

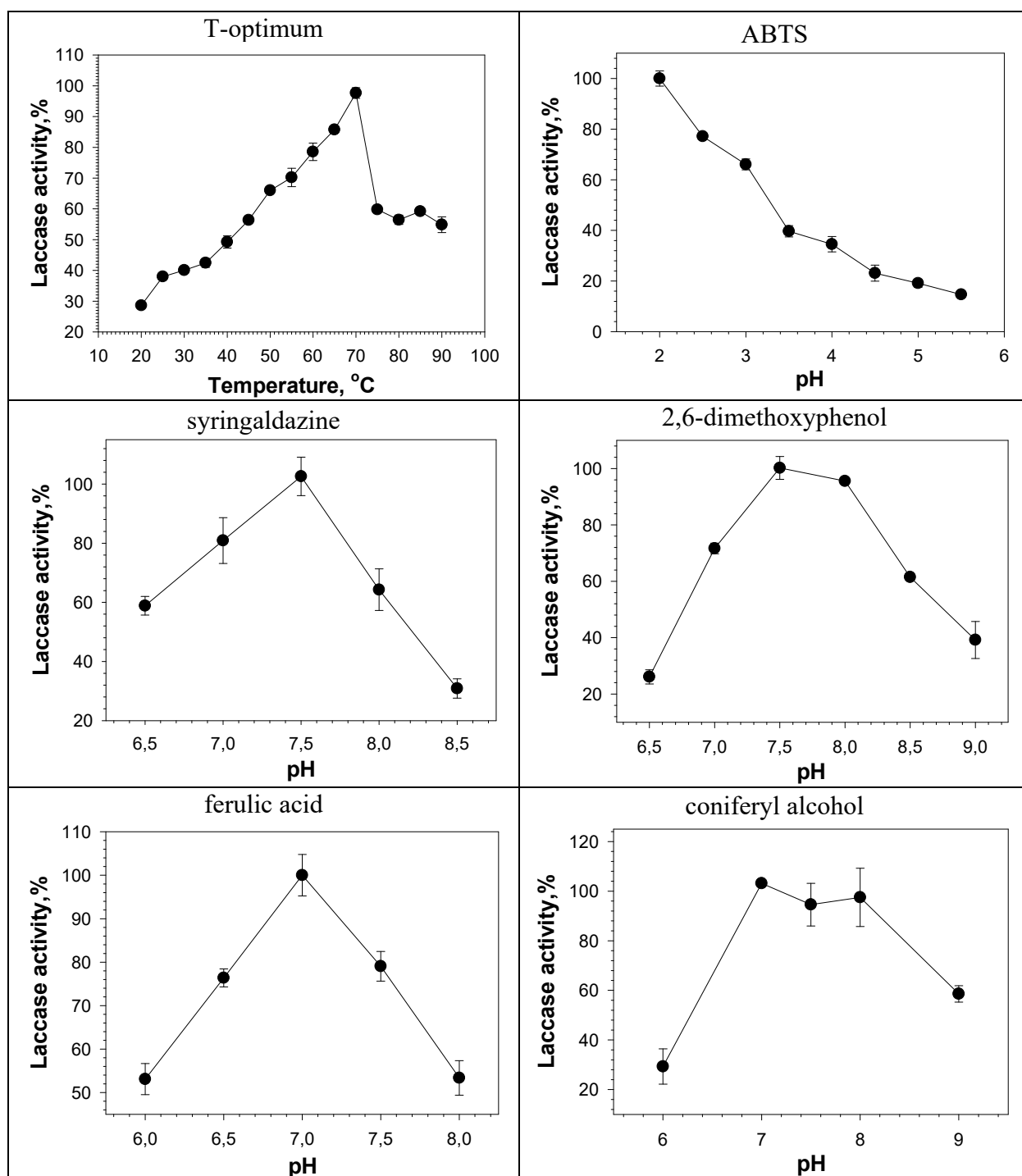
Supplementary material, Table 1. Primers used in the work

| Primers | Sequence | Annealing temperature, °C |
|-----------------------|---------------------------|---------------------------|
| Lac2FOR | GGIACIWIIITGGTAYCAYWSICA | 49 |
| Lac3REV | CCRTGIWKRTGIAWIGGRTGIGG | 49 |
| F3561-20d-SON1-GSP1-F | GATGGCAATGTCACCTTC | 63 |
| F3561-20d-SON1-GSP2-F | CGTCACGTGTTTGCAGTC | 55 |
| F3561-20d-SON2-GSP1-R | TCTTGCATGAACGGCAG | 63 |
| F3561-20d-SON2-GSP2-R | GCATGAAACCAGTCGGTC | 65 |
| F3561-20d-SON3-GSP1-R | GGCCACTTGAGGTCCATATCGGTGT | 60 |
| F3561-20d-SON3-GSP2-R | GTCATCGTACCAGCAGTCTCTTGAT | 63 |
| F3561-20d-Lcc-F | ATGGTCTTTTCAATCCCGAGGGC | 60 |
| F3561-20d-Lcc-R | CTAGCGACGACGCAGACCAGA | 60 |

