Tryptic shaving of *Staphylococcus aureus* unveils immunodominant epitopes on the bacterial cell surface

Annette Dreisbach^{1, #}, Min Wang^{1, #}, Magdalena M. van der Kooi-Pol^{1, #}, Ewoud Reilman^{1, #}, Dennis G.A.M. Koedijk¹, Ruben A.T. Mars^{1, 2}, José Duipmans³, Marcel Jonkman^{3, †}, Joris J. Benschop⁴, Hendrik P.J. Bonarius⁵, Herman Groen⁵, Michael Hecker⁶, Andreas Otto⁶, Katrin Bäsell⁶, Jörg Bernhardt⁶, Jaap Willem Back⁴, Dörte Becher⁶, Girbe Buist¹ and Jan Maarten van Dijl^{1, *}

 ¹Department of Medical Microbiology, University of Groningen, University Medical Center Groningen, Hanzeplein 1, P.O. box 30001, 9700 RB Groningen, the Netherlands
²current address: Division of Gastroenterology and Hepatology, Mayo Clinic, Rochester, MN, 55902, USA
³Department of Dermatology, University of Groningen, University Medical Center Groningen, Hanzeplein 1, Groningen, the Netherlands
⁴Pepscan Therapeutics BV, P.O. Box 2098, 8203 AB Lelystad, the Netherlands
⁵IQ Therapeutics, Rozenburglaan 13a, Groningen, the Netherlands
⁶Institut für Mikrobiologie, Ernst-Moritz-Arndt Universität Greifswald, Friedrich-Ludwig-Jahn-Str.

15, D-17489 Greifswald, Germany

[#]These authors contributed equally to this work

[†]Deceased

*To whom correspondence should be addressed: J.M.van.Dijl01@umcg.nl

Table of Contents

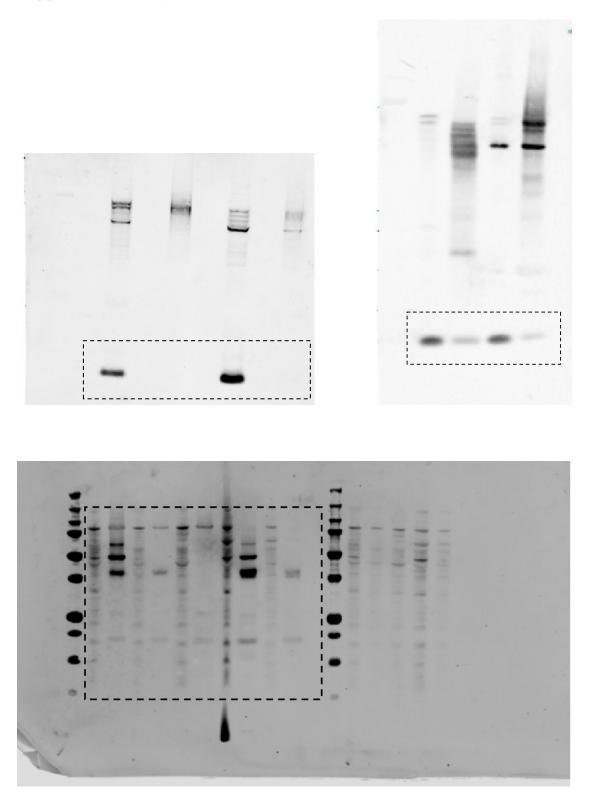
Supplementary Figure S1. Original Western blots
Supplementary Figure S2. Comparison of the p <i>I</i> values of identified proteins and peptides in the different sub-proteome fractions
Supplementary Figure S3. Predicted subcellular localization of the proteins identified with the different approaches for strains USA300 and Newman
Supplementary Figure S4. Comparative overview of the results from the Pepscan analysis. 5
Supplementary Figure S5. Comparison of the results from the proteomic studies and epitope mapping
Supplementary Table S1. Results from the mass spectrometric analyses for the samples derived from <i>S. aureus</i> strain USA300.
Supplementary Table S2. Results from the mass spectrometric analyses for the samples derived from <i>S. aureus</i> strain Newman.
Supplementary Table S3. Comparison of the peptide identifications for S. aureus strains

USA300 and Newman.

Supplementary Table S4. Results from the Pepscan analysis.

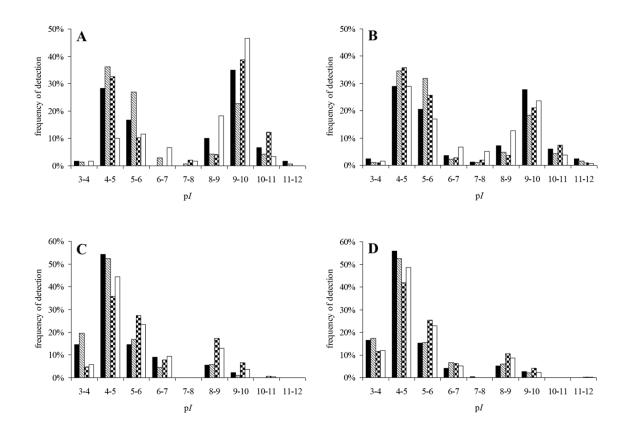
Supplementary Table S5. Comparison of epitope mapping with the peptide identifications from the shaving and exoproteome analyses.

Supplementary Figure S1.



Supplementary Figure S1. Original Western blots. Panel A shows the full blot used to generate Figures 3A, panel B shows the full blot used to generate Figure 3B, and panel C shows the full blot used to generate Figure 4B.

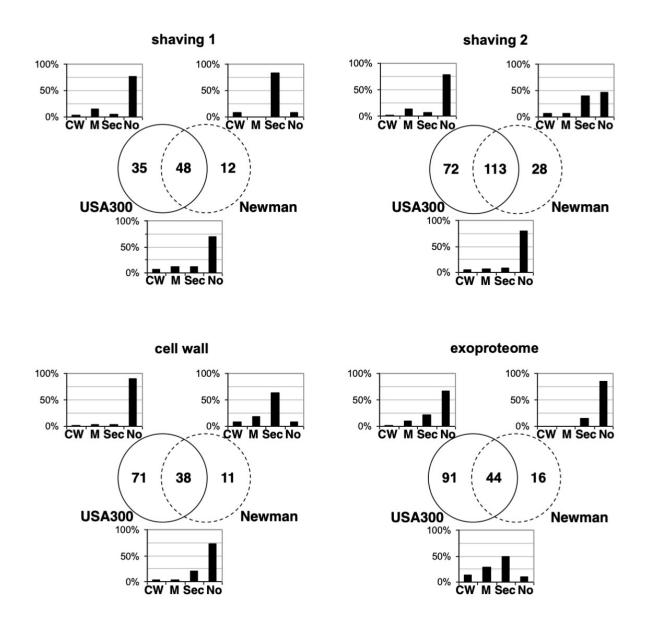
Supplementary Figure S2.



