDL <sup>H</sup> ITVFS <sup>D</sup> GS <sup>A</sup> WPT-----	
<i>Bce</i> -HPP	1	---MKVDYH <sup>I</sup> HLEEGPYS <sup>I</sup> GWLAK <sup>I</sup> INESLQHYEPLKEEKHSMEWLVKIQERLQRRVNEGP	
<i>Bwe</i> -HPP	1	---MKVDYH <sup>I</sup> HLEEGPYS <sup>I</sup> GWLAK <sup>I</sup> INDALQYFEPLKEEKHSMEWLMKTQERLQRRVKEGP	
<i>Mca</i> -HPP	1	---MKVDFH <sup>I</sup> HLEEGPYTNNFNK <sup>I</sup> ITSIDTVKGIQAT-HTLDDIERKAQLFNERMEKGD	
<i>Tth</i> -HPP	1	---MVDSHVHTPLCGHAEGHP-----	
<i>Bsu</i> -HPP	1	---MQKRDGHIHTPF <sup>C</sup> PHGSNDT-----	
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<i>Lla</i> -HPP	23	-----RKHVTEAIAHGLEE <sup>I</sup> CFTEHRD-----	FYFPGMD
<i>Sb</i> -PDE	75	-----LRLAEA <sup>A</sup> HD <sup>L</sup> KFVSFT <sup>E</sup> ED <sup>I</sup> IT-----	PKIRDTGT
<i>Bce</i> -HPP	58	FTTKWIDLYLEEALRKG <sup>I</sup> KEVGI <sup>V</sup> DHLYRFYEAK <sup>E</sup> EY <sup>E</sup> KY <sup>V</sup> DI <sup>S</sup> DSGLGRLQKEWLDQVR	
<i>Bwe</i> -HPP	58	FTAKWIDLYLEEAVRKG <sup>I</sup> KEVGI <sup>V</sup> DHLYRFHEAK <sup>G</sup> Y <sup>E</sup> EY <sup>E</sup> KY <sup>V</sup> DI <sup>S</sup> DSRLGRLQKEWLDQVR	
<i>Mca</i> -HPP	57	YSEWLDLYLEMSLQKGLKQVGI <sup>V</sup> DHLYRFQETRNYFLKYMDVSDTDLGCRQREWLNQVM	
<i>Tth</i> -HPP	19	---EAYLEEARAKGLKGVV <sup>F</sup> TDHSP-----	MPPWYDPESR
<i>Bsu</i> -HPP	21	---LRQYAE <sup>E</sup> ALKKGFES <sup>I</sup> TFTEHAP-----	LPPSFTDPTPLKDSAM
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<i>Lla</i> -HPP	52	FSLNLPEYFQEINQLQAEFKDKIKIKIGLEMGIDLRFKSEINQFIDSA--PFDFVIASVH	
<i>Sb</i> -PDE	106	NKNRSYEIGRAFISSGMLGLGGMKLSLGS <sup>I</sup> ITRAIGHFNCHFLKDANA-----	LNP <sup>G</sup> KV <sup>H</sup>
<i>Bce</i> -HPP	118	VASLHDFTKAIEEAKERWSKRGVTLKLGIEADYF <sup>I</sup> GGEQQLQSLALG--DFDYVIGSVH	
<i>Bwe</i> -HPP	118	VTSIYDFTKAIIEAKERWSKRGITLKLGIADYF <sup>I</sup> EGEQELKGLLALG--DFDYVIGSVH	
<i>Mca</i> -HPP	117	THKMDDFVTFINSQKEKWDKAGVELKLGIEADYF <sup>I</sup> GGEEELKSLAPY--EFDYIIGSVH	
<i>Tth</i> -HPP	51	MRLEALPFYLLALERV <sup>R</sup> ERAQDLVYVIGLEADFH <sup>P</sup> GTEGFLAQLLRRY--PFDYVIGSVH	
<i>Bsu</i> -HPP	60	AGASLERYIHEISGLKKEYRQGLSIR <sup>T</sup> GLEVDYIAEFDEITLFLD <sup>T</sup> YGPYLD <sup>S</sup> ILSVH	
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<i>Lla</i> -HPP	110	EIGDIE-----VYDG--TEFYLQKTKEEAQREYLLACL <sup>D</sup> VVQNFENYNSFGHLDY	
<i>Sb</i> -PDE	161	YS-----TFKQTGGQLRVDWNRTSADEKDL <sup>E</sup> ARF <sup>R</sup> EAKRQGA <sup>I</sup> CQWN <sup>H</sup> PT <sup>I</sup>	
<i>Bce</i> -HPP	176	FLNGWG-----FDNLISACGSI <sup>E</sup> AVYEQYYS <sup>I</sup> YSSIVASLGVYKPKRVGHITL	
