Figure S1

A

```
TanA_Sl        MKKTFISLLSATVILSGCGVGEHQNNNSNHDAKGVNTSNVKIKNYNQASSALQIDNSKWK 60
TanB_Lp        -----------------------MSNRLIFDADWLVPEQVQVAG---------------- 21
                                       .*.  .**. : ..:*:: .

TanA_Sl        YDSKNNVYYQLNISYVSNPQAKNVEKLGIYVPAAYFKGKKNHNGTYTVTVNDAKKVNGYS 120
TanB_Lp        --QAIQYYAARNIQYVQHP-VAAIQVLNVFVPAAYLHG---------------SSVNGYQ 63
                 .  : *   **.**.:* .  :: *.::*****::*               ..****.

TanA_Sl        ARTAPIVYPVNTPGYAEQSAPTSYRYSN------ISKYMKAGFIYVEAGLRGRSMSMGNN 174
TanB_Lp        RATAPILMPNTVGGYLPGPADDPQRVTWPTNAGTIQQALKRGYVVVAAGIRGR------- 116
                 ****: * .. **   .*  . * :       *.: :* *:: * **:***

TanA_Sl        SSNASTKSYETGSPWGVTDLKAAIRYYRFNDSSLPGNSSKIYTFGHSGGGAQSAIAGASG 234
TanB_Lp        TTVDKSGQRVGQAPAFIVDMKAAIRYVKYNQGRLPGDANRIITNGTSAGGATSALAGASG 176
               ::  .: .    :*  :.*:****** ::*:. ***:..:* * * *.*** **:*****

TanA_Sl        DSKLYYKYLEQIGAAMTDKNGKYISDKIDGAMAWCPITSLDQADAAYEWQMGQYGNEGNR 294
TanB_Lp        NSAYFEPALTALGAAP-------ATDDIFAVSAYCPIHNLEHADMAYEWQFNGIN---DW 226
               :*  :   *  :***         :*.* .. *:*** .*::** *****:.  .   :

TanA_Sl        KKNSFQKQLSTDLASSYASYLNKLNLKNGNTTLSLTKSKNGQYTEGSYAKYLKKEIEDSA 354
TanB_Lp        HRYQPVAGTTKNGRPKFEPVSGQLTVEEQALSLALKAQFS------TYLNQLKLTASDGT 280
               :: .     :.:  ..: .  .:*.:::   :*:*. . .      :* : **   .*.:

TanA_Sl        TEFLNNTTFPYKQNSTEQAGMGNGGPSGGKPSGKMGSMPQMRKQSSNKTYKTMDAYLKDL 414
TanB_Lp        HLTLNEAGMGSFRDVVRQLLISS-AQTAFDQGTDIHKYAGFAVTGNQVTDLDLSAYLKSL 339
                  **:: :   ::  ..*  :.. . :. . . .: . . :   ..: *   :.****.*

TanA_Sl        NKKGTWITYDKKTKRAHITSLKDFAKYYKQPSKSVSAFDDLKRSQAENEVFGTSGSDSKL 474
TanB_Lp        TR-----------------------------MKAVPAFDQLDLTSPENNLFGDATAKAKH 370
               .:                              *:*.***:*. :..**::** : :.:*

TanA_Sl        HFDQSLAKLLTENKSNYSKLNGWNSNYVSSYKNDLTKTDKLGTSMSTRMNMYNPMYYLSD 534
TanB_Lp        FTALAQTRSTVTAQLADAEL----------------------------IQAINPLSYLTT 402
               .   : ::  .  :   ::*                            ::  **: **:

TanA_Sl        YYSGYGKSNVANHWRIRTGIQQGDTALNTETNLSLALKERVGSKNVDFKTVWDQGHTMAE 594
TanB_Lp        TSS-----QVAKHWRIRHGAADRDTSFAIPIILAIMLEN--HGYGIDFALPWDIPHSGDY 455
                 *     :**:***** *  : **::     *:: *::   . .:**   **  *:

TanA_Sl        TSGNSDSNFIKWVESINKK 613
TanB_Lp        DLG----DLFSWIDGLCQ- 469
                 *    :::.*::.: :
```