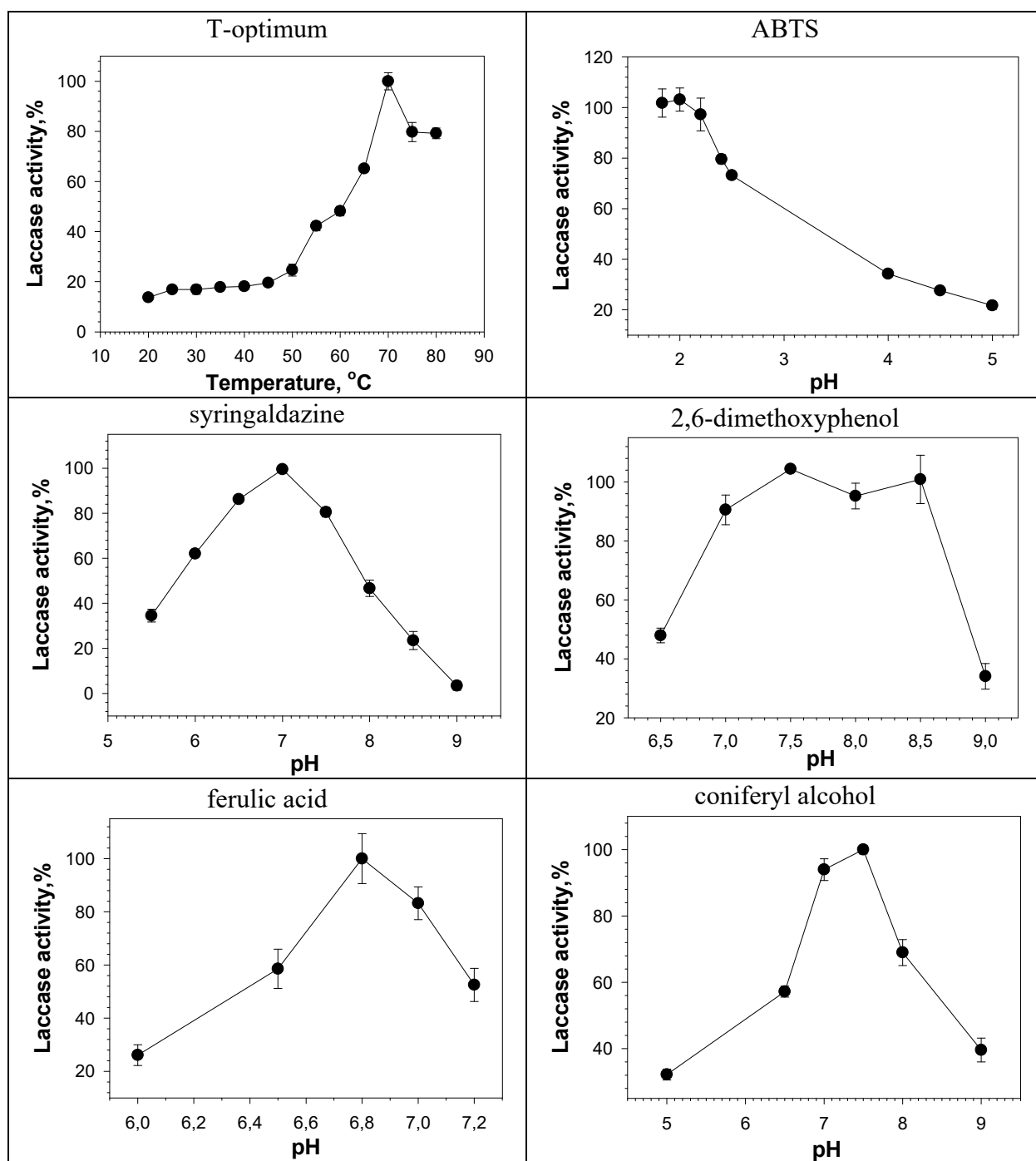
Supplementary material, Table 2. The scheme of purification of the *C. geniculata* VKM F-3561 oxidases (the activity was measured in the reaction with ABTS at pH5.0)

