Restriction_Sites_Hider.py (RSH) also known as Restriction_Sites_Hider_3000 (http://t.me/restriction_sites_hider_3000_BOT)

Instruction

README.md also exist in PDF format -> **README.pdf**

Our team

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Requirements

PYTHON:

- BioPython: `pip install biopython`

Installation

```
git clone https://github.com/trituration/rsh.git
cd rsh/
pip install -e .
```

The source code of the telegram bot is located in the `bot` directory. But it not used for script.

Usage

The command `restriction_sites_hider.py -h` return:

```
usage: restriction_sites_hider.py [-h]

{codon_tables,enzymes,find_known_sites,find_by_pattern,remove_sites,remove_by_
pattern}
                  ...
```

```
positional arguments:

{codon_tables,enzymes,find_known_sites,find_by_pattern,remove_sites,remove_by_
pattern}
                        Available commands:
    codon_tables        Return avalibale codon tables in STDOUT
    enzymes             Return avalibale restriction enzymes in STDOUT
    find_known_sites    Find sites in fasta file for given restriction enzyme
    find_by_pattern     Find sites in fasta file for given restriction enzyme
    remove_known_sites  Return modified FASTA
    remove_by_pattern   Return modified FASTA

optional arguments:
  -h, --help            show this help message and exit
```

Put executable file and database restriction_enzymes_database.tsv in working directory.
Restriction sites removes in several steps:

1. Finding all possible restriction sites in user's sequence
2. Choosing restriction sites that must be hided by User
3. Create new fasta file with hided restriction sites.

Preparatory steps

1. Chose genetic code table
   This programm support different types of genetic code tables. All possible tables user can see by following command:

```
restriction_sites_hider.py codon_tables
```

This command return this table:

```
The Standard Code 1
The Vertebrate Mitochondrial Code 2
The Yeast Mitochondrial Code 3
The Mold, Protozoan, and Coelenterate Mitochondrial Code and the
Mycoplasma/Spiroplasma Code 4
The Invertebrate Mitochondrial Code 5
The Ciliate, Dasycladacean and Hexamita Nuclear Code 6
The Echinoderm and Flatworm Mitochondrial Code 9
The Euplotid Nuclear Code 10
The Bacterial, Archaeal and Plant Plastid Code 11
The Alternative Yeast Nuclear Code 12
The Ascidian Mitochondrial Code 13
The Alternative Flatworm Mitochondrial Code 14
Chlorophycean Mitochondrial Code 16
Trematode Mitochondrial Code 21
Scenedesmus obliquus Mitochondrial Code 22
```

```
Thraustochytrium Mitochondrial Code 23
Rhabdopleuridae Mitochondrial Code 24
Candidate Division SR1 and Gracilibacteria Code 25
Pachysolen tannophilus Nuclear Code 26
Karyorelict Nuclear Code 27
Condylostoma Nuclear Code 28
Mesodinium Nuclear Code 29
Peritrich Nuclear Code 30
Blastocrithidia Nuclear Code 31
Cephalodiscidae Mitochondrial UAA-Tyr Code 33
```

Standard genetic code is set by defeult. If user want to change it to anyone else he/she should set the number on the right side of the table as input paramter to every function.

2. User should choose restriction site or restriction enzyme which sites he wants to hide. In this programm used database Rebase v.110. Obtain list of known restriction enzymes by this command:

```
restriction_sites_hider.py enzymes
```

Restriction sites finding

For restriction sites finding it's possible to use one of the following commands `find_known_sites` or `find_by_pattern`.
If user knew restriction enzyme name he/she use `find_known_sites` command
For example:

```
restriction_sites_hider.py find_known_sites ./NC_005816.fna YenBI test.txt
```

where `./NC_005816.fna` - original fasta, `YenBI` - enzyme's name and `test.txt` - output file

If user don't know restriction enzyme name or it's not present in database - use `find_by_pattern`
For example:

```
restriction_sites_hider.py find_by_pattern ./NC_005816.fna AGCCAG test.txt
```

where `./NC_005816.fna` - original fasta, `AGCCAG` - restriction site and `test.txt` - output file

Additional arguments are:

```
-m MIN, --min MIN - minimal protein length that coded in ORF
-c CODONE, --codone CODONE - index of genetic code table
```

Choose restriction sites to hide by user

Output from previous command `find_known_sites` or `find_by_pattern` (for example `test.txt`) contain table that look like:

```
pos strand  site  region  codone_pos
6899  + GGATCC  in_coding_region  6900
7312  + GGATCC  in_noncoding_region  7312
```

where
`pos` - start of restrictions site
`strand` - + or - strand of DNA
`site` - site that finds
`region` - show is this restriction site in ORF or not

If you don't want to hide some of sites just delete string that conatin it from this file. All remaining sites will be hided.