B

```
TanASl          -MKKTFISLLS----ATVILSGCGVGEHQNNNSNHDAKGVN--TSNVKIKNYNQASSALQ 53
TanALp          MQFRKIVPLMSGLLVMSVGLAACGHSETKTKHPTSTVAKVAKATKQTVTKADVKNAKKLL 60
                   :.::.*:*     :* *:.** .* :.::..  .  *   *.:.  *   : :. *

TanASl          IDNSKWKYDSKNNVYYQLNISYVSNPQAKNVEKLGIYVPAAYFKGKKNHNGTYTVTVNDA 113
TanALp          INQKQWHYNATNKVYYQVGVKYGTKTTSSTYESMGIFIPAKYVNAKASGQKTYTITFNNK 120
                *::.:*:*::.*:****:.:.* ::. :.. *.:**::** *.:.* . : ***:*.*:

TanASl          KKVNGYSARTAPIVYPVNTPGYAEQSAPTSYRYSNISKYMKAGFIYVEAGLRGRSMSMGN 173
TanALp          AKVKGYTAKTAPIVMPVNTPGYAAQTAPTGYDSS-ANKYTKAGFIYVAAGCRGLSQSDKS 179
                 **:**:*:***** ******** *:***.*  *  .** ******* ** ** * *  .

TanASl          NSSNASTKSYETGSPWGVTDLKAAIRYYRFNDSSLPGNSSKIYTFGHSGGGAQSAIAGAS 233
TanALp          NGS----------SPWGVTDLKAAVRTLRLNRSRIAGNTNRVFTFGHSGGGAQSALMGAT 229
                *.*          ***********:*  *:* * :.**:.:::************: **:

TanASl          GDSKLYYKYLEQIGAAMTDKNGKYISDKIDGAMAWCPITSLDQADAAYEWQMGQYGNEGN 293
TanALp          GDSKKYTTYLKAIGAPLATTTGKSTSDAVAGAMAWCPITSLDTANEAYEWNMGQYSNSGT 289
                **** * .**: ***.:: ..**  ** : ************ *: ****:****.*.*.

TanASl          RKKNSFQKQLSTDLASSYASYLNKLNLKNGN-TTLSLTKSKNGQYTEGSYAKYLKKEIED 352
TanALp          RKQGTWTKALSNDMATSYAQYINKLGLKDANGKTLTLKKSTSGIYTSGTYATYLKKEVEQ 349
                **:.:: * **.*:*:***.*:***.**:.* .**:*.**..* **.*:**.*****:*:

TanASl          SATEFLNNTTFPYKQNSTEQAG-------MGNGGPSGGKPSG--KMGSMPQMRKQS---- 399
TanALp          SLNNFLKDTTFPYKATSNEGPSGAASQTLTSGKMPSGSKPSGTAKSGSKPSGSAPSGTAT 409
                * .:**::****** .*.* ..        ..  ***.****  * ** *.    *

TanASl          -----SNKTYKTMDAYLKDLNKKGTWITYDKKTKRAHITSLKDFAKYYKQPSKSVSAFDD 454
TanALp          NSSSTSGETYKTATAYIKALNKNGKWITYNAKKNTATITSVKAFVKHCKTASKDVGAFDG 469
                     *.:****  **:* ***:*.****: *.: * ***:* *.*: * .**.*.***.

TanASl          LKRSQAENEVFGTSGSDSKLHFDQSLAKLLTENKSNYSKLNGWNSNYVSSYKNDLTKTDK 514
TanALp          LTRQQTENKLFATNGS-SANHFDATISKLLTTNQSKYAKLKNYKASYAKAYRSDLKKTDA 528
                *.*.*:**::*.*.** *  *** :::**** *:*:*:**:.:::.*..:*:.**.***

TanASl          LGTSMSTRMNMYNPMYYLSDYYSGYGKSNVANHWRIRTGIQQGDTALNTETNLSLALKER 574
TanALp          QGSSIQKRMNLYNPLYYLTSYYDGYNTSKVAKYWRIRTGINQSDTALTVETNLALTLKQN 588
                *:*:..***:***:***:.**.**..*:**::*******:*.****..****:*:**:.

TanASl          VGSKNVDFKTVWDQGHTMAETSGNSDSNFIKWVESINKK 613
TanALp          SQVKSVDFATVWGQGHTEAERKGNNETNFIKWVNKSLK- 626
                   *.*** ***.**** ** .**.::******:.  *
```