Supplementary Figure S2. Comparison of the pI values of identified proteins and peptides in the different sub-proteome fractions. The percentages of protein (A, B) and peptide (C, D) identifications with a certain pI are displayed for the different sub-proteome fractions of strains Newman (A, C) and USA300 (B, D).

shaving 1, \square shaving 2, \blacksquare cell wall, \square exoproteome.

Supplementary Figure S3.



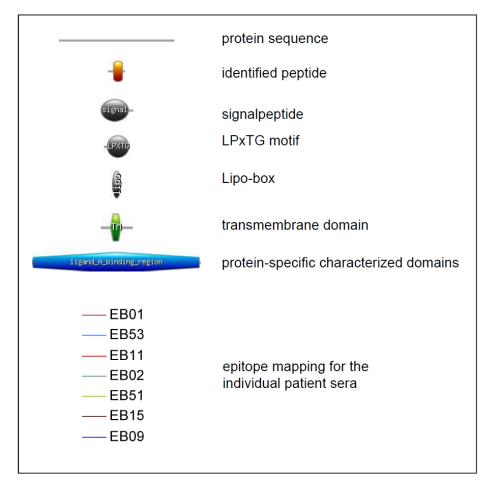
Supplementary Figure S3. Predicted subcellular localization of the proteins identified with the different approaches for strains USA300 and Newman. The overlapping as well as unique proteins identified for the four different sub-proteome fractions from strains USA300 and Newman were analyzed regarding their predicted subcellular localization. CW, covalently cell wall-bound proteins; M, transmembrane- and lipoproteins; Sec, secreted proteins; and No, proteins with no predicted motif for subcellular localization.

Supplementary Figure S4

TPIS_STAAE SDRD_STAAE SBI_STAA RS7_STAAE RS5_STAAF RS13 STAAE Q2FKM6_STAA Q2FKI7_STAA3 PRSA_STAAE PGK STAAE OMP7_STAAE LytM_STAAE HR linea LytM_STAAE HR CLIPS ISDB_STAAE saA STAAF HR lines IsaA_STAAE HR CLIPS . . GCSH_STAAE FLIPR_STAAE . .. ESXA_STAAE ENO_STAAE EMP STAAE EFTU_STAAE EFTS_STAAE EFG_STAAE EBPS_STAAE CIIB STAAE CHIPS_STAAE ALF1_STAAE A6QKF9_STAAE A6QKD3_STAAE A6QK94_STAAE A6QJY9 STAAE A6QJY2_STAAE A6QJV4_STAAE ARO IDE STAAR A6QJE7 STAAE A6QJD9_STAAE A6QHP4_STAAE A6QHG7_STAAE A6QH22 STAAE A6QH01_STAAE A6QG80_STAAE A6QG56_STAAE A6QFU8_STAAE A6QFR2_STAA ABOEC2 STAA A6QFB4 STAAE A6QF81_STAAE A6QF27_STAAE A6QES5_STAAE A6QEF4 STAAE A6QE90_STAAE A6QE54_STAAE • • A6QDQ0_STAAE A6QDK6_STAAE ġ 8

Supplementary Figure S4. Comparative overview of the results from the Pepscan analysis. The binding of antibodies from seven Epidermolysis bullosa patients to immobilized overlapping 15-mer peptide sequences from 54 different staphylococcal surface-exposed proteins were analyzed. For most of the proteins the overlap of consecutive peptides was 11 amino acids. For LytM and IsaA the overlap was 14 amino acids (high resolution, HR). Peptides were synthesizes linearly and with the CLIPSTM technology. The quantified signals were normalized to the signal average per chip and are presented in a bee swarm plot, where the respective proteins are indicated on the y-axis and their normalized signal intensities on the x-axis. • EB01, • EB09, • EB51, • EB11, • EB15, • EB53, • EB02.

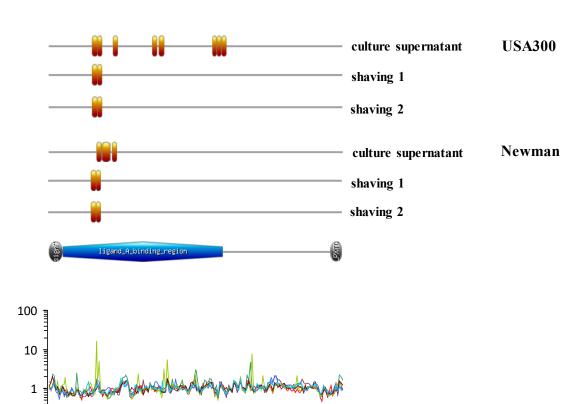
Supplementary Figure S5.



Legend

Figure S5. Comparison of the results from the proteomic studies and epitope mapping. The locations of peptides in particular proteins as identified by the analyses of four different sub-proteome fractions of *S. aureus* strains USA300 and Newman are highlighted in the respective linearly depicted protein sequences. In addition, known protein domains are indicated. The graphs display the signals from the epitope mapping normalized to the median signal of the respective protein and serum for the seven different EB patients.

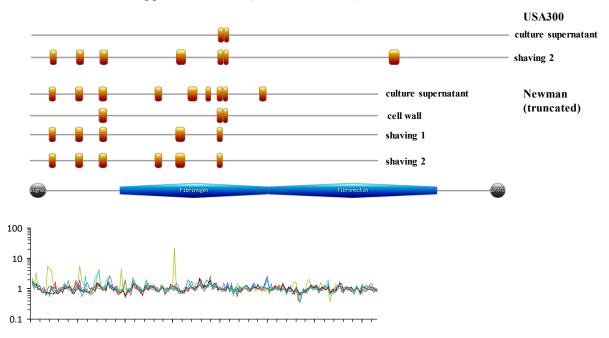
Cell Wall-Anchored Proteins



.

