

Supplemental Figure 1. Multiple sequence alignment of L-AI protein sequences from various *Lactobacillus* species using the T-Coffee algorithm. LRAI, *L. reuteri*; LPIAI, *L. plantarum*, LFAI, *L. fermentum*; LBr, *L. brevis*; LPeAI, *L. pentosus*; LBuAI, *L. buchneri*; LSAI, *L. sakei*. Black shaded areas indicate homology, grey shaded areas indicate amino acids with similar properties.

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LRAI      1  M-DKNEYFWFVVTGSOFLYGEEQLKSVAAADAEDIVNKLNE SGKLPYKVVFKGVMTTAEGI
LPIAI     1  MLSVPDYEFWFVVTGSOHLYGEEQLKSVAKDAQDIADKLNASGKLPYKVVFKDVMTTAESI
LFAI      1  MRKMQDYKFWFVVTGSOPLYGPEALAEVEKDARKVDGLNEGKLDYFVFKLVATTASIS
LBrAI     1  MLSVPDYEFWFVVTGSOHLYGEEQLKSVAKDAQDIADKLNASGKLPYKVVFKDVMTTAESI
LPeAI     1  MLSVPDYEFWFVVTGSOHLYGEEQLKSVAKDAQDIADKLNASGKLPYKVVFKDVMTTAESI
LBuAI     1  MLOVPDYEFWFVVTGSOHLYGEEQLKSVEKDARDVDKLNASGKLPYPIVFKMVATTASIS
LSAI      1  MLNTENYEFWFVVTGSO SLYGEE TL SVEKDAKEIVKLNASRQLPYPIVFKLVATTANI

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LRAI      60  TKFMKEANYNDNVAGVITWMHTFSPAKNWIRGTKLLQKPLLHLATQYLNKI PYDIIDFDY
LPIAI     61  TTFMKEVNYNDKVAGVITWMHTFSPAKNWIRGTELLQKPLLHLATQYLNNI PYADIIDFDY
LFAI      61  TKFMKEANYNDNVAGVITWMHTFSPAKNWIRGTELLQKPLLHLATQFLNNIPI DSIIDMDY
LBrAI     61  TTFMKEVNYNDKVAGVITWMHTFSPAKNWIRGTELLQKPLLHLATQYLNNI PYADIIDFDY
LPeAI     61  TTFMKEVNYNDKVAGVITWMHTFSPAKNWIRGTELLQKPLLHLATQYLNNI PYADIIDFDY
LBuAI     61  TTFMKEVNYNDKVAGVITWMHTFSPAKNWIRGTKLLQKPLLHLATQYLDHI PYDIIDFDY
LSAI      61  TKVMKEANYNDHVAGVITWMHTFSPAKNWIRGTKLLQKPLLHLATQFLNKI PYDIIDFDY

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LRAI      120  MNLNQSAGHDREYAYINARLQKH NKIVYGFWGD E VQEEIADWQNVAVAYNESENIKIVR
LPIAI     121  MNLNQSAGHDREYAYINARLQKH NKIVYGYWGD EDVQEQIARWEDVAVAYNESFKIKVAR
LFAI      121  MNLHQSAGHDREYAYINARLQKH NKIVYGYWGD ADVQEQIADWQH VAVAYNESFHIKVAR
LBrAI     121  MNLNQSAGHDREYAYINARLQKH NKIVYGYWGD EDVQEQIARWEDVAVAYNESFKIKVAR
LPeAI     121  MNLNQSAGHDREYAYINARLQKH NKIVYGYWGD EDVQEQIARWEDVAVAYNESFKIKVAR
LBuAI     121  MNLNQSAGHDREYGF INARLRKNNKIVYGYWGD PEVQEEIADWENI AVAYDESFKIKVAR
LSAI      121  MNLNQSAGHDREYAF INARLRKNNKISGYWGD EDVQKAAKAWMDVAVAYNESFKIKVVT

