Figure S1

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MTH1691       MPDINESMLNQFRPVIRR-FIDPIAD---RIALPADYITLTGFLVACAASAGYASGSLIT
PFU0462       -------MLSNLRPLAKK-PLEKIAEPFSKLGITPNQLTMVGFFLSLLASYEYYLNNQVF
SSO0556       ----MVSMLTRIRRQIKR-VIEPLAKTLAQLKVSANFITMLGLIFAIVYYFEIMRSNTTL
APE1526       -----MGVFNRLRSFYEARIAPTVASFLSRISPDPNIYTLASPVAAAAALPAWLYISPVA
TBHG02550     -----MSKLPFLSRAAFARITTPIARGLLRVGLTPDVVTILGTTASVAGALTLFPMGKLF
SCEPIS1       ---------------MSSNSTPEKVTAEHVLWYIPNKIGYVRVITAALSFFVMKNHPTAF
                                      .     :   .:         :

MTH1691       G-AALLAASGFIDVLDGAVARRRFRPTAFGGFLDSTLDRLSD------GIIIIGITAGGF
PFU0462       G-SLILLLGAFLDALDGSLARLTGRVTKFGGFLDSTMDRLSD------AAIIFGIALGEL
SSO0556       G-IIFLVFSALMDAIDGEVARVSKTVSPLGSFLDSTLDRIED------ILYISAFIFLGF
APE1526       S-LLLIALSLLLDAVDGAVARFTGRVSPLGSFLDSSLDRISD------SLYHATLYIAGV
TBHG02550     AGACVVWFFVLFDMLDGAMARERGGGTRFGAVLDATCDRISDGAVFCGLLWWIAFHMRDR
SCEPIS1       T--WLYSTSCLLDALDGTMARKYNQVSSLGAVLDMVTDRSST------AGLMCFLCVQYP
                  .     ::* :** :**     : :*..**   ** .             :

MTH1691       TGLLTGLLALHSGLMVSYVRARAESLG-IECAVGIAERAERIIIILAGSLAGYL---IHP
PFU0462       VNWKVAFLALIGSYMVSYTRCRAELAGSGTLAVGIAERGERLLILVIAGLFG--------
SSO0556       SSYLVAIAVGLS-LTISYIRAKAESLGLKMEGRGIIERGERIIFVFVILLLYII---VSK
APE1526       H-PLIVIAMLSGGLIVPYLRAKGESLGLEVRGRGLMERGERSIAILAILAIS-I---YNL
TBHG02550     PLVIATLICLVTSQVISYIKARAEASG-LRGDGGFIERPERLIIVLTGAGVSDFPFVPWP
SCEPIS1       QWCVFFQLMLGLDITSHYMHMYASLSAGKTSHKSVGEGESRLLHLYYTRRDVLFTICAFN
                               * :  ..  .      .. *  .* : :

MTH1691       WFMDAAIIVLAALG------YFTMIQRMIYVWQRLK------------------------
PFU0462       -IIDIGVYLVAILS------WITFLQRVYEAKKRLEK-----------------------
SSO0556       QVSLYLFYLFMLLT------AITVIQRFYAVYSLLRK-----------------------
APE1526       QTALALASAAAVLV------WITVIQRMVYIAGELRR-----------------------
TBHG02550     PALSVGMWLLAVAS------VITCVQRLHTVWTSPGAIDRMAIPGKGDR-----------
SCEPIS1       ELFYAGLYLQLFSNSATFGKWTTIISFPGYVFKQTANVVQLKRAALILADNDAKNANEKN
                                   * :.

MTH1691       ---
PFU0462       ---
SSO0556       ---
APE1526       ---
TBHG02550     ---
SCEPIS1       KTY
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Supplemental Figure S1

Multiple alignment of AIP Synthase and PI Synthase. A gene (MTH1691) homologous to the yeast PI synthase gene was identified in the *M. thermautotrophicus* genome. The gene MTH1691 was tentatively annotated as AIP synthase. The amino acid sequence data of MTH1691, *M. thermautotrophicus* (NP_276802)(195 amino acids); PFU0462, *Pyrococcus furiosus* (NP_578191) (187 amino acids); SSO0556, *Sulfolobus solfataricus* (AAK40873)(195 amino acids); APE1526, *Aeropyrum pernix* (NP_148000)(194 amino acids); TBHG02550, *Mycobacterium tuberculosis* (YP_002159588)(217 amino acids); SCEPIS1, *Saccharomyces cerevisiae* (NP_015438)(220 amino acids) were obtained from the NCBI site (WWW.ncbi.nih.gov). Multiple alignment of the six sequences was constructed using the alignment software CLUSTAL W 1.83. Underlined sequences are CDP-alcohol phosphatidyltransferase motif.