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gij213691183 (Phyla) Bifidobacterium longum spp infantis
gij225352176 (PhypA) Bifidobacterium pseudocatenulatum
gij130735 (AppA) Escherichia coli
gij189613 (PAP) Homo sapiens
gij90655301 (LIALP1) Lilium longiflorum
gij18491908 Zea mays
gij37182994 (MINPP1) Homo sapiens
gij41055415 Danio rerio
gij3947867 Schizosaccharomyces pombe
EDT45330 Bifidobacterium dentium
CAQ02958 Clavibacter michiganensis
BAH30792 Rhodococcus erythropolis
YP_004806097.1 Streptomyces sp SirexAA-E
GAA06490 Photobacterium leiognathi
EFL21248 Streptomyces himastatinicus
YP_001339041.1 Marinomonas sp. MWYL1
YP_004393571.1 Aeromonas veronii
ZP_01233650.1 Photobacterium angustum
YP_001809928.1 Burkholderia ambifaria
ZP_04942680.1 Burkholderia cenocepacia
YP_439843.1 Burkholderia thailandensis
YP_004349319.1 Burkholderia gladioli
ZP_06711296.1 Streptomyces sp. e14
ZP_03450126.1 Burkholderia pseudomallei
KAPKGYGPIYTESMARHGSRGLSSYKYDALLMRMAETA--RDGGFKSEAIKAEFVKNLS
AIPSRYHLAYTESVARRHGSRGLSSYKYDALLALMAQSAEENNYAGFVSEVKGKFINNVN
QSEPELKLKESVIVSRHGVRAPTKATQL---MQD---
RSVLAKELKVFVLRHGDORSPI DTFPT-----
SVPDGCRALHNLVARRHGTRAPTKKRIK---EMDQLAI---RLDALLT--DAKEK
SIPDGCRCVIHNLVARRHGTRAPTKKRIK---ELDR LAV---RLEALLK--EANQV
LLEGTCFVQLVALIRHGTRYPTVKQIR---KLRQLHG---LLQARGSRDGGASS
PPSLDCRAIHMVSVIRHGTRYPTTKNVR---KIAQLFD---LVKSDSLRLA---
SFPESCAIKQVHLLQRHGSRNPTGD DTA---TDVSSAQ---YIDIFQNKLLNGSI
KAPGEGYEPITYTESMARHGSRGLSSYKYDALLMKMAEAAE--RDGGFKSDAIKTEFMKNLN
PAPAGFAPVYTESVARHGSRALSSFKYDSLTTQVWEQARSEG---ALTTLGQTLGPEIQ
APPTGYIPVYTESVARHGSRALSSLYKDDLSLQLWEIAEAEN---ALTFVKGKFEFPAALR
QAPKGFVPVFTENVSRHGSRASDREDGDLLALWEKARSEG---QLTRTGERFGGDAE
QAPQGYELVYSELVSRHGSRALSSFKYDDISMQVWREARQKQG---ALTFLGKELGAEIE
REPPAGFAPVFTENVSRHGSRATDGDAGELILALWDKAEAEG---LITARGREFGPEVR