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LRAI      180  FGDTRNVAVTEGDKVEAQIFL GWTVDYWPVSDLVEYVNGISEE EIDAAYKDLASRYEMV
LPIAI     181  FGDTRNVAVTEGDKVEAQIKM GWTVDY YGIGDLVEEINKVSDADVDKEYADLESRYEMV
LFAI      181  FGDTRNDVAVTEGDKVAAQIKL GWTVDY YPTNELVAVVNGIAEDEIDAAYKDLBANYDIV
LBrAI     181  FGDTRNVAVTEGDKVEAQIKM GWTVDY YGIGDLVEEINKVSDADVDKEYADLESRYTMV
LPeAI     181  FGDTRNVAVTEGDKVEAQIKM GWTVDY YGIGDLVEEINKVSDADIDKEYADLESRYEMV
LBuAI     181  FGDTRNVAVTEGDKVEAQIQF GWTVDY YALGDLVESVNAVSESDIDAKYKELQDRYEFV
LSAI      181  FADKMRNVAVTDGDKVEAQIKF GWTVDY YWVGDVLAEVNAVSEADIDAKYADLQKEYLDFV

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LRAI      240  QGDNTKEH YEH SVRYQLREYLG I KRFMDEKGYTFTTNFEDLHGLEELPGLAAQLLMRDG
LPIAI     241  QGDNDATYKHSVRVQLAQYLG I KRFLEGGYTAFTTNFEDLWGMQLPGLASQLLIRDG
LFAI      241  EGDNDHEKYVHNRYQLREYLG I KRFLLDNGYDAFTDNFQDLEGLEQLPGLAVQLLMIDG
LBrAI     241  QGDNDATYKHSVRVQLQQYLG I KRFLEKGGYTAFTTNFEDLWGMQLPGLAAQLLIRDG
LPeAI     241  QGDNDATYKHSVRVQLAQYLG I KRFLEGGYTAFTTNFEDLWGMQLPGLASQLLIRDG
LBuAI     241  QGDNDKDKYEH SVRYQIREYFG I KRFNLDKGNYSFTTNFEDLYGLEQLPGLAAQLLMADG
LSAI      241  EQNTPEKFEHNVKYQIREYFG I KRFMDRRGYTAFTTNFEDLVGLEQLPGLAAQLLMAEG

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LRAI      300  YGFGAEGDWKSAGMDRLK I TAADNVA TAFMEDYTLDLRF GHQA I LGS HMLEVDPPIASDK
LPIAI     301  YGFGAEGDWKTAALGRVMK I MSHNKQ TAFMEDYTLDLRF GHEA I LGS HMLEVDPPIASDK
LFAI      301  YGFGPEGDKMAGLTRLK I TAADNKQ TALMEDYTLDLRF GHEA I MGS HMLEVDPPIASDK
LBrAI     301  YGFGAEGDWKTAALGRVMK I MSHNDR TAFMEDYTLDLRF GHEA I LGS HMLEVDPPIASDK

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LPeAI 301 YGFGAEGDWKTAALGRVIMKIMSHNQATAFMEDYTLDLRFHGHEAILGSHMLEVDPSTIASDK
 LBuAI 301 YGFGAEGDWKTAALDRLLKIMAHNQATAFMEDYTLDLRFHGHEAILGSHMLEVDPSTIASDK
 LSAI 301 YGFAEGDWKTAALDRLLKIMAHNEKTVFMEDYTLDLRFHGHEAILGSHMLEVDPSTIASDK

