Wyniki: beta-3 i beta-1

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Wyniki sekwencjonowania.

kolonia 1

Range 1: 1 to 580 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1213 bits(3138)	0.0	Compositional matrix adjust.	579/580(99%)	579/580(99%)	0/580(0%)

```
Query  1    MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLP  60
Sbjct  1    ............................................................  60

Query  61   FAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD  120
Sbjct  61   ............................................................  120

Query  121  GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDA  180
Sbjct  121  ............................................................  180

Query  181  EVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKGGSG  240
Sbjct  181  ............................................................  240

Query  241  SELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVGRIQMRTRRTLRGHLAKIYAM  300
Sbjct  241  ............................................................  300

Query  301  HWGTDSRLLVSASQDGKLIIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNIC  360
Sbjct  301  .........A..................................................  360

Query  361  SIYNLKTREGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIETGQQTTTFT  420
Sbjct  361  ............................................................  420

Query  421  GHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGMCRQTFTGHESDINAICFFPNGNAF  480
Sbjct  421  ............................................................  480

Query  481  ATGSDDATCRLFDLRADQELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALK  540
Sbjct  481  ............................................................  540

Query  541  ADRAGVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN*  580
Sbjct  541  ....................................*  580
```

Kolonia 2:

Range 1: 1 to 580 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1214 bits(3141)	0.0	Compositional matrix adjust.	580/580(100%)	580/580(100%)	0/580(0%)

```
Query  1    MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLP  60
Sbjct  1    ............................................................  60

Query  61   FAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD  120
Sbjct  61   ............................................................  120

Query  121  GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDA  180
Sbjct  121  ............................................................  180

Query  181  EVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKGGSG  240
Sbjct  181  ............................................................  240

Query  241  SELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVGRIQMRTRRTLRGHLAKIYAM  300
Sbjct  241  ............................................................  300

Query  301  HWGTDSRLLVSASQDGKLIIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNIC  360
Sbjct  301  ............................................................  360

Query  361  SIYNLKTREGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIETGQQTTTFT  420
Sbjct  361  ............................................................  420

Query  421  GHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGMCRQTFTGHESDINAICFFPNGNAF  480
Sbjct  421  ............................................................  480

Query  481  ATGSDDATCRLFDLRADQELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALK  540
Sbjct  481  ............................................................  540

Query  541  ADRAGVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN*  580
Sbjct  541  ....................................*  580
```

beta3:

Score	Expect	Identities	Gaps	Strand
1844 bits(998)	0.0	1015/1023(99%)	1/1023(0%)	Plus/Plus

```
Query  1     ATGGGGGAGATGGAGCAACTGCGTCAGGAAGCGGAGCAGCTCAAGAAGCAGATTGCAGAT  60
Sbjct  1     ................G...A.G.....G.............................  60

Query  61    GCCAGGAAAGCCTGTGCTGACGTTACTCTGGCAGAGCTGGTGTCTGGCCTAGAGGTGGTG  120
Sbjct  61    ............................................................  120

Query  121   GGACGAGTCCAGATGCGGACGCGGCGGACGTTAAGGGGACACCTGGCCAAGATTTACGCC  180
Sbjct  121   ............................................................  180

Query  181   ATGCACTGGGCCACTGATTCTAAGCTGCTGGTAAGTGCCTCGCAAGATGGGAAGCTGATC  240
Sbjct  181   ............................................................  240

Query  241   GTGTGGGACAGCTACACCACCAACAAGGTGCACGCCATCCCACTGCGCTCCTCCTGGGTC  300
Sbjct  241   ............................................................  300

Query  301   ATGACCTGTGCCTATGCCCCATCAGGGAACTTTGTGGCGTGTGGGGGGCTGGACAACATG  360
Sbjct  301   ....................................A.......................  360

Query  361   TGTTCCATCTACAACCTCAAATCCCGTGAGGGCAATGTCAAGGTCAGCCGGGAGCTTTCT  420
Sbjct  361   ............................................................  420

Query  421   GCTCACACAGGTTATCTCTCCTGCTGCCGCTTCCTGGATGACAACAATATTGTGACCAGC  480
Sbjct  421   ............................................................  480

Query  481   TCGGGGGACACCACGTGTGCCTTGTGGGACATTGAGACTGGGCAGCAGAAGACTGTATTT  540
Sbjct  481   ............................................................  540

Query  541   GTGGGACACACGGGTGACTGCATGAGCCTGGCTGTGTCTCCTGACTTCAATCTCTTCATT  600
Sbjct  541   ............................................................  600

Query  601   TCGGGGGCCTGTGATGCCAGTGCCAAGCTCTGGGATGTGCGAGAGGGGACCTGCCGACAG  660
Sbjct  601   ...........................................................T...  660

Query  661   ACTTTCACTGGCCACGAGTCGGACATCAACGCCATCTGTTTCTTCCCCAATGGAGAGGCC  720
Sbjct  661   ............................................................  720

Query  721   ATCTGCACGGGCTCGGATGACGCTTCCTGCCGCTTGTTTGACCTGCGGGCAGACCAGGAG  780
Sbjct  721   ............................................................  780

Query  781   CTGATCTGCTTCTCCCACGAGAGCATCATCTGCGGCATCACGTCTGTGGCCTTCTCCCTC  840
Sbjct  781   ..............................................C.............  840

Query  841   AGTGGCCGCCTACTATTCGCTGGCTACGACGACTTCAACTGCAATGTCTGGGACTCCATG  900
Sbjct  841   ............................................................  900

Query  901   AAGTCTGAGCGTGTGGGCATCCTCTCTGGCCACGATAACAGGGTGAGCTGCCTGGGAGTC  960
Sbjct  901   ............................................................  960

Query  961   ACAGCTGACGGGATGGCTGTGGCCACAGGTTCCTGGGACAGCTTCCTCAAAATCTGGAAC  1020
Sbjct  961   ..............................................-.............  1019

Query  1021  TGA  1023
Sbjct  1020  ...  1022
```