TVPASYILVYTELVARHGSRALSSPKYDDISLKIWAQAKEQN---ALTFLGHEHLGAEIE
PAPQGFSPVSEMVARHGSRALSSPKYDVLTKLVWEAQRQG---ALTFPLQGGLGGKVD
QAPQGYELVYSELVSRHGSRALSSFKYDDISMQVWREARQKQG---ALTFPLGKELGAEIE
APPAGYAPVYTELVARHGSRALSGFKYDGAIYMLVKAADG---ALTALGAQLKADTY
APPAGYAPVYTELVARHGSRALSGFKYDGAIYMLVKAADG---ALTALGAQLKADTY
APPAGYAPVYTEMVARHGSRALSGFKYDGAIYDMLSKADAEG---VITPLGRQLKADTF
APPADYAPVYTELVARHGSRALSGFKYDGAIYMLVKAADG---ALTALGAQLKADTY
RAPRGFVPVFTESVARHGSRASDSEDGDAVLDVLRRAQASD---SLTALGARLGPQVR
APPAGYAPVYTEMLARRHGSRALSGFKYDGAIYDMLQKAGAEG---ALTFPLGRQLKADTF
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A---DGGTIAYQSSGEARATESGENFEKGFNEASG-----GRLIGNVSAFTNP
K---QGLRVSYSQSSGEARATESGENFKLGFQDQASN-----GLLANAVVAFNPF
P---QSQQVAIIADVDERTFRKTGEAFAAGLAPDCA-----ITVHTQADTSSP
Y---KHEQVYIRST'DVDRTLMSAMTNLAALFPPEG-----VSIW-----NP
H---PHIYSIRATQVFRASASAVAFGLGSLFSGRG-----HLGP-----
H---PDVYSIRATQVFRASASAVAFGLGLLSGKG-----KLGQ-----
Y---GRRLRILTSKHKRCMDSSAAFLQGLWQHYY-----PGLP-----
L---RANRIEFMTSSKHKRCVDSVKAFAQEGLHRLWD-----Q-----
-----VYDINTAAQERVVDSAEWFSYGMFGDDM-----Q-----
V---DGGTISYQSSGEARATESGENFEKGFNAASG-----GKLTDSVVKPTDP
A---GSDQVTLLESSGEARATASGKAFAEGLRKADP-----LLASHLP-----
A---QQGTITLTS'SSGVDRAVDSAEAFQGLTGAEF-----AVAGDVA-----
R---NSEQINVVNSGKDRAVDSGTLFAEALAEQDP-----SLKPLIT-----
A---NQRHIVVEYS'GKDRALASANAFT'EGLTENNQ-----DLADLLL-----
K---TSEKIDVVS'GQGR'AVDSGNTFAASLGADAP-----ALKPLIG-----
Q---NQQIAFEYS'GQDR'ARD'SGLAFIQGLENVNF-----ALAPLIS-----
P---HCIKVYTS'GKDRANESAFYFME'SLKR'DVNVYVSDSAQCYLTQDDP'SKID-----
E---NQRHVVEYS'GKDR'ALASANAFT'EGLTENNQ-----DLAGLLL-----
-----GGRQIVVVNSGQDR'AVDSSTYFSAALVAAQF-----ALAAIMLPAAP
-----GNRQVVVVNSGQDR'AVDSSTYFSAALVAAQF-----ALAPAITLPAAP
GAAGGAARRIVVVNSGQDR'AVDSSTYFSGALVAARF-----ALAPAITLPSAP
