

ProtParam - Results

User-provided sequence:

```
10      20      30      40      50      60
MMCYSILGPF FPKEAEKKG A SNTIIGMIFG CFALFELLAS LVFGNYLVHI GAKFMFVAGM

70      80      90     100     110     120
FVSGGVITILF GVLDRVPDGP VFIAMCFLVR VMDAVSFAAA MTASSSILAK AFPNNVATVL

130     140     150     160     170     180
GSLETFSLGL LILGPPVGGF LYQSFGEYEV FIVLGCVVLL MVPLNMYILP NYESDPGEHS

190     200     210     220     230     240
FWKLIALPKV GLIAFVINSL SSCFGFLDPT LSLFVLEKFN LPAGYVGLVF LGMALSYAIS

250     260     270     280     290     300
SPLFGLLSDK RPPLRKWLLV FGNLITAGCY MLLGPVPILH IKSQWLWLLV ILVVSGLSAG

310     320     330     340     350     360
MSIIPTFPEI LSCAHENGFE EGLSTLGLVS GLFSAMWSIG AFMGPTLGGF LYEKIGFEWA

370     380     390     400
AAIQGLWALI SGLAMGLFYL LEYSRRKRSK SQNILSTEE RTTLLPNET
```

[\[Documentation \(/protparam/protparam-doc.html\) / Reference \(/protparam/protpar-ref.html\)\]](#)

Number of amino acids: 409

Theoretical pI: 5.86

Molecular weight: 44203.59

Amino acid composition:

[CSV format](#)

| | | |
|---------|----|-------|
| Ala (A) | 30 | 7.3% |
| Arg (R) | 8 | 2.0% |
| Asn (N) | 12 | 2.9% |
| Asp (D) | 6 | 1.5% |
| Cys (C) | 7 | 1.7% |
| Gln (Q) | 4 | 1.0% |
| Glu (E) | 19 | 4.6% |
| Gly (G) | 43 | 10.5% |
| His (H) | 4 | 1.0% |
| Ile (I) | 27 | 6.6% |
| Leu (L) | 65 | 15.9% |
| Lys (K) | 14 | 3.4% |
| Met (M) | 16 | 3.9% |
| Phe (F) | 34 | 8.3% |
| Pro (P) | 23 | 5.6% |
| Ser (S) | 35 | 8.6% |
| Thr (T) | 14 | 3.4% |
| Trp (W) | 6 | 1.5% |
| Tyr (Y) | 12 | 2.9% |
| Val (V) | 30 | 7.3% |
| Pyl (O) | 0 | 0.0% |
| Sec (U) | 0 | 0.0% |
| (B) | 0 | 0.0% |
| (Z) | 0 | 0.0% |
| (X) | 0 | 0.0% |

Total number of negatively charged residues (Asp + Glu): 25

Total number of positively charged residues (Arg + Lys): 22

Total number of positively charged residues (Arg + Lys): 22

Atomic composition:

| | | |
|----------|---|------|
| Carbon | C | 2078 |
| Hydrogen | H | 3209 |
| Nitrogen | N | 477 |
| Oxygen | O | 537 |
| Sulfur | S | 23 |

Formula: C₂₀₇₈H₃₂₀₉N₄₇₇O₅₃₇S₂₃

Total number of atoms: 6324

Extinction coefficients:

Extinction coefficients are in units of M⁻¹ cm⁻¹, at 280 nm measured in water.

Ext. coefficient 51255

Abs 0.1% (=1 g/l) 1.160, assuming all pairs of Cys residues form cystines

Ext. coefficient 50880

Abs 0.1% (=1 g/l) 1.151, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).

>20 hours (yeast, in vivo).

>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 43.03

This classifies the protein as unstable.

Aliphatic index: 116.33

Grand average of hydropathicity (GRAVY):0.811



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