

ProtParam

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User-provided sequence:

10 20 30 40 50 60
MSSHGNSLFL RESGQRLGRV GWLQRLQESL QQRALRTRLR LQTMLEHVL RFLRRNAFIL
70 80 90 100 110 120
LTVSAVVIGV SLAFALRPYQ LTYRQIKYFS FPGELLMRML QMLVPLIVS SLVTGMASLD
130 140 150 160 170 180
NKATGRMGMR AAVYYMVTII IAVFIGILMV TIIHPGKGSK EGLHREGRIE TIPTADAFMD
190 200 210 220 230 240
LIRNMFPPNL VEACFKQFKT QYSTRVVTRT MVRTENGSEP GASMPPPFVS ENGTSFLENV
250 260 270 280 290 300
TRALGTLQEM LSFEETVPVP GSANGINALG LVVFSVAFGL VIGGMKHKGR VLRDFFDSL N
310 320 330 340 350 360
EAIMRLVGII IWYAPVGILF LIAGKILEME DMAVLGGQLG MYTLTVIVGL FLHAGIVLPL
370 380 390 400 410 420
IYFLVTHRNP FPFIGGMLQA LITAMGTSSS SATLPITFRC LEEGLGVDRR ITRFVLPVGA
430 440 450 460 470 480
TVNMDGTALY EALAAIFIAQ VNNYELNLGQ ITTISITATA ASVGAAGIPQ AGLVTMVIVL
490 500 510 520 530 540
TSVGLPTEDI TLIIAVDWFL DRLRTMTNVL GDSIGAAVIE HLSQRELELQ EAELTLPSLG
550 560
KPYKSLMAQE KGASRGRGGN ESAM

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

Number of amino acids: 564

Molecular weight: 61565.42

Theoretical pI: 9.26

Amino acid composition:		CSV format
Ala (A)	45	8.0%
Arg (R)	36	6.4%
Asn (N)	18	3.2%
Asp (D)	12	2.1%
Cys (C)	2	0.4%
Gln (Q)	20	3.5%
Glu (E)	30	5.3%
Gly (G)	52	9.2%
His (H)	8	1.4%
Ile (I)	41	7.3%
Leu (L)	74	13.1%
Lys (K)	12	2.1%
Met (M)	27	4.8%
Phe (F)	27	4.8%
Pro (P)	23	4.1%
Ser (S)	34	6.0%
Thr (T)	42	7.4%
Trp (W)	3	0.5%
Tyr (Y)	12	2.1%
Val (V)	46	8.2%
Py1 (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): 42

Total number of positively charged residues (Arg + Lys): 48

Atomic composition:

Carbon	C	2775
Hydrogen	H	4491
Nitrogen	N	741
Oxygen	O	775
Sulfur	S	29

Formula: $C_{2775}H_{4491}N_{741}O_{775}S_{29}$

Total number of atoms: 8811

Extinction coefficients:

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

Ext. coefficient 34505

Abs 0.1% (=1 g/l) 0.560, assuming all pairs of Cys residues form cystines

Ext. coefficient 34380

Abs 0.1% (=1 g/l) 0.558, 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 36.33

This classifies the protein as stable.

Aliphatic index: 111.15

Grand average of hydropathicity (GRAVY): 0.399



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[Back to the top](#)