-----GNRQVVVVNSGQDR'AVDSSTYFSAALVAAQF-----ALAPAITLPAAP
A---GHEAVVETSGVFR'AVDSAEAF'GGLVAGEF-----GLTGLVE-----
GTTGGAARKIVVVNSGQDR'AVDSSTYFSGALVAARF-----ALAPAITSPSAI
* :

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ZP_06711296.1 Streptomyces sp. e14
ZP_03450126.1 Burkholderia pseudomallei
DARVN-----G-GSTVATFRFAHAETMMPFAALLGLPGSTQQAPAS-----TTDV
DTRER-----A-G-TAATFRFAHAETIIPFAALLKLP'GSGQQQA-----SEL
TFHP'PQKQAYG-VTLPTSVLFIAGHD'TNLANLGGALEL'NWTLP'GQPDN-----
KRATQ-----IPSYKKLIMYSAHDTTVSGLQ'MALDV-----
EQAIVANEENHKPGNFEKARLRF'FAHAETIVPFTCLLGL--FLEGSEFEQIRAEQPLSLPF
EAIITAREENRADGTFEKARLRF'FAHAETVVPFSCLLGL--FLEGPEIEKIQREALDLP
DKAVEQKQ--RSQPISSPVLQFGHAETLLPLL'SLMGY--FKDKEPLTAY-----NY
DNAAKDH--RFGVEKKTATI'QVGHGETLLPLL'SLMGF--FKDKEPLTSE-----NF
RKGVN-----NASDRKVF'LAFTHDSQII'PVEAALGF--FPDITPEHPLP'DK-----
DERVN-----G-GSTVATFRFAHAETMMPFAALLGLPGSTQQAPAS-----TTDV
DA-RLA-----G-STTAATFRFAHAETIIPFAALLGL'PGST'QQVTP-----EAP
QE-HTG-----DAAVPGADFRFAHAETIIPFAALLKLP'GSTV'SQAE-----GDL
EA-KRA-----GTSTVGAE'LRFTHAEIIP'LAALMEL'PGST'KQVSP-----SRP
EK-IKQ-----GNEQAALKVRF'FAHAETIMPFAANMQLKGS'EEGVDP-----QTT
EA-KRD-----GTSKLGAE'LRFTHAEIIP'LATL'MRL'PGST'KAVTT-----DGP
KG-VQD-----GTNTKAAKIR'FAHAETIIPFAAQ'MQLKGS'ET'GVSR-----DTG
QRQVVE-----GEQSR'RALRF'FAHAETIIP'LAALM'KLG'ESR'QGAS'P-----DQL
EK-IKQ-----GNDQAALKVRF'FAHAETIMPFAANMQLKGS'EEGVDP-----QTT
DA-IAR-----GDLT'RAAKLRFTHAEIIVIPFASIMN'LKNV'FVPT'FQ-----AQT
DA-IAR-----GDLT'HAAKLRFTHAEIIVIPFASIMN'LKNV'FVPT'FQ-----AQT
DA-IAR-----GDLT'NAAKLRFTHAEIIVIPFASIMN'LKNV'FVPT'FQ-----AQT
DA-IAR-----GDLT'HAAKLRFTHAEIIVIPFASIMN'LKNV'FVPT'FQ-----AQT
EA-KAD-----GTGGKGA'VLR'FTHAEIIP'LAALM'LGL'PGST'EP'AP-----GRA
DA-IAR-----GDLT'NAAKLRFTHAEIIVIPFASIMN'LKNV'FVPT'FQ-----AQT
