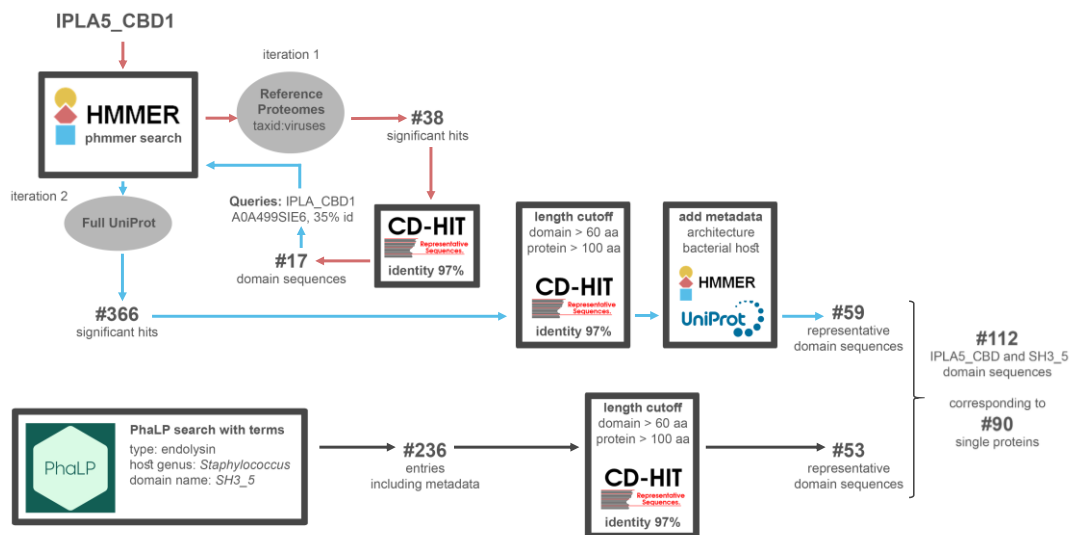


Online Resource 1 from:

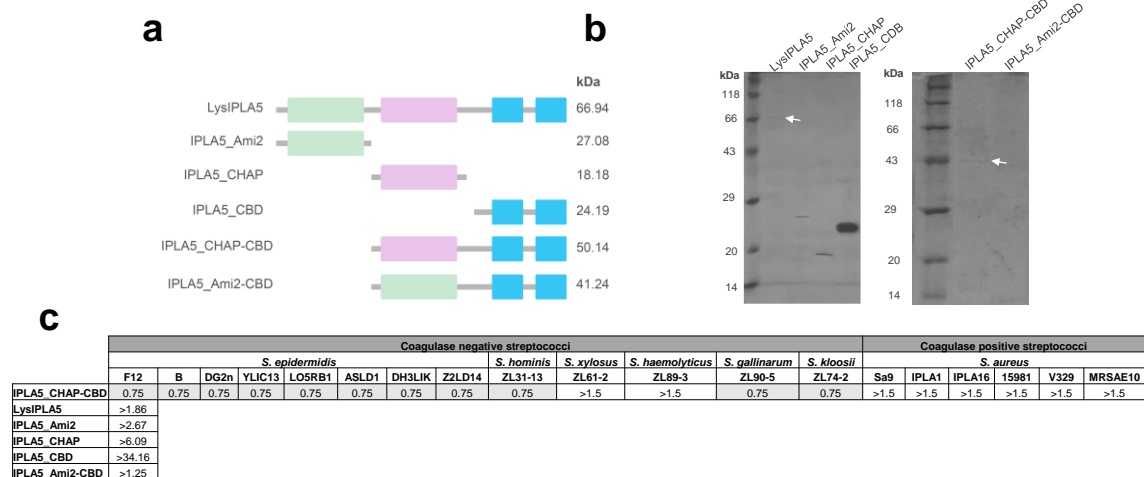
## The new *SH3b\_T* domain increases the structural and functional variability among SH3b-like CBDs from staphylococcal phage endolysins

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Supplementary Fig. S1. Workflow for constructing the datasets of SH3b-like sequences.



**Supplementary Fig. S2.** Functional dissection of LysIPLA5 domains. (a) Scheme of the proteins tested in this experiment. (b) SDS-PAGE depicting the proteins after purification. (c) MIC values calculated for each protein.

**Supplementary Table S1.** Absolute MIC values ( $\mu\text{M}$ ) for the proteins and strains shown in Fig. 4.

Strain	RODI_CHAP	RODI_CHAP-CBD	RODI_CHAP-IPLA5_CBD	C1C_CHAP	C1C_CHAP-CBD	C1C_CHAP-IPLA5_CBD
<i>S. epidermidis</i> F12	6	1.5	0.1875	3	0.375	0.1875
<i>S. epidermidis</i> B	6	6	0.1875	3	0.375	0.1875
<i>S. epidermidis</i> DG2n	6	6	0.1875	3	0.375	0.09375
<i>S. epidermidis</i> YLIC13	12	6	0.1875	3	0.375	0.1875
<i>S. epidermidis</i> LO5RB1	3	3	0.09375	3	0.0468	0.023438
<i>S. epidermidis</i> ASLD1	3	6	0.1875	6	0.375	0.1875
<i>S. epidermidis</i> DH3LIK	6	3	0.1875	3	0.375	0.1875
<i>S. epidermidis</i> Z2LD14	6	3	0.1875	3	0.375	0.09375
<i>S. hominis</i> ZL31-13	1.5	3	0.1875	1.5	0.09375	0.09375
<i>S. xylosum</i> ZL61-2	6	6	3	3	1.5	1.5
<i>S. haemolyticus</i> ZL89-3	3	6	3	3	1.5	1.5
<i>S. gallinarum</i> ZL90-5	3	1.5	1.5	6	1.5	0.75
<i>S. kloosii</i> ZL74-2	3	1.5	1.5	3	1.5	0.75
<i>S. aureus</i> Sa9	3	0.375	3	3	1.5	1.5
<i>S. aureus</i> IPLA1	1.5	1.5	1.5	6	1.5	1.5
<i>S. aureus</i> IPLA16	3	1.5	1.5	6	1.5	1.5
<i>S. aureus</i> 15981	3	1.5	1.5	6	1.5	1.5
<i>S. aureus</i> V329	3	1.5	1.5	3	1.5	1.5
<i>S. aureus</i> MRSAE10	3	3	1.5	3	3	1.5

