

Figure S 1 A-E

| A. Nucleotide and protein sequence from database entry FG090100 | |
|---|--|
| Accession number | FG090100 (EST database), for sequence see below |
| <pre> g ggg ata tca ctc act ctc tat ctc ttt ctc tca tag att ttc att tca aag cta G I S L T L Y L F L S - I F I S K L agt ttg aga aaa atg tcg tgg caa acc tac gtt gat gag cac ctt ttg tgc gat S L R K M S W Q T Y V D E H L L C D atc gaa ggt aat cag ctc act tct gca gcc att atc ggc caa gac ggt agc gtt I E G N Q L T S A A I I G Q D G S V tgg gct cag agc tct tct ttc cct cag ttc aag cct gag gaa ata act gct atc W A Q S S S F P Q F K P E E I T A I gtg aat gac ttt gct gag cct gga tca ctt gct cca act gga tta tat ctc ggt V N D F A E P G S L A P T G L Y L G ggc acg aaa tat atg gtg atc caa ggt gag cca gga gct gtc att cga ggg aaa G T K Y M V I Q G E P G A V I R G K aag ggt cct ggt ggg gtt act gtt aag aag acc aat caa gct ttg atc att ggt K G P G G V T V K K T N Q A L I I G att tat gat gaa cca atg act cca ggc caa tgc aac gtg gta gtt gaa agg ctt I Y D E P M T P G Q C N V V V E R L ggt gat tat ctc att gat acc ggt ctt taa tcc tct tgg taa ttc ttg tta tcg G D Y L I D T G L - S S W - F L L S ttc tta ttt cat tgg ctt tta taa gag gct ttt aca tca act tgc cat gag aat F L F H W L L - E A F T S T C H E N tct tga ttg caa tgt aat aat att atg gct at S - L Q C N N I M A </pre> | |

| B. Nucleotide and protein sequence used for expression | |
|--|--|
| <pre> cat atg tcg tgg caa acc tac gtt gat gag cac ctt ttg tgc gat H M S W Q T Y V D E H L L C D atc gaa ggt aat cag ctc act tct gca gcc att atc ggc caa gac ggt agc gtt I E G N Q L T S A A I I G Q D G S V tgg gct cag agc tct tct ttc cct cag ttc aag cct gag gaa ata act gct atc W A Q S S S F P Q F K P E E I T A I gtg aat gac ttt gct gag cct gga tca ctt gct cca act gga tta tat ctc ggt V N D F A E P G S L A P T G L Y L G ggc acg aaa tat atg gtg atc caa ggt gag cca gga gct gtc att cga ggg aaa G T K Y M V I Q G E P G A V I R G K aag ggt cct ggt ggg gtt act gtt aag aag acc aat caa gct ttg atc att ggt K G P G G V T V K K T N Q A L I I G att tat gat gaa cca atg act cca ggc caa tgc aac gtg gta gtt gaa agg ctt I Y D E P M T P G Q C N V V V E R L ggt gat tat ctc att gat acc ggt ctt ctc gag G D Y L I D T G L L E </pre> | |
| Cleavage sites: | NdeI (cat atg); marked in blue XhoI (ctc gag); marked in blue |
| Expression system: | Expression system: <i>E. coli</i> BL21(DE3), Vector: pET-23b |

