

# Secuencias y Traducción de TYLCV.fna

La secuencia de ADN es:

```
TAATATTACC GGATGGCCGC GCCTTTTCCT TTTATGTGGT CCCCACGAGG
GTTCCACAGA CGTCACTGTC AACCAATCAA ATTGCATACT CAAACGTTAA
ATAAGTG TTC ATTTGTCTTT ATATACTTGG TCCCCAAGTA TTTTGTCTTG
CAATATGTGG GACCCACTTC TAAATGAATT TCCTGAATCT GTTCACGGAT
TTCGTTGTAT GTTAGCTATT AAATATTTGC AGTCCGTTGA GGAAACTTAC
GAGCCCAATA CATTGGGCCA CGATTTAATT AGGGATCTTA TATCTGTTGT
AAGGGCCCGT GACTATGTCG AAGCGACCAG GCGATATAAT CATTTCACAG
CCCGTCTCGA AGGTTCGCCG AAGGCTGAAC TTCGACAGCC CATAACAGCAG
CCGTGCTGCT GTCCCCATTG TCCAAGGCAC AAACAAGCGA CGATCATGGA
CGTACAGGCC CATGTACCGA AAGCCCAGAA TATACAGAAT GTATCGAAGC
CCTGATG TTC CCCGTGGATG TGAAGGCCCA TGTAAAGTCC AGTCTTATGA
GCAACGGGAT GATATTAAGC ACACTGGTAT TGTTCGTTGT GTTAGTGATG
T TACTCGTGG ATCTGGAATT ACTCACAGAG TGGGTAAGAG GTTCTGTGTT
AAATCGATAT ATTTTTTAGG TAAAGTCTGG ATGGATGAAA ATATCAAGAA
GCAGAATCAC ACTAATCAGG TCATGTTCTT TTTGGTCCGT GATAGAAGGC
CCTATGGAAG CAGCCCAATG GATTTTGGAC AGGTTTTTAA TATGTTTCGAT
AATGAGCCCA GTACCGCAAC CGTGAAGAAT GATTTGCGTG ATAGGTTTCA
AGTGATGAGA AAATTTTCATG CAACAGTTAT TGGTGGGCCC TCTGGAATGA
AGGAACAGGC ATTAGTTAAG AGATTTTTTA AAATTAACAG TCATGTAACT
TATAATCATC AGGAGGCAGC CAAGTACGAG AACCATACTG AAAACGCCTT
GTTATTGTAT ATGGCATGTA CGCATGCCTC TAATCCAGTG TATGTAACTA
TGAAAATACG CATCTATTTT TATGATTCAA TATCAAATTA ATAAAATTTA
TATTTTATAT CATGAGTTTC TGTTACATTT ATTGTGTTTT CAAGTACATC
ATACAATACA TGATCAACTG CTCTGATTAC ATTGTTAATG GAAATTACAC
CAAGACTATC TAAATACTTA AGAACTTCAT ATCTAAATAC TCTTAAGAAA
TGACCAGTCT GAGGCTGTAA TGTCGTCCAA ATTCGGAAGT TGAGAAAACA
TTTGTGAATC CCCATTACCT TCCTGATGTT GTGGTTGAAT CTTATCTGAA
TGGAATGAT GTCGTGGTTC ATTAGAAATG GCCGCTGGCT GTGTTCTGTT
ATCTTGAAAT AGAGGGGATT GTTTATCTCC CAAATAAAAA CGCCATTCTC
TGCCTGAGGA GCAGTGATGA GTTCCCCTGT GCGTGAATCC ATGATTGTTG
CAGTTGAGGT GGAGGTAGTA TGAGCAGCCA CAGTCTAGGT CTACACGCTT
ACGCCTTATT GGTTCCTTCT TGGCTATCTT GTGTTGGACC TTGATTGATA
CTTGCGAACA GTGGCTCGTA GAGGGTGACG AAGGTTGCAT TCTTGAGCGC
CCAATTTTTT AAGGATATAT TTTTTTCTTC GTCTAGATAT TCCCTATATG
AGGAGGTAGG TCCTGGATTG CAGAGGAAGA TAGTGGGAAT TCCCCCTTTA
ATTTGAATGG GCTTCCCGTA CTTTGTGTTG CTTTGCCAGT CCCTCTGGGC
CCCCATGAAT TCCTTGAAGT GCTTTAAATA ATGCGGGTCT ACGTCATCAA
TGACGTTGTA CCACGCATCA TTACTGTACA CTTTGGGCT TAGGTCTAGA
TGTCCACATA AATAATTATG TGGGCCTAGA GACCTGGCCC ACATTGTTTT
GCCTGTTCTG CTATCACCCCT CAATGACAAT ACTATTAGGT CTCCATGGCC
GCGCAGCGGA AGACACGACG TTCTCAGCGA CCCACTCTTC AAGTTCATCT
GGA ACTTGAT TAAAAGAAGA AGAAAGAAAT GGAGAAACAT AACTTCTAA
AGGAGGACTA AAAATCCTAT CTAAATTTGA ACTTAAATTA TGAAATTGTA
AAATATAGTC CTTTGGGGCC TTCTCTTTTA ATATATTGAG GCCTCGGAT
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TTATTGCCTG	AATTGAGTGC	TTCGGCATAT	GCGTCGTTGG	CAGATTGCTG
ACCTCCTCTA	GCTGATCTGC	CATCGATTTG	GAAAACTCCA	AAATCAATGA
AGTCTCCGTC	TTTCTCCACG	TAGGTCTTGA	CATCTGTTGA	GCTCTTAGCT
GCCTGAATGT	TCGGATGGAA	ATGTGCTGAT	CTGTTTGGGG	ATACCAGGTC
GAAGAACCGT	TGGTTCTTAC	ATTGGTATTT	GCCTTCGAAT	TGGATAAGCA
CATGGAGATG	TGGTTCCCCA	TTCTCGTGGA	GTTCTCTGCA	AACTTTGATG
TATTTTTTAT	TTGTTGGGGT	TTCTAGGTTT	TTTAATTGGG	AAAGTGCTTC
CTCTTTAGAG	AGAGAACAAT	TGGGATATGT	TAGGAAATAA	TTTTTGGCAT
ATATTTTAAA	TAAACGAGGC	ATGTTGAAAT	GAATCGGTGT	CCCTCAAAGC
TCTATGGCAA	TCGGTGTATC	GGTGTCTTAT	TTATACCTGG	ACACCTAATG
GCTATTTGGT	AATTTTCGTAA	AAGTACATTG	CAATTCAAAA	TTCAAAATTC
	AAAAATCAAA	TCATTAAAGC	GGCCATCCGT	A

Secuencia inversa:

ATGCCTACCG	GCGAAATTAC	TAAACTAAAA	ACTTAAAACT	TAAAACTTAA
CGTTACATGA	AAATGCTTTA	ATGGTTTATC	GGTAATCCAC	AGGTCCATAT
TTATTCTGTG	GCTATGTGGC	TAACGGTATC	TCGAAACTCC	CTGTGGCTAA
GTAAAGTTGT	ACGGAGCAAA	TAAATTTTAT	ATACGGTTTT	TAATAAAGGA
TTGTATAGGG	TTAACAAGAG	AGAGATTTCT	CCTTCGTGAA	AGGGTTAATT
TTTTGGATCT	TTGGGGTTGT	TTATTTTTTA	TGTAGTTTCA	AACGTCTCTT
