

# FASTA reader

This website is made for users that want to make FASTA formatted files

easier to read and visualize the data in the sequence.

Note: This website only works for nucleotide sequences.

By sending a FASTA file to the site, it will give the user 2 graphs and the protein sequence.

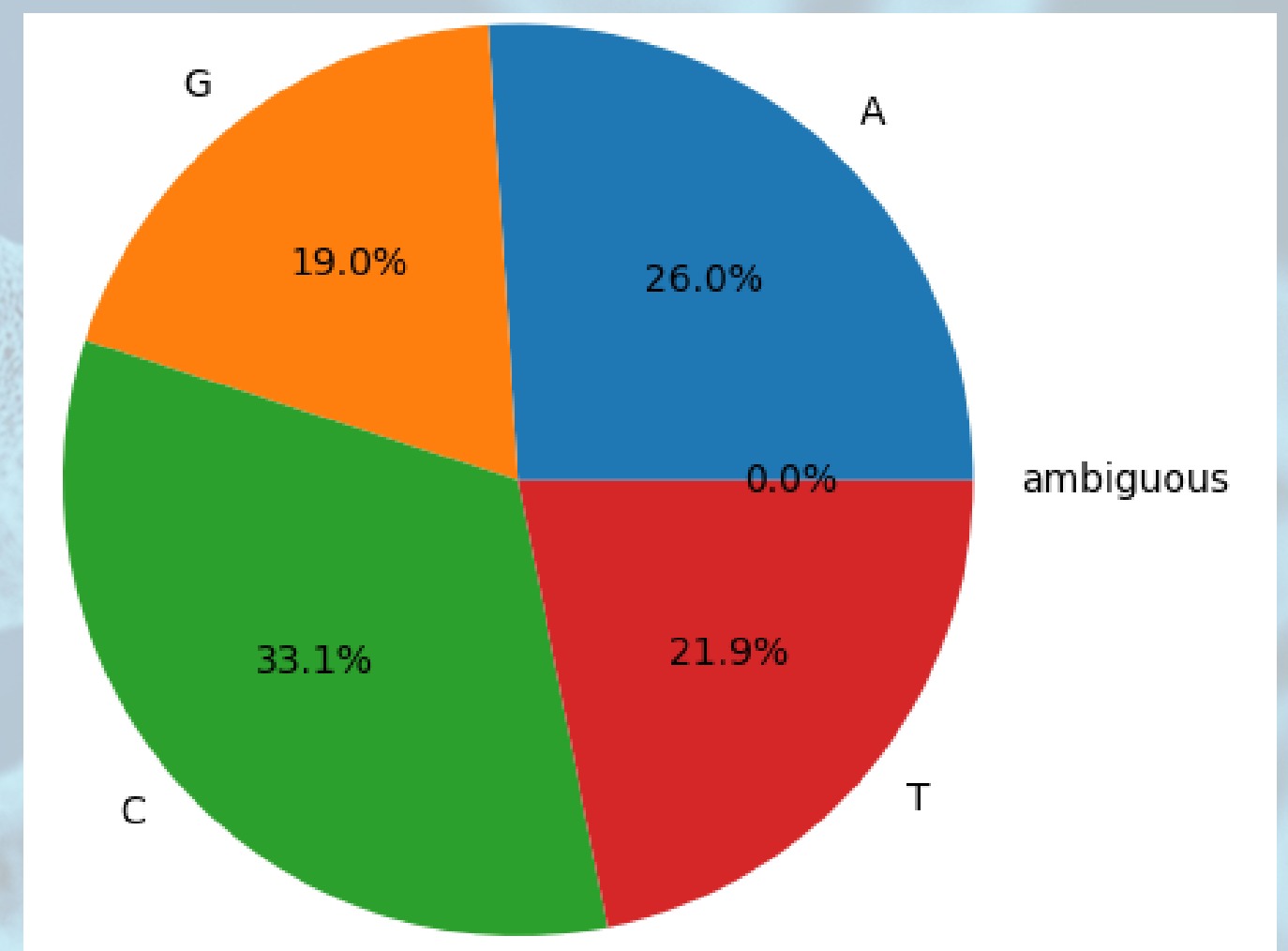
In the first graph, a circle diagram shows the percentage of each nucleic acid.

The second graph shows the frequency of each amino acid. Amino acids are coded by taking 3 consecutive nucleotides from the sequence that count as a codon. On the website, the user can choose which reading frame to use.

