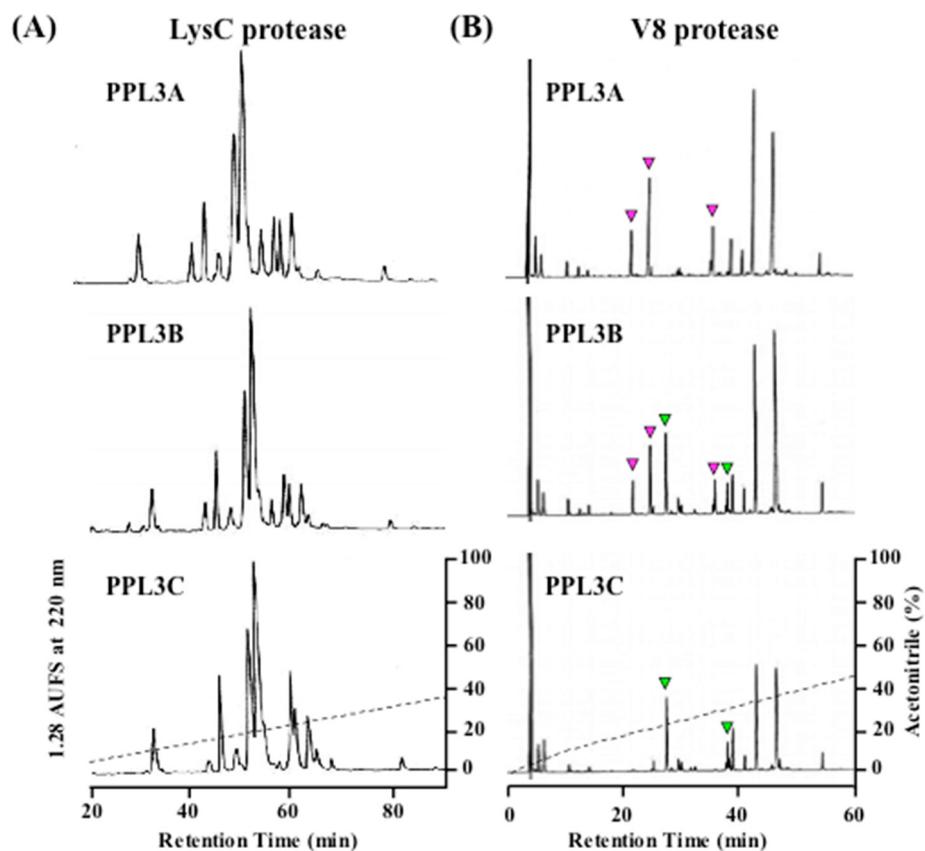
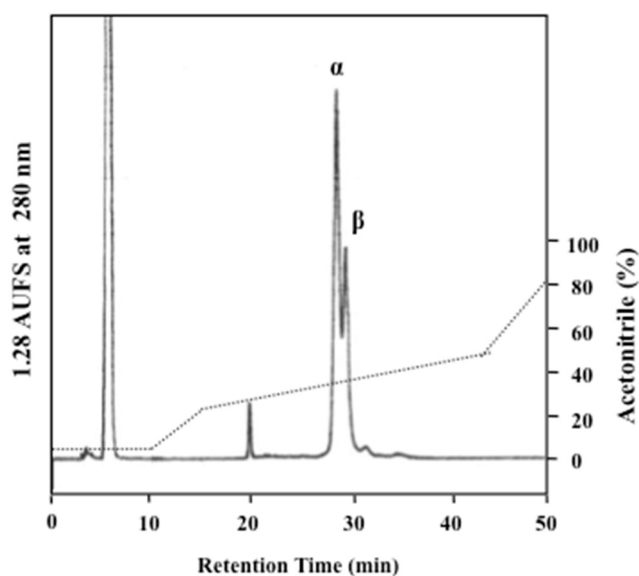




