1. Feed-forward Neural Networks (FNNs): These are the simplest type of neural network and can work well for many tasks. They do not have any memory or recurrent connections, so they might not be the best choice if the order of the amino acids in your sequences is important. However, they are easy to implement and can serve as a good starting point.
2. Convolutional Neural Networks (CNNs): These networks are particularly effective for data with a grid-like topology (like images or time-series data). They can also be used for sequence data like yours, and they might be a good choice if local patterns within the sequences are important for predicting the ddG values.
3. Recurrent Neural Networks (RNNs), Long Short-Term Memory (LSTM) networks, or Gated Recurrent Unit (GRU) networks: These networks are designed to handle sequence data and can capture temporal dependencies between different parts of a sequence. They might be a good choice if the order of the amino acids in your sequences is important.
4. Transformer Models: These models, like BERT or the original Transformer, use self-attention mechanisms to weigh the importance of different parts of a sequence when making predictions. They've been highly successful for many tasks involving sequence data, and they might be a good choice if both local and global patterns within the sequences are important for predicting the ddG values.
5. Graph Neural Networks (GNNs): If you can represent your protein structures as graphs (with amino acids as nodes and some form of connection between them as edges), GNNs can be a powerful tool for prediction. They excel in capturing the relational information between different nodes.