

[Home](#) (/protparam/)[Documentation](#) (/protparam/protparam-doc.html)[Reference](#) (/protparam/protpar-ref.html)[Contact](#) (/contact)

ProtParam - Results

User-provided sequence:

10 20 30 40 50 60
MEALGDLEGP RAPGGDDPAG SAGETPGWLS REQVFVLISA ASVNLGSMMC YSILGPFFPK

70 80 90 100 110 120
EAEKKKGASNT IIGMIFGCFA LFELLASLVF GNYLVHIGAK FMFVAGMFVS GGVTILFGVL

130 140 150 160 170 180
DRVPDGPVFI AMCFLVRVMD AVSFAAAMTA SSSILAKAFP NNVATVLGSL ETFSGLGLIL

190 200 210 220 230 240
GPPVGGFLYQ SFGYEVPFIV LGCVVLLMVP LNMYILPNYE SDPGEHSFWK LIALPKVGLI

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

310 320 330 340 350 360
LRKWLLVFGN LITAGCYMILL GPVPILHIKS QLWLLVLILV VSGLSAGMSI IPTFPEILSC

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

430 440 450
AMGLFYLLLEY SRRKRSKSQN 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%

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



Expasy (<https://www.expasy.org>) is operated by the SIB Swiss Institute of

Bioinformatics (<https://sib.swiss>)

Terms of Use (<https://www.expasy.org/terms-of-use>) | Privacy policy

(<https://www.sib.swiss/privacy-policy>)