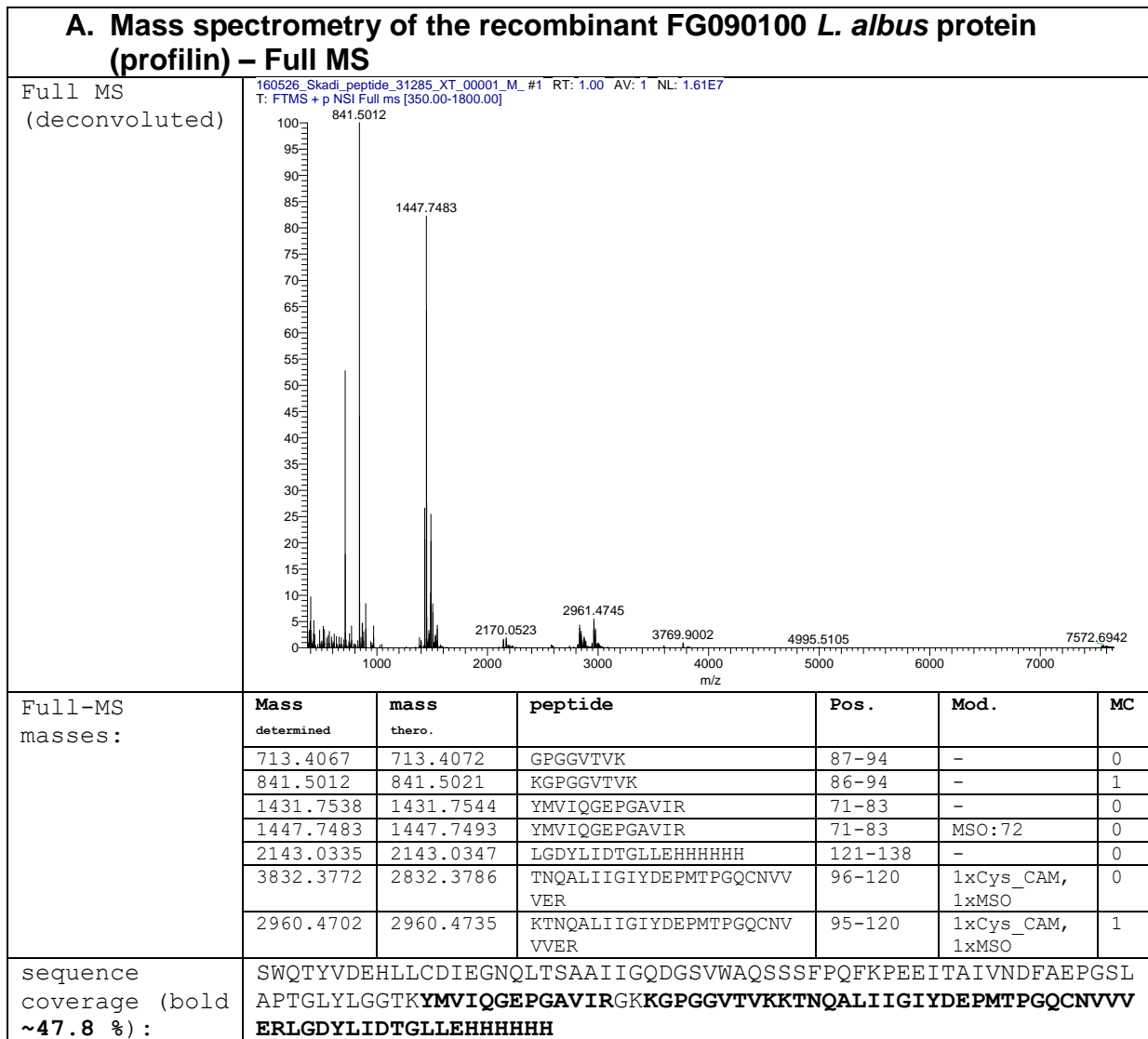
| C. Final protein sequence (after expression) | |
|---|--|
| Incl. His-Tag (black) | SWQTYVDEHLLCDIEGNQLTSAAIIGQDGSVWAQSSSFPPQFKPEEITAIVNDFAE PGLAPTGLYLGGTKYMVIQGEPGA VIRGKKGPGGVTVKKTNQALIIGIYDEPMT PGQCNVVVERLGDYLIDTGLLEHHHHHH |

