Supplemental Text S1. Codon-optimized Bt188 DNA sequence. Restriction sites are underlined.

CATATGAAGTACAAGGTGAAACTGAGCCTGATTCCGATGCTGCTGAAAGGCCTGTATGCCTATAAACATAAAAATTATAACGAGGCCGA
GCGTATTTTTGCACTGCTGCTGGATAAACAGGGCGATAATGCCTATCTGAATTTTCGCTATGGCATGGCCCTGTATAAAAGTAAAAAATG
GGATGAAGCCAACTATTATATCCAGAAAGCAATTAATATCGACCCGAGTAAAAAAAGTTGGCAGGTGCAGCTGGCAACCAGCGAACGTT
ATAAACAGAATAGTGAAAAAGTGAAGGTGGCAGAAGCAAAAAAAGCAGCAATTAAAGATCCGAATAGTCCGGAAGTTATTTGGGAATA
TGCAATTAGTCTGCTGGAAAATAAACAGTATTGGATGGCCAAACTGCAGTTTGAAAAATATCTGATTCTGAAACCGAACAGCGAAAAAG
CATTTGATAATCTGGGTAAAGTTAGTGAAAAGCTGAGTGATTATCCGGAAGCCATTAAATATTTTGAAAAGGCAGCAAGTCTGAGCCCGT
TTAATAGCAATTATAAATATCGCATCGGCTATAGTTACGAATGTCTGGGCGATCTGGAAAATGCCAATACCTATTATGAACTGGTTAGCA
GCTTTGCCAAAAGCAATGATGATGTGGCACTGTTTGGCATTGGCGCACTGCATGCAAAACGTGGCCTGTGGGATAAAGCACTGAATGCA
TATAAACAGTTTCTGGCAAAAACCCAGAGTAATAATCCGGAACTGTATTATCGTATTGGTGTTGCAAATGAACGCCTGTATCTGTGGGAA
GATGCCGGCAAAGCATTTGAACAGGCCGTTAAACTGAGTGAAATTATTACCGCACCGTGGTGTTTTAAATGTGGCCAGGCATACGAACG
CGCCAAAAATTATGCCAAAGCCGTTGAATTTTACCAGAATGCAGTGGCACGCAGTAATAATTATAATGATTATTGGCTGTACCGCCTGGC
CTATAGTATGGAAATGATGGGTAATTTTGAGCAGGCCGCAAAATATTATCAGCAGAGTCGCCGTCGCAAAATTGCCCATGCAGTTGCACC
GAAAGATGTGATTAAAAATAAAGAAGAGGAGTACCTGACCTATTATACCGAATATTATGAAACCCTGGCCGTGAATGAAAAACAGGTTC
TGATTGAAAGTTTCTTTGGTGGTAATATTAGCTGTAATCCGTATGCAATTCTGCTGTATATGCTGGATCATAATTATGATTTCACCTATATC
GTGGTTGTTAAACCGGAAACCGTTATTCCGGATAGCCTGAAATTTAAACAGAATATTATCTTCATCAACCGCGGCAGTGATGCCTATCTGC
GCTATCTGTGTACCGCAAAATATCTGATCAATAATGTTAGTTTCCCGTATTATTTCATCCGCAAAGCCGAACAGATTTATCTGAATACCTGG
CATGGTACCCCGATGAAAACCCTGGGTAAAGATATTAAAAGTCCGTTTCAGGATCATAGTAATGTTAGTCGTAATTTTCTGCAGGCAACC
CATCTGATTAGCCCGAATCGCCATACCACCGATATTATGCTGGAAAAATATGATATCAAGGACCTGTTTAGTGGTGAAATTGCAGAAACC
GGTTATCCGCGTATTGATCTGAGCTTTCTGAGTGAAGAACGCCGCAATGAAATTCGTAAAAAACTGGGTTTTAAGAACAACAAACCGGTG
GTTTTTTATGCCCCGACCTGGCGTGGCACCAGCCAGAGTAAAGATTTTGATACCCAGAAACTGCAGAATGATCTGAAACGCCTGAAAAGC
GATAAATATAATCTGGTGTTTCGCGGCCATCATCTGGTGGAAAGCCTGCTGAGCGAAATTAAACTGGATGTTGTTGTTGCACCGAAGGA
AATTGATAGCAATGAACTGCTGGGTTATTGCGATCTGCTGATTACCGATTATAGTAGCATTATTTACGACTTTCTGGCACTGAATAAACCG
GTTATTAGCTATGTTTATGACTTTGATGAGTACAAAGAGGAACGTGGTCTGTATTTTGAAAAAGATGAAATGGTTGGCGCCGTTTGTAGC
ACCATTAGTGAAGTGCGTCAGGCCATTCTGGAAAATCTGAATAAAAATAAGAGCAACGTGCTGGAACGTGATATTGAAAAATATAGTTA
CCTGGATGACGGCCGTGCAACCCAGCGCACCGTTGATTTTATTTTTAAAAATGACAACCGTTACGTGTACGATTATATTCGTAAAGATACC
GATGTTTTCTTCGTGGGTCCGTTTCTGCAGAATGGTATTACCCGTAGCTTTCTGAATCTGATGAGCACCATTGGTCGCGAAAAAAATATTC
TGGTGCTGATTAATGGCAATGATCTGCAGAGTGATAATAAACGTCTGGAAGAATTTTACCGTCTGCCGAAAGATATTAGTGTTTTTAGCC
GCAGTGGCCGCATGCTGATGACCCTGGAAGAACTGTGGGTGCGCAATAAATTTGATGAAAATTTTAAGTTCTACAGCGAGGAATTTAAG
CGTGTGATTGAAAAAATTTACAAGCGCGAAGCACGCCGTCTGTTTGGTGATAGTAAAATTCGTAATATCATCAACTTCGAGGGCTATGCA
CTGTTTTGGGTTCTGCTGATTAGTCAGGTGAATGCCAAACAGCATATTATTTATCAGCATAATGACAAGTACAAGGAATGGAAAAGTAAA
TTTCCGTATCTGGAAGGTGTTTTTCGCACCTATCGTTATTATGATAAAATCGTTAGCGTGAGTGAAAAAACCATGGAAAATAATCGCAATA

