Supporting Information

Structural Characterization and Pro-inflammatory Activity of a Thaumatin-like Protein from the Pulp Tissues of *Litchi chinensis*

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| Protein IDs | Fasta headers | Peptides | Unique peptides | Sequence coverage [%] | Mol. weight [kDa] | Sequence length | Score | Intensity | percent |
|--------------------------|---|----------|--------------------|-----------------------------|----------------------|--------------------|----------|-----------|----------|
| F8U3U5 | tr F8U3U5 F8U3U5_LITCN Thaumatin-like protein OS=Litchi chinensis OX=151069 GN=TLP PE=2 SV=1 | 12 | 12 | 53.8 | 24.189 | 223 | 323.31 | 1.5E+10 | 72.04815 |
| A0A346D9Z3 | tr A0A346D9Z3 A0A346D9Z3_LITCN Glyceraldehyde-3-phosphate dehydrogenase OS=Litchi chinensis OX=151069 PE=2 SV=1 | 9 | 3 | 31.8 | 36.842 | 340 | 3.5699 | 1.32E+09 | 6.327364 |
| A0A1S5VZG7 | tr A0A1S5VZG7 A0A1S5VZG7_LITCN Calmodulin OS=Litchi chinensis OX=151069 GN=CaM1 PE=2 SV=1 | 5 | 5 | 51 | 16.848 | 149 | 323.31 | 7.58E+08 | 3.645992 |
| Q206Y8 | tr Q206Y8 Q206Y8_LITCN Peroxidase (Fragment) OS=Litchi chinensis OX=151069 GN=POD PE=2 SV=1 | 5 | 3 | 23.5 | 25.09 | 234 | 65.006 | 3.98E+08 | 1.912449 |
| A0A1S5VZH2 | tr A0A1S5VZH2 A0A1S5VZH2_LITCN Cysteine protease OS=Litchi chinensis OX=151069 GN=CP1 PE=2 SV=1 | 6 | 6 | 15.3 | 52.021 | 471 | 196.25 | 3.57E+08 | 1.717139 |
| L0CKN6;G0YC A2 | tr L0CKN6 L0CKN6_LITCN Superoxide dismutase (Fragment) OS=Litchi chinensis OX=151069 GN=Mn-SOD PE=3 SV=1;tr G0YCA2 G0YCA2_LITCN Superoxide dismutase (Fragment) OS=Litchi chinensis OX=151069 PE=2 SV=1 | 3 | 3 | 15.4 | 24.49 | 221 | 82.934 | 3.38E+08 | 1.628191 |
| H2E0Q9;H9TE U3;H9TEU4 | tr H2E0Q9 H2E0Q9_LITCN Copper/zinc superoxide dismutase (Fragment) OS=Litchi chinensis OX=151069 PE=2 SV=1;tr H9TEU3 H9TEU3_LITCN Superoxide dismutase [Cu-Zn] OS=Litchi chinensis OX=151069 PE=2 SV=1;tr H9TEU4 H9TEU4_LITCN Superoxide dismutase [Cu-Zn] OS=Li | 3 | 3 | 25.3 | 15.767 | 154 | 223.59 | 3.34E+08 | 1.607025 |
| A0A1Z1GA30 | tr A0A1Z1GA30 A0A1Z1GA30_LITCN 50S ribosomal protein L33, chloroplastic OS=Litchi chinensis OX=151069 GN=rpl33 PE=3 SV=1 | 2 | 2 | 32.4 | 7.9071 | 68 | 0.013279 | 3.32E+08 | 1.595239 |

Table S1. Information of various protein identified in LPCE.