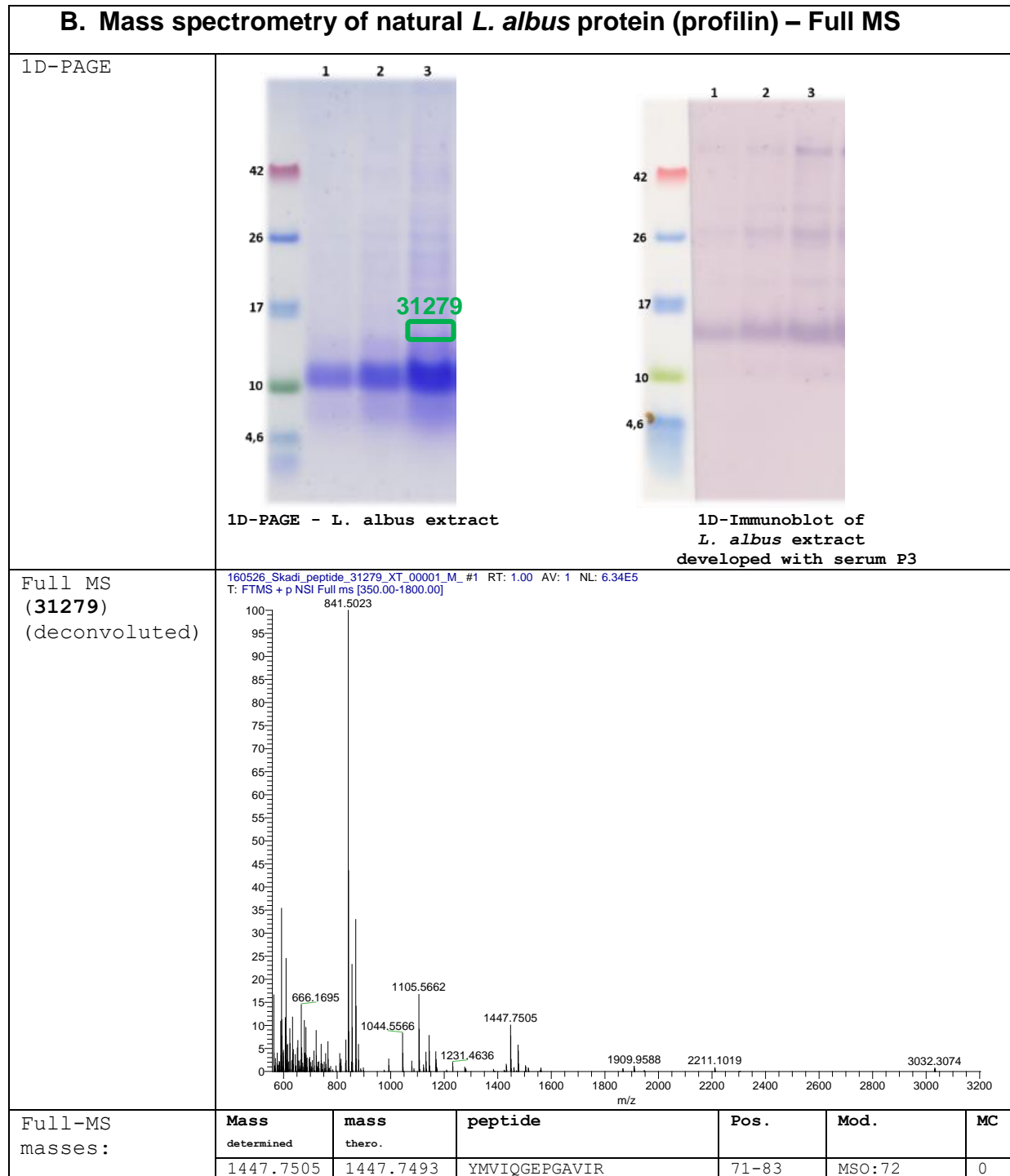
| D. Molecular weight of the expressed protein | |
|---|------------------------------|
| Deduced from sequence | 13.849 kDa (without His-Tag) |
| SDS-PAGE (reduced) | 15 kDa (with His-Tag) |

| E. N-terminal sequencing | |
|---------------------------------|--|
| sequence coverage (bold) : | SWQTYVDEHLLCDIEGNQLTSAAIIGQDGSVWAQSSSFPPQFKPEEITAIVNDFAE PGLAPTGLYLGGTKYMVIQGEPGA VIRGKKGPGGVTVKKTNQALIIGIYDEPMT PGQCNVVVERLGDYLIDTGLLEHHHHHH |