| Purification step | Total protein, mg | Total activity, U | Specific activity, U/mg | Purification, fold | Yield, % |
|--------------------------|--------------------------|--------------------------|--------------------------------|---------------------------|-----------------|
| <i>Culture liquid</i> | 380.0 | 184.0 | 0.3 | 1.0 | 100.0 |
| <i>DE-52</i> | | | | | |
| oxidase I | 45.0 | 27.0 | 0.6 | 2.0 | 14.7 |
| oxidase II | 73.0 | 109.5 | 1.5 | 5.0 | 59.5 |
| <i>Q-Sepharose</i> | | | | | |
| oxidase I | 10.3 | 21.6 | 2.1 | 7.0 | 11.7 |
| oxidase II | 18.1 | 103.2 | 5.7 | 19.0 | 56.1 |
| <i>Resource Q</i> | | | | | |
| oxidase I | - | - | - | - | - |
| oxidase II | 10.7 | 95.2 | 8.9 | 29.7 | 51.7 |
| <i>Superdex 200</i> | | | | | |
| oxidase I | 1.3 | 20.0 | 15.4 | 51.3 | 10.9 |
| oxidase II | 3.7 | 84.7 | 22.9 | 76.3 | 46.0 |

Supplementary material, Figure 1. Dependence of an activity of the purified laccase-like oxidase I of *C. geniculata* VKM F-3561 on temperature (in reaction with ABTS as a substrate) and pH (in the reaction with ABTS, syringaldazine, 2,6-dimethoxyphenol, ferulic acid, and coniferyl alcohol). The error bars represent the standard deviation.



Supplementary material, Figure 2. Dependence of an activity of the purified laccase-like oxidase II of *C. geniculata* VKM F-3561 on temperature (in the reaction with ABTS as a substrate) and pH (in reaction with ABTS, syringaldazine, 2,6-dimethoxyphenol, ferulic acid, and coniferyl alcohol). The error bars represent the standard deviation.