Sites hiding

For hiding restriction sites usr should use one of the following commands: `remove_known_sites` or `remove_by_pattern`.
Choose same command as you used for Restriction sites finding

For example:

```
restriction_sites_hider.py remove_by_pattern ./NC_005816.fna test.txt AGCCAG
new_fasta.fa
```

where
`./NC_005816.fna` is the same fasta file that used for command `python program.py find_by_pattern`
`test.txt` - output from `python program.py find_by_pattern` (optionally edited by user)
`AGCCAG` - restriction enzyme site (same as used for previous command)
`new_fasta.fa` - new fasta file with hided restrictions sites

Another example:

```
restriction_sites_hider.py remove_known_sites ./NC_005816.fna test.txt YenBI
new_fasta.fa
```

Example run

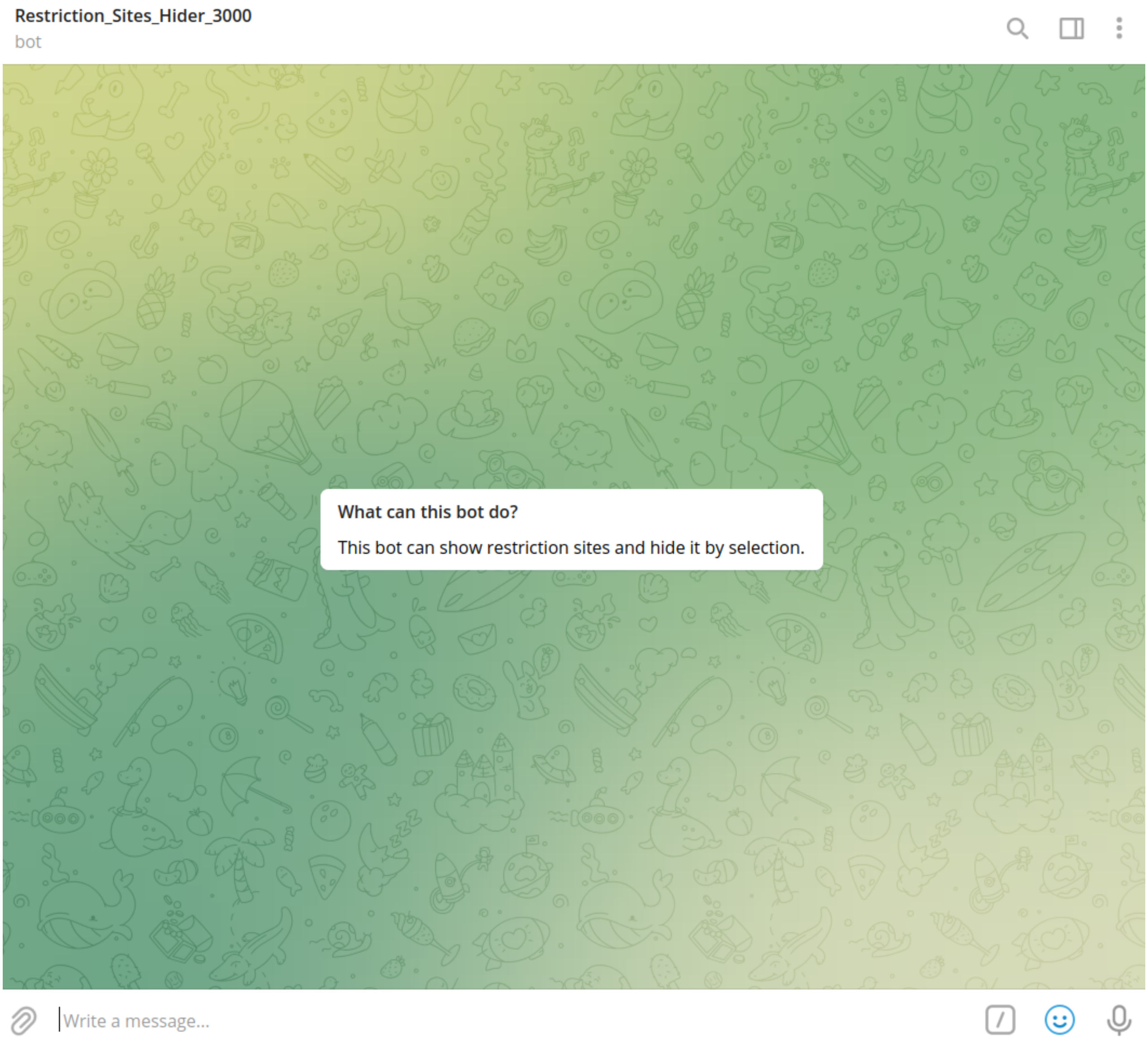
Example data (fasta file of plasmid) and bash script avalibale in `example` directory
In this directoty just run:

```
chmod + x ./example.sh
./example.sh
```

Below described instruction to Teleram bot (http://t.me/restriction_sites_hider_3000_BOT)

This bot hiding restriction sites by users choice. Based on restriction_sites_hider.py (https://github.com/trituration/rsh).