C

```
TanASl       -MKKTFISLLS----ATVILSGCGVGEHQNNNSNHDAKGVN--TSNVKIKNYNQASSALQ 53
TanALp       MQFRKIVPLMSGLLVMSVGLAACGHSETKTKHPTSTVAKVAKATKQTVTKADVKNAKKLL 60
TanBLp       ------------------------------------------MSNRLIFDADWLVPEQVQ 18
                                                        :..   .     .. :

TanASl       IDNSKWKYDSKNNVYYQLNISYVSNPQAKNVEKLGIYVPAAYFKGKKNHNGTYTVTVNDA 113
TanALp       INQKQWHYNATNKVYYQVGVKYGTKTTSSTYESMGIFIPAKYVNAKASGQKTYTITFNNK 120
TanBLp       VAGQAIQYYAAR------NIQYVQHP-VAAIQVLNVFVPAAYLHG--------------- 56
             :  .  :* : .      .:.*  :.     : :.:::** *.:.

TanASl       KKVNGYSARTAPIVYPVNTPGYAEQSAPTSYRYSN------ISKYMKAGFIYVEAGLRGR 167
TanALp       AKVKGYTAKTAPIVMPVNTPGYAAQTAPTGYDSS-------ANKYTKAGFIYVAAGCRGL 173
TanBLp       SSVNGYQRATAPILMPNTVGGYLPGPADDPQRVTWPTNAGTIQQALKRGYVVVAAGIRGR 116
              .*:**   ****: * .. **   .*      :        .:  * *:: * ** **

TanASl       SMSMGNNSSNASTKSYETGSPWGVTDLKAAIRYYRFNDSSLPGNSSKIYTFGHSGGGAQS 227
TanALp       SQSDKSNGS----------SPWGVTDLKAAVRTLRLNRSRIAGNTNRVFTFGHSGGGAQS 223
TanBLp       TTVDKSGQRVG-------QAPAFIVDMKAAIRYVKYNQGRLPGDANRIITNGTSAGGATS 169
             :    ..            :*  :.*:***:*  : * . :.*::.:: * * *.*** *

TanASl       AIAGASGDSKLYYKYLEQIGAAMTDKNGKYISDKIDGAMAWCPITSLDQADAAYEWQMGQ 287
TanALp       ALMGATGDSKKYTTYLKAIGAPLATTTGKSTSDAVAGAMAWCPITSLDTANEAYEWNMGQ 283
TanBLp       ALAGASGNSAYFEPALTALGAAPAT-------DDIFAVSAYCPIHNLEHADMAYEWQFNG 222
             *: **:*:*  :   *  :**. :        * : .. *:*** .*: *: ****::.

TanASl       YGNEGNRKKNSFQKQLSTDLASSYASYLNKLNLKNGN-TTLSLTKSKNGQYTEGSYAKYL 346
TanALp       YSNSGTRKQGTWTKALSNDMATSYAQYINKLGLKDANGKTLTLKKSTSGIYTSGTYATYL 343
TanBLp       INDWHRYQP----------VAGTTKNGRPKFEPVSGQLTVEEQALSLALKAQFSTYLNQL 272
              .:    :           :* :  .   *:   ..: ..     *       .:* . *

TanASl       KKEIEDSATEFLNNTTFPYKQNSTEQAG-------MGNGGPSGGKPSG--KMGSMPQMRK 397
TanALp       KKEVEQSLNNFLKDTTFPYKATSNEGPSGAASQTLTSGKMPSGSKPSGTAKSGSKPSGSA 403
TanBLp       KLTASDGTHLTLNEAGMGSFRDVVRQLL-------------------------------- 300
             *   .:.    *::: :       .

TanASl       QS---------SNKTYKTMDAYLKDLNKKGTWITYDKKTKRAHITSLKDFAKYYKQPSKS 448
TanALp       PSGTATNSSSTSGETYKTATAYIKALNKNGKWITYNAKKNTATITSVKAFVKHCKTASKD 463
TanBLp       ---------------ISSAQTAFDQGTDIHKYAGFAVTGNQVTDLDLSAYLKSLTR-MKA 344
                             .:  : :.  ..  .:  :  . : .   .:. : *  .   *

TanASl       VSAFDDLKRSQAENEVFGTSGSDSKLHFDQSLAKLLTENKSNYSKLNGWNSNYVSSYKND 508
TanALp       VGAFDGLTRQQTENKLFATNGS-SANHFDATISKLLTTNQSKYAKLKNYKASYAKAYRSD 522
TanBLp       VPAFDQLDLTSPENNLFGDATAKAKHFTALAQTRSTVTAQLADAEL-------------- 390
             * *** *   ..**::*.   : :  .   : ::  .  :   ::*

TanASl       LTKTDKLGTSMSTRMNMYNPMYYLSDYYSGYGKSNVANHWRIRTGIQQGDTALNTETNLS 568
TanALp       LKKTDAQGSSIQKRMNLYNPLYYLTSYYDGYNTSKVAKYWRIRTGINQSDTALTVETNLA 582
TanBLp       --------------IQAINPLSYLTTTSS-----QVAKHWRIRHGAADRDTSFAIPIILA 431
                           ::  **: **:   .     :**::**** *  : **::     *:

TanASl       LALKERVGSKNVDFKTVWDQGHTMAETSGNSDSNFIKWVESINKK 613
TanALp       LTLKQNSQVKSVDFATVWGQGHTEAERKGNNETNFIKWVNKSLK- 626
TanBLp       IMLENHG--YGIDFALPWDIPHSGDYDLG----DLFSWIDGLCQ- 469
             : *::.    .:**   *.  *:     *    :::.*::   :
```

