

## Net-SSPredict

Program for secondary structure prediction.

Neural nets based on profile of psiBLAST comparison of the query sequence with NR database.

**!Attention! This program uses SoftBerry web service and requires the computer should be connected to the internet.**

### Example:

```
>T0388
Length=174
```

```
PredSS          bbbbbb      aa      bbbbbbbb      aaa
AA seq          ENLYFQSMINSFYAFEVKDAKGRTVSLEKYKGKVSLLVNVASDCQLTDRN
ProbA           002420022200000000000000000552110000000000110000766
ProbB           00002200000334888851103452000100499999985010000000
```

```
PredSS          aaaaaaaaaa  bbbbbbbb      aaaaaaaaaa  bbb
AA seq          YLGLKELHKEFGPSHFSVLAFFPCNQFGESEPRPSKEVESFARKNYGVTFP
ProbA           77999999998520000000000121301000089899999971100000
ProbB           000000000000038999987310000000000000000000104879
```

```
PredSS          bb          aaaaaaaa      bbbbbb      bbbbbbb
AA seq          IFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEE
ProbA           001000000101158887876430000000000000000000000000000
ProbB           864534422000000000000000000133438988920008999983000
```

```
PredSS          aaaaaaaaaaaaaaaaaa
AA seq          PIEVIRPDIAALVRQVIKKKEDL
ProbA           05568899999999997743000
ProbB           00000000000000000000000000
```

Where:

**PredSS** - secondary structure predicted: **a** - alpha helix, **b** - beta sheet;

**AA seq** - amino acid sequence in one-letter form;

**ProbA** - probability of 'a' structure for the position,

**ProbB** - probability of 'b' structure for the position.

```
>T0388
Length=174
```

```
1 E C 0 0
2 N C 0 0
3 L C 2 0
4 Y C 4 0
5 F C 2 2
6 Q C 0 2
7 S C 0 0
8 M C 2 0
```

9	I	C	2	0
10	N	C	2	0
11	S	C	0	0
12	F	C	0	3
13	Y	C	0	3
14	A	C	0	4
15	F	B	0	8
16	E	B	0	8
17	V	B	0	8
18	K	B	0	8
19	D	B	0	5
20	A	C	0	1
21	K	C	0	1
22	G	C	0	0
23	R	C	0	3
24	T	C	0	4
25	V	C	0	5
26	S	C	0	2
27	L	A	5	0
28	E	A	5	0
29	K	C	2	0
30	Y	C	1	1
31	K	C	1	0
32	G	C	0	0
33	K	C	0	4
34	V	B	0	9
35	S	B	0	9
36	L	B	0	9
37	V	B	0	9
38	V	B	0	9
39	N	B	0	9
40	V	B	0	8
41	A	B	0	5
42	S	C	1	0
43	D	C	1	1
44	C	C	0	0
45	Q	C	0	0
46	L	C	0	0
47	T	C	0	0
48	D	A	7	0
49	R	A	6	0
50	N	A	6	0
51	Y	A	7	0
52	L	A	7	0
53	G	A	9	0
54	L	A	9	0

. . .

Where:

**1 column** - a number of position,

**2 column** - amino acid sequence in one-letter form,

**3 column** - secondary structure predicted: **A** - alpha helix, **B** - beta sheet;

**4 column** - probability of 'A' structure for the position,

**5 column** - probability of 'B' structure for the position.

**Parameters:**

<b>Input</b>	
<b>Sequence</b>	Name of input file with protein sequence in FASTA-format.
<b>Output</b>	
<b>Vertical Prediction</b>	Name of the output file with Vertical Prediction.
<b>Horisontal Prediction</b>	Name of the output file with Horisontal Prediction.