

ProtParam - Results

User-provided sequence:

```
      10      20      30      40      50      60
MEALGDLEGP RAPGGDDPAG SAGETPGWLS REQVFVLISA ASVNLGSMCM YSILGPFFPK

      70      80      90     100     110     120
EAEKKGASNT IIGMIFGCFA LFELLASLVF GNYLVHIGAK FMFVAGMFVS GGVITILFGVL

     130     140     150     160     170     180
DRVDPGPVFI AMCFILVRVMD AVSFAAAMTA SSSILAKAFP NNVATVLGSL ETFSGGLGLIL

     190     200     210     220     230     240
GPPVGGFLYQ SFGYEVPIIV LGCVVLLMVP LNMVILPNYE SDPGEHSFWK LIALPKVGLI

     250     260     270     280     290     300
AFVINSLSSC FGFLDPTLSL FVLEKFNLPV GYVGLVFLGM ALSYAISSPL FGLLSDKRPP

     310     320     330     340     350     360
LRKWLIVFGN LITAGCYMLL GPVPILHIKS QLWLLVLILV VSGLSAGMSI IPTFPEILSC

     370     380     390     400     410     420
AHENGFEELG STLGLVSGLF SAMWSIGAFM GPTLGGFLYE KIGFEWAAAI QGLWALISGL

     430     440     450
AMGLFYLLLE SRRKRKSKQN ILSTEEERTT LLPNET
```

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

Number of amino acids: 456

Theoretical pI: 5.15

Molecular weight: 48868.72

Amino acid composition:

[CSV format](#)

Ala (A)	36	7.9%
Arg (R)	10	2.2%
Asn (N)	13	2.9%
Asp (D)	9	2.0%
Cys (C)	7	1.5%
Gln (Q)	5	1.1%
Glu (E)	23	5.0%
Gly (G)	51	11.2%
His (H)	4	0.9%
Ile (I)	28	6.1%
Leu (L)	70	15.4%
Lys (K)	14	3.1%
Met (M)	17	3.7%
Phe (F)	35	7.7%
Pro (P)	27	5.9%
Ser (S)	40	8.8%
Thr (T)	15	3.3%
Trp (W)	7	1.5%
Tyr (Y)	12	2.6%
Val (V)	33	7.2%
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): 32

Total number of positively charged residues (Arg + Lys): 24

Atomic composition:

Carbon	C	2280
Hydrogen	H	3525
Nitrogen	N	533
Oxygen	O	606
Sulfur	S	24

Formula: C₂₂₈₀H₃₅₂₅N₅₃₃O₆₀₆S₂₄

Total number of atoms: 6968

Extinction coefficients:

Extinction coefficients are in units of M⁻¹ cm⁻¹, at 280 nm measured in water.

Ext. coefficient 56755

Abs 0.1% (=1 g/l) 1.161, assuming all pairs of Cys residues form cystines

Ext. coefficient 56380

Abs 0.1% (=1 g/l) 1.154, 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 41.63

This classifies the protein as unstable.

Aliphatic index: 112.70

Grand average of hydropathicity (GRAVY):0.719



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