1. If you want to start, just send /start or press the start link.

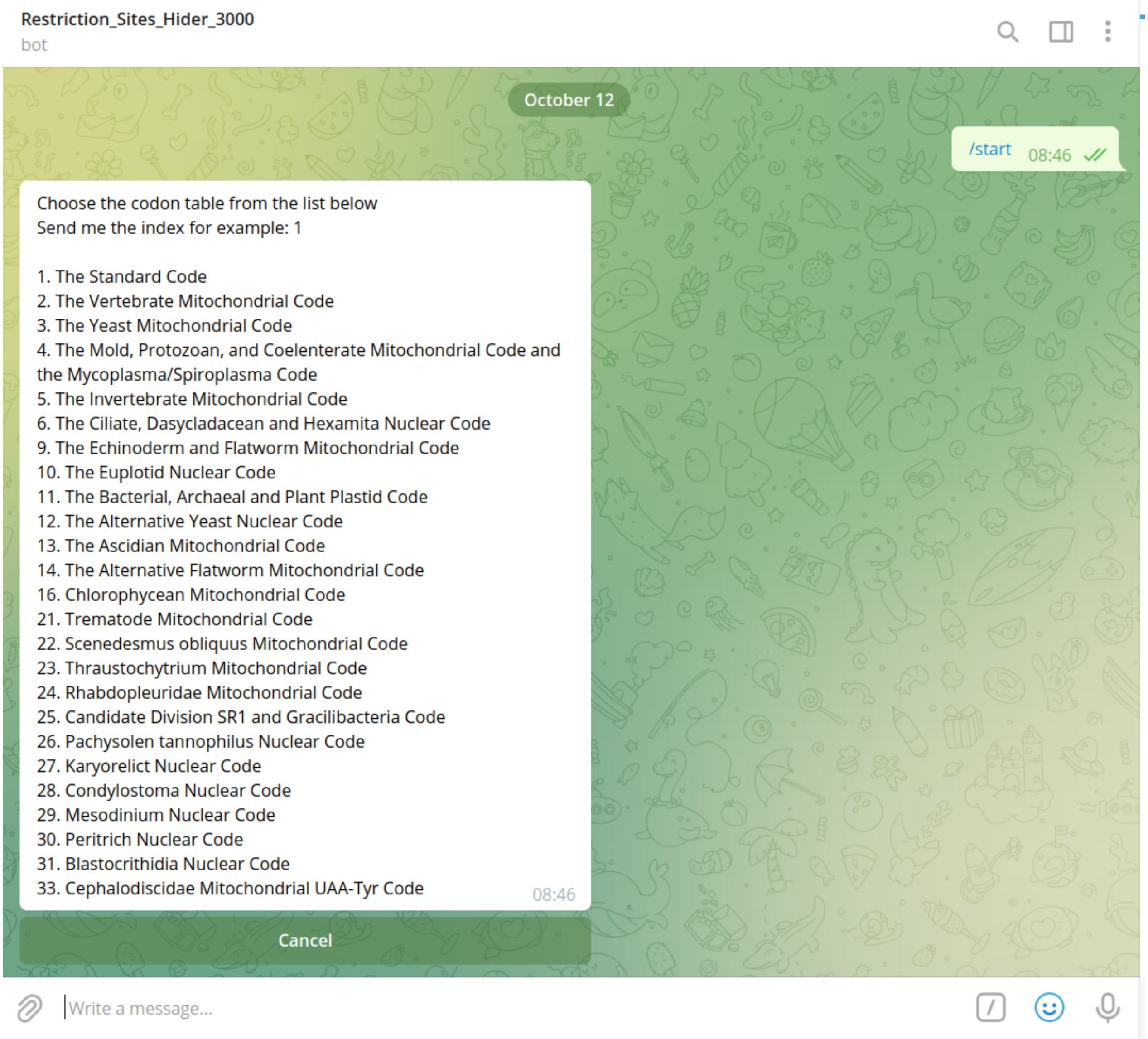


Restriction_Sites_Hider_3000
bot

What can this bot do?

This bot can show restriction sites and hide it by selection.

