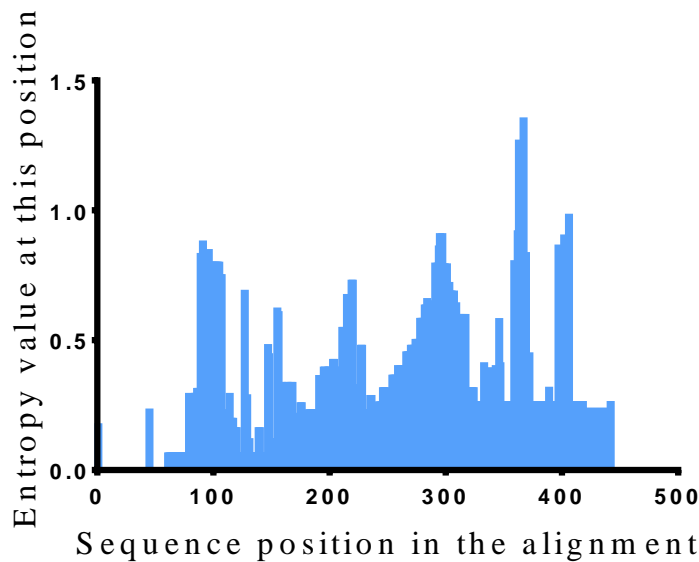
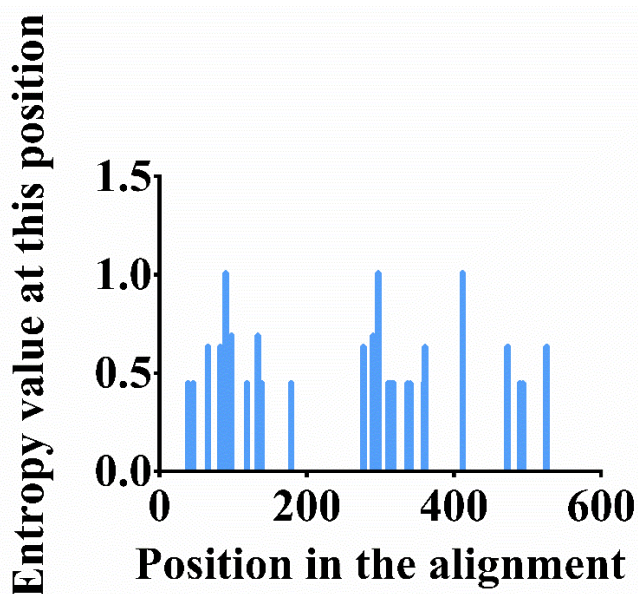


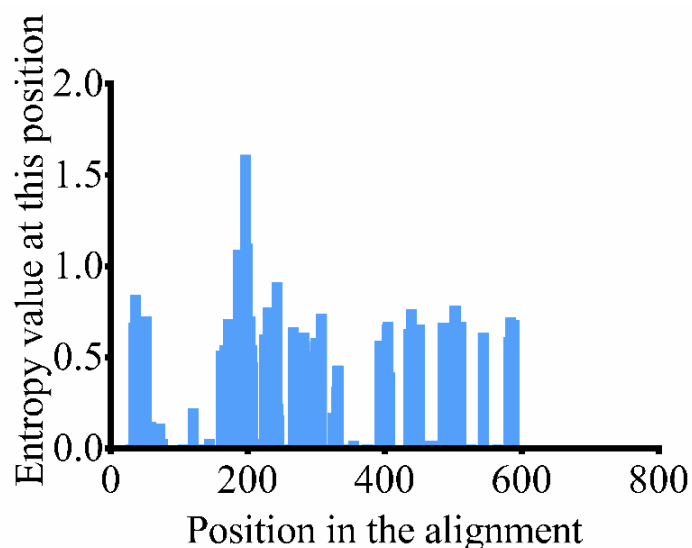
Supplementary figures:



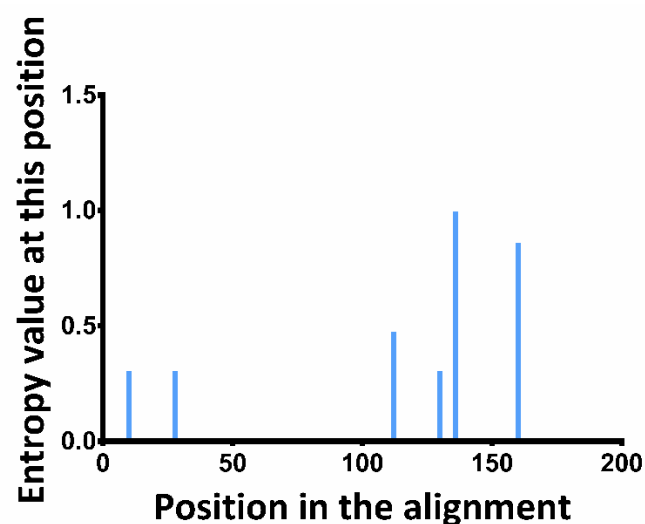
Supplementary figure 1. Entropy map of *P. falciparum* CSP. The entropy value was calculated for each AA position. For this calculation 100 different *P. falciparum* sequences were compared. The first 78 aminoacids are well conserved within the N-terminus. The repeat region differs in the number of NANP repeats. The C-terminus is very entropy-rich. We chose the first 100 sequences available on UniProt for this Shannon Entropy-one calculation by the HIV Sequence database.



Supplementary Figure 2. Entropy map of TRAP. The entropy value was calculated for each AA position. For this calculation 6 different *P. falciparum* sequences were compared. We chose 6 sequences available on UniProt for this Shannon Entropy-one calculation by the HIV Sequence database.



Supplementary Figure 3. Entropy map of *P. falciparum* AMA1. The entropy value was calculated for each AA position. For this calculation 680 different *P. falciparum* sequences of AMA1 were compared. We chose all sequences available on UniProt for this Shannon Entropy-one calculation by the HIV Sequence database.



Supplementary Figure 4. Entropy map of *P. falciparum* EXP1. The entropy value was calculated for each AA position. For this calculation X different *P. falciparum* sequences of EXP1 were compared. We chose all sequences available on UniProt for this Shannon Entropy-one calculation by the HIV Sequence database.