ProtParam

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User-provided sequence:

```
        10         20         30         40         50         60
XFFNALSDAT MKIVQIIMCY MPLGILFLIA GKIIEVEDWE IFRKLGLYMA TVLTGLAIHS

        70         80         90        100        110        120
IVILPLIYFI VVRKNPFRFA MGMAQALLTA LMISSSSATL PVTFRCAEEN NQVDKRITRF

       130        140        150        160        170        180
VLPVGATINM DGTALYEAVA AVFIAQLNDL DLGIGQIITI RDRFRTMVNV LGDAFGTGIV

       190        200        210        220        230        240
EKLSKKELEQ MDVSSEVNIV NPFALESTIL DNEDSDTKKS YVNGGFAVDK SDTISFTQTS


QF
```

References and documentation are available.

Number of amino acids: 242

Molecular weight: 26753.45

Theoretical pI: 4.88

Amino acid composition: CSV format

Ala (A)	20	8.3%
Arg (R)	9	3.7%
Asn (N)	11	4.5%
Asp (D)	14	5.8%
Cys (C)	2	0.8%
Gln (Q)	8	3.3%
Glu (E)	12	5.0%
Gly (G)	14	5.8%
His (H)	1	0.4%
Ile (I)	25	10.3%
Leu (L)	24	9.9%
Lys (K)	11	4.5%
Met (M)	10	4.1%
Phe (F)	16	6.6%
Pro (P)	6	2.5%
Ser (S)	15	6.2%
Thr (T)	17	7.0%
Trp (W)	1	0.4%
Tyr (Y)	5	2.1%
Val (V)	20	8.3%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	1	0.4%

Total number of negatively charged residues (Asp + Glu): 26
Total number of positively charged residues (Arg + Lys): 20

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 13075
Abs 0.1% (=1 g/l) 0.489, assuming all pairs of Cys residues form cystines

Ext. coefficient 12950
Abs 0.1% (=1 g/l) 0.484, 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 28.82
This classifies the protein as stable.

Aliphatic index: 111.20

Grand average of hydropathicity (GRAVY): 0.421