MGEMEQLRQEAEQLKKQIADARKACADVTLA
MHWATDSKLLVSASQDGKLIVWDSYTTNKVHA
CSIYNLKSREGNVKVSRELSAHTGYLSCCRFL
VGHTGDCMSLAVSPDFNLFISGACDASAKLWD
ICTGSDDASCRLFDLRADQELICFSHESIICGIT
KSERVGILSGHDNRVSCLGVTADGMAVATGSW

MGEMEQLRQEAEQLKKQIADARKACADVTLA
MHWATDSKLLVSASQDGKLIVWDSYTTNKVHA
CSIYNLKSREGNVKVSRELSAHTGYLSCCRFL
VGHTGDCMSLAVSPDFNLFISGACDASAKLWD
ICTGSDDASCRLFDLRADQELICFSHESIICGIT
KSERVGILSGHDNRVSCLGVTADGMAVATGSW

Uporządkowanie danych dla donora: *alfa-s-mCitrine*

Odrzucenie danych o skrajnie odstających czasach życia. Uzupelnienie brakujących wartosci przy dopasowaniach monoeksponencjalnych. Brakujące wartosci zastapiono 21 wartosciami wygenerowanymi pseudolosowo, z rozkladu normalnego o sredniej 1.75 i odchyleniu standardowym 0.25. Uzyskane wartosci:

```
##  [1] 2.174721 1.551352 1.837109 1.183650 1.709449 2.0327
##  [8] 1.525208 1.931710 1.547640 1.816771 1.315684 1.3971
## [15] 1.491127 2.090536 1.979364 1.553714 1.893380 1.9795
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.184   1.548   1.709   1.719   1.932   2.175
```

Podsumowanie danych dla donora:

```
##                              samples        amp_1                lft
##  alfa_S_mCitrine_donor_10: 1   Min.    :  462.5   Min.
##  alfa_S_mCitrine_donor_11: 1   1st Qu.: 1907.1   1st Qu.
##  alfa_S_mCitrine_donor_12: 1   Median : 5369.3   Median
##  alfa_S_mCitrine_donor_13: 1   Mean   : 9979.8   Mean
##  alfa_S_mCitrine_donor_14: 1   3rd Qu.:11088.0   3rd Qu.
##  alfa_S_mCitrine_donor_15: 1   Max.   :80546.3   Max.
##  (Other)                  :66   NA's   :21
##      amp_2             lft_2           tau_amp
##  Min.    :  2270   Min.   :3.000   Min.   :2.530
##  1st Qu.:  8874   1st Qu.:3.075   1st Qu.:3.020
##  Median : 17663   Median :3.204   Median :3.040
##  Mean   : 53430   Mean   :3.252   Mean   :3.029
##  3rd Qu.: 49566   3rd Qu.:3.324   3rd Qu.:3.060
##  Max.   :450838   Max.   :3.884   Max.   :3.090
##
```

Odchylenie standardowe czasów życia: 0.07

Porównanie wyników (z akceptorem: beta-3-mCherry)