Figure S2

```
ATCC14917  MQFRKIVPLMSGLLVMSVGLAACGHSETKTKHPTSTVAKVAKATKQTVTKADVKNAKKLL 60
RM35       MQFRKIVPLMSGLLVMSVGLAACGHSETKTKHPTSTVAKVAKATKQTVTKADVKNAKKLL 60
CECT749    MQFRKIVPLMSGLLVMSVGLAACGHSETKTKHPTSTVAKVAKATKQTVTKADVKNAKKLL 60
NC8        MQFRKIVPLMSGLLVMSVGLAACGHSETKTKHPTSTVAKVAKATKQTVTKADVKNAKKLL 60
           ************************************************************

ATCC14917  INQKQWHYNATNKVYYQVGVKYGTKTTSSTYESMGIFIPAKYVNAKASGQKTYTITFNNK 120
RM35       INQKQWHYNATNKVYYQVGVKYGTKTTSSTYESMGIFIPAKYVNAKDSGQKTYTITFNNK 120
CECT749    INQKQWHYNATNKVYYQVGVKYGTKTTSSTYESMGIFIPAKYVNAKASGQKTYTITFNNK 120
NC8        INQKQWHYNATNKVYYQVGVKYGTKTTSSTYESMGIFIPAKYVNAKASGQKTYTITFNNK 120
           ********************************************** *************

ATCC14917  AKVKGYTAKTAPIVMPVNTPGYAAQTAPTGYDSSANKYTKAGFIYVAAGCRGLSQSDKSN 180
RM35       AKVKGYTAKTAPIVMPVNTPGYAAQTAPTGYDSSANKYTKAGFIYVAAGCRGLSQSDKSN 180
CECT749    AKVKGYTAKTAPIVMPVNTPGYAAQTAPTGYDSSANKYTKAGFIYVAAGCRGLSQSDKSN 180
NC8        AKVKGYTAKTAPIVMPVNTPGYAAQTAPTGYDSSANKYTKAGFIYVAAGCRGLSQSDKSN 180
           ************************************************************

ATCC14917  GSSPWGVTDLKAAVRTLRLNRSRIAGNTNRVFTFGHSGGGAQSALMGATGDSKKYTTYLK 240
RM35       GSSPWGVTDLKAAVRTLRLNRSRIAGNTNRVFTFGHSGGGAQSALMGATGDSKKYTTYLK 240
CECT749    GSSPWGVTDLKAAVRTLRLNRSRIAGNTNRVFTFGHSGGGAQSALMGATGDSKKYTTYLK 240
NC8        GSSPWGVTDLKAAVRTLRLNRSRIAGNTNRVFTFGHSGGGAQSALMGATGDSKKYTTYLK 240
           ************************************************************

ATCC14917  AIGAPLATTTGKSTSDAVAGAMAWCPITSLDTANEAYEWNMGQYSNSGTRKQGTWTKALS 300
RM35       AIGAPLATTTGKSTSDAVAGAMAWCPITSLDTANEAYEWNMGQYSNSGTRKQGTWTKALS 300
CECT749    AIGAPLATTTGKSTSDAVAGAMAWCPITSLDTANEAYEWNMGQYSNSGTRKQGTWTKALS 300
NC8        AIGAPLATTTGKSTSDAVAGAMAWCPITSLDTANEAYEWNMGQYSNSGTRKQGTWTKALS 300
           ************************************************************

ATCC14917  NDMATSYAQYINKLGLKDANGKTLTLKKSTSGIYTSGTYATYLKKEVEQSLNNFLKDTTF 360