GAGGTGCTCT	TACCCCTTGG	TGTAGAGGTA	CACGAATAGG	TTAAGCTTCC
GTTTATGGTT	ACATTCTTGG	TTGCCAAGAA	GCTGGACCAT	AGGGGTTTGT
CTAGTCGTGT	AAAGGTAGGC	TTGTAAGTCC	GTCGATTCTC	GAGTTGTCTA
CAGTTCTGGA	TGCACCTCTT	TCTGCCTCTG	AAGTAACTAA	AACCTCAAAA
GGTTTAGCTA	CCGTCTAGTC	GATCTCCTCC	AGTCGTTAGA	CGGTTGCTGC
GTATACGGCT	TCGTGAGTTA	AGTCCGTTAT	TTAGGCTCCG	GGAGTTATAT
AATTTTCTCT	TCCGGGGTTT	CCTGATATAA	AATGTTAAAG	TATTAAATTC
AAGTTTAAAT	CTATCCTAAA	AATCAGGAGG	AAATCTTCAA	ATACAAAGAG
GTAAAGAAAG	AAGAAGAAAA	TTAGTTCAAG	GTCTACTTGA	ACTTCTCACC
CAGCGACTCT	TGCAGCACAG	AAGGCGACGC	GCCGGTACCT	CTGGATTATC
ATAACAGTAA	CTCCCACTAT	CGTCTTGTCC	GTTTTGTTAC	ACCCGGTCCA
GAGATCCGGG	TGTATTAATA	AATACACCTG	TAGATCTGGA	TTCCGGTTTC
CACATGTCAT	TACTACGCAC	CATGTTGCAG	TAATACTGCT	ATCTGGGCGT
AATAAATTTT	GTGAAGTTCC	TTAAGTACCC	CCGGGTCTCC	CTGACCGTTT
CGTTGTGTTT	CATGCCCTTC	GGGTAAGTTT	AATTTCCCCC	TTAAGGGTGA
TAGAAGGAGA	CGTTAGGTCC	TGGATGGAGG	AGTATATCCC	TTATAGATCT
GCTTCTTTTT	TTATATAGGA	ACTTTTTTAA	CCGCGAGTTC	TTACGTTGGA
AGCAGTGGGA	GATGCTCGGT	GACAAGCGTT	CATAGTTAGT	TCCAGGTTGT
GTTCTATCGG	TTCTTCTTTG	GTTATTCCGC	ATTTCGCACAT	CTGGATCTGA
CACCGACGAG	TATGATGGAG	GTGGAGTTGA	CGTTGTTAGT	ACCTAAGTGC
GTGTCCCCTT	GAGTAGTGAC	GAGGAGTCCG	TCTCTTACCG	CAAAAATAAA
CCCTCTATTT	GTTAGGGGAG	ATAAAGTTCT	ATTGTCTTGT	GTCCGTCGCC
GGTAAAGATT	ACTTGGTGCT	GTAGTAAAGG	TAAGTCTATT	CTAAGTTGGT
GTTGTAGTCC	TTCCATTACC	CCTAAGTGTT	TACAAAAGAG	TTGAAGGCTT
AAACCTGCTG	TAATGTCGGA	GTCTGACCAG	TAAAGAATTC	TCATAAATCT
ATACTTCAAG	AATTCATAAA	TCTATCAGAA	CCACATTAAA	GGTAATTGTT

ACATTAGTCT	CGTCAACTAG	TACATAACAT	ACTACATGAA	CTTTTGTGTT
ATTTACATTG	TCTTTGAGTA	CTATATTTTA	TATTTAAAAT	AATTAAACTA
TAACCTAGTA	TCTTTATCTA	CGCATAAAAG	TATCAATGTA	TGTGACCTAA
TCTCCGTACG	CATGTACGGT	ATATGTTATT	GTTCCGCAAA	AGTCATACCA
AGAGCATGAA	CCGACGGAGG	ACTACTAATA	TTCAATGTAC	TGACAATTAA
AATTTTTTAG	AGAATTGATT	ACGGACAAGG	AAGTAAGGTC	TCCCGGGTGG
TTATTGACAA	CGTACTTTAA	AAGAGTAGTG	AACTTTGGAT	AGTGCGTTTA
GTAAGAAGTG	CCAACGCCAT	GACCCGAGTA	ATAGCTTGTA	TAATTTTTTG
ACAGGTTTTA	GGTAACCCGA	CGAAGGTATC	CCGGAAGATA	GTGCTTGGTT
TTTCTTGTAC	TGGACTAATC	ACACTAAGAC	GAAGAACTAT	AAAAGTAGGT
AGGTCTGAAA	TGGATTTTTT	ATATAGCTAA	ATTGTGTCTT	GGAGAATGGG
TGAGACACTC	ATTAAGGTCT	AGGTGCTCAT	TGTAGTGATT	GTGTTGCTTG
TTATGGTCAC	ACGAATTATA	GTAGGGCAAC	GAGTATTCTG	ACCTGAAATG
TACCCGGAAG	TGTAGGTGCC	CCTTGTAAGT	CCGAAGCTAT	GTAAGACATA
TAAGACCCGA	AAGCCATGTA	CCCGGACATG	CAGGTACTAG	CAGCGAACAA
ACACGGAACC	TGTTACCCCT	GTCGTCGTGC	CGACGACATA	CCCGACAGCT
TCAAGTCGGA	AGCCGCTTGG	AAGCTCTGCC	CGCACCTTTA	CTAATATAGC
GGACCAGCGA	AGCTGTATCA	GTGCCCCGGA	ATGTTGTCTA	TATTCTAGGG
ATTAATTTAG	CACCGGGTTA	CATAACCCGA	GCATTCAAAG	GAGTTGCCTG
ACGTTTATAA	ATTATCGATT	GTATGTTGCT	TTAGGCACTT	GTCTAAGTCC
TTTAAGTAAA	TCTTCACCCA	GGGTGTATAA	CGTTCTGTTT	TATGAACCCC
TGGTTCATAT	ATTTCTGTTT	ACTTGTGAAT	AAATTGCAAA	CTCATACGTT
AAACTAACCA	ACTGTCACTG	CAGACACCTT	GGGAGCACCC	CTGGTGTATT
	TTCCTTTTCC	GCGCCGGTAG	GCCATTATAA	T

Secuencia inversa complementaria:

TACGGATGGC	CGCTTTAATG	ATTTGATTTT	TGAATTTTGA	ATTTTGAATT
GCAATGTACT	TTTACGAAAT	TACCAAATAG	CCATTAGGTG	TCCAGGTATA
AATAAGACAC	CGATACACCG	ATTGCCATAG	AGCTTTGAGG	GACACCGATT
CATTTCAACA	TGCCTCGTTT	ATTTAAAATA	TATGCCAAAA	ATTATTTTCT
AACATATCCC	AATTGTTCTC	TCTCTAAAGA	GGAAGCACTT	TCCCAATTAA
AAAACCTAGA	AACCCCAACA	AATAAAAAAT	ACATCAAAGT	TTGCAGAGAA
CTCCACGAGA	ATGGGGAACC	ACATCTCCAT	GTGCTTATCC	AATTCGAAGG
CAAATACCAA	TGTAAGAACC	AACGGTTCTT	CGACCTGGTA	TCCCCAACA
GATCAGCACA	TTTCCATCCG	AACATTCAGG	CAGCTAAGAG	CTCAACAGAT
GTCAAGACCT	ACGTGGAGAA	AGACGGAGAC	TTCAATTGATT	TTGGAGTTTT
CCAAATCGAT	GGCAGATCAG	CTAGAGGAGG	TCAGCAATCT	GCCAACGACG
CATATGCCGA	AGCACTCAAT	TCAGGCAATA	AATCCGAGGC	CCTCAATATA
TTAAAAGAGA	AGGCCCAAAA	GGACTATATT	TTACAATTTT	ATAATTTAAG
TTCAAATTTA	GATAGGATTT	TTAGTCCTCC	TTTAGAAGTT	TATGTTTCTC