Dane dla pomiarów z beta-3-mCherry i gamma2:

```
##      amp_1            lft_1            amp_2                I
##  Min.   : 1438   Min.   :1.364   Min.   :  373.8   Min.
##  1st Qu.: 3597   1st Qu.:2.087   1st Qu.: 7308.0   1st (
##  Median : 7052   Median :2.709   Median :11174.8   Media
##  Mean   : 9393   Mean   :2.758   Mean   :11327.7   Mean
##  3rd Qu.:14768   3rd Qu.:3.279   3rd Qu.:13765.8   3rd (
##  Max.   :22275   Max.   :4.724   Max.   :29005.3   Max.
##     tau_amp
##  Min.   :2.870
##  1st Qu.:2.960
##  Median :2.980
##  Mean   :2.973
##  3rd Qu.:2.990
##  Max.   :3.030
```

Jeszcze trochę czyszczenia

Przed porównaniem srednich czasów życia fluorescencji donora bez i z akceptorem usunięto wyniki mieszczące się poza 99% poziomem ufnosci.

Dla samego donora:

```
## Loading required package: outliers
## Loading required package: dplyr
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:stats':
##
##     filter, lag
##
## The following objects are masked from 'package:base':
##
```

Test t Welcha na statystycznie istotną różnicą między srednimi czasami życia:

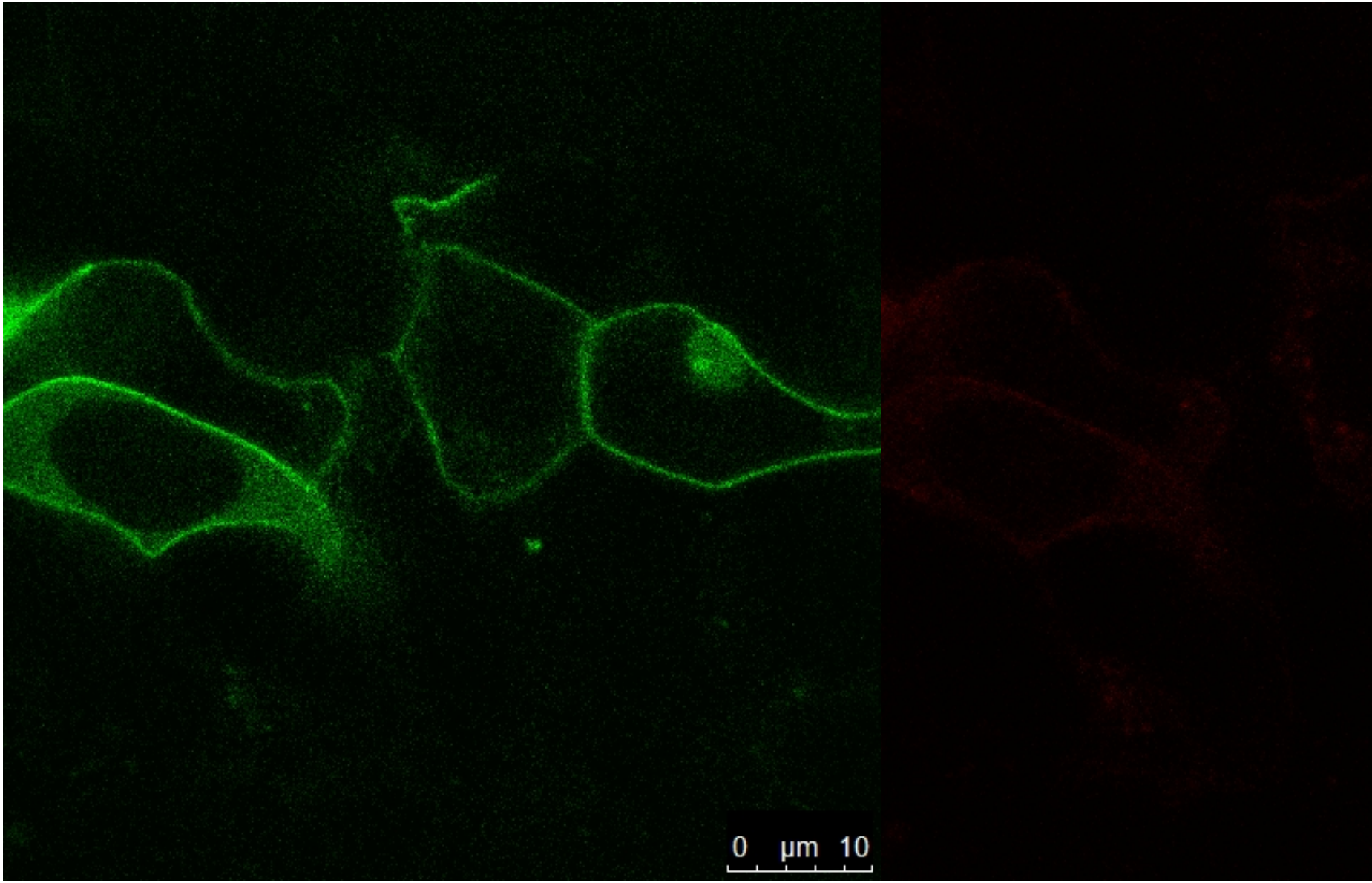
```
##
##  Welch Two Sample t-test
##
## data:  donor$tau_amp and FLIM$tau_amp
## t = 10.18, df = 68.862, p-value = 2.278e-15
## alternative hypothesis: true difference in means is not
## 95 percent confidence interval:
##  0.04801158 0.07141699
## sample estimates:
## mean of x mean of y
##  3.038857  2.979143
```

```
##                  amp_1    lft_1    amp_2    lft_2  tau_ar
## donorout     10087.507 2.074023 54526.34 3.252000 3.03885
## akceptorout   9674.346 2.820800 11043.14 2.913914 2.97914
```