LRAI 360 PRVEVHPLDIGGKDDPARLVFTGREGKAVDVTLSYFNDGKVIIGYSVDCHKPEAETPHLP
 LPlAI 361 PRVEVHPLDIGGKDDPARLVFTGSEGEAIDVTVADEFRDGFKMISYAVDANKPEAETPNLP
 LFAI 361 PRVEVHPLDIGGKDDPARLVFTGAEGKCYDITLSYFDDGKFIIGYPVDCKTPEAETPKLP
 LBrAI 361 PRVEVHPLDIGGKADPARLVFTGSEGDADVTVADEFRDGFKMIGYAVDANKPEAETPNLP
 LPeAI 361 PRVEVHPLDIGGKADPARLVFTGSEGDADVTVADEFRDGFKMISYAVDANKPEAETPKLP
 LBuAI 361 PRVEVHPLDIGGKADPARLVFTGREGDAMDVTISDFGNEYFMIGYAVEGHKAPKTPHLP
 LSAI 361 PRVEVHPLDIGDKDDPARLVFTGMQGDADVDTMADMGDFEFLMSYDVRGNKPEAETPHLP

LRAI 420 VAKQLWTPFTVGLKEGAERWMAAGGGHHTILSFSLKPOQIKDLFGMLDVKVDFTIE
 LPlAI 421 VAKQLWTPKMGGLKKGALFWMQAGGGHHTMLSFSLTEEQMEDYATMVGMTKAFIK
 LFAI 421 VAKQLWTPFTVGLAEGAKQWMAAGGGHHTVLTALSEEQLQLARLKFVDFINIK
 LBrAI 421 VAKQLWTPKMGGLKTGALFWMQAGGGHHTMLSFSLTEEQMEDFATMVGMTKAFIK
 LPeAI 421 VAKQLWTPKMGGLKKGALFWMQAGGGHHTMLSFSLTEEQMEDYATMVGMTKAFIK
 LBuAI 421 VAKQLWTPKMGGLKNGATQWLDGAGGGHHTVLTFNATEQFQDLATMFGLTFNDIK
 LSAI 421 VAKQLWTPKQGLREGAVGWLTVGGGHHTVLSFVDSQQLQDLSHLFDLTYVNIK

Supplemental Figure 2. Multiple sequence alignment of D-XI protein sequences from various *Lactobacillus* species using the T-Coffee algorithm. LRXI, *L. reuteri*; LPIAI, *L. plantarum*, LFAI, *L. fermentum*; LBr, *L. brevis*; LPeAI, *L. pentosus*; LBuAI, *L. buchneri*; LSAI, *L. sakei*. Black shaded areas indicate homology, grey shaded areas indicate amino acids with similar properties.

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LRXI 1  MAD-LWNNIDKIEYEGPHKSIKSGLFYQYYNPDEVILGKKMFDWLRFSVAYWHTFDQRLV
LPI 1  MTNEYWQGVDTIKYICHQ-DKKSGLGFQYYNPDEVIGGKKMFDWLRFSVAYWHTFDQRLV
LFXI 1  MSD-LWGGIDKISYVGNKGSIKSGLGFQYYNPDEEELGKKMFDWLRFSVAYWHTFDQRLV
LBrXI 1  MTEBYWKGVDKIQYVGHQ-DKKSGLGFQYYNPDEEELGKKMFDWLRFAVAYWHTFDQRLV
LPeXI 1  MTNEYWQGVDTIKYICHQ-DKKSGLGFQYYNPDEVIGGKKMFDWLRFSVAYWHTFDQRLV
LBuXI 1  MS--YW-NVDKIKYVGTG-DKKSGLGFQYYNPDEVIGGKKMFDWLRFAVAYWHTFDQRLV
LSXI 1  MT--LQ-NQEKMVYVGNKGLKAGNGFHYYNPNQVINGKKMSEWLKFSVAYWHTMDQRLV