CATTTCTTTC	TTCTTCTTTT	AATCAAGTTC	CAGATGAACT	TGAAGAGTGG
GTGCTGAGAA	ACGTCGTGTC	TTCCGCTGCG	CGGCCATGGA	GACCTAATAG
TATTGTCATT	GAGGGTGATA	GCAGAACAGG	CAAAACAATG	TGGGCCAGGT
CTCTAGGCCC	ACATAATTAT	TTATGTGGAC	ATCTAGACCT	AAGCCCAAAG
GTGTACAGTA	ATGATGCGTG	GTACAACGTC	ATTGATGACG	TAGACCCGCA
TTATTTAAAG	CACTTCAAGG	AATTCATGGG	GGCCCAGAGG	GACTGGCAAA

GCAACACAAA	GTACGGGAAG	CCCATTCAAA	TTAAAGGGGG	AATTCCCCT
ATCTTCCTCT	GCAATCCAGG	ACCTACCTCC	TCATATAGGG	AATATCTAGA
CGAAGAAAAA	AATATATCCT	TGAAAAATTG	GGCGCTCAAG	AATGCAACCT
TCGTCACCCT	CTACGAGCCA	CTGTTCGCAA	GTATCAATCA	AGGTCCAACA
CAAGATAGCC	AAGAAGAAAC	CAATAAGGCG	TAAGCGTGTA	GACCTAGACT
GTGGCTGCTC	ATACTACCTC	CACCTCAACT	GCAACAATCA	TGGATTCACG
CACAGGGGAA	CTCATCACTG	CTCCTCAGGC	AGAGAATGGC	GTTTTTATTT
GGGAGATAAA	CAATCCCCTC	TATTTCAAGA	TAACAGAACA	CAGCCAGCGG
CCATTTCTAA	TGAACCACGA	CATCATTTCC	ATTCAGATAA	GATTCAACCA
CAACATCAGG	AAGGTAATGG	GGATTACAA	ATGTTTTCTC	AACTTCCGAA
TTTGGACGAC	ATTACAGCCT	CAGACTGGTC	ATTTCTTAAG	AGTATTTAGA
TATGAAGTTC	TTAAGTATTT	AGATAGTCTT	GGTGTAATTT	CCATTAACAA
TGTAATCAGA	GCAGTTGATC	ATGTATTGTA	TGATGTACTT	GAAAACACAA
TAAATGTAAC	AGAAACTCAT	GATATAAAAT	ATAAATTTTA	TTAATTTGAT
ATTGAATCAT	AGAAATAGAT	GCGTATTTTC	ATAGTTACAT	ACACTGGATT
AGAGGCATGC	GTACATGCCA	TATACAATAA	CAAGGCGTTT	TCAGTATGGT
TCTCGTACTT	GGCTGCCTCC	TGATGATTAT	AAGTTACATG	ACTGTTAATT
TTAAAAAATC	TCTTAACTAA	TGCCTGTTCC	TTCATTCCAG	AGGGCCCCACC
AATAACTGTT	GCATGAAATT	TTCTCATCAC	TTGAAACCTA	TCACGCAAAT
CATTCTTCAC	GGTTGCGGTA	CTGGGCTCAT	TATCGAACAT	ATTAAAAACC
TGTCCAAAAT	CCATTGGGCT	GCTTCCATAG	GGCCTTCTAT	CACGGACCAA
AAAGAACATG	ACCTGATTAG	TGTGATTCTG	CTTCTTGATA	TTTTTCATCCA
TCCAGACTTT	ACCTAAAAAA	TATATCGATT	TAACACAGAA	CCTCTTACCC
ACTCTGTGAG	TAATTCCAGA	TCCACGAGTA	ACATCACTAA	CACAACGAAC
AATACCAGTG	TGCTTAATAT	CATCCCGTTG	CTCATAAGAC	TGGACTTTAC
ATGGGCCTTC	ACATCCACGG	GGAACATCAG	GGCTTCGATA	CATTCTGTAT
ATTCTGGGCT	TTCGGTACAT	GGGCCTGTAC	GTCCATGATC	GTCGCTTGTT
TGTGCCTTGG	ACAATGGGGA	CAGCAGCACG	GCTGCTGTAT	GGGCTGTCTGA
AGTTCAGCCT	TCGGCGAACC	TTCGAGACGG	GCGTGGAAT	GATTATATCG
CCTGGTCGCT	TCGACATAGT	CACGGGCCCT	TACAACAGAT	ATAAGATCCC
TAATTAAATC	GTGGCCCAAT	GTATTGGGCT	CGTAAGTTTC	CTCAACGGAC
TGCAATATTT	TAATAGCTAA	CATACAACGA	AATCCGTGAA	CAGATTCAGG
AAATTCATTT	AGAAGTGGGT	CCCACATATT	GCAAGACAAA	ATACTTGGGG
ACCAAGTATA	TAAAGACAAA	TGAACACTTA	TTTAACGTTT	GAGTATGCAA
TTTGATTGGT	TGACAGTGAC	GTCTGTGGAA	CCCTCGTGGG	GACCACATAA
AAGGAAAAGG CGCGGCCATC CGGTAATATT A				

Porcentajes:

- Secuencia:

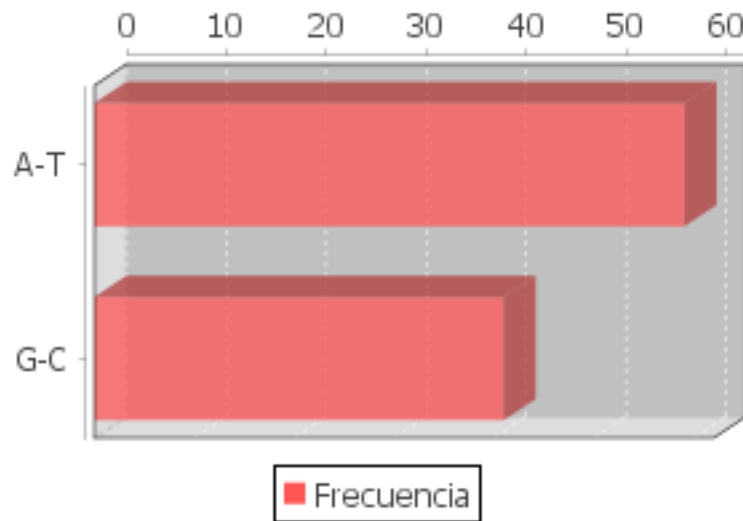
- A: 27.436174%
- C: 19.237684%
- T: 31.607336%
- G: 21.718805%

- Secuencia inversa complementaria:

- A: 31.607336%

- C: 21.718805%
  - T: 27.436174%
  - G: 19.237684%
- Porcentajes agrupados por nucleótidos complementarios:
- A-T: 59.04351%
  - G-C: 40.95649%

Diagrama de barras:



La traducción de esta secuencia se muestra a continuación:

**Marco de lectura 1:**

**Secuencia:**

```
*YRMAAPFP FMWSPRGFHR RHCQPIKLHT QTLNKCSFVF IYLVPKYFVL
QYVGPTSK*I S*ICSRISLY VSY*IFAVR* GNLRAQYIGP RFN*GSYICC
KGP*LCRSDQ AI*SFPRPSR RFAEG*TSTA HTAAVLLSPL SKAQTSDDHG
RTGPCTESPE YTECIEALMF PVDVKAHVKS SLMSNGMILS TLVLFVVLVM
LLVDLELLTE WVRGSVLNRY IF*VKSGWMK ISRSRITLIR SCSFWSVIEG
PMEAAQWILD RFLICSIMSP VPQP*RMICV IGFK**ENFM QQLLVGPLE*
RNRH*LRDFL KLTVM*LIII RRQPSTRIL KTPCYCIWHV RMPLIQCM*L
*KYASISMIQ YQINKIYILY HEFLLHLLCF QVHHTIHDQL L*LHC*WKLH
QDYLNT*ELH I*ILLRNDQS EAVMSSKFGS *ENICESPLP S*CCG*ILSE
WK*CRGSLEM AAGCVLLS*N RGDCLSPK*K RHSLPEEQ** VPLCVNP*LL
QLRWR*YEQP QSRSTRRLI GFFLAILCWT LIDTCEQWLV EGDEGCILER
PIFQGYIFFF V*IFPI*GGR SWIAEEDSGN SPFNLNGLPV LCVALPVPLG
PHEFLEVL*I MRVYVINDVV PRIITVHLWA *V*MST*IIM WA*RPGPHCF
ACSAITLNDN TIRSPWPRSG RHDVLSDFLF KFIWNLIKRR RKKWRNINF*
RRTKNPI*I* T*IMKL*NIV LWGLLF*YIE GLGFIA*IEC FGICVVGRL