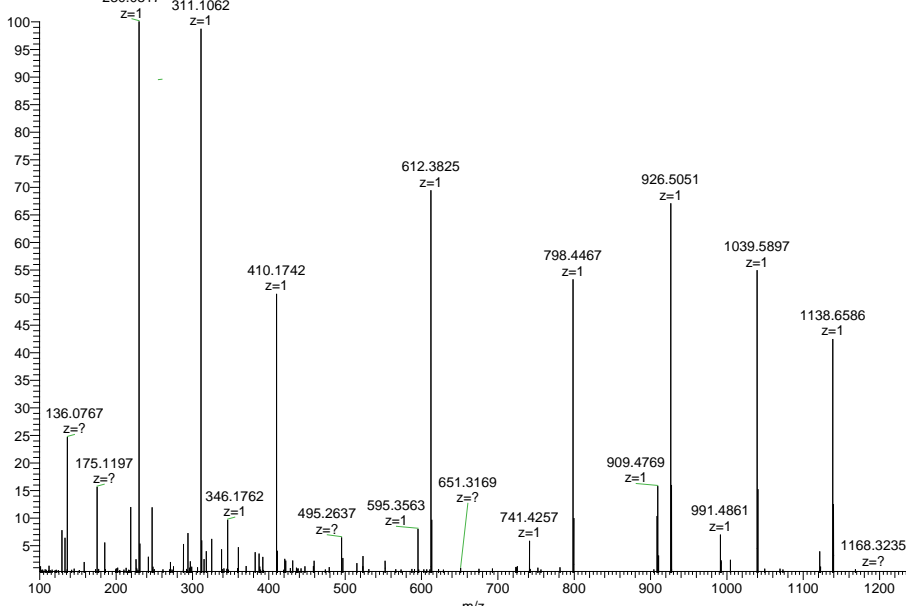
Figure S 1 A-E. Identification of the sequence information on *L. albus* (A) available from the EST data base, (B) sequence used for recombinant expression of the authentic protein and (C-E) preparation for mass spectrometry analysis