2. Bot will ask you to choose the codon table which supposed to be used



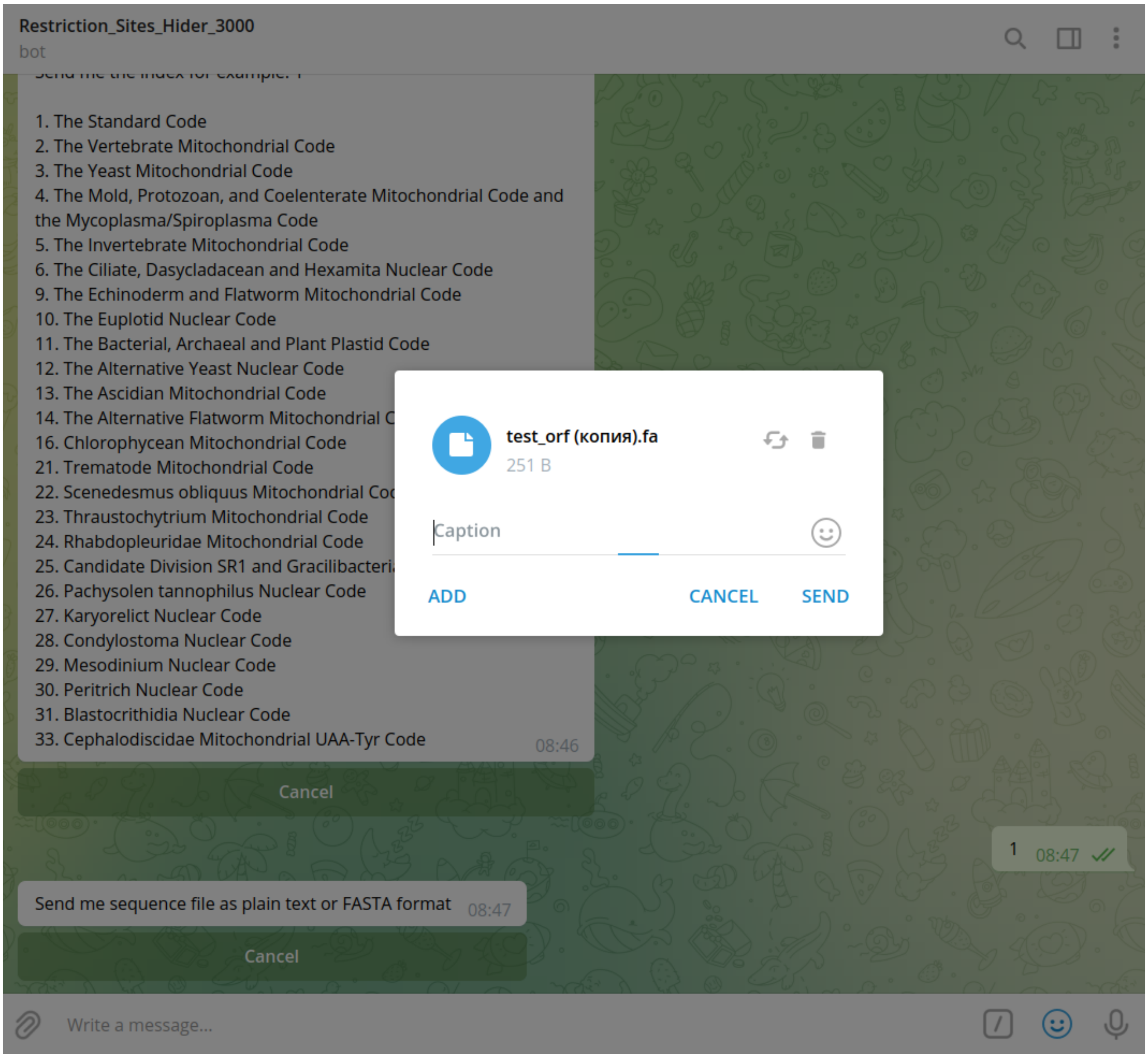
/start 08:46

Choose the codon table from the list below
Send me the index for example: 1

1. The Standard Code
2. The Vertebrate Mitochondrial Code
3. The Yeast Mitochondrial Code
4. The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code
5. The Invertebrate Mitochondrial Code
6. The Ciliate, Dasycladacean and Hexamita Nuclear Code
9. The Echinoderm and Flatworm Mitochondrial Code
10. The Euplotid Nuclear Code
11. The Bacterial, Archaeal and Plant Plastid Code
12. The Alternative Yeast Nuclear Code
13. The Ascidian Mitochondrial Code
14. The Alternative Flatworm Mitochondrial Code
16. Chlorophycean Mitochondrial Code
21. Trematode Mitochondrial Code
22. Scenedesmus obliquus Mitochondrial Code
23. Thraustochytrium Mitochondrial Code
24. Rhabdopleuridae Mitochondrial Code
25. Candidate Division SR1 and Gracilibacteria Code
26. Pachysolen tannophilus Nuclear Code
27. Karyorelict Nuclear Code
28. Condylostoma Nuclear Code
29. Mesodinium Nuclear Code
30. Peritrich Nuclear Code
31. Blastocrithidia Nuclear Code
33. Cephalodiscidae Mitochondrial UAA-Tyr Code

08:46

3. Upload your sequence txt file as plain text or FASTA format. Bot support only DNA fasta with 1 sequence. MultiFasta will work in an unforeseen way.