RM35       NDMATSYAQYINKLGLKDANGKTLTLKKSTSGIYTSGTYATYLKKEVEQSLNNFLKDTTF 360
CECT749    NDMATSYAQYINKLGLKDANGKTLTLKKSTSGIYTSGTYATYLKKEVEQSLNNFLKDTTF 360
NC8        NDMATSYAQYINKLGLKDANGKTLTLKKSTSGIYTSGTYATYLKKEVEQSLNNFLKDTTF 360
           ************************************************************

ATCC14917  PYKATSNEGPSGAASQTLTSGKMPSGSKPSGTAKSGSKPSGSAPSGTATNSSSTSGETYK 420
RM35       PYKATSNEGPSGAASQTLTSGKMPSGSKPSGTAKSGSKPSGSAPSGTATNSSSTSGETYK 420
CECT749    PYKATSNEGPSGAASQTLTSGKMPSGSKPSGTAKSGSKPSGSAPSGTATNSSSTSGETYK 420
NC8        PYKATSNEGPSGAASQTLTSGKMPSGSKPSGTAKSGSKPSGSAPSGTATNSSSTSGETYK 420
           ************************************************************

ATCC14917  TATAYIKALNKNGKWITYNAKKNTATITSVKAFVKHCKTASKDVGAFDGLTRQQTENKLF 480
RM35       TATAYIKALNKNGKWITYNAKKNTATITSVKAFVKHCKTASKDVGAFDGLTRQQTENKLF 480
CECT749    TATAYIKALNKNGKWITYNAKKNTATITSVKAFVKHCKTASKDVGAFDGLTRQQTENKLF 480
NC8        TATAYIKALNKNGKWITYNAKKNTATITSVKAFVKHCKTASKDVGAFDGLTRQQTENKLF 480
           ************************************************************

ATCC14917  ATNGSSANHFDATISKLLTTNQSKYAKLKNYKASYAKAYRSDLKKTDAQGSSIQKRMNLY 540
RM35       ATNGSSANHFDATISKLLTTNQSKYAKLKNYKASYAKAYRSDLKKTDAQGSSIQKRMNLY 540
CECT749    ATNGSSANHFDATISKLLTTNQSKYAKLKNYKASYAKAYRSDLKKTDAQGSSIQKRMNLY 540
NC8        ATNGSSANHFDATISKLLTTNQSKYAKLKNYKASYAKAYRSDLKKTDAQEVRFRSGT--- 537
           *************************************************   ::.

ATCC14917  NPLYYLTSYYDGYNTSKVAKYWRIRTGINQSDTALTVETNLALTLKQNSQVKSVDFATVW 600
RM35       NPLYYLTSYYDGYNTSKVAKYWRIRTGINQSDTALTVETNLALTLKQNSQVKSVDFATVW 600
CECT749    NPLYYLTSYYDGYNTSKVAKYWLIQTGINQSDTALTVETNLALTLKQNSQVKSVDFATVW 600
NC8        ----YITHYIIPVIMTVITRARPSTGGFGR------VSIRVILRLLRPTHRNKIHKLKVF 587
               *:* *      : :::      *:.:      *. .: * * : :: :.:.  .*:

ATCC14917  GQGHTEAERKGNNETNFIKWVNKSLK 626
RM35       GQGHTEAERKGNNETNFIKWVNKSLK 626
CECT749    GQGHTEAERKGNNETNFIKWVNKSLK 626
NC8        --------------------------
```