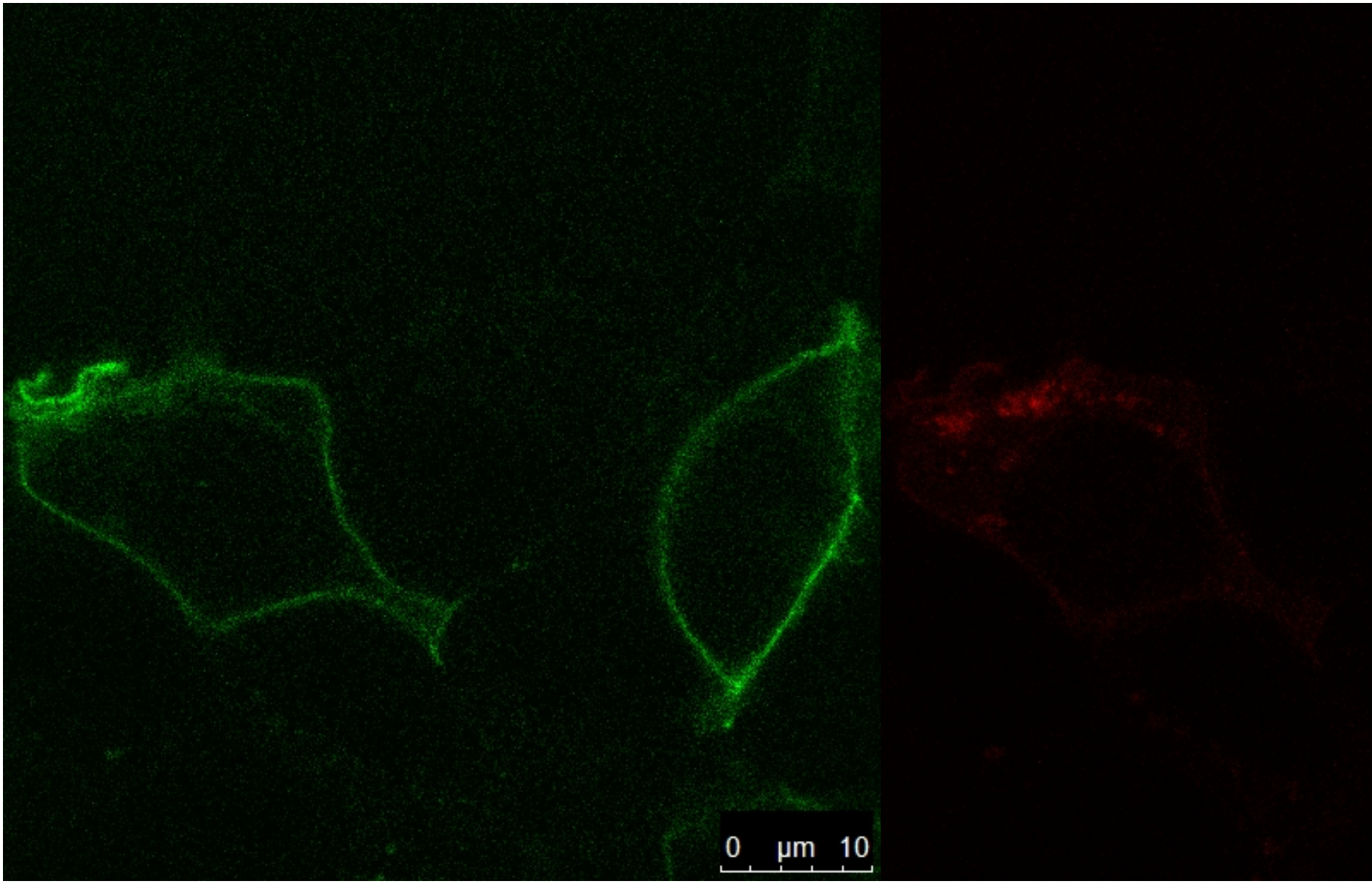
Transfer energii: 1.97%

Co z tym transferem?

