

```

T. maritimum MKNKLPFILMLLOLLIFTGCNDDVSLGETTKEFKKRASSISTNTNITLSILSYNI FHLPSIASIYHYKEYRAEAQKNFFN
B. cereus MEVWNVKCKLLKGVLSLGVG----LGALYSGTSAQA--EVSTNQNDTLKVMTHNVYMLSTNLYPNW-G----QTERADLIG
S. aureus M-VKKTKSNLSKKVATLALANLLLVGALTD-NSSKA-ESKDDTD-LKLVSHNVYMLSTVLYPNW-G----QYKRADLIG
          * : : . : * . . : * . . . : . * . . . . : * : : * : : * . : : : .
          : : :

T. maritimum TREISENMDIIIVQEA FNRY--VPIISNGLTSFINQSGLVGLYCGSWTMNRSDNYFDKMSLSNCSNSPFTVNGGVKIYS
B. cereus AADYIKNQDVVILNEVFDNSASDRLLGNLKKKEYPNQTAVLGRSSGSEW-----DKT--LGNY-SSSTPEDGGVAIVS
S. aureus QSSYIKNNDVVI FNEAFDNGASDKLLSNVKKEYPYQTPVLGRSQS-GW-----DKT--EGSY-SSTVAEDGGVAIVS
          . : * * : * : * : * . . . : * : : * . . . . . ** . . . * . : * * * * *
          : : :

T. maritimum KWPIEYDEQLIFKNSLRGTADYLSNKGASYVRINKNGKFFHIIGTHLQADEAKKDGSGIRKLQDELQYWIAQKIKSGKI
B. cereus KWPIAEKIQYVFAKCG--PDNLSNKG FVYTKIKKNDRFVHVIIGTHLQAEDSMCGKTPASVRTDQLKE-IQDFIKNKNI
S. aureus KYPIKEKIQHVFKSGCG--FDNDSNKG FVYTKIEKNGKNVHVIIGTHTQSEDSRCGAGHDKIRAEQMKE-ISDFVKKKNI
          * : * * . * : * . . . * * * * * * . : * : * * : . * : * * * * * * : : : . . : : : : * : : * . : *
          : : :

T. maritimum PSNEPIIFAGDFNIPH-----YDIEKIKEMTTILQSNEVKLQGDLSYDESQNTILQSNGNKYPPQTLDYILVSKQKQP
B. cereus PNNEYVLIGGDMNVNKINAENKNDSEYASMFKTLNASVPSYTGHTATWDATTNSIAKYNFPDSPA EYLDYIIASKDHANP
S. aureus PKDETVYIGGDINVN-----KGTPEFKDMLKNLNVNDVLYAGHNSTWDPQSNSIAKYNYPNGKPEHLDYIFTDKDHKQP
          * . : * : : . * : * : . . . : . * . : : * * : * : * . . : * * * : . . * : : *
          : : :

T. maritimum LFIPTFSHTTFR-----AKNTNATEDLSDHHPKQTFYFSY
B. cereus SYIENKVLQPKSPQWTVTSWFQKYTYNDYS DHYPVEATISM-K
S. aureus KQLVNEVVTEKPKPVDVYAFPYYYVYNDFS DHYPIKAYS---K
          : . . . : * * * : * : :
          : : :

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Figure S3A - Comparison of amino acid sequences of sphingomyelinase from *T. maritimum* NCIMB 2154^T, *B. cereus* ATCC 14579 and *S. aureus* RN4220. The sequences were aligned with the program ClustalW. Signal peptides are squared in red; the residues corresponding to the central metal-binding sites were retrieved from Ago *et al.*, 2006 and are boxed in blues.

