ProtParam

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User-provided sequence:

```
        10         20         30         40         50         60
XEENLGIDKR VTRFVLPVGA TINMDGTALY EAVAAIFIAQ MNGVVLDGGQ IVTVRDRMRT

        70         80         90        100        110        120
SVNVVGDSFG AGIVYHLSKS ELDTIDSQHR VHEDIEMTKT QSIYDDMKNH RESNSNQCVY

       130        140        150
AAHNSVIVDE CKVTLAANGK SADCSVEEEP WKREK
```

References and documentation are available.

Number of amino acids: 155

Molecular weight: 17127.41

Theoretical pI: 5.05

Amino acid composition: CSV format

Ala (A)	12	7.7%
Arg (R)	8	5.2%
Asn (N)	9	5.8%
Asp (D)	12	7.7%
Cys (C)	3	1.9%
Gln (Q)	5	3.2%
Glu (E)	12	7.7%
Gly (G)	10	6.5%
His (H)	5	3.2%
Ile (I)	10	6.5%
Leu (L)	7	4.5%
Lys (K)	8	5.2%
Met (M)	5	3.2%
Phe (F)	3	1.9%
Pro (P)	2	1.3%
Ser (S)	11	7.1%
Thr (T)	9	5.8%
Trp (W)	1	0.6%
Tyr (Y)	4	2.6%
Val (V)	18	11.6%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	1	0.6%

Total number of negatively charged residues (Asp + Glu): 24
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 11585
Abs 0.1% (=1 g/l) 0.676, assuming all pairs of Cys residues form cystines

```
Ext. coefficient    11460
Abs 0.1% (=1 g/l)   0.669, 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 27.76
This classifies the protein as stable.



Aliphatic index: 84.19

Grand average of hydropathicity (GRAVY): -0.325
```

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