

Eindopdracht

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Inleiding

- Taakverdeling

- Opdracht in het kort;

helix & sheet naar output

helix, sheet en volledige sequence → graph

Alle functies

<code>read()</code>	- Inlezen en openen bestand
<code>pro_sequence()</code>	- Aanmaken proteïne sequentie
<code>helix()</code>	- Aanmaken Helix sequentie
<code>sheet()</code>	- Aanmaken Sheet sequentie
<code>printer()</code>	- Header aanmaken + Wegschrijven naar ander bestand
<code>graph()</code>	- Maken van histogram m.b.v. sequentie
<code>graph_helix()</code>	- Maken van histogram m.b.v. sequentie
<code>graph_sheet()</code>	- Maken van histogram m.b.v. sequentie

helix()

```
def helix():
    global helix_sequence
    helix_list = []
    helix_start = 0
    helix_stop = 0
    helix_count = 0
    helix_sequence = ''
    file_obj = open(file)
    for line in file_obj:
        helix_count = 0
        if line.startswith('HELIX'):
            helix_list = line.split()
            helix_start = int(helix_list[5])
            helix_stop = int(helix_list[8])
            for char in protein_letters:
                if helix_count >= helix_start and helix_count <= helix_stop:
                    helix_sequence += char
                helix_count += 1
```

sheet()

```
def sheet():
    global sheet_sequence
    sheet_count = 0
    sheet_sequence = ''
    file_obj = open(file)
    for line in file_obj:
        sheet_count = 0
        if line.startswith('SHEET'):
            letter = False
            sheet_list = []
            sheet_start = ''
            sheet_stop = ''
            sheet_list = line.split()
            for char in sheet_list[6]:
                if char.isalpha():
                    letter = True
                    break
            else:
                sheet_start += char
                sheet_stop = sheet_list[9]

            if letter == True:
                for char in sheet_list[5]:
                    if not char.isalpha():
                        sheet_start += char
                for char in sheet_list[7]:
                    if not char.isalpha():
                        sheet_stop += char

            for char in protein_letters:
                if sheet_count >= int(sheet_start) and sheet_count <= int(sheet_stop):
                    sheet_sequence += char
                sheet_count += 1
    file_obj.close()
```

SHEET	1	AA1	2	VAL	A	393	THR	A	398	0	
SHEET	2	AA1	2	GLU	A	479	LYS	A	483	-1	O
SHEET	1	AA2	5	ILE	A	488	CYS	A	491	0	
SHEET	2	AA2	5	LEU	A	568	ASP	A	572	1	O
SHEET	3	AA2	5	ARG	A	600	VAL	A	603	1	O
SHEET	4	AA2	5	LEU	A	453	GLY	A	458	1	N
SHEET	5	AA2	5	LYS	A	615	LEU	A	619	1	O
SHEET	1	AA3	3	ALA	A	A1225	ILE	A	A1234	0	
SHEET	2	AA3	3	MET	A	A1210	LYS	A	A1218	-1	N
SHEET	3	AA3	3	ASN	A	A1262	GLN	A	A1268	-1	O
SHEET	1	AA4	6	PHE	A	A1286	ILE	A	A1289	0	
SHEET	2	AA4	6	ILE	A	A1366	ASP	A	A1370	1	O
SHEET	3	AA4	6	THR	A	A1396	CYS	A	A1400	1	O
SHEET	4	AA4	6	ARG	A	A1239	LEU	A	A1243	1	N
SHEET	5	AA4	6	GLN	A	A1412	GLU	A	A1417	1	O
SHEET	6	AA4	6	LYS	A	A1420	TYR	A	A1424	-1	O

graph()

```
def graph():
    h = '#'
    total_p = 0
    count_dict = {'C': 0, 'D': 0, 'S': 0,
                  'Q': 0, 'K': 0, 'I': 0,
                  'P': 0, 'T': 0, 'F': 0,
                  'N': 0, 'G': 0, 'H': 0,
                  'L': 0, 'R': 0, 'W': 0,
                  'A': 0, 'V': 0, 'E': 0,
                  'Y': 0, 'M': 0, '-': 0}

    for p in protein_letters:
        total_p += 1
        count_dict[p] += 1

    print('\nGrafiek voor de protein sequence:')
    for key in count_dict.keys():
        pro_p = count_dict[key] / total_p * 100
        print(key, count_dict[key], ' ', h * int(round(pro_p)), (round(pro_p)), "%")
```

```
Grafiek voor de protein sequence:
C 18      # 1 %
D 58      #### 4 %
S 125     ##### 8 %
Q 68      ##### 5 %
K 92      ##### 6 %
I 119     ##### 8 %
P 45      ### 3 %
T 83      ##### 6 %
F 86      ##### 6 %
N 55      ##### 4 %
G 84      ##### 6 %
H 25      ## 2 %
L 185     ##### 12 %
R 78      ##### 5 %
W 23      ## 2 %
A 83      ##### 6 %
V 91      ##### 6 %
E 94      ##### 6 %
Y 40      ### 3 %
M 37      ## 2 %
- 19      # 1 %
```