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FIG. S1 Refined multiple sequence alignment of PhypA from *B. pseudocatenulatum* ATCC 27919, Phyla from *B. longum* spp *Infantis* ATCC 15697 and different phosphatases from the HAP family. Non-homologous regions were eliminated with GBlocks. Invariant conserved sequences in all members of the family and conserved sequences that differ between members are boxed.

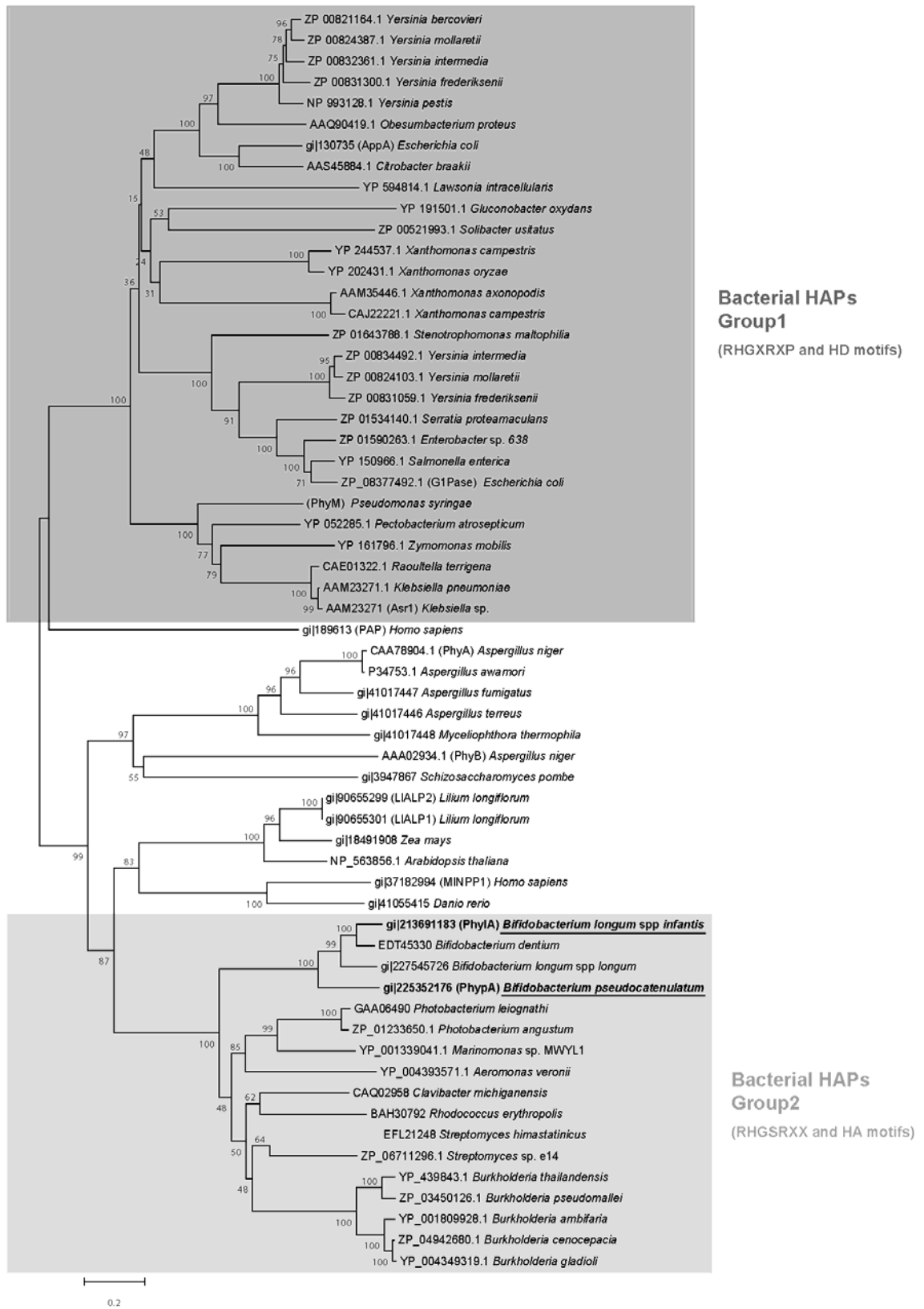


FIG. S2 Phylogenetic analysis of phosphatases from different origins belonging to the branch 2 HAP group, including PhylA and PhypA from bifidobacteria. Amino acid sequences were aligned with the EBI ClustalW2 tool and sequence trimming was done with GBlocks. The phylogenetic trees were constructed with MEGA4 (Poisson correction model, pairwise deletion and 1000 replicates).

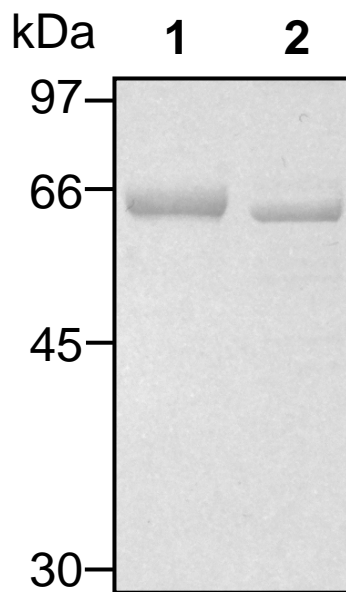
A**B**

FIG. S3 (A) Schematic representation of the PhylA and PhypA phytases and the truncated 6X(His)-tagged version lacking the signal peptide (sp) and the hydrophobic C-terminal region (tm). The (+) symbol at the C-terminal part represent positively charged amino acids. Signature sequences of the different conserved motifs are also shown (HAPs RHGSRGL and HA domains and the C-terminal cell-wall anchoring domains (LAXTG)); (B) SDS-PAGE analysis of purified 6X(His) truncated phytases. Lane 1, 6x(His)⁴⁹PhypA⁶¹² from *B. pseudocatenulatum*; lane 2, 6x(His)³²PhylA⁵⁹⁹ from *B. longum* spp *infantis*. The calculated molecular weight of the truncated enzymes is 61.8 and 62.2 kDa, respectively. Attempts to express in *E. coli* the N-terminal deleted proteins carrying the C-terminal hydrophobic helices (6x(His)⁴⁹PhypA⁶³⁹ and 6x(His)³²PhylA⁶²³) which form part of the sortase-dependent cell wall anchoring motif, always rendered insoluble inclusion bodies.