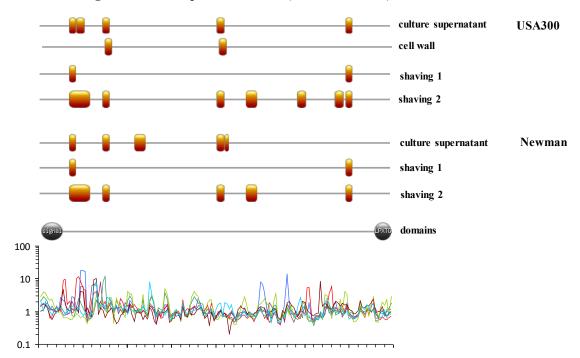
Clumping factor B, ClfB (Q2FDM9, CLFB)

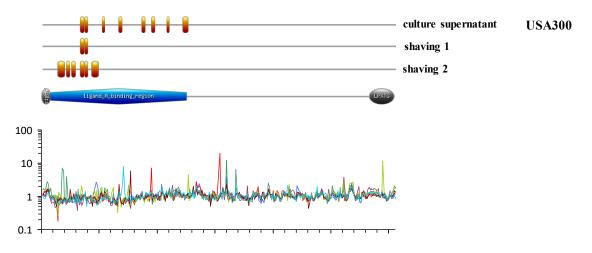
0.1 -



Fibronectin binding protein A, FnbA (Q2FE03, A6QJY9)

Iron-regulated surface protein B, IsdB (Q2FHV2, ISDB)

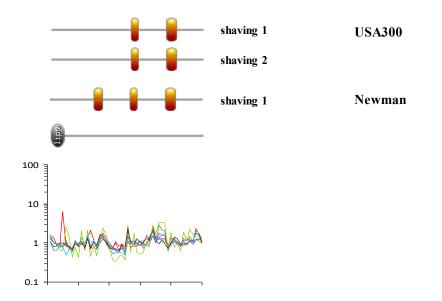




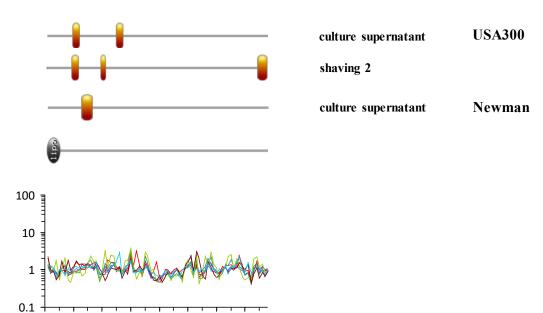
Serine-aspartate repeat-containing protein D, SdrD (Q2FJ78)

Lipoproteins

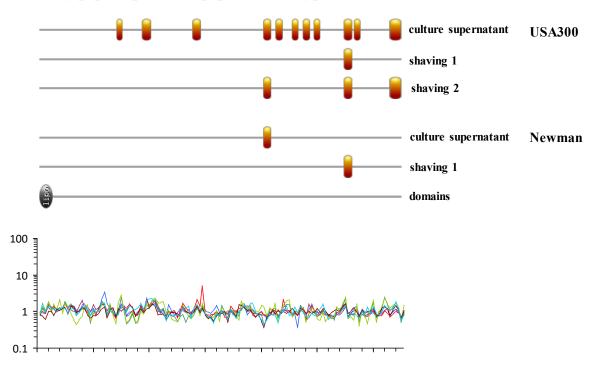
Cell wall binding lipoprotein (YkyA-like) (Q2FHY8, A6QFU8)

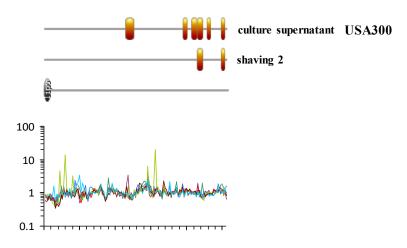






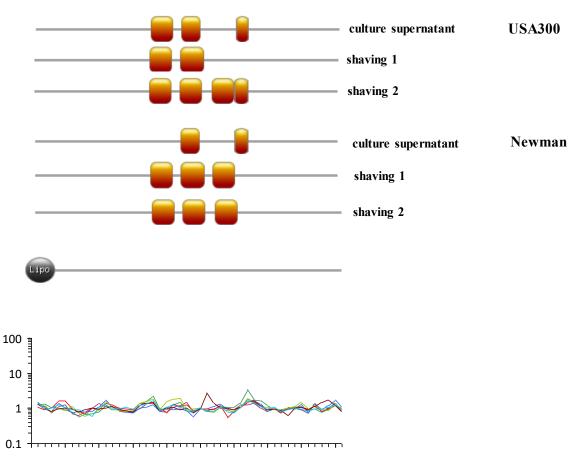
Oligopeptide permease peptide binding protein (Q2FE32, A6QJV4)

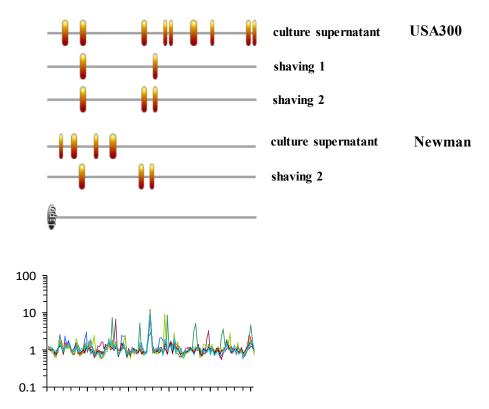




Peptide ABC transporter, peptide binding protein (Q2FKI7)



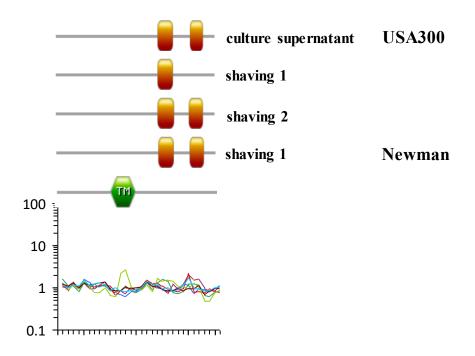


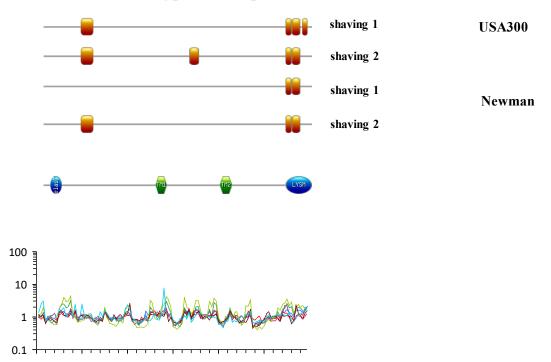


Zn-binding lipoprotein AdcA-like protein (Q2FE92, A6qjp6)