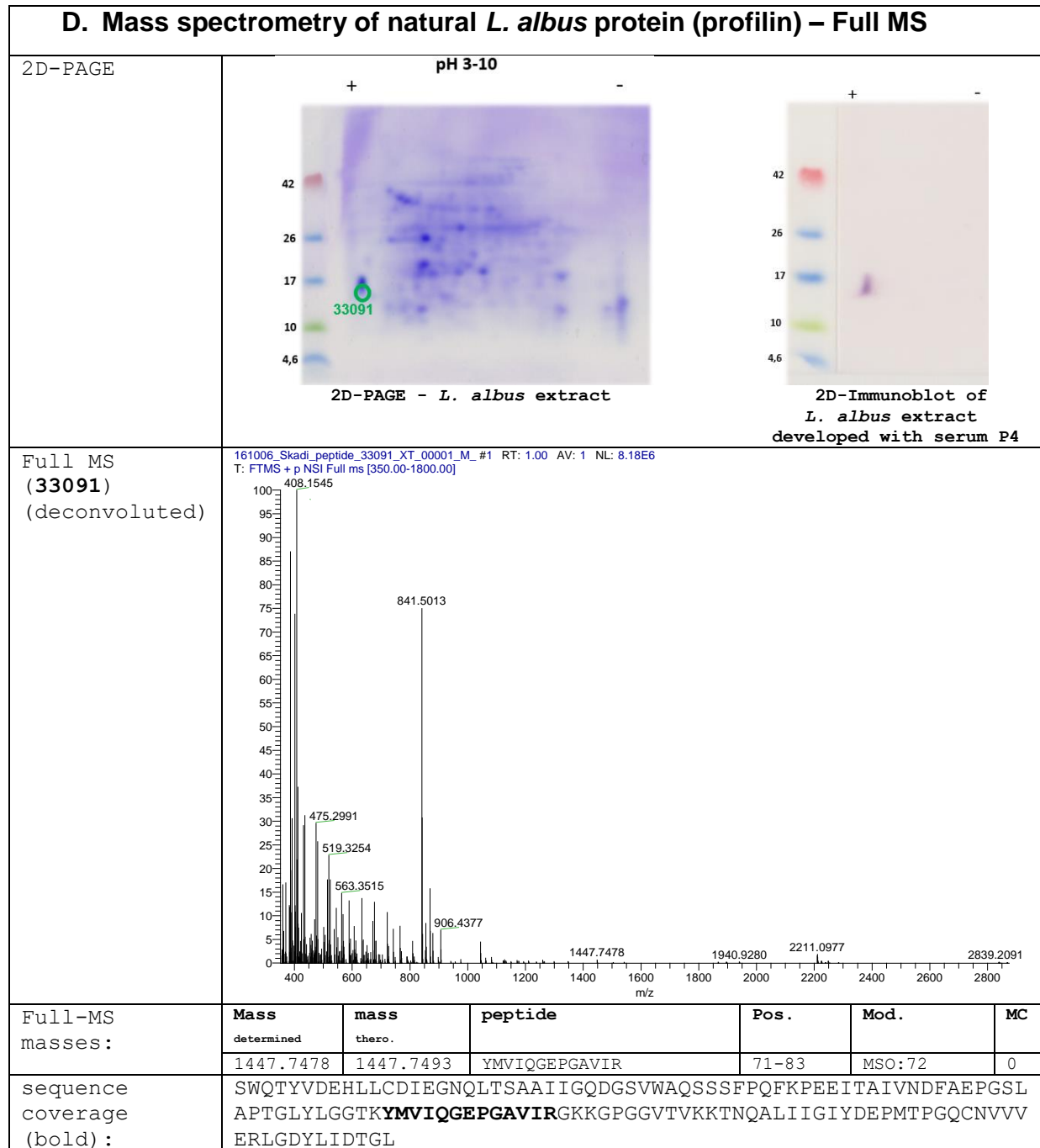
Figure S 2 A-E

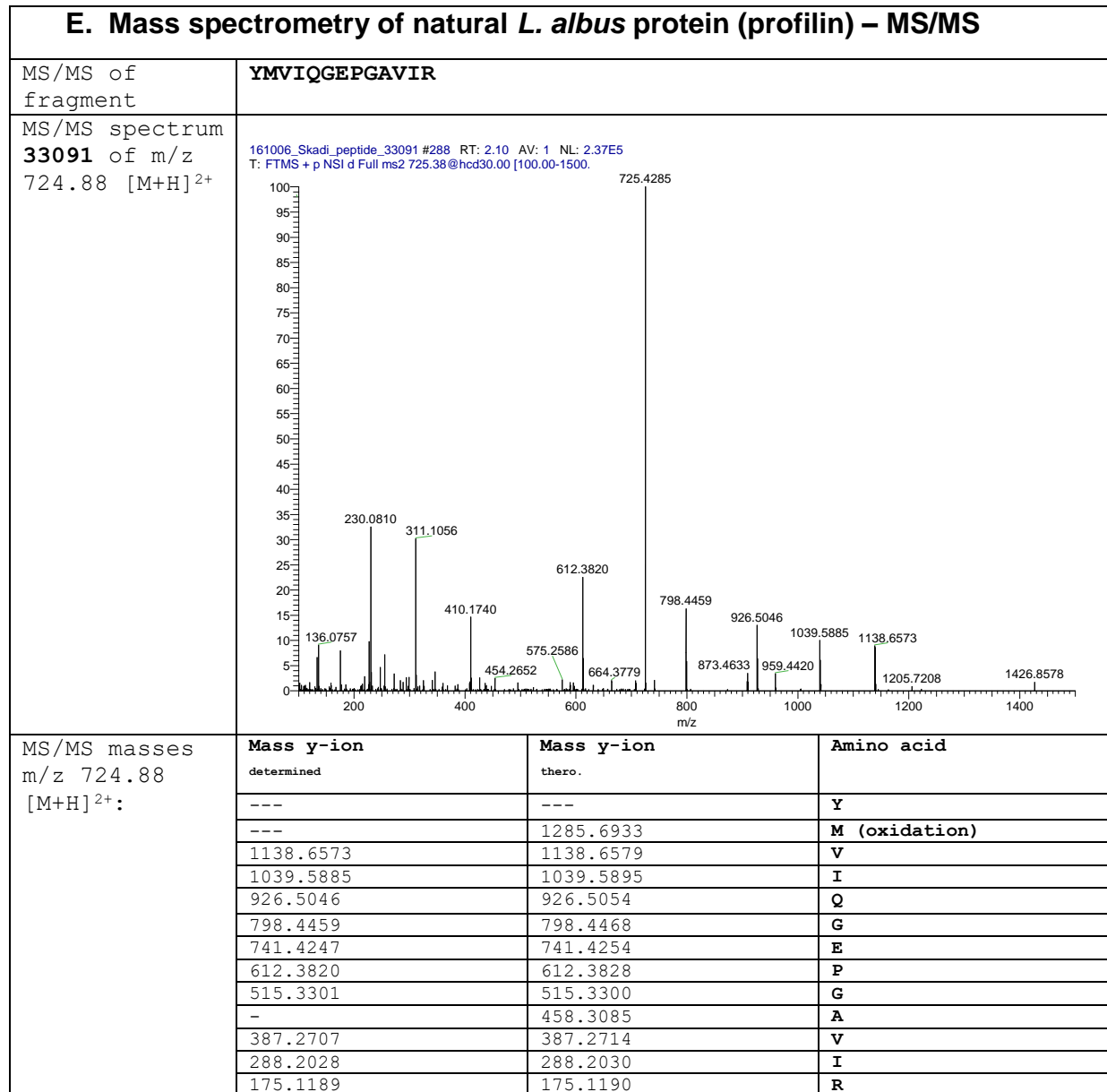




C. Mass spectrometry of natural *L. albus* protein (profilin) – MS/MS

| MS/MS of fragment | YMVIQGEPGA VIR | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|-----------------------|-------------------|------------|-----|-----|----------|-----|-----------|----------------------|-----------|-----------|----------|-----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|--|--|
| MS/MS spectrum 31279 of m/z 724.88 [M+H] ²⁺ | <p>160526_Skadi_peptide_31279 #51 RT: 0.69 AV: 1 NL: 8.97E4 T: FTMS + p NSI d Full ms2 724.88@hcd30.00 [99.67-1495.00]</p>  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| MS/MS masses m/z 724.88 [M+H] ²⁺ : | <table border="1"> <thead> <tr> <th>Mass y-ion determined</th> <th>Mass y-ion thero.</th> <th>Amino acid</th> </tr> </thead> <tbody> <tr><td>---</td><td>---</td><td>Y</td></tr> <tr><td>---</td><td>1285.6933</td><td>M (oxidation)</td></tr> <tr><td>1138.6586</td><td>1138.6579</td><td>V</td></tr> <tr><td>1039.5897</td><td>1039.5895</td><td>I</td></tr> <tr><td>926.5051</td><td>926.5054</td><td>Q</td></tr> <tr><td>798.4467</td><td>798.4468</td><td>G</td></tr> <tr><td>741.4257</td><td>741.4254</td><td>E</td></tr> <tr><td>612.3825</td><td>612.3828</td><td>P</td></tr> <tr><td>515.3312</td><td>515.3300</td><td>G</td></tr> <tr><td>458.3088</td><td>458.3085</td><td>A</td></tr> <tr><td>387.2711</td><td>387.2714</td><td>V</td></tr> <tr><td>288.2032</td><td>288.2030</td><td>I</td></tr> <tr><td>175.1197</td><td>175.1190</td><td>R</td></tr> </tbody> </table> | Mass y-ion determined | Mass y-ion thero. | Amino acid | --- | --- | Y | --- | 