Davis

input\_csv\_path = "/content/drive/MyDrive/Kd\_Meshari/UniProt/uniprot\_sequences\_with\_deletions11.csv"

input\_csv\_path = "/content/drive/MyDrive/Kd\_Meshari/data/davis/proteins.txt"

original\_ligands\_path = "/content/drive/MyDrive/Kd\_Meshari/data/davis/ligands\_can.txt"

input\_file = '/content/drive/MyDrive/Drug-Target-Binding-Affinity/UniProt/input\_data.csv'

test\_fold = json.load(open(fpath + "folds/test\_fold\_setting" + str(setting\_no)+".txt"))

train\_folds = json.load(open(fpath + "folds/train\_fold\_setting" + str(setting\_no)+".txt"))

Kiba

input\_csv\_path = "/content/drive/MyDrive/Kd\_Meshari/data/kiba/proteins.txt"

input\_csv\_path = "/content/drive/MyDrive/Kd\_Meshari/proccessed\_kiba/combined\_data.csv"

input\_csv\_path = "/content/drive/MyDrive/Kd\_Meshari/proccessed\_kiba/domain\_binding\_site\_summary\_updated\_manually.csv"

original\_ligands\_path = "/content/drive/MyDrive/Kd\_Meshari/data/kiba/ligands\_can.txt"

test\_fold = json.load(open(fpath + "folds/test\_fold\_setting" + str(setting\_no)+".txt"))

train\_folds = json.load(open(fpath + "folds/train\_fold\_setting" + str(setting\_no)+".txt"))