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T. maritimum M-KFOKTPRFLFLLFLFIFOINYSSNNYTIGVGISDITGQIAESAFFGYGDPFFKNGGIRDQRQYARAYIVKDIHQN-SV
P. aeruginosa MSRSFTALLLSCVLLALSMPARADDLPYRFGLGKADITGEAAEVGMGYSLEQKTAGIHMRQWARAFVIEEAAASGRRL
* : * . : * ::* : : : . . * : * : * : * * * : * * . . : * . * * : * : * * : : : : . . :

T. maritimum VVVSIDKGATEQSVNLAVIEKLREAYGNLYTDTNVVISAHHTHVSPPGGYSHYGLYNTSTGGFYKTNFTILVDGIFNAIQQ
P. aeruginosa VVNTDLGMIEQAVHLKVLARLKAKYPGVYDENVMLAATHHTHSGPGGESHYAMYNLSVLGFQEKTFNAIVDGVIRSIER
* * * . * * * . . . * . . * * : : : * : . . * : : * * : : * * * * * * . * * . * * . : * * * . . : * :

T. maritimum AHN LAPGRIYYNTGSLTNASINRSLVAYNLNADANDYI-SIDDQMTVLKFIQGDTEV-GMISWFAVHPTNLSNSYKYAS
P. aeruginosa A QARLQPGRLFYGSGELRNANRNRSLLSHLKNPDI VGYEDGIDPQMSVLSFVDANGELAGAISWFPVHSTSMTNANHLIS
* : . * * * : : * : . * * * . * * . * * * : : * . * . * * . * * . * : : : * : * * * * . * * . : *

T. maritimum GDNKGHASLKFERRHKGASYGKGAATFVAAFSNSNAGDMSPNLNQLPLSDLYTNATGPGNNEEEESTEIGNRQYYKALDLY
P. aeruginosa PDNKGYASYHWEHDVSL---RKSG-FVAAFAQTNAGNISPNLNK-----PGSGPFDNEFDNTR EIGLRQFAKAYEIA
* * * . * * . : : * : . : : . * * * : : * * : * * * . . : * * : * * . * * * : * :

T. maritimum NNAHIQLIGTIKAVSRYSYDYNILVSPKFTDGYQSTCKAALGIFRAGA-EDGRSGIGKE-GQTRSN-----PTA--G
P. aeruginosa GQAQEELVGLDSRFRFVDFTRLPIRPEFTDQPRQLCTAAIGTSLAAGSTEDGPGPLGLEEGNNPFLSALGLLTGVP
. : * : : : * : : . * : * : : : : * : * * * . . * . * * : * : * * * . : * * * * :

T. maritimum FEVDRCHEKPIDPLFYVGANNNDPKTPKILPITSILKIGQLGILAAPAEFTVMAGRRVKATVL-ENKNTEIQYTVFAGYS
P. aeruginosa QELVQCQAEKTI--LADTGNKKPYPWTPTVLP IQMFRIGQLLELLGAPAEFTVMAGVRIRRAVQAASEAAGIRHVVFNGYA
* : . * : * * . * . * : : * * * . * * . : : * * * * : * . * * * * * * * . : : * : . * * * * :

T. maritimum DAYSCYVVTREEEYASQQYEGASTQFGPWTLAAYRQEFEKLT SILADPNVTPWDTPAPIPPRKNYIGSDKTVPI LFDDIPW
P. aeruginosa NAYASYVTREEEYAAQEYEGGSTLYGPWTQAAYQQLFVDM AVALRERL--PVETSA-IAPDLSCCMNFQ TGVVADDPYI
: * : . * * * * * * * : * : * * * * * * * * * * : : * : : * : * * * * . : : *

T. maritimum FKSFGSIFSN TNDNYSTDEIAEVTFWGAPNNNDPKTNSTYFRVQKKIGDSW---VSKYEDSDTNTKLIWNRDGVANSKIT
P. aeruginosa GKSFGDVLQQPRESYRIGDKVTVAFTGHPKNDL RTEKTFLEVVNIGKDGKQTPETVAIDNDWNTYRWERVGISASKAT
* * * . : : * * * . : * * * * : : * * * * * * : * . : * * * * : * * * * : * *

T. maritimum IQFKITS DVESGHYRIIHHGKWKNGWNGKLTPTYTGISNTFYIHQNFRNAVPTS KNTINNILLIYPNPTSGAFTI INERLLT
P. aeruginosa ISWSIPPGETEPGHYYIRHYGNK NFWTQKISEIGGSTRSF EVLGTTP-----
* . : . * . . . . * . * * * * * : * : * * * * * : * : : * :

T. maritimum GNY SITNAMGQIVKKGKLSKSHHLINMDVLP GMYFIKTI FQNGETNTISIVK
P. aeruginosa -----

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Figure S3B – Comparison of amino acid sequences of the ceramidase from *T. maritimum* NCIMB 2154^T and *Pseudomonas aeruginosa* PAO1. The sequences were aligned with ClustalW. *P. aeruginosa* protein motifs were retrieved from the Uniprot entry (UniProtKB: Q9I596). The signal peptides of each protein are boxed in red, the conserved amino-acids involved in metal binding are boxed in blue, those involved in substrate binding are boxed in black, the active site is boxed in green and the predicted CTD1 of *T. maritimum* is boxed in orange.