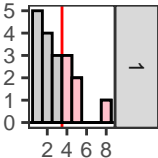
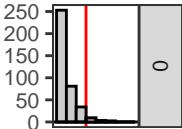


Number of positions  
in first 400 residues



Number of different  
amino acids in data