ProtParam - Results

User-provided sequence:

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

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

       130        140        150        160        170        180
GSLETFSGLG LILGPPVGGF LYQSFGYEVP 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 IKSQLWLLVL ILVVSGLSAG

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

       370
AAIQGLWALI SYF
```

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

Number of amino acids: 373
Theoretical pI: 5.57
Molecular weight: 40085.90

Amino acid composition: CSV format

Ala (A)	29	7.8%
Arg (R)	4	1.1%
Asn (N)	10	2.7%
Asp (D)	6	1.6%
Cys (C)	7	1.9%
Gln (Q)	3	0.8%
Glu (E)	14	3.8%
Gly (G)	41	11.0%
His (H)	4	1.1%
Ile (I)	26	7.0%
Leu (L)	58	15.5%
Lys (K)	12	3.2%
Met (M)	15	4.0%
Phe (F)	34	9.1%
Pro (P)	22	5.9%
Ser (S)	31	8.3%
Thr (T)	10	2.7%
Trp (W)	6	1.6%
Tyr (Y)	11	2.9%
Val (V)	30	8.0%
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): 20

Total number of positively charged residues (Arg + Lys): 16

Atomic composition:

Carbon	C	1902
Hydrogen	H	2910
Nitrogen	N	424
Oxygen	O	479
Sulfur	S	22

Formula: $C_{1902}H_{2910}N_{424}O_{479}S_{22}$
Total number of atoms: 5737

Extinction coefficients:
Extinction coefficients are in units of M^{-1} cm^{-1}, at 280 nm measured in water.
Ext. coefficient 49765
Abs 0.1% (=1 g/l) 1.241, assuming all pairs of Cys residues form cystines

Ext. coefficient 49390
Abs 0.1% (=1 g/l) 1.232, 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 36.25
This classifies the protein as stable.

Aliphatic index: 118.93
Grand average of hydropathicity (GRAVY):0.967