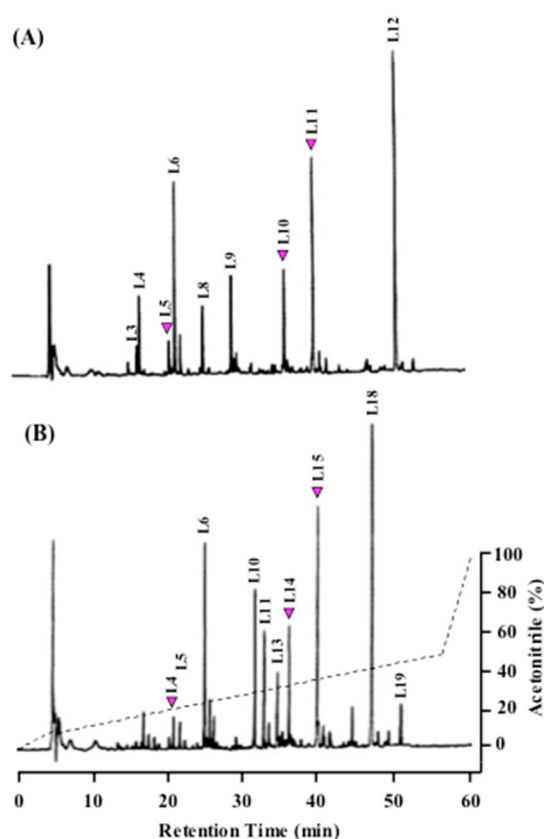
Supplementary Figure S1. Peptide maps of CAM-PPL3A($\alpha+\alpha$), 3B($\alpha+\beta$), and 3C($\beta+\beta$) digested by *Achromobacter* protease I (A) and *Staphylococcus aureus* V8 protease (B). Peptides were separated by reversed-phase HPLC on COSMOSIL® Protein-R column ($\varnothing$ 4.6 $\times$ 250 mm) using a linear gradient of acetonitrile in 0.1% trifluoroacetic acid. Common peaks between α and β subunits were marked by magenta and green-colored arrow heads, respectively.

PPL3 α ATGATTTCTGGACTATATCTGGTAATTGCAGTGATTCTACCAAAATGCAGTGTATCACAG 60
 M I S G L Y L V I A V I L P N A V L S Q
 PPL3 β ATGATTTCTGGACTATATCTGGTGTGGCAGTGATTCTACCAAAATGCAGTGTATCACAG
 M I S G L Y L V V A V I L P N A V L S Q
 Signal sequence L E
 PPL3 α GTTGCCCTCTGAATATCTTGGAGGACCAGGAGGCGACGCTTTTGACGATAAAGCAGTAGCA 120
 V A S E Y L G G P G G D A F D D K A V A V14
 PPL3 β GTTGCCCTCTGAATATCTTGGAGGACCAGGAGGCGATGCTTTTGATGATAAAGCATTAGCA L10
 V A S E Y L G G P G G D A F D D K A L A V16
 I L11
 PPL3 α CAAAATGGTGACATAACAAGAATTGAGATGCAATGTACAGATGTTGCAACCTATATCAAA 180
 Q N G D I T R I E M Q C T D V A T Y I K V19
 PPL3 β CAAAATGGTGACATAACAAGAATCGAGATGCAATGTACAGATGTTGCTACCTATATCAAA 180
 Q N G D I T R I E M Q C T D V A T Y I K V19
 PPL3 α CTTCGTATGGGAAAGTAGATAGCAGGCAATGGGGATGGGCAAATGAGAATTGTATACAG 240
 L R Y G K V D S R Q W G M A N E N C I Q V7
 PPL3 β CTTCGTATGGGAAAGTAGATAGCAGGCAATGGGGATGGGCAAATGAGAATTGTATACAG V8
 L R Y G K V D S R Q W G M A N E N C I Q V10
 PPL3 α TGGTCAAAAAGGGAGAGAAAAGTTGTCCACGAGTTGAGTAGTGGTGAATACATCACAAGC 300
 W S K K G E K V V H E L S S G E Y I T S
 PPL3 β TGGTCAAAAAGGGAGAGAAAAGTTGTCCACGAGTTGAGTAGTGGTGAATACATCACAAGC
 W S K K G V K V V H E L S S G E Y I T S
 PPL3 α GCTATTGTACATATGGTAAATATGTACAATCCATTACTTTCAAGACCAACAAAAGAACA 360
 A I V T Y G K Y V Q S I T F K T N K R T V21
 PPL3 β GCTATTGTACATATGGTAAATATGTACAATCCATTACTTTCAAGACCAACAAAAGAACA V21
 A I V T Y G K Y V Q S I T F K T N K R T L4
 PPL3 α CTTCCAAGATGCGGAACCACTGCCACTGAAAAATCCGTCACAGTTTAAATCCTGGAGGC 420
 L P R C G T S A T E K S V T V L I P G G
 PPL3 β CTTCCAAGATGCGGAACCACTGCCACTGAAAAATCCGTCACAGTTTAAATCCTGGAGGC
 L P R C G T S A T E K S V T V L I P G G
 PPL3 α CTGAAATACATTCTGGAAGATGGGGTTGTAGAATTGATGGATTGCGATTTCATGCTAAA 480
 L K Y I S G R M G C R I D G L R F H A K V20
 PPL3 β CTGAAATACATTCTGGAAGATGGGGTTGTAGAATTGATGGATTGCGATTTCATGCTAAA V20
 L K Y I S G R M G C R I D G L R F H A K L8
 TGTTGA 486
 PPL3 α C *
 PPL3 β TGTTGA C *