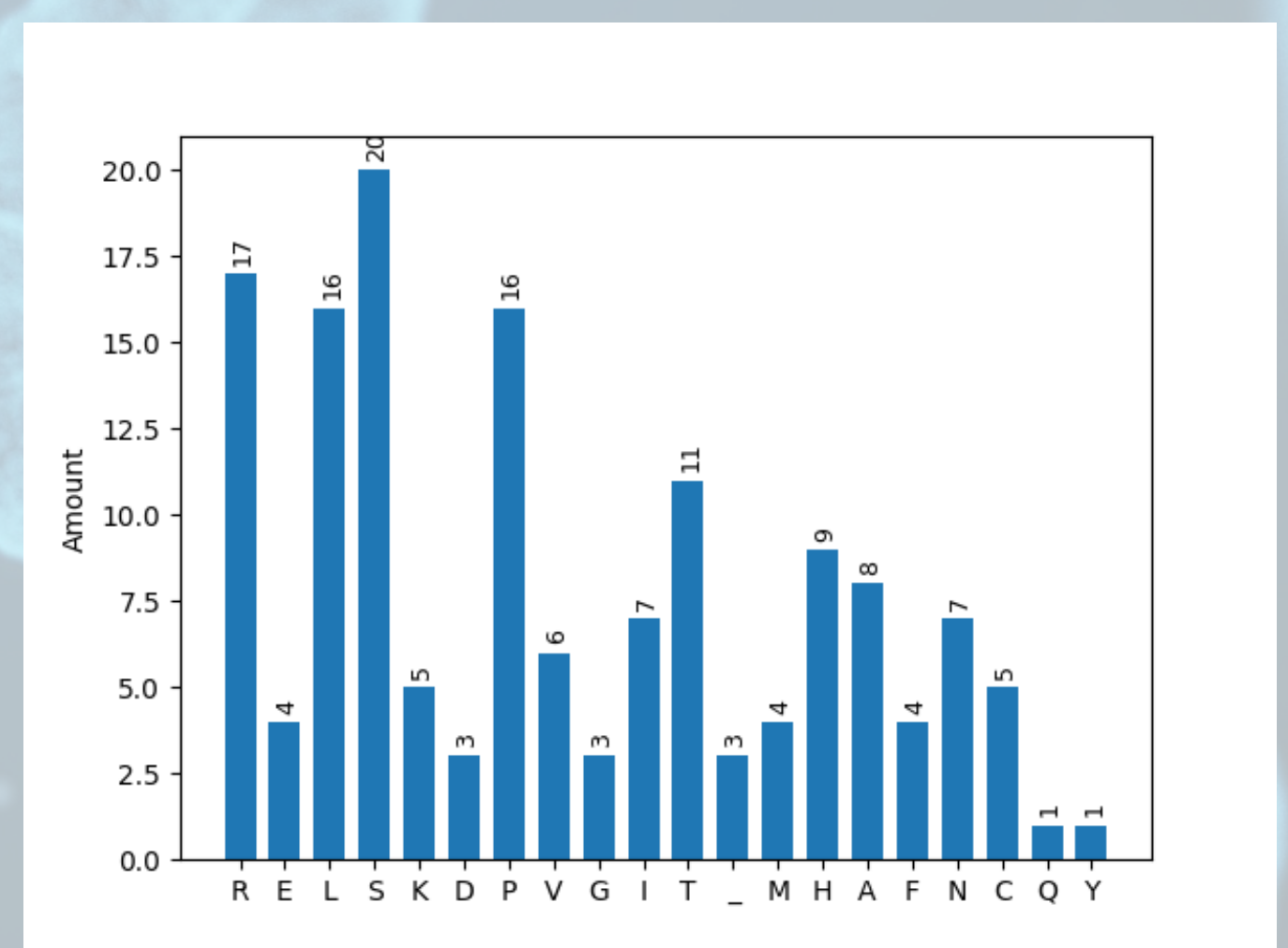
The last result is the protein sequence. It is a simple text box and translates the nucleotide sequence to amino acids depending on the reading frame the user submits.

```
Header >VIT_201s0011g03530.1
Sequence AATTAAGCATAAAATACTCACTCTTACCCCTTATTTTCTTATCTCTCATCACTTTTGGTGCGAAG
GACCATGAGAACAAGCTGCAATGGGTGTAGGGTTCTTCGCAAGGCATGCAGCCAAGACTGCATCA
Header >VIT_201s0011g03540.1
Sequence CAGGTAGCGTGAAGTTAAACCCTAGCGCTTTAGACAAACAGCTGTAGTCACCGCCCACAAACACC
AGCCTCTGAGACACCACCTCAAACCTTTCCACTTAAATACACATCCCTCACACCCTTTTCAATTC
Header >VIT_201s0011g03550.1
Sequence CATGCAAAGCTGAACGCGATGCTGTGATTGGTGGTAAGTGGTAGTTGAGTAAATTTGACAGTGAA
GCCGAAATGGTAAAAGACTAAGGCTAGAAGTAGAATACCACTGTTCTTCTCATCACGTGGGCCCA
```

Example of a FASTA formatted file



Pie chart with percentages of each nucleic acid



Bar chart with amounts of each amino acid

```
Protein sequence
>ref|NT_111909.2|MmX_110779_37:c2447217-2446765 Mus musculus chromosome X genomic
contig, strain C57BL/6J
RELSLEKLDLPVLRSSRREGITP_MRMHTRTLKAGLFSASSEALVRFHP_SRSSAPSPTRHRFSLRKTTT
GSVSLNPHNSVRALCNLRSPQHHTYAHSSPPISRNV_MCLPTDPIPKNRRPLDNRNCSIKSITAHTITNF
MCLLACPIPH
```

Textbox with the header from the original file and its protein sequence