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Supplemental Information

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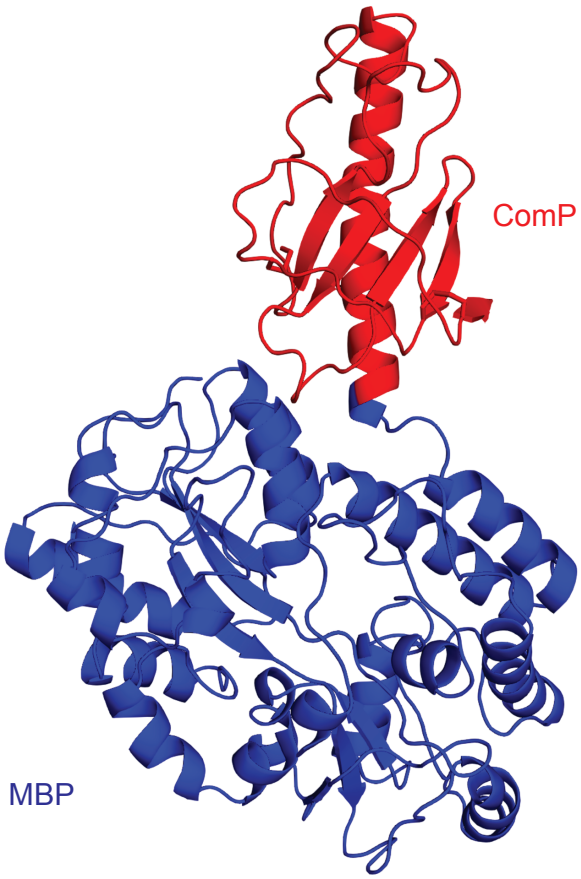

Figure S1, related to Figure 3. Full 3D structure of the MBP-ComP fusion protein. The crystal structure is shown as a cartoon drawing. The ComP moiety is highlighted in red, while the MBP moiety is highlighted in blue.