1285.6933 | M (oxidation) | 1138.6586 | 1138.6579 | V | 1039.5897 | 1039.5895 | I | 926.5051 | 926.5054 | Q | 798.4467 | 798.4468 | G | 741.4257 | 741.4254 | E | 612.3825 | 612.3828 | P | 515.3312 | 515.3300 | G | 458.3088 | 458.3085 | A | 387.2711 | 387.2714 | V | 288.2032 | 288.2030 | I | 175.1197 | 175.1190 | R | | |
| Mass y-ion determined | Mass y-ion thero. | Amino acid | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| --- | --- | Y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| --- | 1285.6933 | M (oxidation) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1138.6586 | 1138.6579 | V | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1039.5897 | 1039.5895 | I | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 926.5051 | 926.5054 | Q | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 798.4467 | 798.4468 | G | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 741.4257 | 741.4254 | E | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 612.3825 | 612.3828 | P | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 515.3312 | 515.3300 | G | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 458.3088 | 458.3085 | A | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 387.2711 | 387.2714 | V | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 288.2032 | 288.2030 | I | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 175.1197 | 175.1190 | R | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |





As submitted to the WHO/IUIS allergen nomenclature sub-committee, 2016

Figure S 2 A-E. Synopsis of the mass spectrometry analyses of *L. albus* recombinant profilin and the *L. albus* profilin purified from the natural source.

