

**Figure S1. Alignment of PTP2 amino acid sequences identified in *A. algerae*.** Corresponding proteins were incomplete in their N-terminal region. A 5'-RACE-PCR approach allowed to identify the lacking sequence coding for the N-terminal part of PTP2c (sequence in red). PTP2c predicted signal peptide is boxed. PTP2 proteins have a conserved C-terminal region and a variable N-terminal region due to insertions/deletions events in repeated motifs rich in glycine and serine residues. Identical amino acids are highlighted in grey and the eight cysteine residues in conserved position are highlighted in black. The two sequences underlined in black correspond to regions that were selected for the expression of recombinant polypeptides in *E. coli*. Specific peptides for each PTP2 were identified by mass spectrometry analysis and are underlined in red. This confirms the presence of the three PTP2 in the *A. algerae* polar tube. Amino acids are numbered on the right. The accession number for the full-length PTP2c is WAQ68435.1. The contig names for PTP2a and PTP2b are KI0AQA2Y004FM1\_3..1481 and KI0ALA25YH17FM1:c(216..1571), respectively and are available under the accession number GCA\_000313815.1.

PTP2c	<u>MRKPVLLAILLVFYQSQA</u> <u>SYSWSSSSRRSSSGGSRGGGSSGGAS</u> SSGGSGGASMSGVSSGG	60
PTP2b	-----	0
PTP2a	-----	0
PTP2c	SSMSFSGGSSGGASSGGSSSHGSGGSGSGSSGHGSGSGGGAPGKSSGSESGSGAPGGGS	120
PTP2b	-----GGSGSGSGSGSGHSGSGGGAPG-----GSGSGAPGGGS	35
PTP2a	-----GSGSGHSGSGSGGGAPGGSGHSGSGTTPGGGS	34
PTP2c	<u>GS</u> SGSGSGHSGSGGGAPGGGSGNGSGSGSGHSGSGGGAPGGGSGSGAPGGGSGGGSG	180
PTP2b	GGSGSGSGHSGSGGGAPGGGSGNGSGAGSNG-----SGSGAPGGGSGSGPG	84
PTP2a	<u>GS</u> GPSSGSGHSGSGGGAPGGGSDSGAGSGAQGGSSAGE-----	75
PTP2c	<u>SGSGHSGSGGGAPGGGSDSGAGSGAQGGSSAGEGSGAKGSGSAGEGSGAQGGSSAG</u>	239
PTP2b	<u>SGSGHSGSGGGAPGGGSDSGAGSGAQGGSSAGEGSGAKGSGSAGEGSGAQGGSSAGE</u>	144
PTP2a	<u>-----GSGAKG-----SGSAGEGSGAQGGSSAGEGSGAKGSGSAGEGSGAQGGSSAG</u>	122
PTP2c	<u>-----EGSGAKGSGSAGEGNAPEKGAEGSGQAQKPGIGQAGPGNAAAQGDSTGA</u>	288
PTP2b	<u>GSGAKGGSSAGEGSGALGSGSAGEGNAPEKGAEGSGQAQKPGIGQAGPGNAAAQGDSTGA</u>	204
PTP2a	<u>-----EGSGAQGSGSAGEGNAPEKGAEGSGQAQKPGIGQAGPGNAAAQGDSTGA</u>	171
PTP2c	ANDLVALETHKALKTALNQSMANSVSPQTANEFNLAGNPECNQQAVEGNWVKVINEKIKQEC	348
PTP2b	ANDLVALETHKALKTALNQSMANSVSPQTANEFNLAGNPECNQQAVEGNWVKVINEKIKQEC	264
PTP2a	ANDLVALETHKALKTALNQSMANSVSPQTANEFNLAGNPECNQQAVEGNWVKVINEKIKQEC	231
PTP2c	RNKMNERKAKAEQIAKFITKPTPDKCVKKNLPNALVCCQALTMNTIIKQPRFKIDLIGSN	408
PTP2b	RNKNVNERKAKAEQIAKFITKPTPDKCVKKNLPNALVCCQALTMNTIIKQPRFKIDLIGSN	324
PTP2a	RNKNVNERKAKAEQIAKFITKPTPDKCVKKNLPNALVCCQALTMNTIIKQPRFKIDLIGSN	291
PTP2c	VVEIKKDGSPILLGVAESLNYNVTMKMRKRYNPLKNPTARLEFNELGSLKQEGEIPKPK	468
PTP2b	VVEIKKDGSPILLGVAESLNYNVTMKMRKRYNPLKNPTARLEFNELGSLKQEGEIPKPK	384
PTP2a	VVEIKKDGSPILLGVAESLNYNVTMKMRKRYNPLKNPTARLEFNELGSLKQEGEIPKPK	351
PTP2c	RLDFCGSCLLEKLSKKAQVEGEKDMCGGC <del>D</del> ALMELNSLKRGSFNNLQ <del>T</del> ENKKPEVTP <del>T</del> ETT	528
PTP2b	RLDFCGSCLLEKLSKKAQVEGEKDMCGGC <del>D</del> ALMELNSLKRGSFNNLQ <del>T</del> ENKKPEVTP <del>T</del> ETT	444
PTP2a	RLDFCGSCLLEKLSKKAQVEGEKDMCGGC <del>D</del> ALMELNSLKRGSFNNLQ <del>T</del> ENKKPEVTP <del>T</del> ETT	411
PTP2c	<u>KAAEESK</u>	535
PTP2b	<u>KAAEESK</u>	451
PTP2a	<u>KAAEESK</u>	418