ACATCAGTTACGAATTCGGTATTGCAGAAAAACGCTTTGTTTTTTGCAATAATCCGATTAATATCGATCAGATTATCAGCAATGCCAAAGATGATATTGAAATTGAAGACGAATTCGATAACTTCGCAGGTACCAAATTTATTAATATCGGCCGTATGAGTCATGAAAAAGATCAGCTGAAACTGATTGAAGCATTTGCAGAAGTTAATAAAAAGCATAAGGACACCCGCCTGTTTATTCTGGGCGATGGTCCGCTGAAACAGGAACTGATTACCCGTATTAAAAAACTGAGCTTAGAAAAAGACGTGTTTCTGCTGGGCCAGAAAACCAATCCGTTTGCATATCTGAAACAGGCAGATATTTTTGTGCTGAGTAGTAATCATGAAGGCCAGCCGATGGTTCTGCTGGAAAGCCTGACCCTGGGTACCCCGATTATTGCAACCGATATTGTGGGCAATCGCAGCATTCTGGGCGACAAATATGGCCTGCTGGTTGAAAATAGCAAACAGGGTCTGATTAATGGTATGAATGAATATCTGGAAAACGGCAGTAAACAGGATAATTTTGATCCGATTGCATATCAGAAAGATGCAATGGATAAATTTTACGCCCTGCTGAATGAACTCGAG

