

#NS5 already downloaded and loaded from Uniprot in this example.

(<https://www.uniprot.org/uniprot/A0A0B4ZYS0>)

```
> # print the rnaframesZikaSet
```

```
> rnaframesZikaSet
```

```
A RNAStringSet instance of length 6
```

```
width seq names
```

```
[1] 10794 AGUUGUUGAUCUGUGUGAGUCAG...GUGUGGGGAAAUCCAUGGUUUCU Pos 1
```

```
[2] 10794 AGAAACCAUGGAUUUCCCCACAC...CUGACUCACACAGAUAACAACU Neg 1
```

```
[3] 10793 GUUGUUGAUCUGUGUGAGUCAGA...GUGUGGGGAAAUCCAUGGUUUCU Pos 2
```

```
[4] 10793 GAAACCAUGGAUUUCCCCACACC...CUGACUCACACAGAUAACAACU Neg 2
```

```
[5] 10792 UUGUUGAUCUGUGUGAGUCAGAC...GUGUGGGGAAAUCCAUGGUUUCU Pos 3
```

```
[6] 10792 AAACCAUGGAUUUCCCCACACCG...CUGACUCACACAGAUAACAACU Neg 3
```

```
>
```

```
> # translate all 6 reading frames
```

```
> AAzika6F <- translate(rnaframesZikaSet)
```

```
> AAzika6F
```

```
A AAStringSet instance of length 6
```

```
width seq names
```

```
[1] 3598 SC*SV*VRLRQFESEARANNSIN...PPRWPPGTDRTSAAGVGKSMVS Pos 1
```

```
[2] 3598 RNHGFPHTGRRSSAICAWRPAWW...VDTVSSSRFRLELSQSDSHRSTT Neg 1
```

```
[3] 3597 VVDLCESDCDSSSLKRELTTVST...FHHAGRQAQIAELRRPVWGNPWF Pos 2
```

```
[4] 3597 ETMDFPTPAAEVRRSVPGGQRGG...LLILLALASDSNCRSLTHTDQQ Neg 2
```

```
[5] 3597 MLICVSQTATVRV*SES*QQYQQ...STTLAARHRSPNFGGRCGEIHGF Pos 3
```

```
[6] 3597 KPWISPHRPPKFGDLCLAASVVE...C*YCC*LSLQTRTVAV*LTQINN Neg 3
```

```
>
```

```
> # Count the matches allowing 15 mismatches
```

```
> vcountPattern(pattern = ns5, subject = AAzika6F, max.mismatch = 15)
```

```
[1] 0 0 1 0 0 0
```

```
>
```

```
> # Select the frame that contains the match
```

```
> selectedSet <- AAzika6F[3]
```

```
>
```

```
> #Convert this frame into a single sequence
```

```
> selectedSeq <- unlist(selectedSet)
```

*****THIRD FRAME HOLDS THE PATTERN. Use selectedSet and selectedSeq to look at the match*****

```
> # Use vmatchPattern with the set
```

```
> vmatchPattern(pattern = ns5, subject = selectedSet, max.mismatch = 15)
```

MIndex object of length 1

\$`Pos 2`

IRanges object with 1 range and 0 metadata columns:

	start	end	width
	<integer>	<integer>	<integer>
[1]	3023	3347	325

>

> # Use matchPattern with the single sequence

> matchPattern(pattern = ns5, subject = selectedSeq, max.mismatch = 15)

Views on a 3597-letter AAStrng subject

subject:

VVDLCESDCDSSSLKRELTTVSTGLIWIWKREFL...IDVGKTRDSMSFHHAGRQAQIAELRRPV
WGNPWF

views:

	start	end	width
[1]	3023	3347	325

[SRAIWYMWLGARFLEFEALGFLNEDHW...HRRDLRLMANAICSAVPVDWVPTGRTT]

###The above shows an NS5 protein sequence found in Zika virus.