

# ProtParam

## ProtParam

### User-provided sequence:

```

      10      20      30      40      50      60
XNMFPPNLVE ACFKQVCPRG YSLPDCWEDC GDGRHGCDWG AACHVHRDCH CWLTHSRSHR

      70      80      90     100     110     120
LATPLLLGNT EKPLGFYWRV AASTHHRSGD LFKFCHPTHH LQVPGREQWR GQARHQIRAP

RRSHH

```

[References](#) and [documentation](#) are available.

Number of amino acids: 125

Molecular weight: 14488.59

Theoretical pI: 9.01

Amino acid composition:

[CSV format](#)

Ala (A)	8	6.4%
Arg (R)	13	10.4%
Asn (N)	3	2.4%
Asp (D)	6	4.8%
Cys (C)	9	7.2%
Gln (Q)	5	4.0%
Glu (E)	4	3.2%
Gly (G)	10	8.0%
His (H)	14	11.2%
Ile (I)	1	0.8%
Leu (L)	10	8.0%
Lys (K)	3	2.4%
Met (M)	1	0.8%
Phe (F)	5	4.0%
Pro (P)	9	7.2%
Ser (S)	6	4.8%
Thr (T)	5	4.0%
Trp (W)	5	4.0%
Tyr (Y)	2	1.6%
Val (V)	5	4.0%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

(B)	0	0.0%
(Z)	0	0.0%
(X)	1	0.8%

Total number of negatively charged residues (Asp + Glu): 10

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

### Atom composition:

As there is at least one ambiguous position (B,Z or X) in the sequence considered, the atomic composition cannot be computed.

### Extinction coefficients:

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

Ext. coefficient	30980
Abs 0.1% (=1 g/l)	2.138, assuming all pairs of Cys residues form cystines

Ext. coefficient      30480  
Abs 0.1% (=1 g/l)    2.104, assuming all Cys residues are reduced

**Estimated half-life:**

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

Due to the presence of an N-terminal ambiguity, the estimated half-life can not be computed.

**Instability index:**

The instability index (II) is computed to be 58.92  
This classifies the protein as unstable.

**Aliphatic index:** 52.32

**Grand average of hydropathicity (GRAVY):** -0.764



Expasy is operated by the [SIB Swiss Institute of Bioinformatics](#) | [Terms of Use](#)  
[Back to the top](#)