TSSS*SAIDL ENSKINEVSV FLHVGLDIC* ALSCLNVRME MC*SVWGYQV
EEPLVLTLLVF AFELDKHMEM WFPILVEFSA NFDVFFICWG F*VF*LGKCF
LFRERTIGIC *EIIIFGIYFK *TRHVEMNRC PSKLYGNRCI GVLFI PGHLM
AIW*FRKSTL QFKIQNSKIK SLKRPSV
```

Las longitudes exactas de los fragmentos son:

Fragmento	Posición	Longitud	Secuencia
F01	[001,057]	57	YRMAAPFPFMWSPRGFHRHRCQPIKLHTQTLNKCSFVFIYLVPKYFVLQYVGPTSK
F02	[059,060]	02	IS
F03	[062,072]	11	ICSRISLYVSY
F04	[074,078]	05	IFAVR
F05	[080,092]	13	GNLRAQYIGPRFN
F06	[094,102]	09	GSYICCKGP
F07	[104,111]	08	LCRSDQAI
F08	[113,124]	12	SFPRPSRRFAEG
F09	[126,221]	96	TSTAHTAAVLLSPLSKAQTSDDHGRTGPCTESPEYTECIEALMF PVDVKAHVKSSLMSNGMILSTLVLFVVLVM LLVDLELLTEWVRGSVLNRYIF
F10	[223,273]	51	VKSGWMKISRSRITLIRSCSFWSVIEGPMEEAAQWILD RFLICSIMSPVPQP

F11	[ 275 , 283 ]	09	RMICVIGFK
F12	[ 286 , 298 ]	13	ENFMQQLLVGPLE
F13	[ 300 , 303 ]	04	RNRH
F14	[ 305 , 314 ]	10	LRDFLKLTVM
F15	[ 316 , 347 ]	32	LIIIRRQPSTRITILKTPCYCIWHVRMPLIQCM
F16	[ 349 , 349 ]	01	L
F17	[ 351 , 390 ]	40	KYASISMIQYQINKIYILYHEFLLHLLCFQVHHTIHD QLL
F18	[ 392 , 394 ]	03	LHC
F19	[ 396 , 405 ]	10	WKLHQDYLNT
F20	[ 407 , 410 ]	04	ELHI
F21	[ 412 , 429 ]	18	ILLRNDQSEAVMSSKFGS
F22	[ 431 , 440 ]	10	ENICESPLPS
F23	[ 442 , 444 ]	03	CCG
F24	[ 446 , 451 ]	06	ILSEWK
F25	[ 453 , 467 ]	15	CRGSLEMAAGCVLLS
F26	[ 469 , 477 ]	09	NRGDCLSPK
F27	[ 479 , 487 ]	09	KRHSLPEEQ
F28	[ 490 , 496 ]	07	VPLCVNP
F29	[ 498 , 504 ]	07	LLQLRWR
F30	[ 506 , 560 ]	55	YEQPQSRSTRRLRIGFFLAILCWTLIDTCEQWLVEGD EGCILERPIFQGYIFFFV
F31	[ 562 , 565 ]	04	IFPI
F32	[ 567 , 607 ]	41	GGRSWIAEEDSGNSPFNLNGLPVLCVALPVPLGPHEF LEVL
F33	[ 609 , 629 ]	21	IMRVYVINDVVPRIITVHLWA
F34	[ 631 , 631 ]	01	V
F35	[ 633 , 635 ]	03	MST
F36	[ 637 , 641 ]	05	IIMWA
F37	[ 643 , 698 ]	56	RPGPHCFACSAITLNDNTIRSPWPRSGRHDVLSDPLF KFIWNLIKRRRKKWRNINF
F38	[ 700 , 706 ]	07	RRTKNPI
F39	[ 708 , 708 ]	01	I
F40	[ 710 , 710 ]	01	T
F41	[ 712 , 715 ]	04	IMKL
F42	[ 717 , 725 ]	09	NIVLWGLLF
F43	[ 727 , 735 ]	09	YIEGLGFIA
F44	[ 737 , 753 ]	17	IECFGICVVGRLLTSSS
F45	[ 755 , 778 ]	24	SAIDLENSKINEVSVFLHVGLDIC
F46	[ 780 , 791 ]	12	ALSCLNVRMEMC
F47	[ 793 , 840 ]	48	SVWGYQVEEPLVLTTLVFAFELDKHMEMWFPILVEFSA NFDVFFICWGF
F48	[ 842 , 843 ]	02	VF
F49	[ 845 , 859 ]	15	LGKCFLFRERTIGIC
F50	[ 861 , 869 ]	09	EIIFGIYFK
F51	[ 871 , 902 ]	32	TRHVENNRCP SKLYGNRCIGVLFIPGHLMAIW
F52	[ 904 , 926 ]	23	FRKSTLQFKIQNSKIKSLKRPSV

## Marco de lectura 2:

### Secuencia:

NITGWPRFL LCGPHEGSTD VTVNQSNCIL KR\*ISVHLSL YTWSPSILSC  
 NMWDPLLNEF PESVHGFRM LAIKYLSQVE ETYPEPNTLGH DLIRDLISVV  
 RARDYVEATR RYNHFHARLE GSPKAELRQP IQQPCCCPHC PRHKQATIMD  
 VQAHVPKAQN IQNVSKP\*CS PWM\*RPM\*SP VL\*ATG\*Y\*A HWYCSLC\*\*C  
 YSWIWNYSQS G\*EVL\*IDI FFR\*SLDG\*K YQEAESH\*SG HVLF\*GP\*\*KA  
 LWKQPN\*GF\*GF\*YVR\*\*AQ YRNREE\*FA\* \*VSSDEKISC NSYWWALWNE  
 GTGIS\*EIF\* N\*QSCNL\*SS GGSQVREPY\* KRLVIVYGMV ACL\*SSVCNY  
 ENTHLFL\*FN IKLIKFI\*FYI MSFCYIYCVF KYIIQYMINC SDYIVNGNYT  
 KTI\*ILKNFI SKYS\*EMTSL RL\*CRPNSEV EKTFVNPHYL PDVVVESYLN  
 GNDVVVH\*KW PLAVFCYLEI EGIVYLPNKN AILCLRSSDE FPCA\*IHDCC  
 S\*GGGSMSSH SLGLHAYALL VSSWLSCVGP \*LILANSGS\* RVTKVAFLSA  
 QFFKDIFFSS SRYSLYEEVG PGLQRKIVGI PPLI\*MGFPY FVLLCQSLWA  
 PMNSLKCFK\* CGSTSSMTLY HASLLYTFGL RSRCPHK\*LC GPRDLAHIVL  
 PVLLSPSMTI LLGLHGAAE DTTFSATHSS SSSGT\*LKEE ERNGET\*TSK  
 GGLKILSKFE LKL\*NCKI\*S FGAFSFNILR ASDLLPELSA SAYASLADC\*  
 PPLADLPSIW KTPKSMKSPS FST\*VLTSVE LLAA\*MFGWK CADLFGDTRS  
 KNRWFLHWYL PSNWISTWRC GSPFSWSSLQ TLMYFLFVGV SRFFNWESAS  
 SLEREQLGYV RK\*FLAYILN KRGMLK\*IGV PQSSMAIGVS VSYLYLDT\*W  
 LFGNFVKVHC NSKFKIQKSN H\*SGHP

Las longitudes exactas de los fragmentos son:

Fragmento	Posición	Longitud	Secuencia