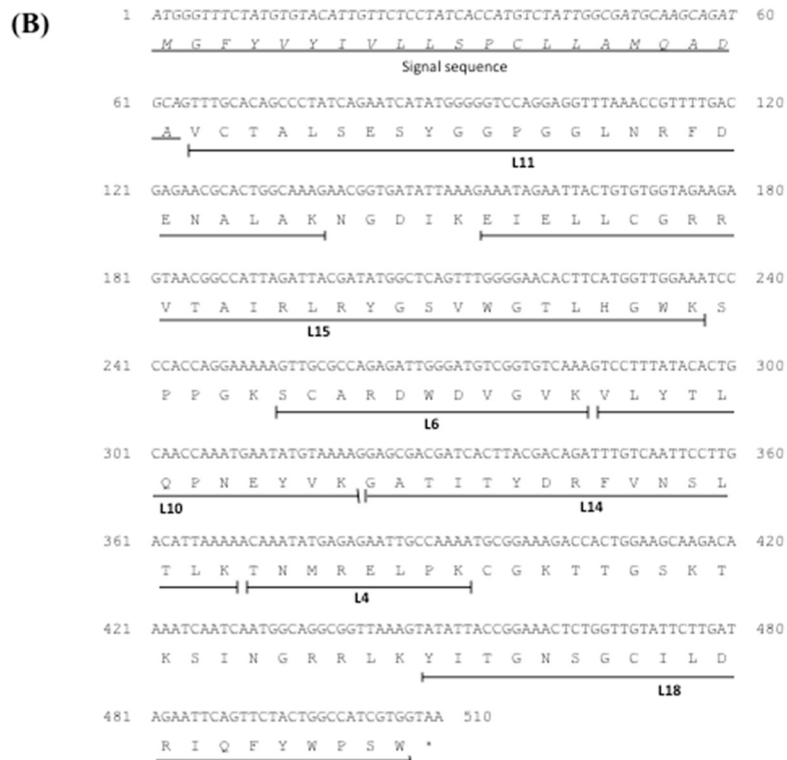
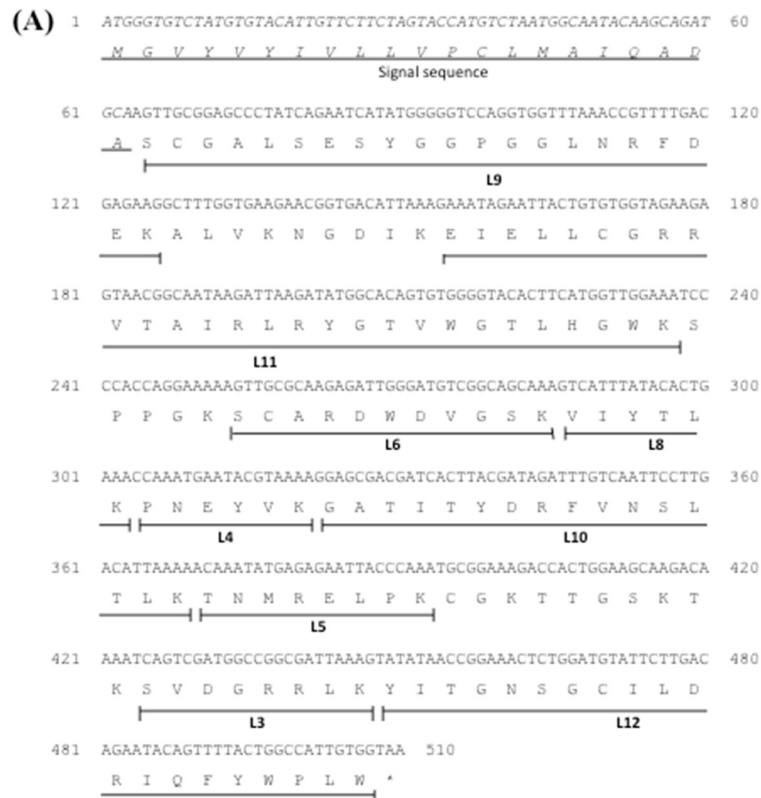
Supplementary Figure S2. Nucleotide sequences of cDNAs and the corresponding amino acid sequences of PPL3 subunits. Nucleotide residues and amino acid residues different from PPL3 α and β subunits are indicated by bold characters, respectively. Peptide fragments generated by digestion with *Achromobacter* protease I (L) and *S. aureus* V8 protease (V), respectively, are indicated by lines. Italic letter with underline indicates the signal peptide region. Asterisk indicates the stop codon.