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LRXI 60  DPFGDGTAQRPYDKYS DPMDCALAKVDYAFEFYHKLGVDFLCFHDRDLAPEGDTLRETNK
LPI 60  DPFGDGTAQRPYDHI TDPMDLALAKVDAAAFEFYHKLGVDFLCFHDRDLAPEGDTLRETNR
LFXI 60  DPFGDGTAIRPYDKYTDPMDLALAKVDYAFEFYHKLGVDFLCFHDRDLAPEGDTLRETSNA
LBrXI 60  DPFGDGTAQRPYDKYTDPMDLALAKVDAAAFEFYHKLGVDFLCFHDRDLAPEGDTLRETNA
LPeXI 60  DPFGDGTAQRPYDHI TDPMDLALAKVDAAAFEFYHKLGVDFLCFHDRDLAPEGDTLRETNR
LBuXI 57  DPFGDGTAIRPYDKYTDPMDLALAKVDAAAFEFYHKLGVDFLCFHDRDLAPEGDTLRETNR
LSXI 58  DPFGDGTAQRPDITIEDPMDLALAKVDYLFEFLNKINVEYFAFHDRDLAPEGDTLRETNQ

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LRXI 120  NLDKVVVDKIVEYQKATGMKVLWNTSNLFTNPRFVSGACTAESSKIYAYAAAQLKHSLEIVG
LPI 120  NLDKVIDKIVDYQKQATGMKVLWNTSNLFTNPRFVAGAAATSEADVFAYAAAQLKHSLEIG
LFXI 120  NLDKVIDKIVENQKATGMKVLWNTSNLFTNPRFVSGACTAESSKIYAYACAQLKHSLEIVG
LBrXI 120  NLDKVVVDKIVEYQKTS GMKVLWNTSNLFTNPRFVAGAAATSEYADVFAYSAAQLKHSLEIG
LPeXI 120  NLDKVIDKIVDYQKQATGMKVLWNTSNLFTNPRFVAGAAATSEADVFAYAAAQLKHSLEIG
LBuXI 117  NLDKVVVDKIVENQKTS GMKVLWNTSNLFTNPRFVAGAAATSEYADIFAYSAAQLKHSLEIG
LSXI 118  NLDIVVDKIVAKMQETGKVLWNTSSLFTNPRFVAGAAATSEYADIFAYSAAQLKHSLEIA

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LRXI 180  KRVGSENYVFWGGREGYESLWNTMKREQSHIAKFFHMAKDYANEIGFDAQMLLEPKPKE
LPI 180  KRVGSENYVFWGGREGYESLWNTMKLEQEHAAKFFHMAKDYANEIGFDAQMLLEPKPKE
LFXI 180  KRVGSENYVFWGGREGYESLWNTMKREQAHIKMFHMAKDYANEIGFDAQMLLEPKPKE
LBrXI 180  KRVGSENYVFWGGREGYESLWNTMKLEQEHAAKIFHMAKDYANEIGFDAQMLLEPKPKE
LPeXI 180  KRVGSENYVFWGGREGYESLWNTMKLEQEHAAKFFHMAKDYANEIGFDAQMLLEPKPKE
LBuXI 177  KRVGSENYVFWGGREGYESLWNTMKREQEHAAKLFHMAKDYANEIGFDAQMLLEPKPKE
LSXI 178  KRVNSESYVFWGGREGYESLWNTMKLEQDHIKFFRMAKDYANEIGYTCQFLLEPKPKE

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LRXI 240  PTHQYDFDAATTINFMCEYGLDKDFKLNLEGNHANLAGHTYQHEIRVAREAGLLGSLDA
LPI 240  PTHQYDFDAATTIAFMKEYLDLKDDFKLNLEGNHANLAGHTYQHEIRVAREANLLGSLDA
LFXI 240  PTHQYDFDAATTIAFMKEYGLDKDFKLNLEGNHANLAGHTYQHEIRVAREAGLLGSLDA
LBrXI 240  PTHQYDFDAATTIAFMKEYALDKDFKLNLEGNHANLAGHTYQHEIRVAREAGLLGSLDA
LPeXI 240  PTHQYDFDAATTIAFMKEYLDLKDDFKLNLEGNHANLAGHTYQHEIRVAREANLLGSLDA
LBuXI 237  PTHQYDFDAATTIAFMKEYGLDKDFKLNLEGNHANLAGHTYQHEIRVAREAGLLGSLDA
LSXI 238  PMSHQYDFDAATTIAFMKEYGLDKDFKLNLEGNHANLAGHTYQHEIRVAREAGLLGSLDA