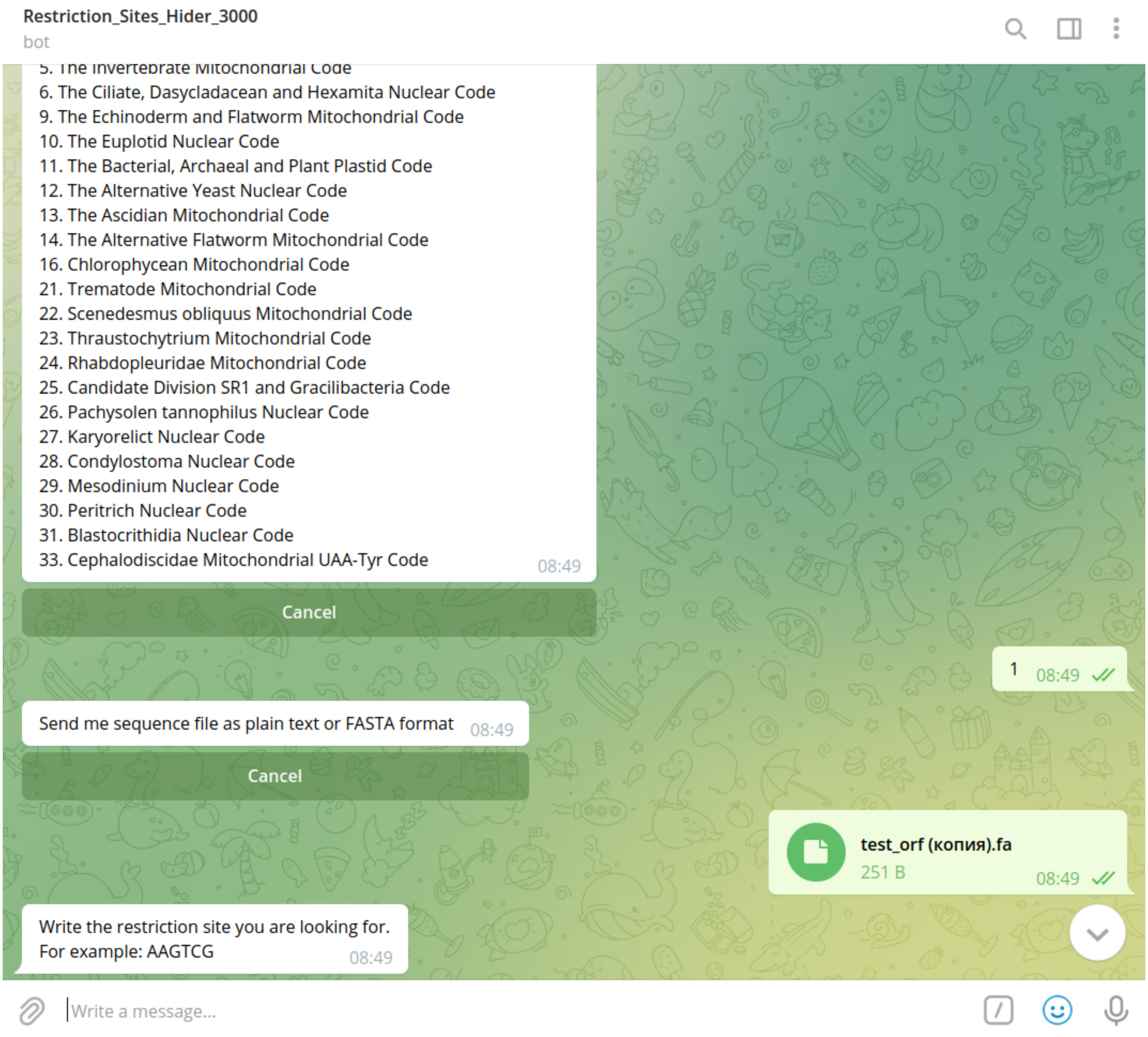
Send me the index for example: 1

1. The Standard Code
2. The Vertebrate Mitochondrial Code
3. The Yeast Mitochondrial Code
4. The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code
5. The Invertebrate Mitochondrial Code
6. The Ciliate, Dasycladacean and Hexamita Nuclear Code
9. The Echinoderm and Flatworm Mitochondrial Code
10. The Euplotid Nuclear Code
11. The Bacterial, Archaeal and Plant Plastid Code
12. The Alternative Yeast Nuclear Code
13. The Ascidian Mitochondrial Code
14. The Alternative Flatworm Mitochondrial C
16. Chlorophycean Mitochondrial Code
21. Trematode Mitochondrial Code
22. Scenedesmus obliquus Mitochondrial Coc
23. Thraustochytrium Mitochondrial Code
24. Rhabdopleuridae Mitochondrial Code
25. Candidate Division SR1 and Gracilibacteri
26. Pachysolen tannophilus Nuclear Code
27. Karyorelict Nuclear Code
28. Condylostoma Nuclear Code
29. Mesodinium Nuclear Code
30. Peritrich Nuclear Code
31. Blastocrithidia Nuclear Code
33. Cephalodiscidae Mitochondrial UAA-Tyr Code 08:46

1 08:47

Send me sequence file as plain text or FASTA format 08:47

4. Enter site of restriction by typing it as message. You could use upper and lower case.



5. The Invertebrate Mitochondrial Code
6. The Ciliate, Dasycladacean and Hexamita Nuclear Code
9. The Echinoderm and Flatworm Mitochondrial Code
10. The Euplotid Nuclear Code
11. The Bacterial, Archaeal and Plant Plastid Code
12. The Alternative Yeast Nuclear Code
13. The Ascidian Mitochondrial Code
14. The Alternative Flatworm Mitochondrial Code
16. Chlorophycean Mitochondrial Code
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26. Pachysolen tannophilus Nuclear Code
27. Karyorelict Nuclear Code
28. Condylostoma Nuclear Code
29. Mesodinium Nuclear Code
30. Peritrich Nuclear Code
31. Blastocrithidia Nuclear Code
33. Cephalodiscidae Mitochondrial UAA-Tyr Code 08:49