Membrane Proteins

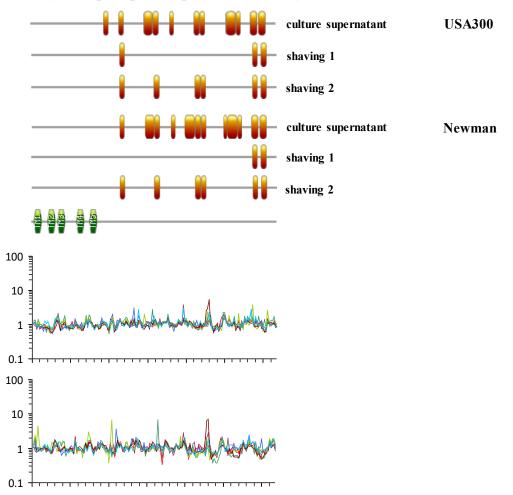
Cell divison protein FtsL (Q2FHQ7, A6QG80)

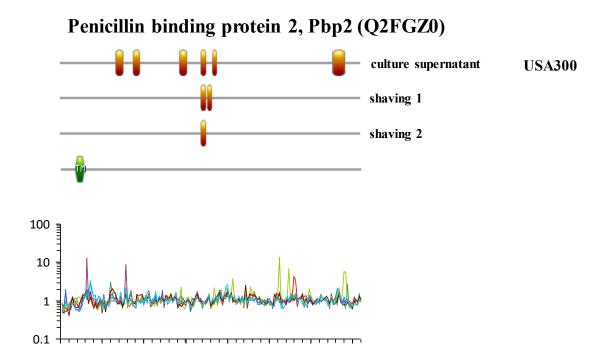




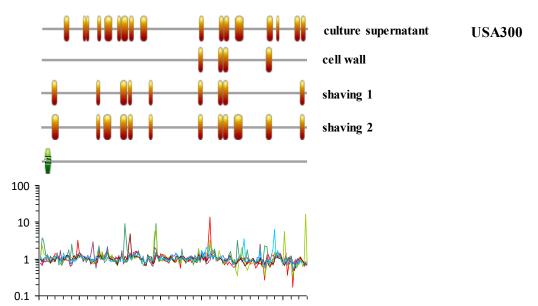
Elastin binding protein, EbpS (Q2FGW1, EBPS)

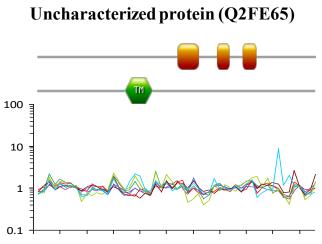
Glycerol phosphate lipoteichoic acid synthase, LtaS (Q2FIS2, A6QF27)





Penicillin binding protein 2', Pbp2A(Q2FKM6)

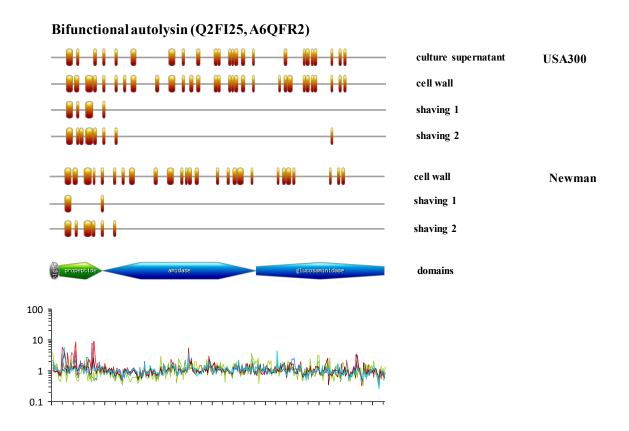




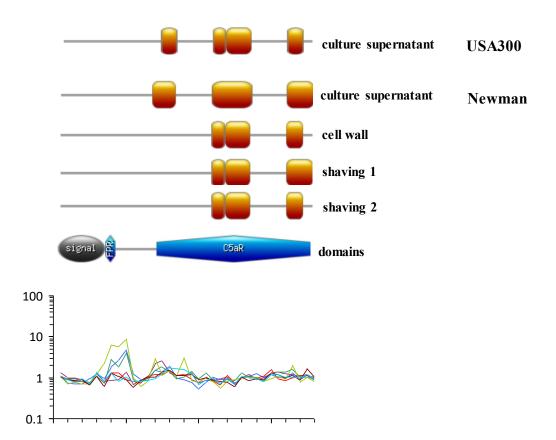
culture supernatant

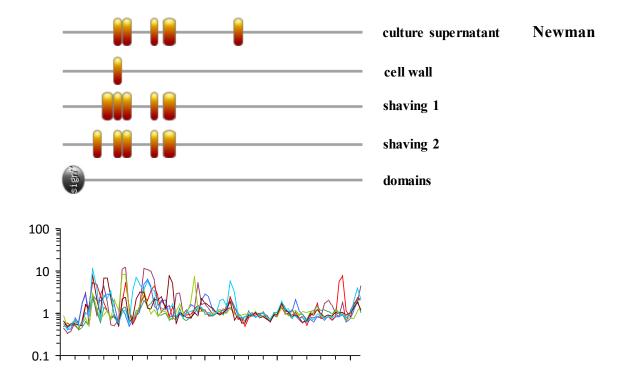
USA300

Secreted Proteins



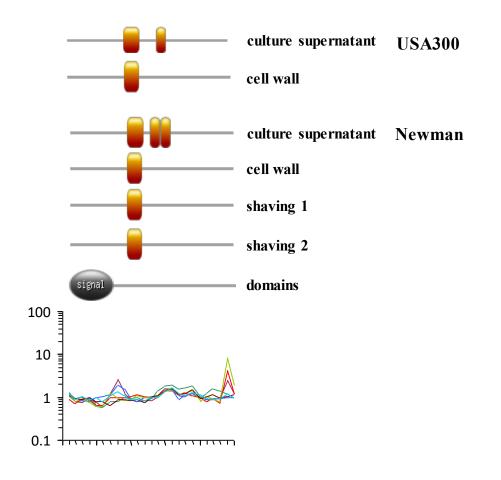
Chemotaxis inhibitory protein, CHIPS (Q2FFF7, CHIPS)