Figure S3

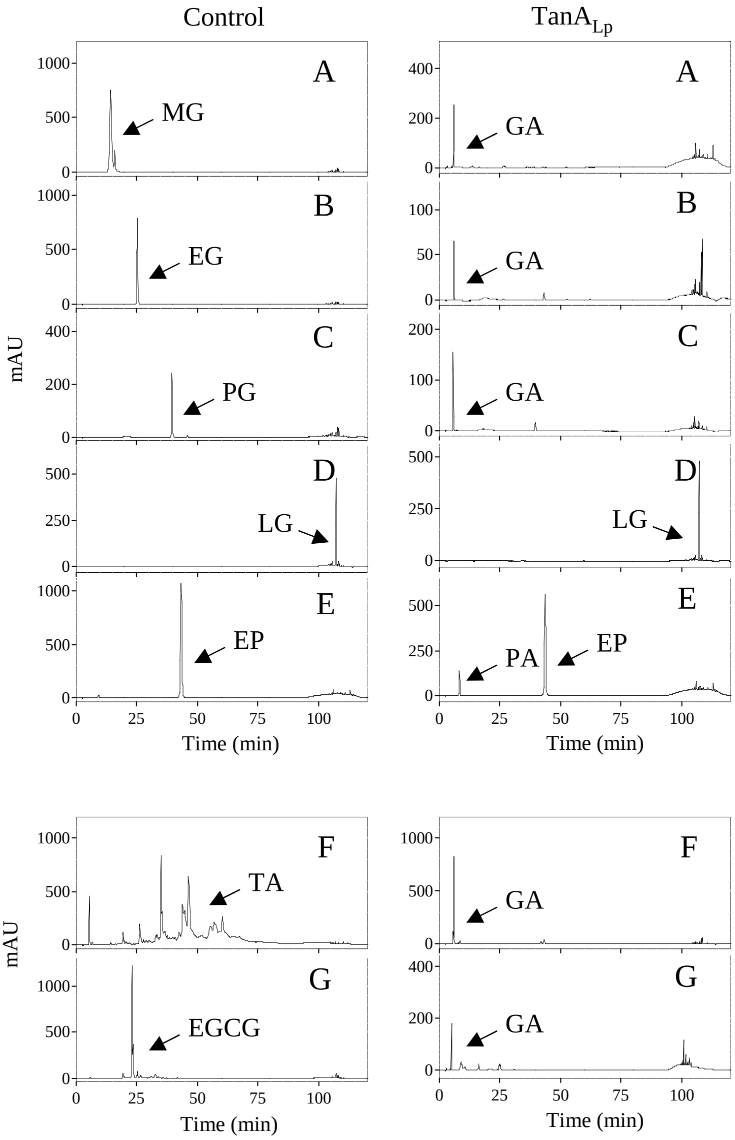
Control
TanA$_{Lp}$
mAU
A
B
C
D
E
F
G
MG
EG
PG
LG
EP
TA
EGCG
GA
PA
Time (min)
0
25
50
75
100
1000
500
400
250
200
100
50

Figure legends for supplementary material

FIG S1. Comparison of amino acid sequences of bacterial tannases. TanA_{Sl} from *Staphylococcus lugdunensis*, and TanA_{Lp} and TanB_{Lp} from *Lactobacillus plantarum*. Multiple alignments were done using the program ClustalW2 after retrieval of sequences from BLAST homology searches. Alignment of TanA_{Sl}-TanB_{Lp} (A), TanA_{Sl}-TanA_{Lp} (B), and TanA_{Sl}-TanB_{Lp}-TanA_{Lp} (C). Residues that are identical (*), conserved (:) or semiconserved (.) in all sequences are indicated. Dashes indicated gaps introduced to maximize similarities. The serine hydrolase conserved motif is highlighted in yellow; residues of the catalytic triad identified in the structure of TanB_{Lp} are highlighted in blue; and residues which make contacts with the three hydroxyl groups of gallic acid are highlighted in pink color.

FIG S2. Comparison of amino acid sequences of TanB_{Lp} proteins from different *L. plantarum* strains. Residues that are identical (*), conserved (:) or semiconserved (.) in all sequences are indicated. Dashes indicated gaps introduced to maximize similarities. The amino acid changes in relation to *L. plantarum* ATCC 14971^{T} TanB_{Lp} sequence are highlighted in colour.

FIG S3. Enzymatic activity of *L. plantarum* TanA_{Lp} protein. Esterase activity of purified TanA_{Lp} protein compared with control reactions on which the enzyme was omitted. HPLC chromatograms of TanA_{Lp} (50 μg) incubated in 50 mM phosphate buffer pH 6, 1mM $CaCl_2$, and 1 mM of methyl gallate (A), ethyl gallate (B), propyl gallate (C), lauryl gallate (D), ethyl protocatechuate (E), tannic acid (F), and epigallocatechin gallate (G). The methyl gallate (MG), ethyl gallate (EG), propyl gallate

(PG), lauryl gallate (LG), ethyl protocatechuate (EP), tannic acid (TA), epigallocatechin gallate (EGCG), gallic acid (GA), and protocatechuic acid (PA) detected are indicated. The chromatograms were recorded at 280 nm.