F01	[000,031]	032	NITGWPRFLLCGPHEGSTDVTVNQSNCILKR
F02	[033,166]	134	ISVHLSLYTWSPSILSCNMWDPLLNEFPESVHGFRMLAIKYLQSVETTYPEPNTLGHDLIRDLISVVRARDYVEATTRYNHFHARLEGSPKAELRQPIQQPCCCPHCPRHKQATIMDVQAHVPKAQNIQNVSKP
F03	[168,172]	005	CSPWM
F04	[174,176]	003	RPM
F05	[178,181]	004	SPVL
F06	[183,185]	003	ATG
F07	[187,187]	001	Y
F08	[189,196]	008	AHWYCSLC
F09	[199,210]	012	CYSWIWNYSQSG
F10	[212,215]	004	EVL
F11	[217,222]	006	IDIFFR
F12	[224,227]	004	SLDG
F13	[229,236]	008	KYQEAESH
F14	[238,245]	008	SGHVLF*GP
F15	[248,261]	014	KALWKQPN*GF*GF



F16	[263,265]	003	YVR
F17	[268,275]	008	AQYRNREE
F18	[277,278]	002	FA
F19	[281,304]	024	VSSDEKISCNSYWWALWNEG TGIS
F20	[306,308]	003	EIF
F21	[310,310]	001	N
F22	[312,316]	005	QSCNL
F23	[318,328]	011	SSGGSQVREPY
F24	[330,342]	013	KRLVIVYGYACL
F25	[344,356]	013	SSVCNYENTHLFL
F26	[358,402]	045	FNIKLIKFI FYIMSFCYIYCVFKYIIQYMINCSDYIV NGNYTKTI
F27	[404,413]	010	ILKNFISKYS
F28	[415,421]	007	EMTSLRL
F29	[423,456]	034	CRPNSEVEKTFVNPHYLPDVVVESYLN GNDVVVH
F30	[458,493]	036	KWPLAVFCYLEIEGIVYLPKNAILCLRSSDEFFPCA
F31	[495,500]	006	IHDCCS
F32	[502,529]	028	GGGSMSSHSLGLHAYALLVSSWLSCVGP
F33	[531,538]	008	LILANSGS
F34	[540,583]	044	RVTKVAFLSAQFFKDIFFSSSRYSLYEEVGPGLQRKI VGIPPLI
F35	[585,608]	024	MGFPYFVLLCQSLWAPMNSLKC FK
F36	[610,636]	027	CGSTSSMTLYHASLLYTFGLRSRCPHK
F37	[638,684]	047	LCGPRDLAHIVLPVLLSPSMTILLGLHGRAAEDTTFS ATHSSSSSGT
F38	[686,695]	010	LKEEERNGET
F39	[697,712]	016	TSKGGLKILSKFELKL
F40	[714,717]	004	NCKI
F41	[719,748]	030	SFGAFS FNILRASDLLPELSASAYASLADC
F42	[750,772]	023	PPLADLPSIWKTPKSMKSPSFST
F43	[774,783]	010	VLTSVELLAA
F44	[785,861]	077	MFGWKCADLFGDTRSKNRWFLHWYLP SNWISTWRCGS PFSWSSLQTLMYFLFVGVS RFFNWESASSLEREQ LGY VRK
F45	[863,875]	013	FLAYILNKR GMLK
F46	[877,897]	021	IGVPQSSMAIGVSVS YLYLDT
F47	[899,920]	022	WLFGNFVKVHCNSKFKIQKSNH
F48	[922,925]	004	SGHP

### Marco de lectura 3:

Secuencia:

ILPDGRAFSF YVVPTRVPQT SLSTNQIAYS NVK\*VFICLY ILGPQVFCLA  
ICGTHF\*MNF LNLFTDFVVC \*LLNIC SPLR KLTSPIH WAT I\*LGILYLL\*  
GPVTMSKRPG DIIISTPVSK VRRRLNFDSP YSSRAAVPIV QGTNKRRSWT  
YRPMYRKPRI YRMYRSPDVP RGCEGPCKVQ SYEQRDDIKH TGIVRCVSDV

TRGSGITHRV GKRFCVKSIIY FLGKVWMDEN IKKQNHNTNQV MFFLVRDRRP  
 YGSSPMDFGQ VFNMFNDNEPS TATVKNDLRD RFQVMRKFHA TVIGGPSGMK  
 EQALVKRFFK INSHVTYNHQ EAAKYENHTE NALLLYMACT HASNPVYVTM  
 KIRIIFYDSI SN\*\*NLYFIS \*VSVTFIVFS STSYNT\*STA LITLLMEITP  
 RLSKYLRTSY LNTLKK\*PV\* GCNVVQIRKL RKHL\*IPITF LMLWLNLI\*M  
 EMMSWFIRNG RWLCSVILK\* RGLFISQIKT PFSA\*GAVMS SPVRESMIVA  
 VEVEVV\*AAT V\*VYTLTPYW FLLGYLVLDL D\*YLRTVARR G\*RRLHS\*AP  
 NFSRIYFFLR LDIPYMRR\*V LDCRGR\*WEF PL\*FEWASRT LCCFASPSGP  
 P\*IP\*SALNN AGLRHQ\*RCT THHYCTPLGL GLDVHINNYV GLETWPTLFC  
 LFCYHPQ\*QY Y\*VSMAAQRK TRRSQRPTLQ VHLELD\*KKK KEMEKHKLLK  
 ED\*KSYLNLN LNYEIVKYSP LGPSLLIY\*G PRIYCLN\*VL RHMRRWQIAD  
 LL\*LICHRFG KLQNQ\*SLRL SPRRS\*HLLS S\*LPECSDBG VLICLGIPGR  
 RTVGSYIGIC LRIG\*AHGDV VPHSRGVLC L\*CIFYLLGF LGFLIGKVLP  
 L\*RENNWDML GNNFWHIF\*I NEAC\*NESVS LKALWQSVYR CLIYTWTPNG  
 YLVIS\*KYIA IQNSKFKNQI IKA AIR

Las longitudes exactas de los fragmentos son:

Fragmento	Posición	Longitud	Secuencia
F01	[000,032]	033	ILPDGRAFSFYVVPTRVPQTSLSNQAISNVK
F02	[034,055]	022	VFICLYILGPQVFCLAICGTHF
F03	[057,069]	013	MNFLNLF TDFVVC
F04	[071,090]	020	LLNICSP LRKLTSP IHWATI
F05	[092,098]	007	LGILYLL
F06	[100,361]	262	GPVTMSKRPGDIIISTPVSKVRRRLNFDSPYSSRAAV PIVQGTNKRRSWTYRPMYRKPRIYRMYRSPDVPRGCE GPCKVQSYEQRDDIKHTGIVRCVSDVTRGSGITHRVG KRFCVKSIIYFLGKVWMDENIKKQNHNTNQVMFFLVRDR RPYGSSPMDFGQVFNMFNDNEPSTATVKNDLRDRFQVM RKFHATVIGGPSGMKEQALVKRFFKINSHVTYNHQEA AKYENHTENALLLYMACTHASNPVYVTMKIRIIFYDS ISN
F07	[364,369]	006	NLYFIS
F08	[371,385]	015	VSVTFIVFSSTSYNT