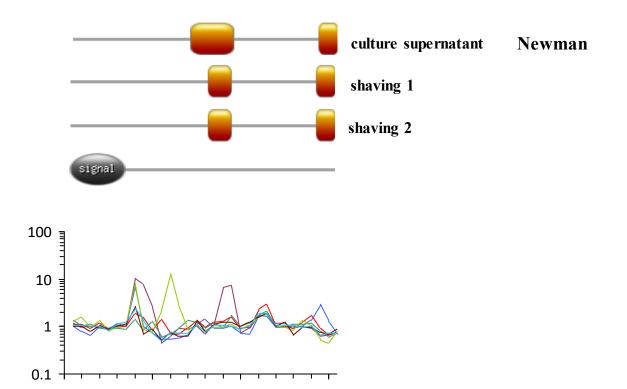


Extracellular matrix binding protein, Emp(EMP)

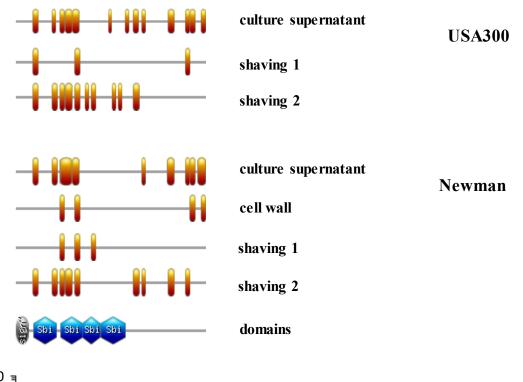
Fibrinogen binding related protein (Q2FHS8, A6QG56)

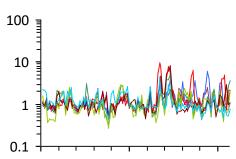


FPRL1 inhibitory protein, FLIPR (FLIPR)

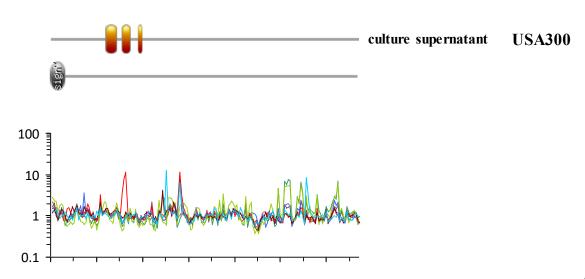


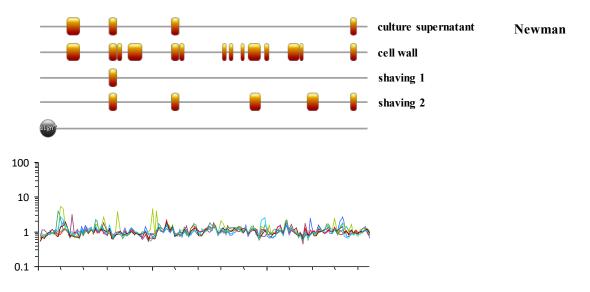
IgG binding protein, Sbi (Q2FE79, SBI)





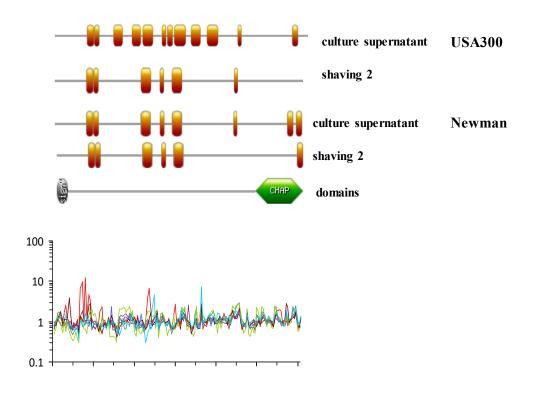
Lipase, Lip (Q2FDJ1)

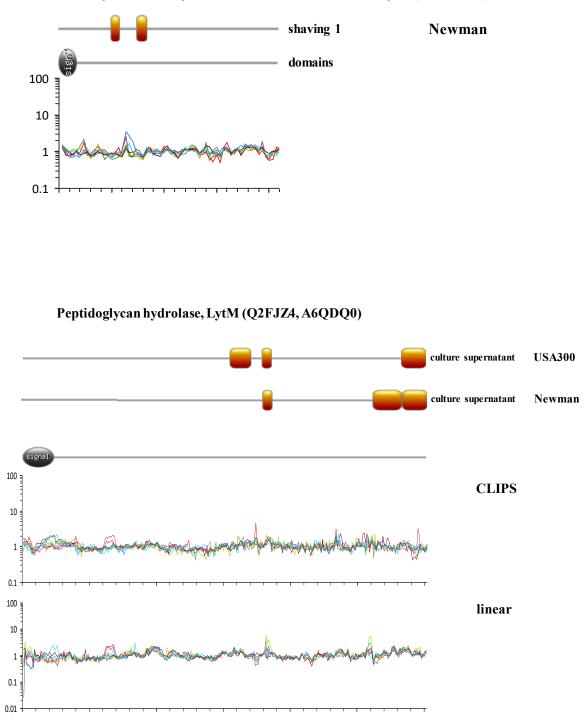




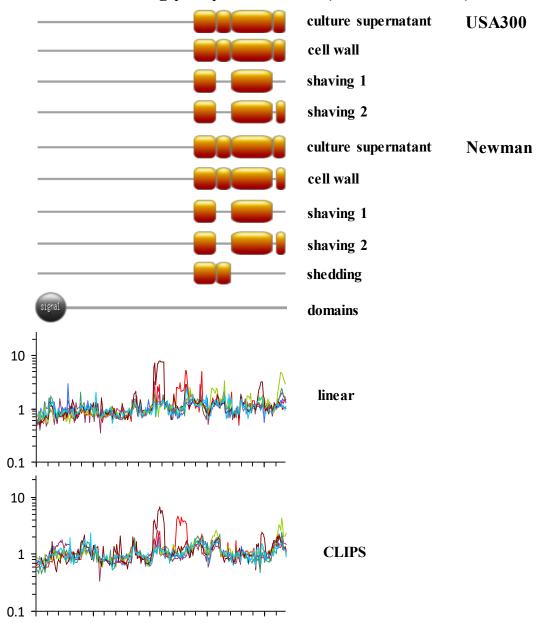
MHC class II analog protein, Omp7 (OMP7)

N-acetylmuramoyl-L-alanine amidase domain proteins (Q2FDL5, A6QKD3)

