ProtParam

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User-provided sequence:

```
        10         20         30         40         50         60
MTKSNGEEPK MGGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAF VLLTVTAVIV

        70         80         90        100
GTILGFTLRP YRMSYREVKY FSFPGELLMR MLQMLVLPLI ISSLVT
```

References and documentation are available.

Number of amino acids: 106

Molecular weight: 12249.73

Theoretical pI: 10.48

Amino acid composition: CSV format

Ala (A)	3	2.8%
Arg (R)	9	8.5%
Asn (N)	3	2.8%
Asp (D)	1	0.9%
Cys (C)	0	0.0%
Gln (Q)	4	3.8%
Glu (E)	6	5.7%
Gly (G)	7	6.6%
His (H)	0	0.0%
Ile (I)	5	4.7%
Leu (L)	14	13.2%
Lys (K)	9	8.5%
Met (M)	7	6.6%
Phe (F)	6	5.7%
Pro (P)	4	3.8%
Ser (S)	6	5.7%
Thr (T)	8	7.5%
Trp (W)	0	0.0%
Tyr (Y)	4	3.8%
Val (V)	10	9.4%
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): 7
Total number of positively charged residues (Arg + Lys): 18

Atomic composition:

Carbon	C	556
Hydrogen	H	917
Nitrogen	N	149
Oxygen	O	146
Sulfur	S	7

Formula: $C_{556}H_{917}N_{149}O_{146}S_7$
Total number of atoms: 1775

Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that
this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of M^{-1} cm^{-1}, at 280 nm measured in water.

Ext. coefficient 5960
Abs 0.1% (=1 g/l) 0.487

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 36.82
This classifies the protein as stable.

Aliphatic index: 100.09

Grand average of hydropathicity (GRAVY): 0.036