Table S4. Examples for how Protein complexes may be modified (time, post-translational, ribonucleoproteins). (**a**) Heterogeneous complexes: Ribonucleoproteins; (**b**) Changes over time and in metabolic adaptation. There is variation in protein complexes during time and different modes regulate this.

(a)

–RNAse P *in S. aureus:* It removes the leader pre-tRNA sequence. It forms a complex with RNAseP protein. In *S. aureus* even the 3D structure of the RNA P holoenzyme with its single-stranded RNA is known (1D6T; [1])
–tmRNA in S. aureus: Ssra/tmRNA, base pairing to crtMN mRNA, but having an interaction (regulation of translation) with proteins leading to carotenoid pigment *crtM* and *crtN* genes, a key feature of pathogenic S. aureus [2]; furthermore, there is also a RNA-protein interaction involved: SmpB (small protein B) can bind *ssrA* and is involved in ssrA biological function in *Escherichia coli;* in *S. aurues* this is present according to Rfam prediction (RFAM family RF00023).
–summary number on sRNAs: thirty are well known and involved in translational but also protein interactions including central regulation of metabolism RsaE [3] to coordinate metabolism when carbon sources get low. New sRNAs have been discovered recently, for instance ArtR [4], which regulates a-toxin expression via the untranslated region of the sarT mRNA.

(b)

Example 1: The diauxic shift leads to a reassembly of aldolase and pyruvate dehydrogenase complexes as well as changes the activities of the transaminases, amino acid synthesis complexes etc.
Example 2: Redox changes affect protein complexes via Rex-family of repressors [5]. This has then impact on numerous protein complexes, in particular global protein synthesis and on the activity of fermentation pathways under aerobic and anaerobic conditions.
Example 3: Anaerobic conditions The *Staphylococcus aureus* SrrAB two-component system promotes resistance to nitrosative stress and hypoxia. [6].
A general repository: Much more data on these condition-specific proteome changes (without looking at individual protein complexes as analyzed here) can be found in Aureolib [7]. In infection biology of course protection against *S. aureus* is important, we analyze for this the human monoclonal antibody targeting the conserved staphylococcal antigen IsaA (cleaving peptidoglycan) protects mice against *Staphylococcus aureus* bacteremia [8]. Interestingly, the IsaA protein is present in all five strains and has a key interaction with SACOL2583 acetyltransferase. Further predicted interactions include a suitable transporter and cell wall protein ScdA. In particular the latter could boost a potential vaccine further.

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