F09	[387,415]	029	STALITLLMEITPRLSKYLRTSYLNTLKK
F10	[417,418]	002	PV
F11	[420,433]	014	GCNVVQIRKL RKHL
F12	[435,447]	013	IPITFLMLWLNLI
F13	[449,468]	020	MEMMSWFIRNGRWLCSVILK
F14	[470,483]	014	RGLFISQIKTPFSA
F15	[485,505]	021	GAVMSSPVRESMIVAVEVEVV
F16	[507,510]	004	AATV
F17	[512,530]	019	VYTLTPYWFLGGLVLDLD
F18	[532,540]	009	YLRTVARRG
F19	[542,546]	005	RRLHS
F20	[548,567]	020	APNFSRIYFFLRDLIPYMRR
F21	[569,575]	007	VLDCRGR

F22	[577,581]	005	WEFPL
F23	[583,600]	018	FEWASRTLCCFASPSGPP
F24	[602,603]	002	IP
F25	[605,615]	011	SALNNAGLRHQ
F26	[617,656]	040	RCTTHHYCTPLGLGLDVHINNYVGLETWPTLFCCLFCY HPQ
F27	[658,660]	003	QYY
F28	[662,685]	024	VSMAAQKTRRSQRPTLQVHLELD
F29	[687,701]	015	KKKKEMEKHKLLKED
F30	[703,727]	025	KSYLNLNLNLYEIVKYSPLGPSLLIY
F31	[729,736]	008	GPRIYCLN
F32	[738,751]	014	VLRHMRRWQIADLL
F33	[753,764]	012	LICHRFGKLQOQ
F34	[766,774]	009	SLRLSPRRS
F35	[776,780]	005	HLLSS
F36	[782,813]	032	LPECSDGNVLICLGIPGRRTVGSYIGICLRIG
F37	[815,830]	016	AHGDVVPHSRGVLCKL
F38	[832,850]	019	CIFYLLGFLGFLIGKVLPL
F39	[852,867]	016	RENNWDMLGNFWHIF
F40	[869,873]	005	INEAC
F41	[875,904]	030	NESVSLKALWQSVYRCLIIYTWTPNGYLVIS
F42	[906,925]	020	KYIAIQNSKFKNQIIKAAIR

## Marco de lectura -1:

### Secuencia:

YGWPL\*\*FDF \*ILNFELQCT FTKLPNSH\*V SRYK\*DTDTP IAIEL\*GTPI  
 HFNMPRLFKI YAKNYFLTYP NCSLSKEEAL SQLKNLETPT NKKYIKVCRE  
 LHENGEPHLH VLIQFEGKYQ CKNQRFFDLV SPNRSAHFHP NIQAAKSSTD  
 VKTYVEKDGD FIDFGVFQID GRSARGGQQS ANDAYAEALN SGNKSEALNI  
 LKEKAPKDYI LQFHNLSNL DRIFSPPLEV YVSPFLSSSF NQVPDELEEW  
 VAENVVSSAA RPWRPNSIVI EGDSRTGKTM WARSLGPHNY LCGHLDLSPK  
 VYSNDAWYNV IDDVDPHYLK HFKEFMGAQR DWQSNTKYGK PIQIKGGIPT  
 IFLCNPPTS SYREYLDEEK NISLKNWALK NATFVTLYEP LFASINQGPT  
 QDSQEETNKA \*ACRPRLWLL ILPPPQLQQS WIHAQGNSSL LLRQMAFLF  
 GR\*TIPTISR \*QNTASGHF\* \*TTTSFPFR\* DSTTTSGR\*W GFTNVFSTSE  
 FGRHYSRLV IS\*EYLDMKF LSI\*IVLV\*F PLTM\*SEQLI MYCMMYLKTQ  
 \*M\*QKLMI\*N INFINLILNH RNRCVFS\*LH TLD\*RHAYMP YTITRRFQYG  
 SRTWLPPDDY KLHDC\*F\*KI S\*LMPVPSFQ RAHQ\*LLHEI FSSLETYHAN  
 HSSRLRYWAH YRTY\*KPVQN PLGCFHRAFY HGPKRT\*PD\* CDSAS\*YFHP  
 SRLYLKNISI \*HRTSYPLCE \*FQIHE\*HH\* HNEQYQCA\*Y HPVAKHTGLY  
 MGLHIHGEHQ GFDTFCIFWA FGTWACTSMI VACLCLGQWG QQHGCCMGCR  
 SSAFGEPSRR AWK\*LYRLVA ST\*SRALTTD IRSLIKSWPN VLGS\*VSSTD  
 CKYLIANIQR NP\*TDGNSF RSGSHILQDK ILGDQVYKDK \*TLI\*RLSMQ  
 FDWLTVTSVE PSWGPHKRKR RGHPVIL

Las longitudes exactas de los fragmentos son:

Fragmento	Posición	Longitud	Secuencia
F01	[000,004]	005	YGWPL
F02	[007,009]	003	FDF
F03	[011,027]	017	ILNFELQCTFTKLPNSH
F04	[029,033]	005	VSRYK
F05	[035,044]	010	DTDTPIAIEL
F06	[046,409]	364	GTPIHFNMPRLFKIYAKNYFLTYPNCSLSKEEALSQ KNLETPTNKKYIKVCRELHENGEPHLHVLIQFEGKYQ CKNQRFDDLVSPPNRSAPFHPNIQAASSTDVKTYVEK DGDFFIDFGVFQIDGRSARGGQQSANDAYAEALNSGNK SEALNILKEKAPKDYILQFHNLSNLDRIFFSPPLEVY VSPFLSSSFNQVPDELEEWVAENVVSSAARPWRPNSI VIEGDSRTGKTMWARSLGPHNYLCGHLDLSPKVYSND AWYNVIDDVPDHYLKHFKFEMGAQRDWQSNTRYGKPI QIKGGIPTIFLCNPGPTSSYREYLDEEKNI SLKNWAL KNATFVTLYEPLFASINQGPTQDSQEETNKA
F07	[411,451]	041	ACRPRLWLLILPPPQLQQSWIHAQGNSSLLLRQRMAL LFGR
F08	[453,459]	007	TIPSISR
F09	[461,468]	008	QNTASGHF
F10	[471,478]	008	TTTSFPFR
F11	[480,487]	008	DSTTTSGR
F12	[489,511]	023	WGFTNVFSTSEFGRHYSLRLVIS
F13	[513,522]	010	EYLDMKFLSI
F14	[524,527]	004	IVLV
F15	[529,533]	005	FPLTM
F16	[535,549]	015	SEQLIMYCMMYLKTQ
F17	[551,551]	001	M
F18	[553,557]	005	QKLMI
F19	[559,576]	018	NINFINLILNHRNRCVFS
F20	[578,582]	005	LHTLD
F21	[584,614]	031	RHAYMPYTITRRFQYGSRTWLPDDYKLHDC
F22	[616,616]	001	F
F23	[618,620]	003	KIS
F24	[622,633]	012	LMPVPSFQRAHQ
F25	[635,663]	029	LLHEIFSSLETYHANHSSRLRYWAHYRTY
F26	[665,685]	021	KPVQNPLGCFHRAFYHGPKRT
