Although deep learning approaches have had tremendous success in image, video and audio processing, computer vision, and speech recognition, their applications to three-dimensional (3D) biomolecular structural data sets have been hindered by the geometric and biological complexity. To address this problem we introduce the element-specific persistent homology (ESPH) method. ESPH represents 3D complex geometry by one-dimensional (1D) topological invariants and retains important biological information via a multichannel image-like representation. This representation reveals hidden structure-function relationships in biomolecules. We further integrate ESPH and deep convolutional neural networks to construct a multichannel topological neural network (TopologyNet) for the predictions of protein-ligand binding affinities and protein stability changes upon mutation. To overcome the deep learning limitations from small and noisy training sets, we propose a multi-task multichannel topological convolutional neural network (MM-TCNN). We demonstrate that TopologyNet outperforms the latest methods in the prediction of protein-ligand binding affinities, mutation induced globular protein folding free energy changes, and mutation induced membrane protein folding free energy changes.AVAILABILITY: weilab.math.msu.edu/TDL/.