1 ATGGTCTTTTCAATCCCGAGGGCGGTACCGCACTGGGGCTTCTCTGCCTACTGTACCTCTGTTGCCCTATCT 75
M V F S I P R A V T A L G L L L P T V T S V A L S
76 TATGAAGGCCGCGCACCCATAACACCTCCCGTCCCTTGGAAAGATACTGGACTCTTCTCTGGACACGTGAGCCGA 150
Y E G R A P I T P P V P W K D T G L F S G H V S R
151 TCAGGATATCCAACCTTTTGCATAATGGTCCACAATCAAGAGACTGCTGGTACGATGACTTCAACATCGACACC 225
S G Y P T F C N N G P Q S R D C W Y D D F N I D T
226 GATATGGACCTCAAGTGGCCCGACACTGGCAATACAGTCAAGTACCACCTGACTATCACAACTCTACCGGTGCT 300
D M D L K W P D T G N T V K Y H L T I T N S T G A
301 CCCGATGGTTTCGAGAGACCAATATCCTTGATCAACGGTCAATACCCAGGACCAGTAAAGTGTATACAAACGATA 375
P D G F E R P I S L I N G Q Y P G P
376 **CCGATAGTTCTTCTCTAATGAAATGTAGACAATACTGGCTGATTGGGGAGACGATTTGGAAATCACTGTTACCAA** 450
интрон T I L A D W G D D L E I T V T N
451 CGGTTTGGAGAACAACGGAACAGGTATTTCATTGGCATGGATTGCGACAACCTCGGATCAAACGAGCAAGATGGAGT 525
G L E N N G T G I H W H G L R Q L G S N E Q D G V
526 GAACGGCATCACTGAATGCCCAATCGCGCCCGGCGACTCCAAAGTCTACAAGTTCAAGGCAACACAATACGGCAC 600
N G I T E C P I A P G D S K V Y K F K A T Q Y G T
601 CTCTGTAAGTATCAGAAATTGTCTGACATGTTGAATGAAGACGACTGACCGTCACAGTGGTATCACACGCACTAC 675
S интрон W Y H T H Y
676 TCCGTACAGTATGGCGACGGTATTGTAGGACCTTTAATCATCCGAGGACCTGCAACAGCAAACACTAGATATTGAT 750
S V Q Y G D G I V G P L I I R G P A T A N Y D I D
751 CTCGGCGCCCTTCCAATGACCGACTGGTTTTCATGCGACCACTTTCACTGTGAACGCTGCTGCCGTTTCATGCAAGA 825
L G A L P M T D W F H A T T F T V N A A A V H A R
826 GGTCTCCAACCTCGGACAACGTTCTGATCAACGGCTCCATGACTTCGTCTTTTGGTGGAAATACGCTGAAACA 900
G P P T A D N V L I N G S M T S S F G G K Y A E T
901 ATTCTAACCCCTGGAAAGGCCCACTTGTGCGCCTGATGAACGTTGGCATCAACAATATCTCCATGTCGGTCTC 975
I L T P G K A H L L R L M N V G I N N Y L H V G L
976 GATGGACACAAGTTCAGGTCAATTCGCGGACTTTACCCCATCGAACCATTCTACACCGACAACCTGGTTCTC 1050
D G H K F Q V I S A D F T P I E P F Y T D N L V L
1051 GCAGTCGGTCAACGCTATGAAGTCATCATTAAATGCAACCGAGGCTGTTGGTAACACTGCGCTTCGCGTGGTACT 1125
A V G Q R Y E V I I N A T E A V G N Y W L R V G T
1126 GGTGGTTCTTGTGATGGTCCCAACGCCAACGCGGCAAACATCAGGAGTATCTTCCGATACGCTGGCGCCCTGCT 1200
G G S C D G P N A N A A N I R S I F R Y A G A P A
1201 ATGGAGCCCAACACGACTGGTACCCTTCCATCGGGCTGCTACGATGAGACTGTTGTGCCCCACGCCAAACAACT 1275
M E P N T T G T L P S G C Y D E T V V P H A K T T
1276 GTTCCTCAGGACATGCCTGAATTGCTCAGTGTGGGCTTCAACCCCAACTGGACCAGCGACGTGACGCAAAACAG 1350
V P Q D M P E L L S V G F N P N W T S D V T Q N Q
1351 GGCTTGGTTCAATGGCTTGTCAACGCGACCCCTATGAATGTCGACCTTGAAGTCCCCACACTACAGTCAGTATTG 1425
G L V Q W L V N G D P M N V D L E V P T L Q S V L
1426 GATGGCAATGTCACCTTCGGAACAACCGTCACGTGTTTGCAGTCGACGAGACAAACAAGGTATGTCATCTCTTG 1500
D G N V T F G N N R H V F A V D E T N K
1501 **CGCTCGATATCATTCTTCCGTGACTAACACAACACTCCAGTGGCAATACTGGGTCAATCAACAAAACAGCTCCAA** 1575
интрон W Q Y W V I Q Q N S S N
1576 CCCAGCCCTTCCCCACCCCATCCACCTTCACGGCCACGACTTCTACGTCTCGCCGACGAAGAAAACGAGTCTG 1650
P A L P H P I H L H G H D F Y V L A Q Q E N A V W
1651 GAACGGCGACATTTCCACCTTGAAGACCGACAACCCCATCCGTGCGATACAGCCGACCTTCCCGCCAACGGCTA 1725
N G D I S T L K T D N P I R R D T A D L P A N G Y
1726 CCTGGTCCTTGCTTTCGAGTCTGACAACCCAGGTGCATGGCTCATGCACTGCCACATCCCTTCCACGTTGCCGC 1800
L V L A F E S D N P G A W L M H C H I P F H V A A
1801 TGGTCTTGGCGTCCAGTTCCTGGAACGCCAGTCCGAAATCAAGGCCAGGATGGATTTGCAGAGATGAAGAGGAC 1875
G L G V Q F L E R Q S E I K A Q D G F A E M K R T
1876 CTGTGCAAACTGGAAGTCTTGGCGCTACCAGTTCATCCCAATGGTATCTTATTCCTGGTGACTCTGGTCTGCG 1950
C A N W K S W R Y Q F H P N G I L F P G D S G L R
1951 TCGTCGCTAG 1960
R R *

Supplementary material, Figure 3. Nucleotide sequence of the laccase gene and translated amino acid sequence of the laccase from the fungus *C. geniculata* VKM F-3561. The intron is shown in bold. The putative signal peptide is shaded, possible N-glycosylation sites are in rectangles. The conservative amino acid sequences responsible for the binding of copper ions in the active site of the enzyme are underlined.