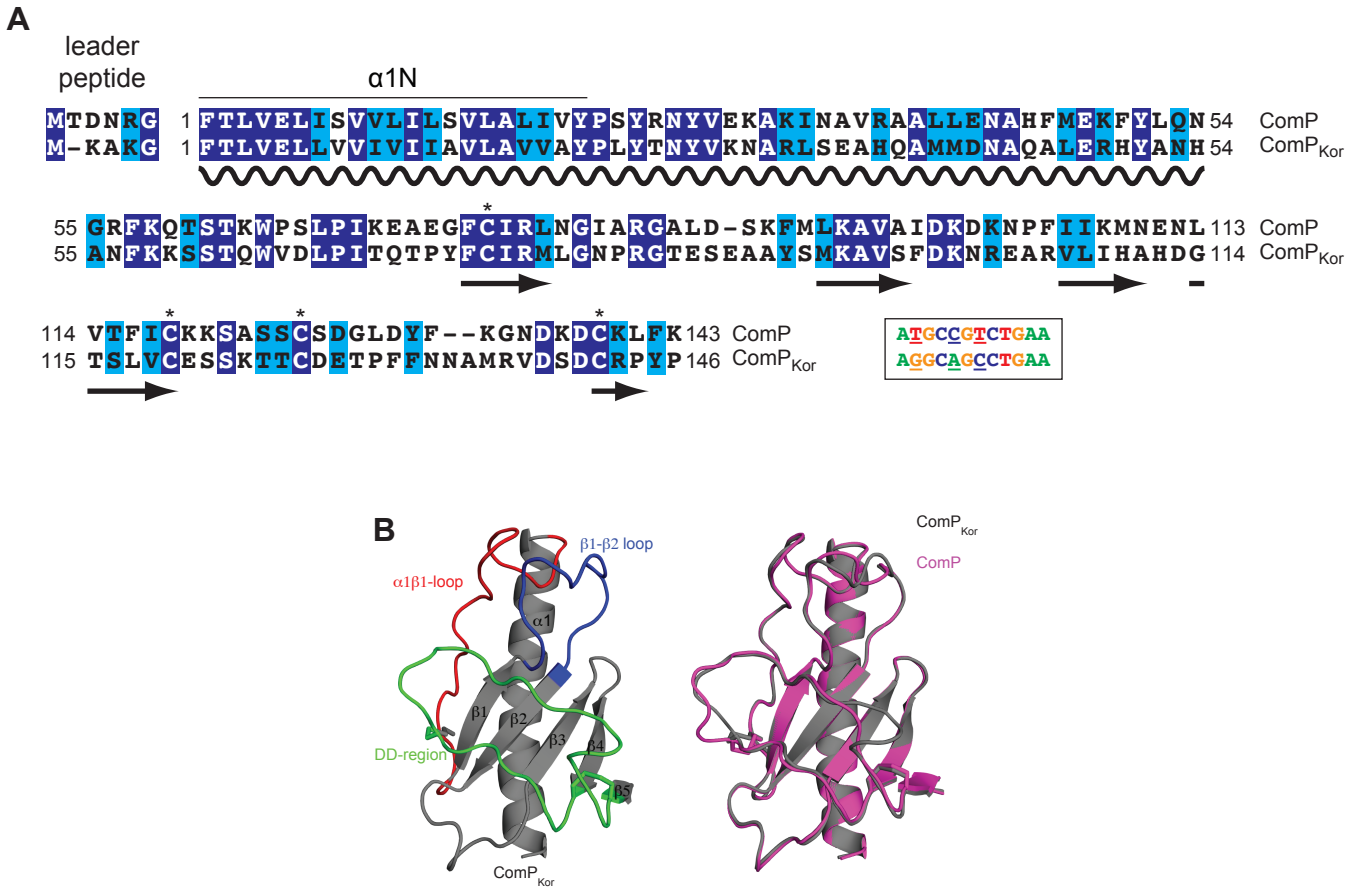

Figure S2, related to Figures 3 and 4. Homology modelling of the structure of the ComP$_{Kor}$ ortholog from *K. oralis*. (A) Sequence alignment of ComP$_{Kor}$ with ComP from *N. meningitidis* 8013, produced using Clustal Omega. Amino acids were shaded in dark blue (when identical), in light blue (when highly similar) or non-shaded (when non-conserved). Relevant structural and functional features have been highlighted. The four Cys residues that form two crucial disulfide bonds are identified by *. The inset represents a sequence alignment of DUS and the DUS variant found in *K. oralis*. These motifs differ by three base, which have been underlined. (B) Cartoon drawing representation of the homology model of ComP$_{Kor}$ and of its superposition with the ComP crystal structure.

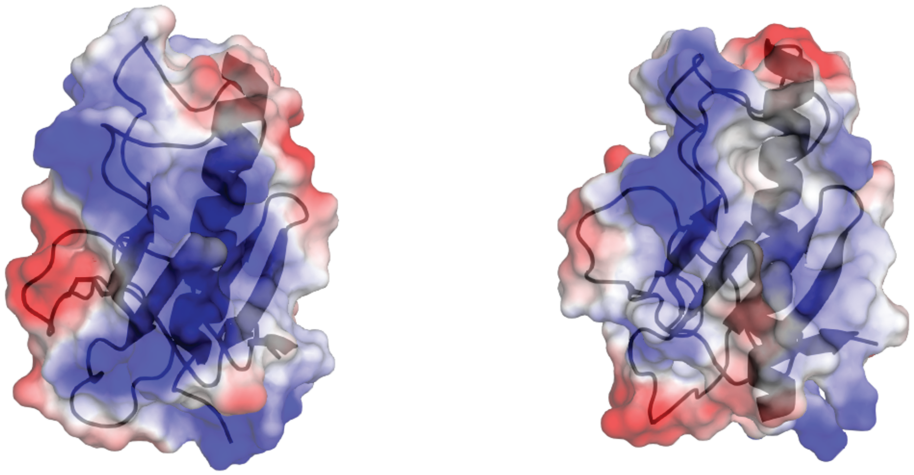

Figure S3, related to Figures 3 and 4. Surface charge representation of the ComP and ComP$_{sub}$ structures. Positively charged residues are represented in blue, negatively charged residues in red, while neutral residues are not coloured.

Table S1, related to Figures 3 and 4. Structural data collection and refinement parameters.

MBP-ComP		
Resolution range (Å)	58.05-1.43 (1.47-1.43)	
Space group	$P2_12_12_1$	
Unit cell dimensions	63.57, 68.44, 109.58; 90, 90, 90	
Total observations	415,797 (28,880)	
Total unique	88,446 (6,445)	
Multiplicity	4.7 (4.5)	
Completeness (%)	99.5 (99.2)	
I/σ(I)	15 (1.2)	
Wilson B factor		21.3
R_{merge}	0.039 (1.096)	
R_{meas}	0.049 (1.384)	
R_{work}		0.16
R_{free}		0.19
Ramachandran favoured (%)		97.2
Ramachandran outliers (%)		0
Average B factor		29
His_6-$ComP_{sub}$		
Number of distance restraints		2,017
intra-residual		744
sequential		445
medium range		273
long range		555
NOE violations >0.5 Å		1
Dihedral violations >5º		0
Ramachandran favoured (%)		75.5
Ramachandran allowed (%)		20.6
Ramachandran generously allowed (%)		3.9
Ramachandran disallowed (%)		0

Table S2, related to the Experimental proocedures. Primers used in this study.

Name	Sequence[a]
Cloning	
opt*comP*-F	gg**gaattc**GAAAAAGCCAAAATTAACGCAGTT
opt*comP*-R	gg**aagctt**TTATTTAAACAGTTTGCAGTCTTTG
$comP_{sub}$-pMalF	gg**gaattc**CGCTCGGCCAACCTGCGTG
$comP_{sub}$-pMalR	gg**aagctt**TCACCCCGTAAAAGGCCGA
his$comP_{sub}$-pETF	gg**ccatgg**atcatcatcatcatcatcatCGCTCGGCCAACCTGCGTG
his$comP_{sub}$-pETR	cc**ggatcc**TCACCCCGTAAAAGGCCGA
DNA-binding assay (EMSA/SPR)	
$DUS_{var1}1$[b]	tgaccAGGCCGTCTGAAcaaac
$DUS_{var1}2$	gtttgTTCAGACGGCCTggtca
SUD1[b]	tgaccACGACTTATAATcaaac
SUD2	gtttgATTATAAGTCGTggtca
SDU1[b]	tgaccAAGGCCTGTCATcaaac
SDU2	gtttgATGACAGGCCTTggtca
NMR titration	
$DUS_{var1}1$bis	cAGGCCGTCTGAAc
$DUS_{var1}2$bis	gTTCAGACGGCCTg

[a]Overhangs are in lower case, with restriction sites in bold.

[b]When indicated, these primers were 5'-labelled with biotin.