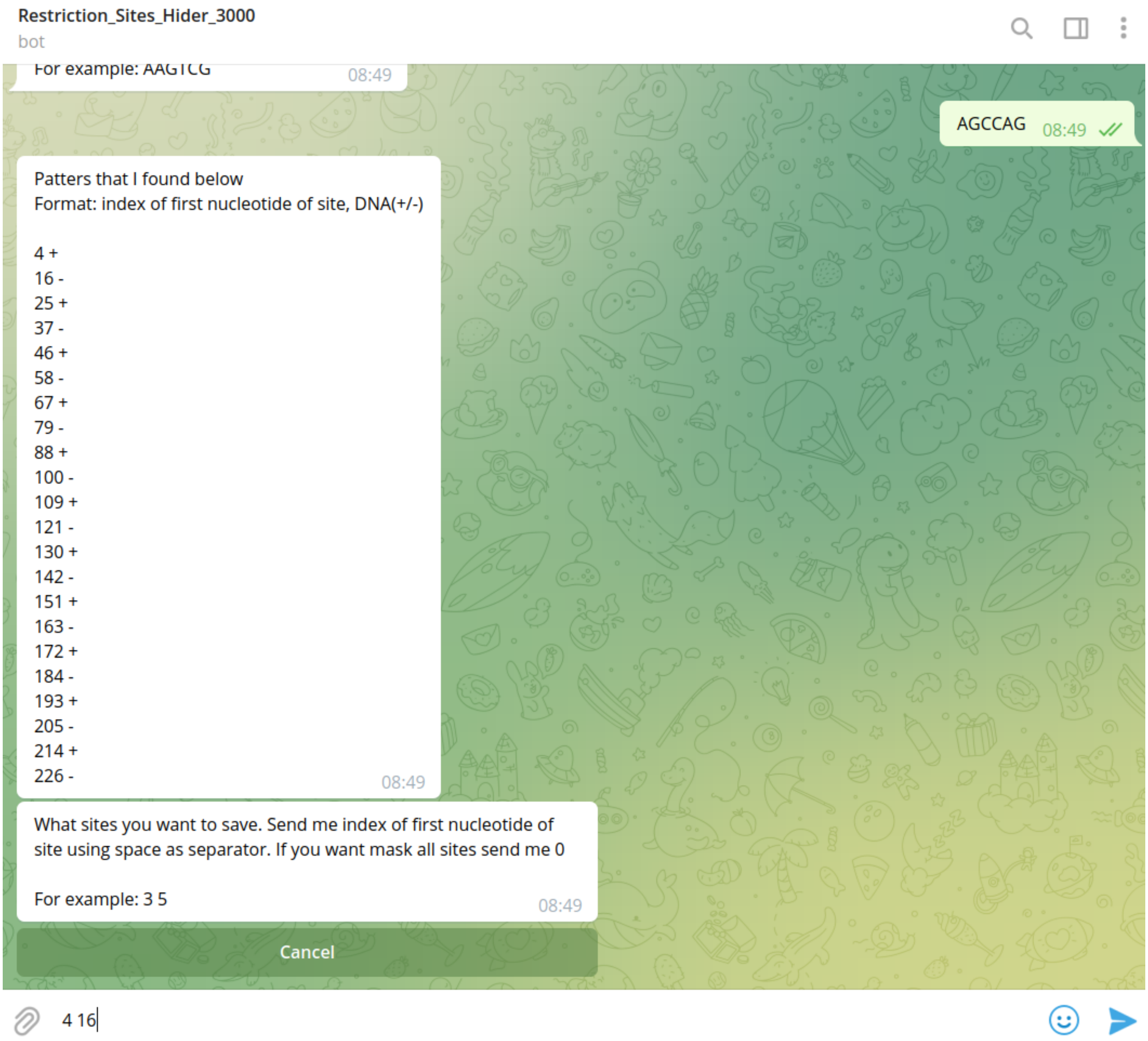
1 08:49

Send me sequence file as plain text or FASTA format 08:49

test_orf (копия).fa
251 B 08:49

Write the restriction site you are looking for.
For example: AAGTCG 08:49

5. Choose site or sites which you want to save.



For example: AAGTCG 08:49

AGCCAG 08:49

Patters that I found below
Format: index of first nucleotide of site, DNA(+/-)

```
4 +
16 -
25 +
37 -
46 +
58 -
67 +
79 -
88 +
100 -
109 +
121 -
130 +
142 -
151 +
163 -
172 +
184 -
193 +
205 -
214 +
226 -
```