| A0A2P9JY09 | tr A0A2P9JY09 A0A2P9JY09_LITCN Sucrose-phosphate synthase 3 OS=Litchi chinensis OX=151069 GN=SPS3 PE=2 SV=1 | 3 | 3 | 5.1 | 120.04 | 1069 | 0.33133 | 2.31E+08 | 1.108888 |
|-------------------|--|----|---|------|--------|------|----------|----------|----------|
| G3FSZ8 | tr G3FSZ8 G3FSZ8_LITCN Glyceraldehyde-3-phosphate dehydrogenase OS=Litchi chinensis OX=151069 GN=GAPDH PE=2 SV=1 | 10 | 2 | 34.8 | 36.612 | 336 | 22.802 | 2.04E+08 | 0.98314 |
| A0MMD6 | tr A0MMD6 A0MMD6_LITCN Xyloglucan endotransglucosylase/hydrolase OS=Litchi chinensis OX=151069 GN=XET1 PE=2 SV=1 | 3 | 3 | 10.2 | 32.778 | 294 | 20.071 | 1.56E+08 | 0.751269 |
| B0FYI8 | tr B0FY18 B0FY18_LITCN Superoxide dismutase [Cu-Zn] OS=Litchi chinensis OX=151069 PE=2 SV=1 | 3 | 3 | 30.3 | 15.285 | 152 | 5.1335 | 1.53E+08 | 0.735154 |
| A0A023GU60 | tr A0A023GU60 A0A023GU60_LITCN Glutathione reductase OS=Litchi chinensis OX=151069 PE=2 SV=1 | 5 | 5 | 14.1 | 53.414 | 497 | 54.848 | 1.49E+08 | 0.716344 |
| S5SXA4 | tr S5SXA4 S5SXA4_LITCN TFL1-1 OS=Litchi chinensis OX=151069 PE=2 SV=1 | 3 | 3 | 30.6 | 19.381 | 173 | 0.095179 | 1.33E+08 | 0.639856 |
| F8V3J0 | tr F8V3J0 F8V3J0_LITCN Phospholipase D OS=Litchi chinensis OX=151069 GN=PLD delta PE=2 SV=1 | 2 | 2 | 5.1 | 98.323 | 865 | 2.18E-06 | 1.03E+08 | 0.49347 |
| A0A1S5VZG0 | tr A0A1S5VZG0 A0A1S5VZG0_LITCN NAC transcription factor 13 OS=Litchi chinensis OX=151069 GN=NAC13 PE=2 SV=1 | 2 | 2 | 7.4 | 41.154 | 366 | 0.10176 | 85484000 | 0.411228 |
| B7UCP4 | tr B7UCP4 B7UCP4_LITCN Peroxidase OS=Litchi chinensis OX=151069 PE=2 SV=1 | 3 | 3 | 13.1 | 39.313 | 358 | 1.1911 | 71848000 | 0.345631 |
| G8FRT0;Q0PW W8 | tr G8FRT0 G8FRT0_LITCN 3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Litchi chinensis OX=151069 GN=HMG2 PE=2 SV=1;tr Q0PWW8 Q0PWW8_LITCN 3-hydroxy-3-methylglutaryl-coenzyme A reductase (Fragment) OS=Litchi chinensis OX=151069 GN=hmg2 PE=2 SV=1 | 2 | 2 | 3.7 | 60.665 | 568 | 0.079528 | 60440000 | 0.290752 |

| B3V945 | tr B3V945 B3V945_LITCN Pectin acetylesterase OS=Litchi chinensis OX=151069 PE=2 SV=1 | 4 | 4 | 23.8 | 43.889 | 399 | 11.686 | 59494000 | 0.286201 |
|--|---|---|---|------|--------|-----|----------|----------|----------|
| B6E500 | tr B6E500 B6E500_LITCN Peroxidase OS=Litchi chinensis OX=151069 GN=POD5 PE=2 SV=2 | 3 | 3 | 11.2 | 36.068 | 329 | 9.5567 | 59187000 | 0.284724 |
| A0A248XBI5;A 0A248XBG7;A 0A248XBI2 | tr A0A248XBI5 A0A248XBI5_LITCN Beta-fructofuranosidase, insoluble isoenzyme CWINV4 OS=Litchi chinensis OX=151069 PE=2 SV=1;tr A0A248XBG7 A0A248XBG7_LITCN Beta-fructofuranosidase, insoluble isoenzyme CWINV1 OS=Litchi chinensis OX=151069 PE=2 SV=1;tr A0A248X | 2 | 2 | 7.9 | 62.661 | 558 | 0.045502 | 57050000 | 0.274444 |
| Q1HB06 | tr Q1HB06 Q1HB06_LITCN 3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Litchi chinensis OX=151069 GN=HMG1 PE=2 SV=2 | 2 | 2 | 7.3 | 60.241 | 562 | 0.15474 | 55678000 | 0.267844 |
| A0A1L5YQR0 | tr A0A1L5YQR0 A0A1L5YQR0_LITCN BHLH1 OS=Litchi chinensis OX=151069 GN=bHLH1 PE=2 SV=1 | 2 | 2 | 2.6 | 73.812 | 657 | 9.002 | 52341000 | 0.251791 |
| A0A1Z1GA21 | tr A0A1Z1GA21 A0A1Z1GA21_LITCN Photosystem I assembly protein Ycf4 OS=Litchi chinensis OX=151069 GN=ycf4 PE=3 SV=1 | 2 | 2 | 12.5 | 21.525 | 184 | 0.67487 | 50186000 | 0.241424 |
| A0A126X326 | tr A0A126X326 A0A126X326_LITCN Putative LOV domain-containing protein OS=Litchi chinensis OX=151069 PE=2 SV=1 | 3 | 3 | 4.6 | 75.208 | 669 | 0.016664 | 44088000 | 0.212089 |
| A4GWU6 | tr A4GWU6 A4GWU6_LITCN Expansin OS=Litchi chinensis OX=151069 GN=Exp2 PE=2 SV=1 | 2 | 2 | 8.6 | 27.677 | 256 | 0.13358 | 41469000 | 0.19949 |
| F2XI26;E7E819 ;F2XI27 | tr F2XI26 F2XI26_LITCN Actin OS=Litchi chinensis OX=151069 GN=ACT4 PE=2 SV=1;tr E7E819 E7E819_LITCN Actin OS=Litchi chinensis OX=151069 GN=ACT PE=2 SV=1;tr F2XI27 F2XI27_LITCN Actin OS=Litchi chinensis OX=151069 GN=ACT7 PE=2 SV=1 | 3 | 3 | 9.3 | 41.725 | 377 | 57.705 | 33795000 | 0.162574 |