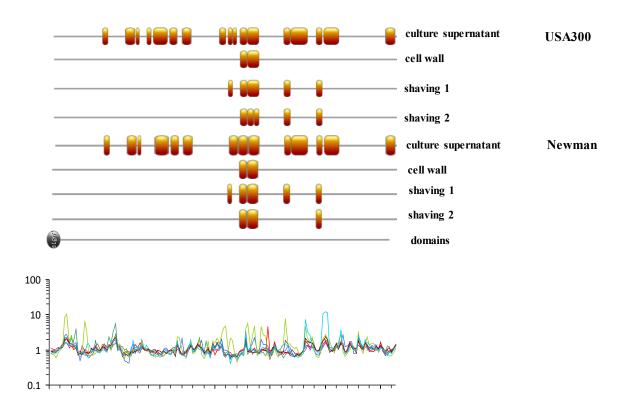




N-acetylmuramoyl-L-alanine amidase, family 4 (A6QJE7)

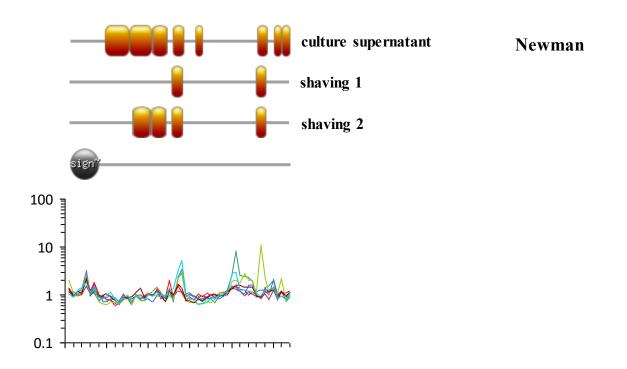


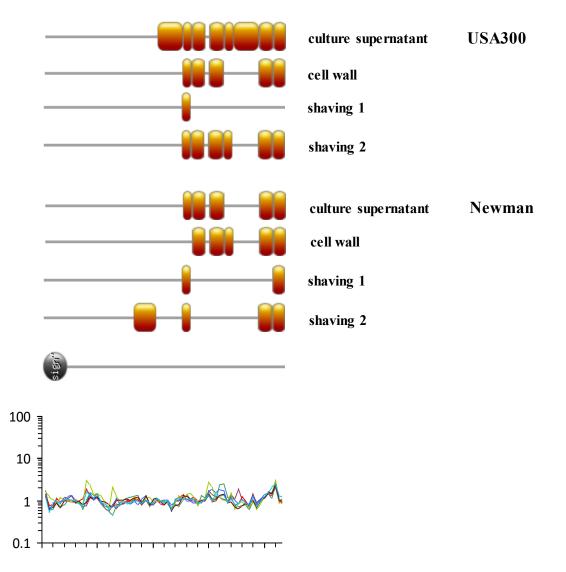
Probable transglycosylase A, IsaA (Q2FDT8, ISAA)



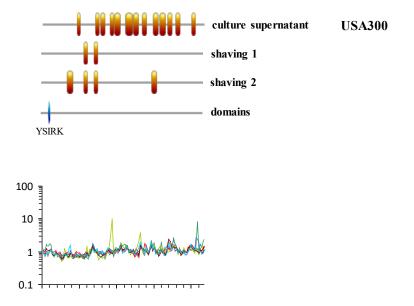
Staphylocoagulase, Coa (Q2FK40, A6QDK6)

Staphylococcal enterotoxin-like toxin (A6QE90)



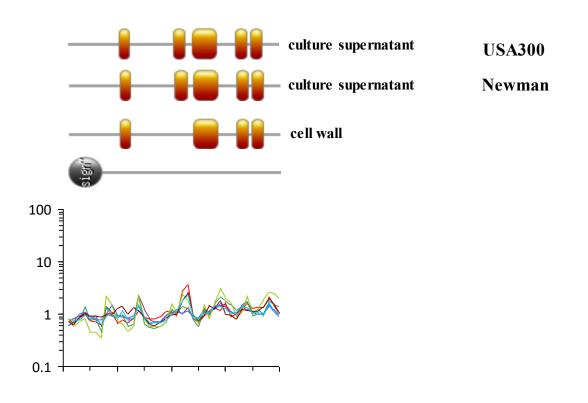


Staphylococcal secretory antigen, SsaA (Q2FEJ4, A6QJD9)

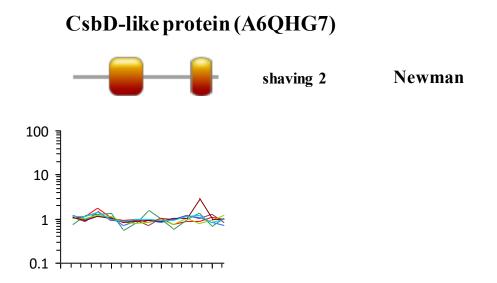


Truncated putative cell wall surface anchor protein, truncated SasG (Q2FE08)

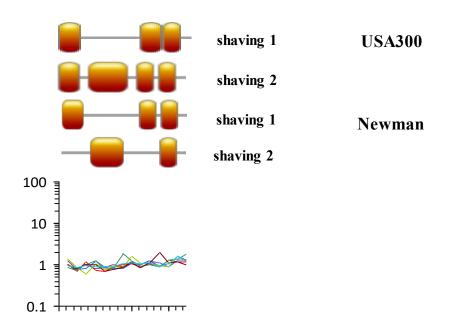
uncharacterized protein (Q2FJ23, A6QES5)



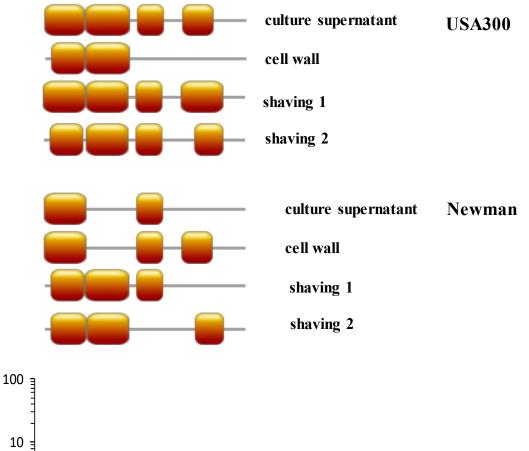
"Cytosolic" Proteins

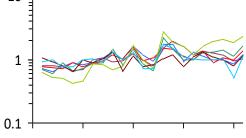


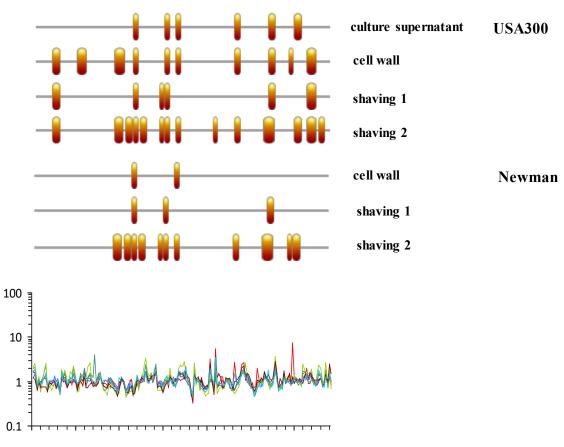
CsbD-like superfamily protein (Q2FIG2, A6QFC3)