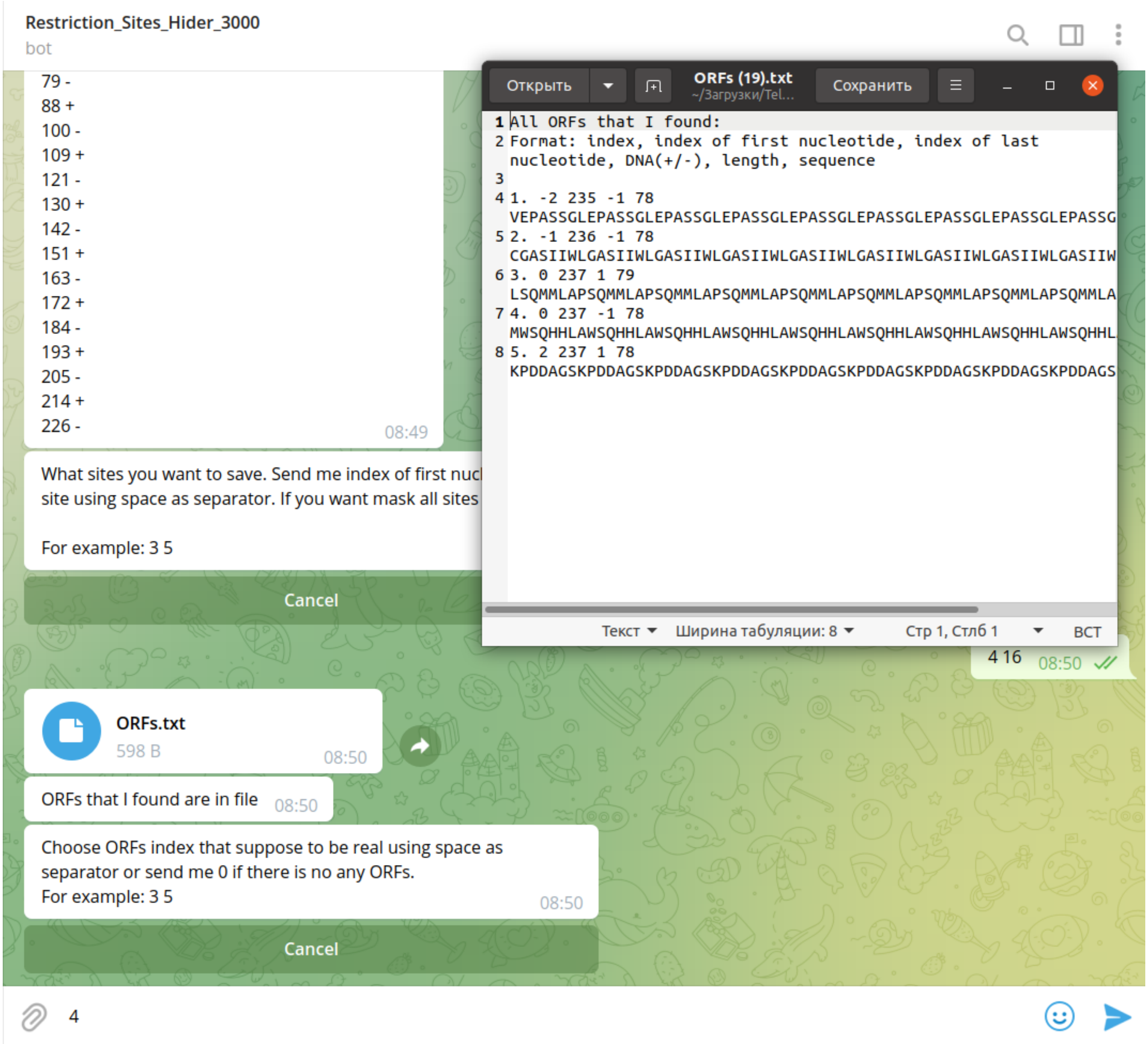
08:49

What sites you want to save. Send me index of first nucleotide of site using space as separator. If you want mask all sites send me 0

For example: 3 5 08:49

4 16

6. Choose open reading frame.



```
79 -
88 +
100 -
109 +
121 -
130 +
142 -
151 +
163 -
172 +
184 -
193 +
205 -
214 +
226 -
```

08:49

What sites you want to save. Send me index of first nuc
site using space as separator. If you want mask all sites

For example: 3 5

```
All ORFs that I found:
Format: index, index of first nucleotide, index of last
nucleotide, DNA(+/-), length, sequence

1. -2 235 -1 78
VEPASSGLEPASSGLEPASSGLEPASSGLEPASSGLEPASSGLEPASSGLEPASSGLEPASSG
2. -1 236 -1 78
CGASIIWLGASIIWLGASIIWLGASIIWLGASIIWLGASIIWLGASIIWLGASIIWLGASIIW
3. 0 237 1 79
LSQMMLAPSQMMLAPSQMMLAPSQMMLAPSQMMLAPSQMMLAPSQMMLAPSQMMLAPSQMMLA
4. 0 237 -1 78
MWSQHHLAWSQHHLAWSQHHLAWSQHHLAWSQHHLAWSQHHLAWSQHHLAWSQHHLAWSQHHL
5. 2 237 1 78
KPDDAGSKPDDAGSKPDDAGSKPDDAGSKPDDAGSKPDDAGSKPDDAGSKPDDAGSKPDDAGS
```