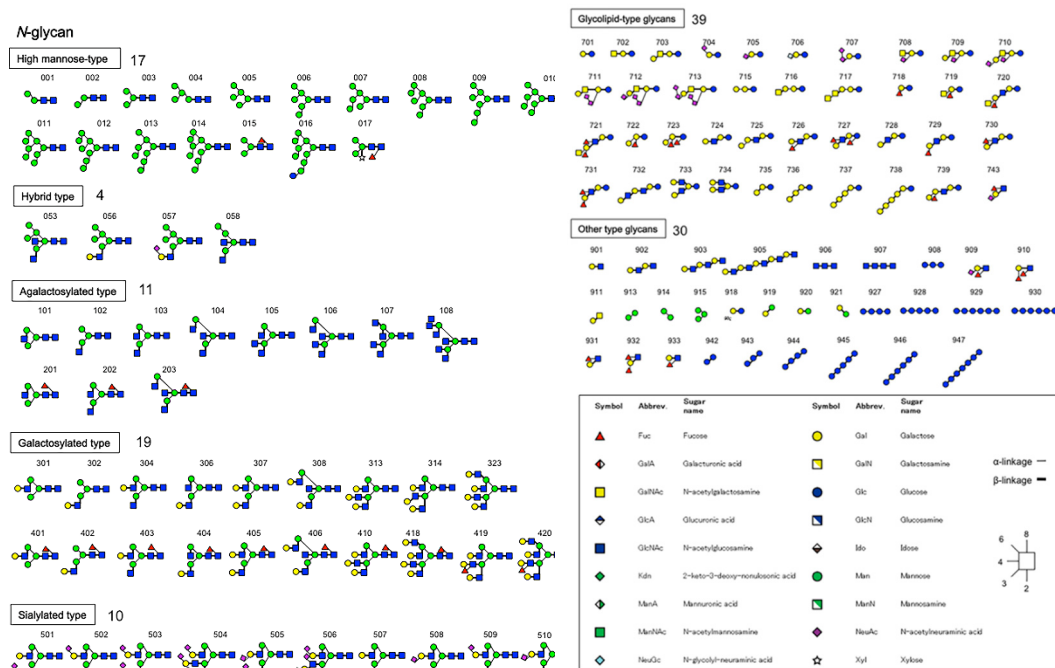
Supplementary Figure S3. Separation of CAM-PPL4 α and β subunits by reversed-phase HPLC. Separation of CAM-PPL4 subunits was conducted by HPLC on a CAPCELL PAK (C8) column (ϕ 4.6 $\times$ 150 mm) using graded linear gradient of acetonitrile in 0.1 % TFA.



Supplementary Figure S4. Peptide maps of CAM-PPL4 α (A) and β (B) subunits digested by *Achromobacter* protease I. Peptides were separated by reversed-phase HPLC on COSMOSIL[®] Protein-R column (ϕ 4.6 $\times$ 250 mm) using a linear gradient of acetonitrile in 0.1% trifluoroacetic acid. Common peaks between α and β subunits were marked by magenta arrow heads.



Supplementary Figure S5. Nucleotide sequences of cDNAs and the corresponding amino acid sequences of PPL4 α (A) and β (B) subunits. Peptide fragments generated by *Achromobacter* protease I (L) digestion are indicated by lines. Italic letter with underline indicates the signal peptide region. Asterisk indicates the stop codon.