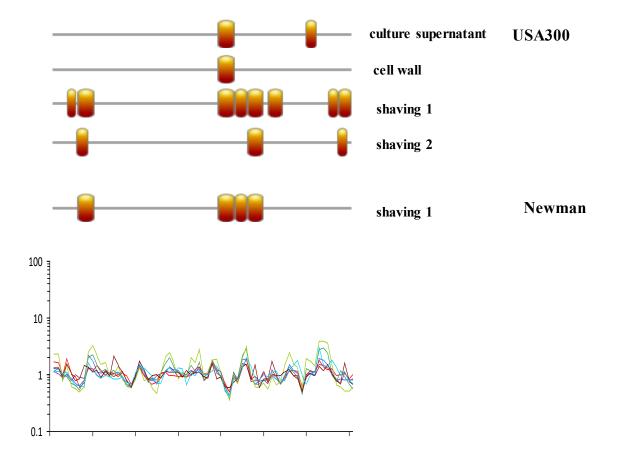
DNA-binding protein HU (Q2FGW9, A6QH22)





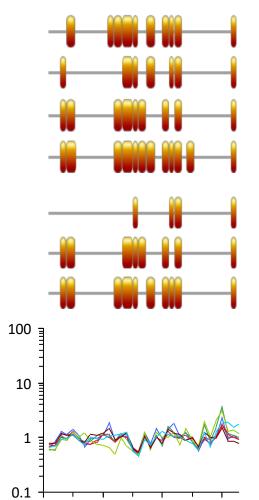


Elongation factor, Ef-G (Q2FJ93, EFG)

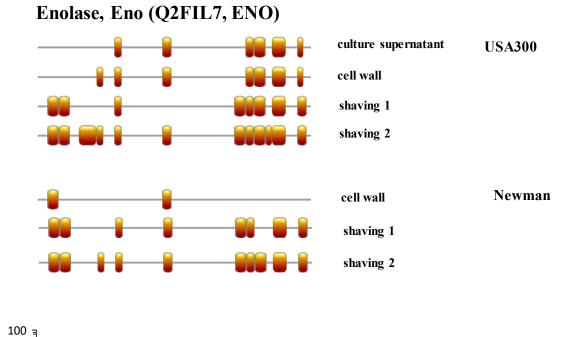


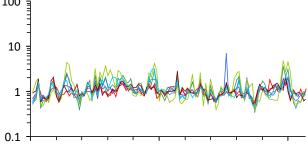
Elongation factor Ts, Ef-Ts (Q2FHI1, EFTS)

Elongation factor Tu, Ef-Tu (Q2FJ92, EFTU)

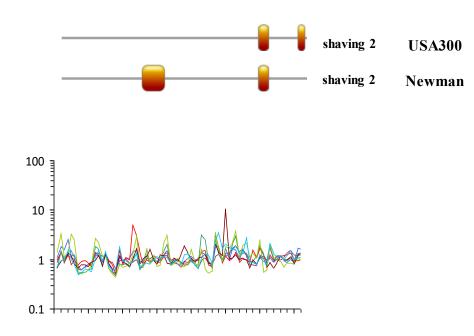


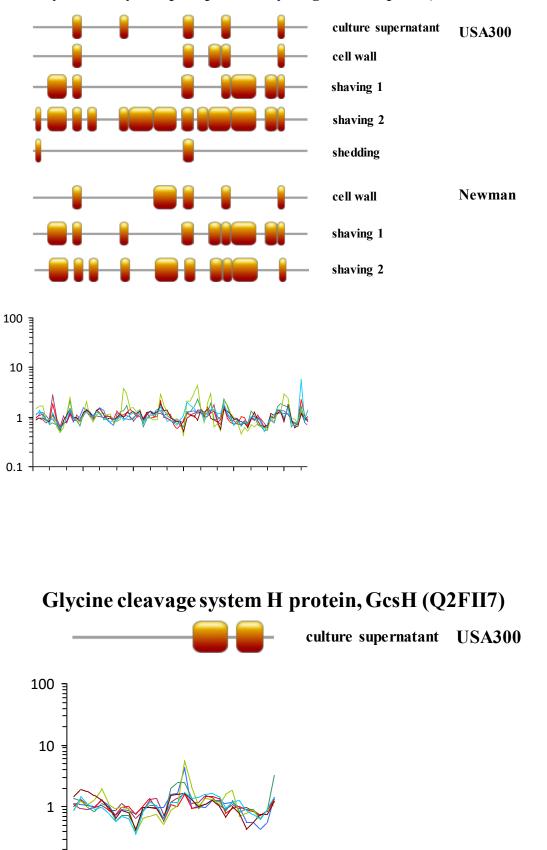
culture supernatant	USA300
cell wall	
shaving 1	
shaving 2	
cell wall	Newman
shaving 1	
shaving 2	





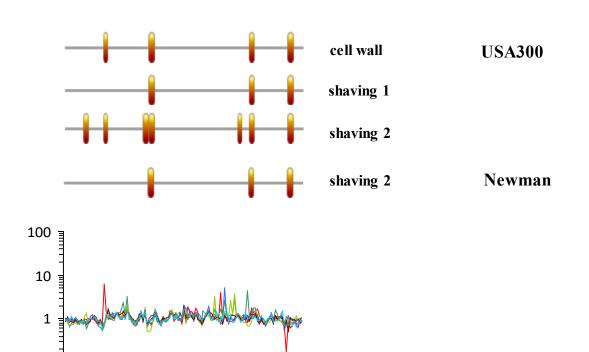
Fructose-bisphosphate-aldolase, Alf1 (Q2FF03, A6QIW9)





