## needcoffee

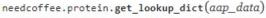
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Protein module

build dict out of aminoacid properties dataframe :param aap\_data: :return:

lookup\_dict: holdes mapping dicts for diff properties

class needcoffee.protein.protein(protein\_id, lookup\_dict)

The class protein allows for analysing and ... .. attribute:: protein\_id

identifying code used by uniprot to assign a specific pos to the protein that is being looked up

type: str lookup\_dict

dictionary providing the aminoacid to value references of the chosen properties

Type: dict

sq

protein sequence

Type: str

def get\_data():

pulls sequence form uniprot based on the protein id

def map(self, prop):

builds a list of values using the sequence and mapping dict to link sequence and values

def map\_sld\_wdw(self, prop, wd):

builds a list of property values following the sequence using a sliding window

def plot(self, prop, sld=False, wd=None):

plots a selected properties values against the sq of the protein that was created as instance the plot will be shown in a browser setting

get data()

[A] pulls sq form uniprot given an id name inspired by paul for prettyness :return: said proteins sq

map (prop)

[B] builds a list of values using the sq and mapping dict to link sq and values :param prop: property to be analysed :return: prop\_val\_sq: property value sq

map\_sld\_wdw(prop, wd)

[D] builds list of property values following sq using a sliding window :param prop: property to be analysed :param wd: width of analysing window :return:

plot(prop, sld=False, wd=None)

plots a selected properties values against the sq of the protein that was created as instance the plot will be shown in a browser setting :param prop: name of the property of the aminoacid properties that we want to plot :param sld: do you want to use a sliding window approach please set this to True :param wd: width of the sliding window should you decide to go with said option :return:

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