Figure S 3 A-D

A. Database protein sequence (XP_019446786.1)

PREDICTED: non-specific lipid-transfer protein 1-like [Lupinus angustifolius]

NCBI Reference Sequence: XP_019446786.1
[Identical Proteins](#) [FASTA](#) [Graphics](#)

[Go to:](#)

LOCUS XP_019446786 116 aa linear PLN 16-DEC-2016
DEFINITION PREDICTED: non-specific lipid-transfer protein 1-like [Lupinus angustifolius].
ACCESSION XP_019446786
VERSION XP_019446786.1
DBLINK BioProject: [PRJNA356456](#)
DBSOURCE REFSEQ: accession [XM_019591241.1](#)
KEYWORDS RefSeq.
SOURCE Lupinus angustifolius (narrow-leaved blue lupine)
ORGANISM [Lupinus angustifolius](#)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
COMMENT MODEL [REFSEQ](#): This record is predicted by automated computational analysis. This record is derived from a genomic sequence ([NC_032009.1](#)) annotated using gene prediction method: Gnomon.
Also see: [Documentation](#) of NCBI's Annotation Process

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI
Annotation Status :: Full annotation
Annotation Version :: [Lupinus angustifolius Annotation Release 100](#)
Annotation Pipeline :: NCBI eukaryotic genome annotation pipeline
Annotation Software Version :: [7.2](#)
Annotation Method :: Best-placed RefSeq; Gnomon
Features Annotated :: Gene; mRNA; CDS; ncRNA
##Genome-Annotation-Data-END##
COMPLETENESS: full length.