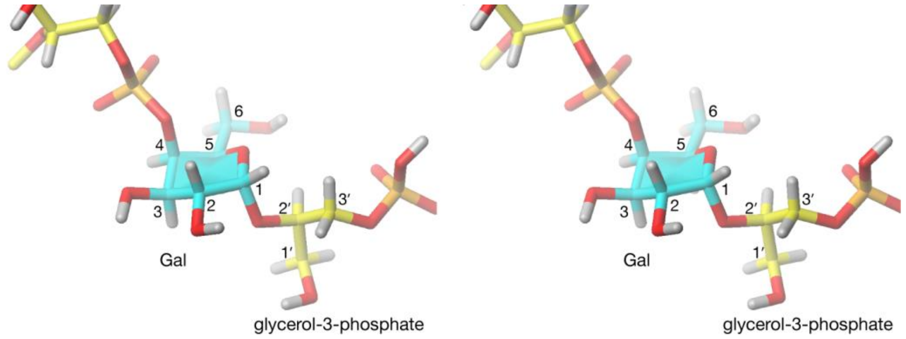

Fig. S1. Stereoview of a repeating unit of a [→4)-α-Gal-(1→2)-Gro-(3-PO$_4^-$] (*App*3) hexamer. The distances between Gal H1 and the surrounding protons in the model are in good agreement to the distances derived from NOE cross-peak intensities from 2D NOESY spectra shown in Fig. 3g (H1-H2’, H1-H3a’, H1-H3b’ all < 3.0 Å) according to (Aeschbacher T, Zierke M, Smieško M, Collot M, Mallet J-M, Ernst B, Allain FHT, Schubert M. 2017, Chemistry, 23:11598–11610, doi: 10.1002/chem.201701866). The model was generated using CarbBuilder (Kuttel MM, Ståhle J, Widmalm G. 2016, J Comput Chem, 37:2098–105, doi: 10.1002/jcc.24428), was further refined by a molecular dynamics calculation using Yasara (Krieger E, Vriend G. 2015, J Comput Chem, 36:996–1007, doi: 10.1002/jcc.23899) and the image was generated using Molmol (Koradi R, Billeter M, Wüthrich K. 1996, J Mol Graph, 14:51–5, 29–32, doi: 10.1016/0263-7855(96)00009-4).

Supplemental Table S1

Strains, enzymes and recombinant constructs generated and used in this study.

Strain (Ref.)	Serotype	Protein	Accession number	Plasmid	Identifier	Recombinant construct	MW	Primer	Restriction site
Actinobacillus pleuropneumoniae S1421	*App*3	Cps3B	Genbank: ABY70165.1	*p*cps3B-His$_6$	5113	Cps3B-His$_6$	17.5 kDa	TF117 / TF116	NdeI/XhoI
				*p*cps3B-H14A-His$_6$	5715	Cps3B-H14A-His$_6$	17.5 kDa	CL243 / CL244	
				*p*cps3B-H17A-His$_6$	5716	Cps3B-H17A-His$_6$	17.5 kDa	CL245 / CL246	
				*p*cps3B-K44A-His$_6$	5717	Cps3B-K44A-His$_6$	17.5 kDa	CL247 / CL248	
				*p*cps3B-K46A-His$_6$	5718	Cps3B-K46A-His$_6$	17.5 kDa	CL249 / CL250	
				*p*cps3B-R113A-His$_6$	5719	Cps3B-R113A-His$_6$	17.5 kDa	CL251 / CL252	
		Cps3D	Genbank: KY807157	*p*MBP-cps3D- His$_6$	5360	(1)			
				*p*MBP-cps3D-R982A-His$_6$	5393	MBP-Cps3D-R982A-His$_6$	176 kDa	CL219 / CL220	
Actinobacillus pleuropneumoniae AP76	*App*7	Cps7B	Genbank: ACE62293.1	*p*cps7B-His$_6$	5152	Cps7B-His$_6$	17.5 kDa	TF117 / TF116	NdeI/XhoI
		Cps7D	Genbank: ACE62291.1	*p*MBP-cps7D-His$_6$	4887	(1)			
				*p*MBP-cps7D-H743A-His$_6$	5055	(1)			
		Glpk	Genbank: ACE61051	*p*glpk-His$_6$	5797	Glpk-His$_6$	57 kDa	TF180 / TF181	
Actinobacillus pleuropneumoniae 56153 (2, 3)	*App*11	Cps11D	UniParc: UPI0001E49633	*p*MBP-cps11D-His$_6$	5402	MBP-Cps11D-His$_6$	176 kDa	TF156 / TF157	BamHI / XhoI
non-serotyped *Bibersteinia trehalosi* strain USDA-ARS-USMARC-188 (4)		Bt188	GenBank: AHG82487.1	*p*Bt188-His$_6$	5419	Bt188-His$_6$	134 kDa	Synthesized (*General Biosystems*)	NdeI/XhoI