F27	[687,688]	002	PD
F28	[690,694]	005	CDSAS
F29	[696,709]	014	YFHPSRLYLKNISI
F30	[711,719]	009	HRTSYPLCE
F31	[721,725]	005	FQIHE
F32	[727,728]	002	HH
F33	[730,737]	008	HNEQYQCA

F34	[739,812]	074	YHPVAHKTGLYMGLHIHGEHQGFDTFCIFWAFGTWAC TSMIVACLCLGQWGQQHGCCMGCRSSAFGEPSRRAWK
F35	[814,821]	008	LYRLVAST
F36	[823,843]	021	SRALTDIRSLIKSWPNVLGS
F37	[845,861]	017	VSSTDCKYLIANIQRNP
F38	[863,889]	027	TDSGNSFRSGSHILQDKILGDQVYKDK
F39	[891,893]	003	TLI
F40	[895,926]	032	RLSMQFDWLTVTSVEPSWGPBKRKRGRHPVIL

## Marco de lectura -2:

### Secuencia:

TDGRFNDLIF EF\*ILNCNVL LRNYQIAIRC PGINKTPIHR LP\*SFEGHRF  
 ISTCLVYLKY MPKIIS\*HIP IVLSLKRKHF PN\*KT\*KPQQ IKNTSKFAEN  
 STRMGNHISM CLSNSKANTN VRTNGSSTWY PQTDQHISIR TFRQLRAQQM  
 SRPTWRKTET SLILEFSKSM ADQLEEVSNL PTHMPKHSI QAINPRPSIY  
 \*KRRPQRTIF YNFII\*VQI\* IGFLVLL\*KF MFLHFFLLLL IKFQMNLSKG  
 SLRTSCLPLR GHGDLIVLSL RVIAEQAKQC GPGL\*AHIII YVDI\*T\*AQR  
 CTVMRGTTT LMT\*TRII\*S TSRNSWGPRG TGKATQSTGS PFKLKGEFPL  
 SSSAIQDLPP HIGNI\*TKKK IYP\*KIGRSR MQPSSPSTSH CSQVSIKVQH  
 KIAKKKPIRR KRVDLDCGCS YYLHLNCCNH GFTHRGTHHC SSGREWRFYL  
 GDKQSPFLQD NRTQPAAISN EPRHHFHSK IQPQHQEGNG DSQMFSQLPN  
 LDDITASDWS FLKSI\*I\*SS \*VFR\*SWCNF H\*QCNQSS\*S CIV\*CT\*KHN  
 KCNRNS\*YKI \*ILLI\*Y\*II EIDAYFHSYI HWIRGMRTCH IQ\*QGVFSMV  
 LVLGCLLMII SYMTVNFKKS LN\*CLFLHSR GPTNNCCMKF SHHLKPITQI  
 ILHGCGTGLI IEHIKNLSKI HWAASIGPSI TDQKEHDLIS VILLLDIFIH  
 PDFT\*KIYRF NTEPLTHSVS NSRSTSNITN TTNNTSVLNI IPLLIRLDFT  
 WAFTSTGNIR ASIHSVYSGL SVHGPVRP\*S SLVCALDNGD SSTAAVWAVE  
 VQPSANLRDG RGNDYIAWSL RHSHGPLQQI \*DP\*LNRGPM YWARKFPQRT  
 ANI\*\*LTYNE IREQIQEIHL EVGPTYCKTK YLGTKYIKTN EHLFNV\*VCN  
 LIG\*Q\*RLWN PRGDHIKKGK AAIR\*Y

Las longitudes exactas de los fragmentos son:

Fragmento	Posición	Longitud	Secuencia
F01	[000,011]	012	TDGRFNDLIFEF
F02	[013,041]	029	ILNCNVLLRNYQIAIRCPGINKTPIHRLP
F03	[043,065]	023	SFEGHRFISTCLVYLKYMPKIIS
F04	[067,081]	015	HIPIVLSLKRKHFNP
F05	[083,084]	002	KT
F06	[086,199]	114	KPQQIKNTSKFAENSTRMGNHISMCLSNSKANTNVRT NGSSTWYPQTDQHISIRTFRQLRAQQMSRPTWRKTET SLILEFSKSMADQLEEVSNLPTTHMPKHSIQAINPRP SIY

F07	[ 201 , 214 ]	014	KRRPQRTIFYNFII
F08	[ 216 , 218 ]	003	VQI
F09	[ 220 , 226 ]	007	IGFLVLL
F10	[ 228 , 283 ]	056	KFMFLHFFLLLLIKFQMNLSGSLRTSCLPLRGHGD IVLSLRVIAEQAKQCGPGL
F11	[ 285 , 293 ]	009	AHIIIYVDI
F12	[ 295 , 295 ]	001	T
F13	[ 297 , 312 ]	016	AQRCTVMMRGTTSLMT
F14	[ 314 , 317 ]	004	TRII
F15	[ 319 , 364 ]	046	STSRNSWGPRGTGKATQSTGSPFKLKGEFPLSSSAIQ DLPPHIGNI
F16	[ 366 , 372 ]	007	TKKKIYP
F17	[ 374 , 514 ]	141	KIGRSRMQPSSPSTSHCSQVSIKVQHKIAKKKPIRRK RVDLDCGCSYYLHLNLCNNHGFTHRGTHHCSSGREWRF YLGDKQSPLFQDNRTQPAAISNEPRHHFHSDKIQPQH QEGNGDSQMFSQLPNLDDITASDWSFLKSI
F18	[ 516 , 516 ]	001	I
F19	[ 518 , 519 ]	002	SS
F20	[ 521 , 523 ]	003	VFR
F21	[ 525 , 530 ]	006	SWCNFH
F22	[ 532 , 537 ]	006	QCNQSS
F23	[ 539 , 542 ]	004	SCIV
F24	[ 544 , 545 ]	002	CT
F25	[ 547 , 555 ]	009	KHNKCNRNS
F26	[ 557 , 559 ]	003	YKI
F27	[ 561 , 564 ]	004	ILLI
F28	[ 566 , 566 ]	001	Y
F29	[ 568 , 591 ]	024	II EIDAYFHSYIHWIRGMRTCHIQ
F30	[ 593 , 621 ]	029	QGVFSMVLVLGCLLMIISYMTVNFKKSLN
F31	[ 623 , 703 ]	081	CLFLHSRGPTNNCCMKFSHHLKPITQIILHGC GTGLI IEHIKNLSKIHWAASIGPSITDQKEHDLISVILLLDI FIHPDFT
F32	[ 705 , 777 ]	073	KIYRFNTEPLTHSVSNSRSTSNITNTTNTSVLNIIP LLIRLDFTWAFTSTGNIRASIHSVYSGLSVHGVPVRP
F33	[ 779 , 829 ]	051	SSLVCALDNGDSSTA AVWAVEVQPSANLRDGRGNDYI AWSLRHSHG PLQOI
F34	[ 831 , 832 ]	002	DP
F35	[ 834 , 852 ]	019	LNRGPMYWAR KFPQRTANI
F36	[ 855 , 895 ]	041	LTYNEIREQIQEIHLEVGP TYCKTKYLGTKYIKTNEH LFNV
F37	[ 897 , 902 ]	006	VCNLIG
F38	[ 904 , 904 ]	001	Q
F39	[ 906 , 923 ]	018	RLWNPRGDHIK GKGA AIR
F40	[ 925 , 925 ]	001	Y

