

**P037** Docking analysis applied to the interaction between polyphenols and mammalian 20S proteasome.  
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Molecular docking of small ligands to macromolecules represent an useful device to predict interactions between potential partners. Previous studies reported on the role of polyphenols as inhibitors of the mammalian 20S proteasome. On such basis, we performed a molecular docking analysis between some flavonoids, demonstrated to have the highest binding affinity, and both constitutive and inducible proteasome active subunits in order to gain insight into the potential mechanism of interaction. The models for the 20S proteasome inducible subunits were obtained by homology modeling.

Among all flavonoids used, EGCG showed the highest affinity for the proteasome subunits, in particular  $\beta 5$  and  $\beta 5i$  subunits (-66 kcal/mol and -83,9 kcal/mol respectively), known to be related to the chymotrypsin-like and BrAAP activities. Overall, flavonoids showed a higher affinity for the inducible subunits, confirming the trend reported by *in vitro* studies.

The contribution of the various types of interaction (van der Waals, electrostatic, H-bonds) to the stability of the flavonoid-proteasome complex was dissected.

The differences between the *in vitro* measured affinities and the predicted values obtained by docking analysis have been discussed in terms of conformational changes upon ligand binding.