4 16 08:50

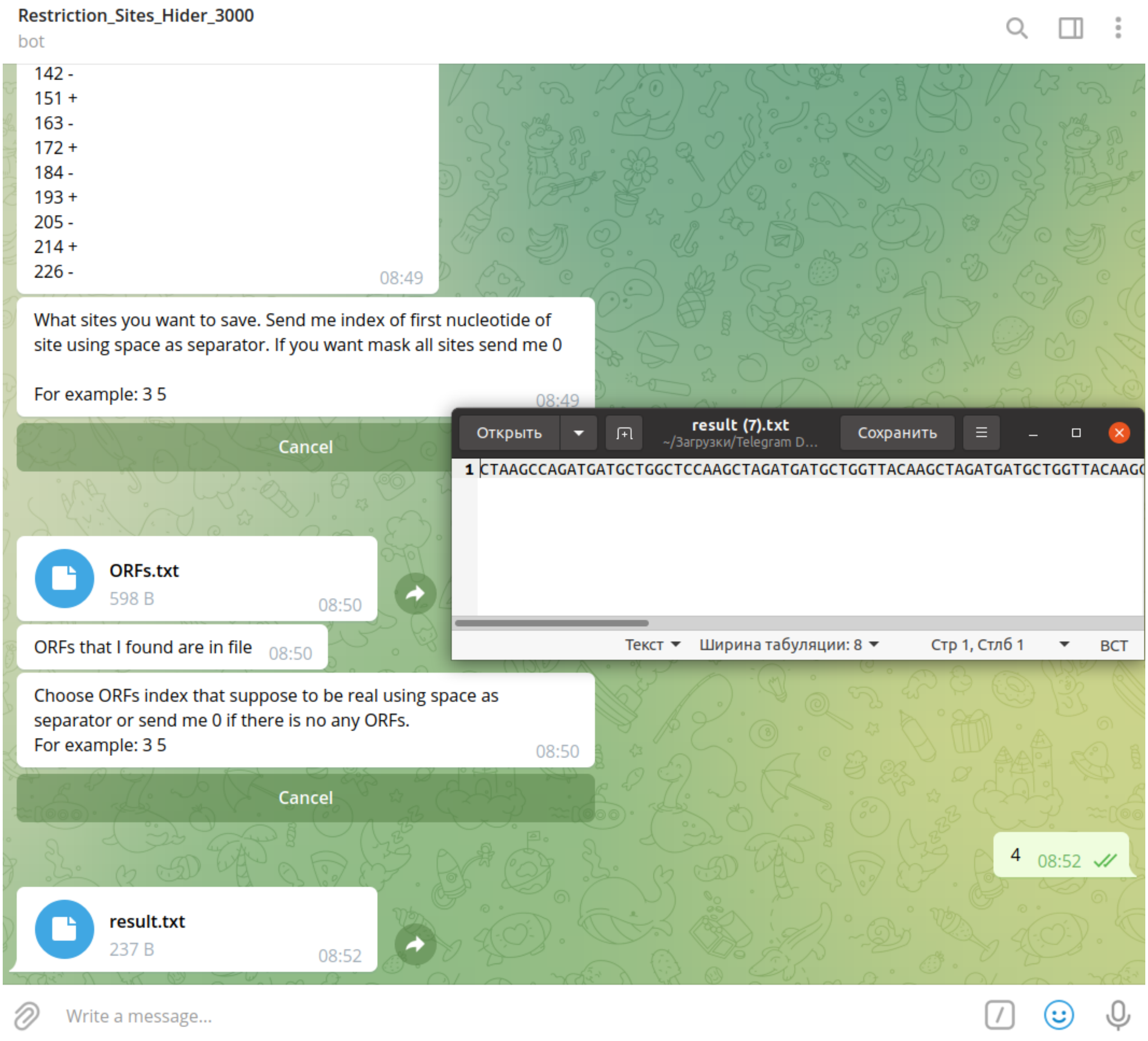
ORFs.txt
598 B 08:50

ORFs that I found are in file 08:50

Choose ORFs index that suppose to be real using space as separator or send me 0 if there is no any ORFs.
For example: 3 5 08:50

4

7. Your result is ready, you are wonderful!



```
142 -
151 +
163 -
172 +
184 -
193 +
205 -
214 +
226 -
```

08:49

What sites you want to save. Send me index of first nucleotide of site using space as separator. If you want mask all sites send me 0

For example: 3 5

08:49

```
CTAAGCCAGATGATGCTGGCTCCAAGCTAGATGATGCTGGTTACAAGCTAGATGATGCTGGTTACAAG
```

ORFs that I found are in file 08:50

Choose ORFs index that suppose to be real using space as separator or send me 0 if there is no any ORFs.
For example: 3 5

08:50

4 08:52