| E3W5V8 | tr E3W5V8 E3W5V8_LITCN Flavanone 3-hydroxylase OS=Litchi chinensis OX=151069 GN=F3H PE=2 SV=1 | 2 | 2 | 7.7 | 40.927 | 363 | 0.20491 | 31470000 | 0.151389 |
|------------|--|---|---|------|--------|------|---------|----------|----------|
| A0A023GU61 | tr A0A023GU61 A0A023GU61_LITCN Lipoxygenase OS=Litchi chinensis OX=151069 PE=2 SV=1 | 2 | 2 | 6.2 | 98.907 | 872 | 0.12116 | 26932000 | 0.129559 |
| W8FS36 | tr W8FS36 W8FS36_LITCN Glycosyltransferase OS=Litchi chinensis OX=151069 PE=2 SV=1 | 2 | 2 | 6.1 | 49.453 | 446 | 0.9359 | 22770000 | 0.109537 |
| A0A1Z1GA65 | tr A0A1Z1GA65 A0A1Z1GA65_LITCN Protein Ycf2 OS=Litchi chinensis OX=151069 GN=ycf2 PE=3 SV=1 | 3 | 3 | 2.9 | 268.33 | 2286 | 0.47818 | 22230000 | 0.106939 |
| A0A1L5YQR7 | tr A0A1L5YQR7 A0A1L5YQR7_LITCN BHLH2 OS=Litchi chinensis OX=151069 GN=bHLH2 PE=2 SV=1 | 2 | 2 | 2.9 | 77.786 | 700 | 1.0913 | 21765000 | 0.104702 |
| A0A023GU59 | tr A0A023GU59 A0A023GU59_LITCN Polyphenol oxidase OS=Litchi chinensis OX=151069 PE=2 SV=1 | 2 | 2 | 10.7 | 67.036 | 599 | 0.13578 | 21518000 | 0.103514 |
| W8FRI3 | tr W8FRI3 W8FRI3_LITCN UDP-glycosyltransferase 3 OS=Litchi chinensis OX=151069 PE=2 SV=1 | 2 | 2 | 3.5 | 50.636 | 458 | 0.82307 | 12034000 | 0.057891 |
| A0A1Z1GA07 | tr A0A1Z1GA07 A0A1Z1GA07_LITCN ATP synthase subunit alpha, chloroplastic OS=Litchi chinensis OX=151069 GN=atpA PE=3 SV=1 | 2 | 2 | 4.7 | 55.572 | 507 | 0.14185 | 7838800 | 0.037709 |
| A0A1Z1GA11 | tr A0A1Z1GA11 A0A1Z1GA11_LITCN DNA-directed RNA polymerase subunit beta OS=Litchi chinensis OX=151069 GN=rpoB PE=3 SV=1 | 2 | 2 | 1.9 | 120.77 | 1070 | 1.9692 | 5066100 | 0.024371 |
| A0A2R4K351 | tr A0A2R4K351 A0A2R4K351_LITCN Squamosa promoter binding-like protein OS=Litchi chinensis OX=151069 GN=SPL-7 PE=2 SV=1 | 3 | 3 | 5.6 | 118.4 | 1062 | 1.2421 | 4446300 | 0.021389 |

| F1DG64 | tr F1DG64 F1DG64_LITCN Phospholipase D OS=Litchi chinensis OX=151069 GN=PLDbeta PE=2 SV=1 | 2 | 2 | 4.9 | 95.659 | 851 | 0.11124 | 3146100 | 0.015135 |
|--------|--|---|---|-----|--------|-----|---------|---------|----------|
|--------|--|---|---|-----|--------|-----|---------|---------|----------|

