Text till rapporten

Quality assessments of protein models can be divided into three subfields, clustering-based methods, single-model methods and quasi single-model methods. The clustering methods are based on the assumption that high quality structure models are more likely to be similar, whilst low quality models are expected to be significantly different. As suggested by the name, single-model methods use only the model being evaluated, and its intrinsic properties, for example a contact map. A quasi single-model method adopts the single-model method for selecting a number high-quality protein models and thereafter use them as reference in further evaluations, resembling a fusion of the clustering and the single-model method. <https://www.nature.com/articles/srep31571>