The proteasome controls a multitude of cellular processes through protein degradation and has been identified as a therapeutic target in oncology (1). However, our understanding of its function and the development of specific modulators are hampered by the lack of a straightforward method to determine the overall proteasome status in biological samples.

Although the cylindrical α7β7β7β7 barrel-like structure of the 20S catalytic core proteasome has been preserved throughout evolution, the oligomeric protease has evolved, resulting in a higher heterogeneity of subunit compositions in mammals.

The cylindrical α7β7β7β7 barrel-like structure of the 20S catalytic core proteasome has been preserved throughout evolution, the oligomeric protease has evolved, resulting in a higher heterogeneity of subunit compositions in mammals.

The cylindrical α7β7β7β7 barrel-like structure of the 20S catalytic core proteasome has been preserved throughout evolution, the oligomeric protease has evolved, resulting in a higher heterogeneity of subunit compositions in mammals.

The cylindrical α7β7β7β7 barrel-like structure of the 20S catalytic core proteasome has been preserved throughout evolution, the oligomeric protease has evolved, resulting in a higher heterogeneity of subunit compositions in mammals.

The cylindrical α7β7β7β7 barrel-like structure of the 20S catalytic core proteasome has been preserved throughout evolution, the oligomeric protease has evolved, resulting in a higher heterogeneity of subunit compositions in mammals.