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LRXI 300 NQGDKLI~~GW~~DIDEYPSNLYETTAAMWEVIQNGSIGPRGGLNFD~~AK~~PRRISF~~KPV~~DLFYGH
 LP1 300 NQGDKLI~~GW~~DIDEF~~PS~~DLYEATAAMYEVVENGSI~~G~~PRGGLNFD~~AK~~PRRSSFAAN~~DL~~FYGH
 LFXI 300 NQGDKLI~~GW~~DIDEF~~PS~~NLYETTAAMWEVVENGQIGPRGGLNFD~~AK~~PRRIS~~W~~QAE~~DL~~FYSH
 LBrXI 300 NQGDKLI~~GW~~DIDEYPSNLYETTAAMYEVVENGSI~~G~~PRGGLNFD~~AK~~PRRSSFAPE~~DL~~FLGH
 LPeXI 300 NQGDKLI~~GW~~DIDEF~~PS~~DLYEATAAMYEVVENGSI~~G~~PRGGLNFD~~AK~~PRRSSFAAN~~DL~~FYGH
 LBUXI 297 NQGDKLI~~GW~~DIDEYPSNLYETTAAMTEVVENGSI~~G~~PRGGLNFD~~AK~~PRRSSFEP~~DL~~FYGH
 LSXI 298 NM~~G~~DKLI~~GW~~DIDEFPNDIYEATLVMYEMLKNGGL-PTGGLNFD~~SK~~PRRQSFDM~~DL~~FLAH

LRXI 360 IVGMD~~S~~FAAGLRVAAAMKEDGFLDDIKERYSTWDEGLCKSI~~ED~~GNENFASLEKVIDTP
 LP1 360 IVGMD~~T~~FAAGLRVALKMKODGFLEKLVADRYRSYQSGVGAIEAGTADFKSLESVAIDKP
 LFXI 360 IVGMD~~S~~FAAGLRVAAAMKEDGFLDDV~~L~~KTRYASTWDEGLCKSI~~ED~~GKEDFKSLEKVIDTP
 LBrXI 360 IVGMD~~S~~FAAGLRVAAAMKODGFLDSIKADRYSSYKSGVGAIESGKADLKSLEVAIDKP
 LPeXI 360 IVGMD~~T~~FAAGLRVALKMKODGFLEKLVADRYSSYQSGVGAIEAGTADFKSLESVAIDKP
 LBUXI 357 IVGMD~~S~~FAAGLRVAVAMKNDGV~~L~~DDIVKNRYSSFD~~S~~G~~V~~GAIESGKAS~~M~~ADLENVSTDKT
 LSXI 357 AAGMD~~T~~YAAGLLVANKIIE~~D~~RV~~ED~~DDVLD~~D~~RYGSEKIGVGAIEAGKVTFKDFEDVIDKP

LRXI 420 QSEL~~A~~AATHSDHLEEIKDTINHYIIE~~T~~LAK
 LP1 420 QSEL~~A~~AATS~~S~~SDHLEE~~V~~KDTINHYIIE~~T~~LAK
 LFXI 420 QAE~~L~~R~~A~~AATQSDHLEQIKDTINHYIIQ~~T~~LAK
 LBrXI 420 QSEL~~A~~AATHSDHLEEIKDTINHYIID~~T~~LAK
 LPeXI 420 QSEL~~A~~AATS~~S~~SDHLEE~~V~~KDTINHYIIE~~T~~LAK
 LBUXI 417 QK~~D~~L~~R~~DATHSDHLEEIKDTINHYIIQ~~T~~L-K
 LSXI 417 QSEL~~A~~AATKSGHLEQIKATINNYIYTVLGR