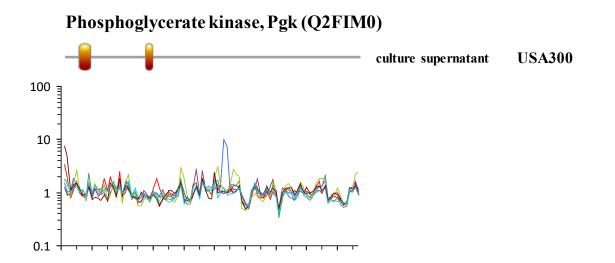
0.1 +

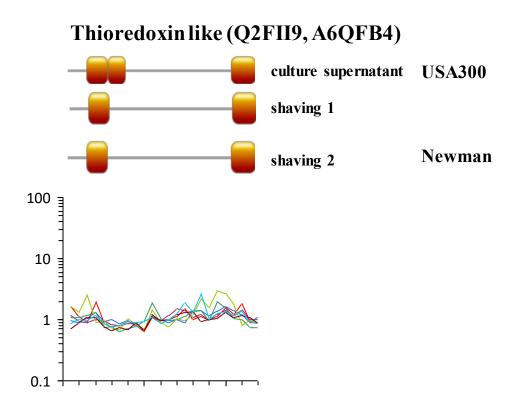
Glyceraldehyde 3-phosphate dehydrogenase GapDH (Q2FIM1, A6QF81)



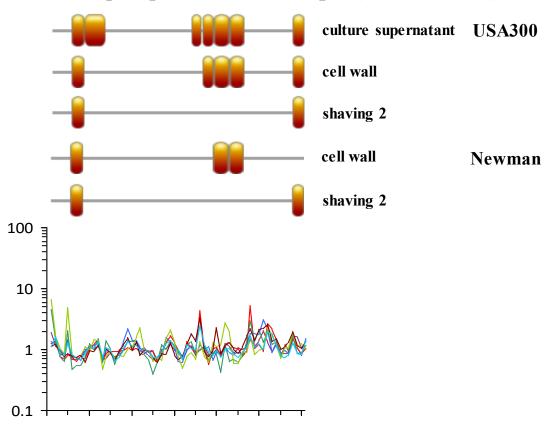
0.1

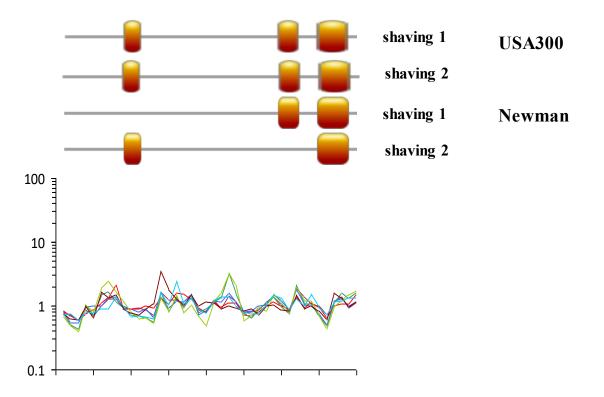
Mqo malate:quinone oxidoreductase (Q2FDQ3, A6QK94)





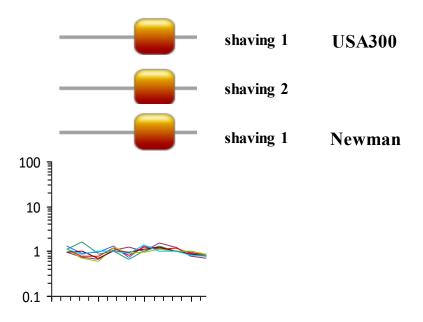
Triosephosphate isomerase, TpiS (Q2FIL9, TPIS)



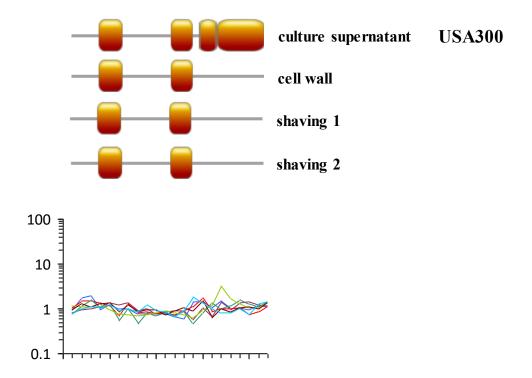


universal stress protein, Y1819 (Q2FG28, A6QHP4)

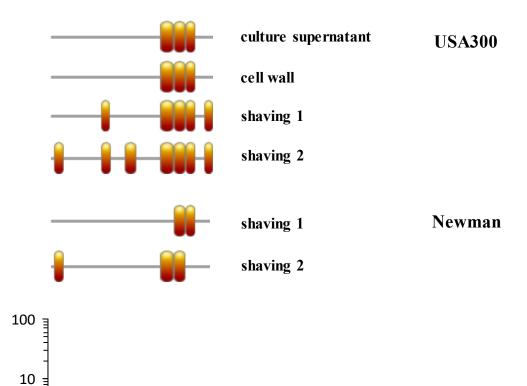
UPF0337protein (A6QHG6)



Virulence factor, EsxA (Q2FJY6)



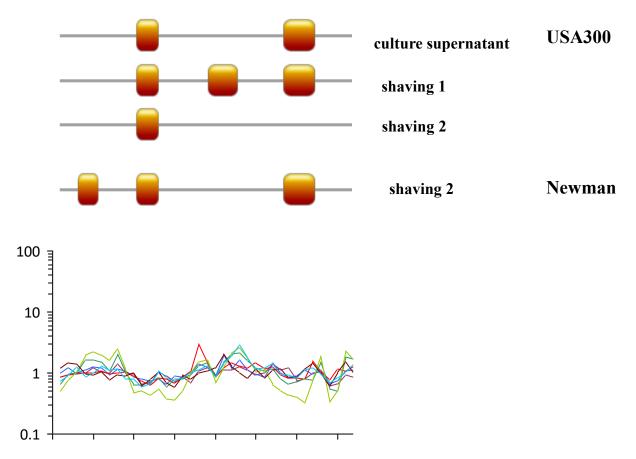
30S ribosomal protein S5, RS5 (Q2FEQ6, RS5)



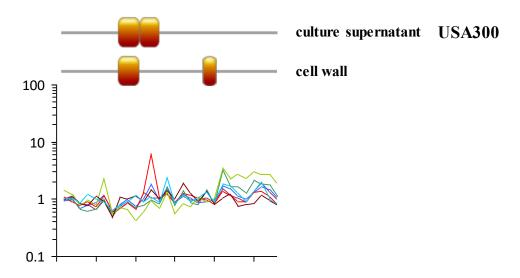
1

0.1 +





30S ribosomal protein S13, RS13 (Q2FER3)



50S ribosomal protein L25 (Ctc) (Q2FJE0, A6QEF4)