Supplementary Figure S6. Schematic representation of oligosaccharide structures. Note that the reducing terminal is pyridylaminated for FAC analysis. Symbols used to represent pyranose rings of monosaccharides are shown in the box at the bottom. Anomeric carbon, i.e. position 1, is placed at the right side, and 2, 3, 4 are placed clockwise. Thin and thick bars represent α-linkage and β-linkage, respectively.

Supplementary Table S1. The amino acid sequences and masses of the peptides generated by cleavage of the CAM-PPL3B with *Achromobacter* protease I (A) and *S. aureus* V8 protease (B).

(A) *Achromobacter* protease I

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
L4	YVQSITFK	984.55	987.10
L5	EIASEYLGGPGGDAFDDK	1839.84	1844.19
L8	YISGRWGCRIDGLRFHAK	2192.18	2196.43
L9	VDSRQWGWANENCIQWSK	2264.09	2269.28
L10	AVAQNGDITRIEMQCTDVATYIK	2597.33	2601.46
L11	ALAQNQDITRIEMQCTDVATYIK	2611.34	2616.13

(B) *S. aureus* V8 protease

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
V7	NCIQWSKKGE	1250.64	1250.01
V8	NCIQWSKKGEKVVHE	1842.97	1842.29
V9	ITFKTNKRLPRCGTSATE	2182.18	2181.85
V10	NCIQWSKKGVKVVHE	1813.00	1812.06
V14	YLGPGGDAFDDKAVAQNGDITRIE	2579.24	2579.64
V16	YLGPGGDAFDDKALAQNGDITRIE	2593.25	2593.96
V17	VATYIKLRYGKVDSRQGWANE	2640.37	2640.23
V19	MQCTDVATYIKLRYGKVDSRQGWANE	3276.61	3276.47
V20	KSVTVLIPGGLKYISGRWGCRIDGLRFHAKC	3546.99	3545.02
V21	LSSGEYITSAIVTYGKYVQSITFKTNKRLPRCGTSATE	4329.26	4325.63

Common peptides between PPL3A (α+α) and PPL3B (α+β), and between PPL3B (α+β) and PPL3C (β+β) are indicated by magenta and green boxes, respectively.

Supplementary Table S2. The amino acid sequences and masses of the peptides generated by cleavage of the CAM-PPL4 α (A) and β (B) subunits with *Achromobacter* protease I.

(A) PPL4 α

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
L3	SVDGRRLK	929.56	932.82
L4	PNEYVK	748.40	773.46
L5	TNMRELPK	987.54	991.19
L6	SCARDWDVGSK	1280.62	1283.11
L8	VIYTLK	735.48	760.08
L9	SCGALSESYGPGGLNRFDEK [N terminus]	2201.05	2203.56
L10	GATTITYDRFVNSLTk	1797.99	1802.24
L11	EIELLCGRRTAIRLRYGTWGTlHGWK	3340.88	3344.89
L12	YITGNSGCILDRIQFYWPLW	2502.28	2506.58

(B) PPL4 β

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
L4	TNMRELPK	987.54	990.42
L6	SCARDWDVGK	1292.66	1295.40
L10	VLYTLQPNEYVK	1465.81	1469.29
L11	VCTALSESYGPGGLNRFDENALAK [N terminus]	2626.31	2630.86
L14	GATTITYDRFVNSLTk	1797.99	1802.24
L15	EIELLCGRRTAIRLRYGSVWGTlHGWK	3326.86	3331.88
L18	YITGNSGCILDRIQFYWPSW	2476.23	2478.06

Common peptides between PPL4 α and β subunits are indicated by magenta boxes.

Supplementary Table S3. Properties of lectin-immobilized columns used for FAC analysis.

Lectin name	Amount of Immobilized		Bt (nmol)	Kd (M)	R ² ^a	Used carbohydrate
	lectin (mg/ml gel)					
PPL2A	0.05		0.02	2.0 x 10 ⁻⁷	0.996	1M2M-5NC-Asn Fmoc
PPL3	0.5		0.63	3.01 x 10 ⁻⁵	0.985	1M2M-5NC-Asn Fmoc
PPL4	1.0		0.98	2.0 x 10 ⁻⁵	0.996	ManαpNP

^a the coefficient of determination quantified the degree of linear correlation obtained from a Woolf-Hofstee-type plot in each concentration-dependent analysis. B_t and K_d values were calculated from those determined by concentration-dependent analysis.