<i>Bwe</i> -HPP	176	FIDGWG-----FDNPD <sup>T</sup> KEYFKEHDL <sup>Y</sup> ALYD <sup>T</sup> FFKTVECAVRSE <sup>L</sup> FD <sup>I</sup> IAHL <sup>D</sup> N	
<i>Mca</i> -HPP	175	FNHWG-----FDNPD <sup>T</sup> KEYFG <sup>T</sup> HELHT <sup>L</sup> YHT <sup>F</sup> FATVESAVRSE <sup>L</sup> FD <sup>I</sup> IAHL <sup>D</sup> N	
<i>Tth</i> -HPP	109	YLGAWP-----LDHPELENKFNEYDLV <sup>K</sup> LYD <sup>H</sup> FN <sup>T</sup> VIKAAESGIF <sup>S</sup> IAHL <sup>D</sup> N	
<i>Bsu</i> -HPP	120	FLRTDSSYLCLDYDEHTFKEPDHQEEYAWRDLKEVFRAYFQ <sup>E</sup> VEKAARSGLFHAIGHLDL	
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<i>Lla</i> -HPP	158	VARYGPYTDKSIKFAENREILFEILRALASKEKALEINT-RLFDDPKTEQFYSDLLINFK	
<i>Sb</i> -PDE	207	PSSSPG-----EAVTPFLERMFSEGLLSGIEVAQSD-----	FIHPSAMDVA
<i>Bce</i> -HPP	225	IKVFN----YRLDENEQISYYKKIARALVETNTATEINAGLYRYPVREMCPSPLYLQVL	
<i>Bwe</i> -HPP	225	IKVFN----YRLDENEQLSYYKEIARALVETNTATEINAGLYRYPVREMCPSPLYLQVL	
<i>Mca</i> -HPP	224	LKVFN----YRPEEALLIPL <sup>Y</sup> EQVAEALAKNDVATEVNVGLKYRYPVKEQCPSERFIKVL	
<i>Tth</i> -HPP	158	PKKFG----HRLPEEALLEAL <sup>E</sup> PALRAVAEAGLFDVNT-AGLRRPAKEVYPAPALLRRA	
<i>Bsu</i> -HPP	280	VQKFIK-LFPYSMSEHIRGLVSLCLNAIEENGMELDFNTSGLR <sup>K</sup> TYAGGIYIEDWMLNEA	
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<i>Lla</i> -HPP	217	RLGGKFITLGTDSHIAKRDWLSIHKARTLIKKAGFHELATFSGMKIDKNKKS <sup>I</sup> EKELAA	
<i>Sb</i> -PDE	249	LKYNLYIAATTD <sup>A</sup> LGTALEQEAAGMDHRVATLFLTQGEDEAAFKDALEKRR <sup>T</sup> VGLFRD-	
<i>Bce</i> -HPP	281	AKHEVPI <sup>T</sup> LSSDAHYPNDLGKYVEENIKTLRNH <sup>D</sup> IAHLATFT--KRVRTMRLL <sup>E</sup> EV <sup>T</sup> ISK	
<i>Bwe</i> -HPP	281	AKHGVP <sup>I</sup> LSSDAHYPNDLGKYVEENIKTLRNH <sup>D</sup> ISHIATFT--KRVRTMRLL <sup>E</sup> EEV <sup>I</sup> IS	
<i>Mca</i> -HPP	280	SEYDVKFTTSSDSHFPHDIGIYNDEIRNLLKRN <sup>G</sup> VKSIVTFS--KMKREEKDIKSIH--	
<i>Tth</i> -HPP	213	RELGI <sup>L</sup> VLGSDAHRPEEVGFAP <sup>E</sup> VQALLAGLGFREAYYFV--EGSPVAYPLSRAS--	
<i>Bsu</i> -HPP	239	KQKKIPLVFGSDAHQAGDVGYAYEAFLERC-----	
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<i>Lla</i> -HPP	277	LE	
<i>Sb</i> -PDE	--		
<i>Bce</i> -HPP	339	--	
<i>Bwe</i> -HPP	339	K-	
<i>Mca</i> -HPP	--		
<i>Tth</i> -HPP	--		
<i>Bsu</i> -HPP	--		

**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* II1403 (accession no. NP\_267372); *Bce*, *Bacillus cereus* (WP\_000861821); *Bwe*, *B. weihenstephanensis* (WP\_078175627); *Mca*, *Micrococcus 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* II1403 are indicated by triangles. Putative metal coordination residues of *Sb*-PDE are shown in reverse letters.