Output command line

Grafiek voor de protein sequence:

C 18	# 1 %
D 58	#### 4 %
S 125	##### 8 %
Q 68	##### 5 %
K 92	##### 6 %
I 119	##### 8 %
P 45	### 3 %
T 83	##### 6 %
F 86	##### 6 %
N 55	#### 4 %
G 84	##### 6 %
H 25	## 2 %
L 185	##### 12 %
R 78	##### 5 %
W 23	## 2 %
A 83	##### 6 %
V 91	##### 6 %
E 94	##### 6 %
Y 40	### 3 %
M 37	## 2 %
- 19	# 1 %

Grafiek voor de helix sequence:

C 11	# 1 %
D 25	### 3 %
S 56	##### 7 %
Q 36	#### 4 %
K 49	##### 6 %
I 72	##### 9 %
P 18	## 2 %
T 37	#### 4 %
F 58	##### 7 %
N 20	## 2 %
G 37	#### 4 %
H 15	## 2 %
L 124	##### 15 %
R 48	##### 6 %
W 17	## 2 %
A 60	##### 7 %
V 59	##### 7 %
E 34	#### 4 %
Y 23	### 3 %
M 29	#### 4 %
- 0	0 %

Grafiek voor de sheet sequence:

C 2	## 2 %
D 4	#### 4 %
S 7	##### 8 %
Q 2	## 2 %
K 4	#### 4 %
I 12	##### 13 %
P 1	# 1 %
T 5	##### 5 %
F 3	### 3 %
N 2	## 2 %
G 6	##### 7 %
H 2	## 2 %
L 15	##### 16 %
R 1	# 1 %
W 0	0 %
A 4	#### 4 %
V 9	##### 10 %
E 8	##### 9 %
Y 3	### 3 %
M 1	# 1 %
- 0	0 %

Uitkomst printer()

```
1 >5UAK MEMBRANE PROTEIN, HYDROLASE HELIX
2 VVSKLFFSTRPILRKGYRQRADNLSEKLEREWDRELASKKLINALRRCFFWRFMFYGIFLYLGEVTKAVQ
3 LLLGRIIASYDRSIAIYLGIGLCLLFIVRTL LLLHPAIFGLHHIGMQMRIAMFSLIYKKT LKLSRVLDKIG
4 LVSLLSNNLNKFDEGLALAHFVWIAPLQVALLMGLIWSAFCGLGFLIVLALFQAGLGRMMM KYRDQRAGK
5 SERLVITSEMIENIIQSVKAYCWAMEKMIENLRQTELKLTRKAAYVRYFNSSAFFFSGFFV VFLSVLPYA
6 IKGRKIFTTISFCIVLRMAVTRQQFPWAVQ TWYDSLGAINKIQDFLQKKTSLLMVIMGEIKENI IFGEYR
7 RSVIKACQLEEDISKFAGGQRARISLARAVYKDVLTEKEIFESCVCCKLMAMEHLKKADFSELQNLQPPDF
8 SKLMGWNTYLRYITVSLIFVLIWCLVIFLAEVAASLVVLWLLYIYVGVAADTLLAPLVHTLITVSKILHH
9 MLHSV LQMSTLNTLKAGGILNRF SKDIAILD D LLLPLTIFDFIQ LLLIVIGAI AVVAVLQPIFVATVPVI
10 AFIMLRAYFLQTSQQ LKQLESEGRSPIFTHLVTSLKGLLWTLRAFG RQPYFETLFHKALNLHTANWFLYL
11 TLRWFQMRIEMIFVIF FIAVTFISILT TGRVGIILT LAMNIMMSTLQWAVNSSIDVDSL MRSVSRVFKFI
12 MPKSTLLSAFLRLLQQWRKFRKNLDPDQE IWKVADEVGRSVIEQFVDGGCHGHKQLMCLARSVLSKPSAH
13 DPVTYQIIRRTLKQAF AEAMLEIQKLLNERSLFLEKASVVSKLFFSW
14
15 >5UAK MEMBRANE PROTEIN, HYDROLASE SHEET
16 MENVTAGKIKHSFCSYLLDSILVTLAVAGSILILHILENISFSISTVKDLTAKYTEGEIQIGVIPLLLDE
17 ILCEVGLLGFLVIEEVRQYD
18
19
```