References

1. Litschko C, Oldrini D, Budde I, Berger M, Meens J, Gerardy-Schahn R, Berti F, Schubert M, Fiebig T. 2018. A New Family of Capsule Polymerases Generates Teichoic Acid-Like Capsule Polymers in Gram-Negative Pathogens. MBio 9:16017.
2. Xu Z, Chen X, Li L, Li T, Wang S, Chen H, Zhou R. 2010. Comparative genomic characterization of Actinobacillus pleuropneumoniae. J Bacteriol 192:5625–36.
3. Frey J, Nicolet J. 1990. Hemolysin patterns of Actinobacillus pleuropneumoniae. J Clin Microbiol 28:232–6.
4. Harhay GP, McVey DS, Koren S, Phillippy AM, Bono J, Harhay DM, Clawson ML, Heaton MP, Chitko-McKown CG, Korlach J, Smith TPL. 2014. Complete Closed Genome Sequences of Three Bibersteinia trehalosi Nasopharyngeal Isolates from Cattle with Shipping Fever. Genome Announc 2.

Supplemental Table S2

Primers used in this study. Restriction sites are underlined.

Primer	Sequence
TF117	5’-GCATCTCATATGAAAAAAGTATTAACCTATGGAACC-3’
TF116	5’-GCATCTCTCGAGCTCTTTTTCGTGAATTTGTTTTTGTC-3’
TF156	5’-GCATCTGGATCCTTATTAAAAAGCGAGAACTTTAAAATGAAACATAATG-3’
TF157	5’-GCATCTCTCGAGATTTGTTAATAATGAATAAAACTTCGCCATAGC-3’
TF180	5’-ACGAGCACTTCACCAACAAGGACCATAGCATATGACTAAAGAATACATTATTGCGTTAGACCAAGG-3’
TF181	5’-TGGTGGTGGTGGTGGTGCTCGAGTTCCTCTGCGTCTTCTTTTGCCCATTC-3’
CL243	5’-TGATTTATTAGCACATGGGCATATTCGTTTATTAGAAAGAGCAAG-3’
CL244	5’-ATGCCCATGTGCTAATAAATCAAAGGTTCCATAGGTTAATAC-3’
CL245	5’-ACACCATGGGGCTATTCGTTTATTAGAAAGAGCAAGATCATTAG-3’
CL246	5’-TCTAATAAACGAATAGCCCCATGGTGTAATAAATCAAAGGTTCC-3’
CL247	5’-AACTTAGGAGCAGGCAAAGTATGCGCTTATACTTACGAAGAGAG-3’
CL248	5’-ACTTTGCCTGCTCCTAAGTTAAATTGATCGGTAGAAATAGCAACAG-3’
CL249	5’-AGGAAAAGGCGCAGTATGCGCTTATACTTACGAAGAGAGAGCG-3’
CL250	5’-AAGCGCATACTGCGCCTTTTCCTAAGTTAAATTGATCGGTAGAAATAGC-3’
CL251	5’-AGTTTATTTACCTGCAACTCCTGATATTTCAACCACTCAAG-3’
CL252	5’-ATCAGGAGTTGCAGGTAAATAAACTACTTCGCAATAATCTGCTAAG-3’
CL219	5’-AATATTGGCGCGATGTCGCAC-3’
CL220	5’-AATAAACTTCTGGCCATTGAATAAAGTAAACTC-3’