Marco de lectura -3:

Secuencia:

RMAALMI\*FL NFEF\*IAMYP YEITK\*PLGV QV\*IRHRYTD CHRALRDTDS  
 FQHASFI\*NI CQKLFNPISQ LFSL\*RGSTF PIKKPRNPKN \*KIHQSLQRT  
 PREWGTTSPC AYPIRRQIPM \*EPTVLRPGI PKQISTFPSE HSGS\*ELNRC  
 QDLRGERRRL H\*FWSFPNRW QIS\*RRSAIC QRRICRSTQF RQ\*IRGPQYI  
 KREGPKGLYF TIS\*FKFKFR \*DF\*SSFRSL CFSISFFFF\* SSSR\*T\*RVG  
 R\*ERRVFRCA AMET\*\*YCH\* G\*\*QNRQNNV GQVSRPT\*LF MWTSRPKPKG  
 VQ\*\*CVVQRH \*\*RRPALFKA LQGIHGGPEG LAKQHKVREA HSN\*RGNSHY  
 LPLQSRTYLL I\*GISRRRKK YILEKLGAQE CNLRHPLRAT VRKYQSRST  
 R\*PRRNQ\*GV SV\*T\*TVAAH TTSTSTATIM DSRTGELITA PQAENGVFIW  
 EINNPLYFKI TEHSQRPFLM NNDIISIQIR FNHNIRKVMG IHKCFNLNRI  
 WTTLQPQTGH FLRVFRYEV LKYLDLGLVIS INNVIRAVDH VLYDVLENTI  
 NVTETHDIKY KFY\*FDIES\* K\*MRIFIVTY TGLEACVHAI YNNKAFSVWF  
 SYLAAS\*\*L\* VT\*LLILKNL LTNACSFIE GPPITVA\*NF LIT\*NLSRKS  
 FFTVAVLGLS SNILKTCPKS IGLLP\*GLLS RTKKNMT\*LV \*FCFLIFSSI  
 QTLPKKYIDL TQNLPLTL\*V IPDPRVTSLT QRTIPVCLIS SRCS\*DWTLLH  
 GPSHPRGTSG LRYILYILGF RYMGlyVHDR RLFVPWTMGT AARLLYGLSK  
 FSLRRTFETG VEMIISPGRF DIVTGPYNRY KIPN\*IVAQC IGLVSFLNGL  
 QIFNS\*HTTK SVNRFKFI\* KWVPHIARQN TWGPSI\*RQM NTYLTFEYAI  
 \*LVDSVDVCGT LVGTT\*KEKA RPSGNI

Las longitudes exactas de los fragmentos son:

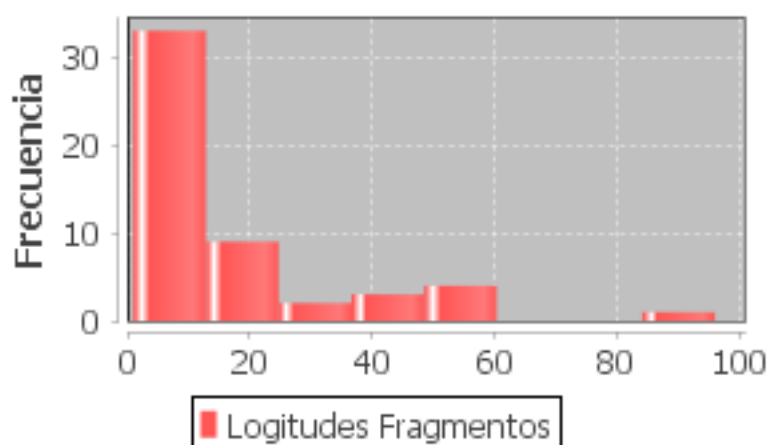
Fragmento	Posición	Longitud	Secuencia
F01	[000,006]	007	RMAALMI
F02	[008,013]	006	FLNFEF
F03	[015,024]	010	IAMYPYEITK
F04	[026,031]	006	PLGVQV
F05	[033,056]	024	IRHRYTDCHRALRDTDSFQHASFI
F06	[058,073]	016	NICQKLFNPISQLFSL
F07	[075,089]	015	RGSTFPIKKPRNPKN
F08	[091,119]	029	KIHQSLQRTPREWGTTSPCAYPIRRQIPM
F09	[121,143]	023	EPTVLRPGIPKQISTFPSEHSGS
F10	[145,160]	016	ELNRCQDLRGERRRLH
F11	[162,172]	011	FWSFPNRWQIS
F12	[174,191]	018	RRSAICQRRICRSTQFRQ
F13	[193,212]	020	IRGPQYIKREGPKGLYFTIS
F14	[214,219]	006	FKFKFR
F15	[221,222]	002	DF
F16	[224,238]	015	SSFRSLCFSISFFFF
F17	[240,243]	004	SSSR
F18	[245,245]	001	T
F19	[247,250]	004	RVGR
F20	[252,263]	012	ERRVFRCAAMET
F21	[266,268]	003	YCH
F22	[270,270]	001	G

F23	[ 273 , 286 ]	014	QNRQNNVGQVSRPT
F24	[ 288 , 301 ]	014	LFMWTSRPKPKGVQ
F25	[ 304 , 309 ]	006	CVVQRH
F26	[ 312 , 342 ]	031	RRPALFKALQGIHGGPEGLAKQHKVREAHSN
F27	[ 344 , 360 ]	017	RGNSHYLPLQSRITYLLI
F28	[ 362 , 400 ]	039	GISRRRKKYILEKLGAQECNLRHPLRATVRKYQSRSN TR
F29	[ 402 , 406 ]	005	PRRNQ
F30	[ 408 , 411 ]	004	GVSV
F31	[ 413 , 413 ]	001	T
F32	[ 415 , 562 ]	148	TVAAHTTSTSTATIMDSRTGELITAPQAENGVIWEI NNPLYFKITEHSQRPFLMNHDIISIQIRFNHNIRKVM GIHKCFLNFRIWTTLPQTGHFLRVFRYEVLKYLDL GVISINNVIRAVDHVLYDVLENTINVTETHDIKYKFY
F33	[ 564 , 568 ]	005	FDIES
F34	[ 570 , 570 ]	001	K
F35	[ 572 , 605 ]	034	MRIFIVTYTGLEACVHAIYNNKAFSVWFSYLAAS
F36	[ 608 , 608 ]	001	L
F37	[ 610 , 611 ]	002	VT
F38	[ 613 , 636 ]	024	LLILKNLLTNACSFIEGPPITVA
F39	[ 638 , 642 ]	005	NFLIT
F40	[ 644 , 674 ]	031	NLSRKSFFTVAVLGSLSNILKTCPKSIGLLP
F41	[ 676 , 686 ]	011	GLLSRTKKNMT
F42	[ 688 , 689 ]	002	LV
F43	[ 691 , 717 ]	027	FCFLIFSSIQTLPKKYIDLTQNLPLTL
F44	[ 719 , 743 ]	025	VIPDPRVTSLTQRTIPVCLISSRCS
F45	[ 745 , 833 ]	089	DWTLHGPHPRGTSGRLRYILYILGFRYMGLYVHDRRL FVPWTMGTAARLLYGLSKFSLRRTFETGVEMIISPGR FDIVTGPYNRYKIPN
F46	[ 835 , 854 ]	020	IVAQCIGLVSFLNGLQIFNS
F47	[ 856 , 868 ]	013	HTTKSVNRFRKFI
F48	[ 870 , 885 ]	016	KWVPHIARQNTWGPSI
F49	[ 887 , 899 ]	013	RQMNTYLTFEYAI
F50	[ 901 , 914 ]	014	LVDSDVCGTLVGTT
F51	[ 916 , 925 ]	010	KEKARPSGNI

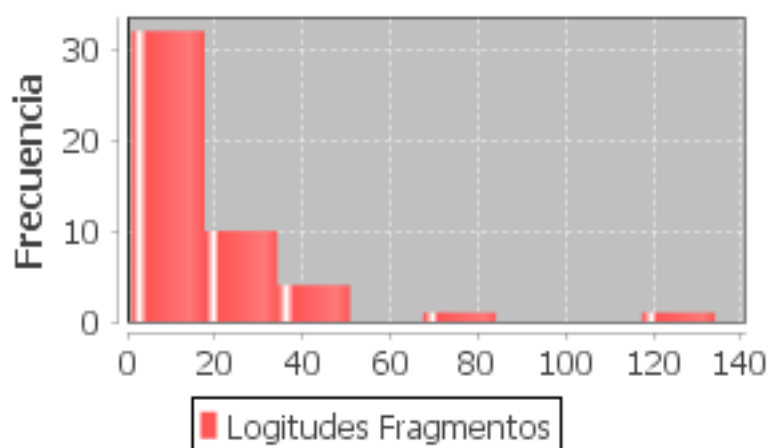
Histogramas:



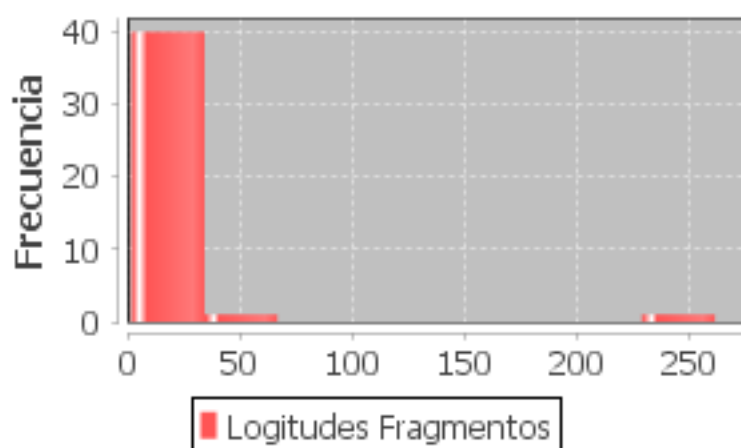
## Histograma ML 1



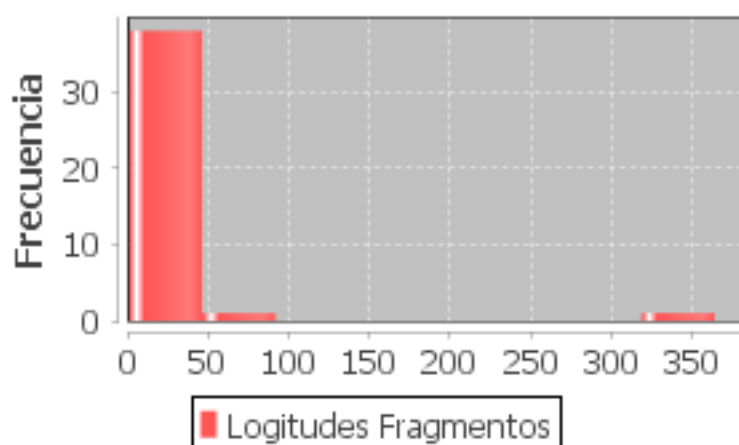
## Histograma ML 2



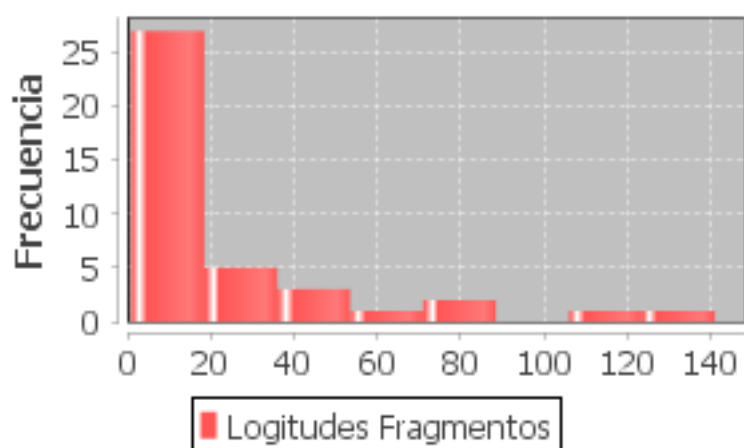
## Histograma ML 3



## Histograma ML -1



## Histograma ML -2



## Histograma ML -3