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|---------------------------------------|---------------------------|---------------------------------------|-------------------------|
| I able SZ. Information of the mRINA | genomic sequences of TTP | ' genes identified in <i>Litch</i> i | <i>cheninse</i> genome. |
| I wole Sat Information of the mite of | genomie sequences of f El | Series racintinea in Brien | ententitise genomet |

| Protein names | mRNA genomic sequences |
|----------------------|--|
| | ATGAAGCTCTTCAAAATCCTCCTTTCCTTTTTTGCCATTGCACTCTCCACCACCTTGGTTTATGCAGCCAAATTTGACATCACCAACAAC |
| | TGTCCTGAGACTATTTGGGCAGCTGCCGTGCCTGGTGGTGGCAAGAAACTAGACAAAGGCGAAACATGGACCATAACTGCCGCCCCAG |
| ΤΙΡ | GTACCAAAGAAGCCAGAATTTGGGGACGTACCAAGTGCAATTTCGATGCCAGCGGGAAAGGCAAGTGTGAGACAGGTGACTGCAACG |
| (GenBank: | GCGTCCTCGAGTGCCAAGGCTATGGATCCCCTCCCAATACCTTGGCTGAGTACGCGTTGCAGCAGTTCAACAACATGGACTTCATTGAC |
| (OeliDalik, EP77700) | ATGTCCAACATTGAT <u>GGTTTTAATGTCCCAATGGAGTTCAGCTC</u> CACCTCTCCTGGATGCAACCGTGTGATCAAATGCACGGGTGAC |
| ALD///09.1) | TTGGTAGGGCAGTGCCCTAATGAGCTCAAAGTACCAGGAGGATGTCAAGGGCCATGCTGGGTGTTCAAGACCAACGAGCACTGTTGCA |
| | ATTCTGGTAGTTGTGGACCTACAGATTTCTCCAGGTTTTTCAAAGATAGGTGCCCGGATGTTTATAGTTATCCAAAAGATGATGCAACA |
| | AGTGTTTTTACTTGCCCTAGTGGAACAGACTATAAGGTTGTCTTTTGCCCCTGA |
| | ATGAAGCTCTTCAAAATCCTCCTTTCCTTTTTTGCCATTGCACTCTCCACCACCTTGGTTTATGCAGCCAAATTTGACATCACCAACAAC |
| | TGTCCTGAGACTATTTGGGCAGCTGCCGTGCCTGGTGGTGGCAAGAAACTAGACAAAGGCGAAACATGGACCATAACTGCCGCCCCAG |
| | GTACCAAAGAAGCCAGAATTTGGGGACGTACCAAGTGCAATTTCGATGCCAGCGGGAAAGGCAAGTGTGAGACAGGTGACTGCAACG |
| LPP | GCGTCCTCGAGTGCCAAGGCTATGGATCCCCTCCCAATACCTTGGCTGAGTACGCGTTGCAGCAGTTCAACAACATGGACTTCATTGAC |
| | ATGTCCAACATTGAT <u>GGTTTTAATGTCCC(A/G)ATGGAGTTCAGCTC</u> CACCTCTCCTGGATGCAACCGTGTGATCAAATGCACGGGTG |
| | ACTTGGTAGGGCAGTGCCCTAATGAGCTCAAAGTACCAGGAGGATGTCAAGGGCCATGCTGGGTGTTCAAGACCAACGAGCACTGTTG |
| | CAATTCTGGTAGTTGTGGACCTACAGATTTCTCCAGGTTTTTCAAAGATAGGTGCCCGGATGTTTATAGTTATCCAAAAGATGATGCAA |
| | CAAGTGTTTTTACTTGCCCTAGTGGAACAGACTATAAGGTTGTCTTTTGCCCCTGA |



Figure S1. Total ion chromatogram for identification of LPCE.



Figure S2. Ramachandran plot and statistics of the LcTLP three dimension structure.