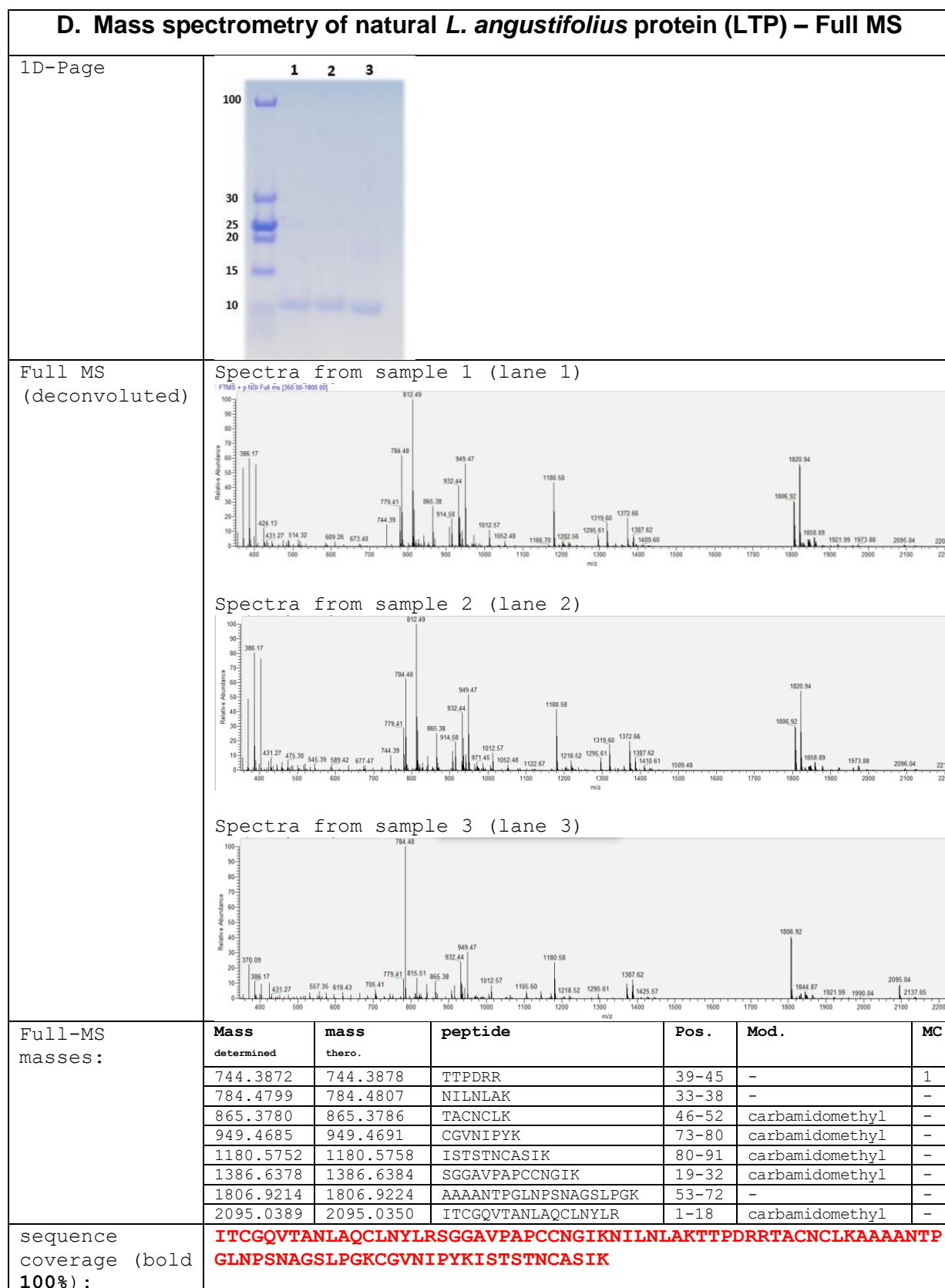
FEATURES Location/Qualifiers
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/cultivar="Tanjil"
/db_xref="taxon:[3871](#)"
/chromosome="LG01"
/tissue_type="whole plant"
/dev_stage="seedling"
/country="Australia: Western Australia"
[Protein](#) 1..116
/product="non-specific lipid-transfer protein 1-like"
/calculated_mol_wt=11589
[CDS](#) 1..116
/gene="LOC109350101"
/coded_by="XM_019591241.1:78..428"
/db_xref="GeneID:[109350101](#)"

ORIGIN
1 magivklaca vlicmvvsa pltkaitcgq vtanlaqcln ylrsggavpa pccngiknil
61 nlakttppdr tacnclkaa antpglnpsn agslpgkcvv nipykistst ncasik
//

>XP_019446786.1 PREDICTED: non-specific lipid-transfer protein 1-like [Lupinus angustifolius]
MAGIVKLACAVLICMVVVSAPLTKAITCGQVTANLAQCLNLYLRSGGAVPAPCCNGIKNILNLAKTTPDRR
TACNCLKAAAANTPGLNPSNAGSLPGKCVNIPYKISTSTNCASIK
Signal peptide, mature sequence

| B. Molecular weight of the mature protein | |
|--|---|
| 1D-Page | <p>SDS-PAGE of <i>L. angustifolius</i> LTP under reducing (R) and non-reducing (N) conditions</p> |
| Deduced from sequence | 9.23 kDa (monoisotopic mass) |
| SDS-PAGE (reduced) | ~11.00 kDa |
| SDS-PAGE (non-reduced) | ~16.00 kDa |

| C. N-terminal sequencing | |
|---------------------------------|--|
| sequence coverage (bold) :13.2% | ITCGQVTANLAQ CLNYLRSGGAVPAPCCNGIKNILNLAKTTPDRRTACNCLKAAAANTP GLNPSNAGSLPGKCGVNIPIYKISTSTNCASIK |



As submitted to the WHO/IUIS allergen nomenclature sub-committee, 25/09/2019.

Figure S 3 A-D. *Lupinus angustifolius* lipid transfer protein (LTP): (A) database protein sequence, (B) molecular weight determination of the mature protein (under reducing and non-reducing conditions), (C) N-terminal sequencing, and (D) mass spectrometry.