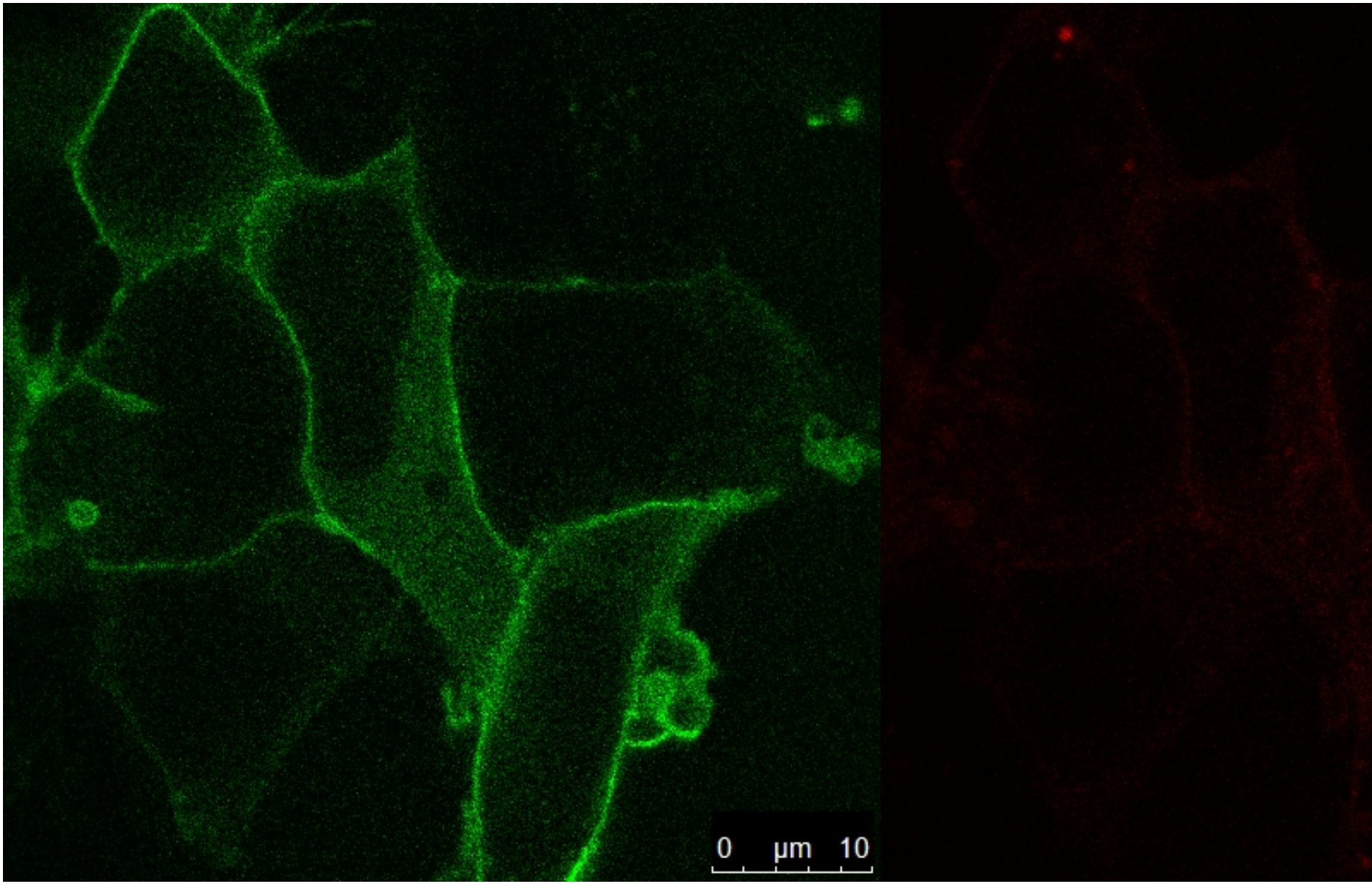
alfa-s z mCitrine, beta-3 z mCherry:



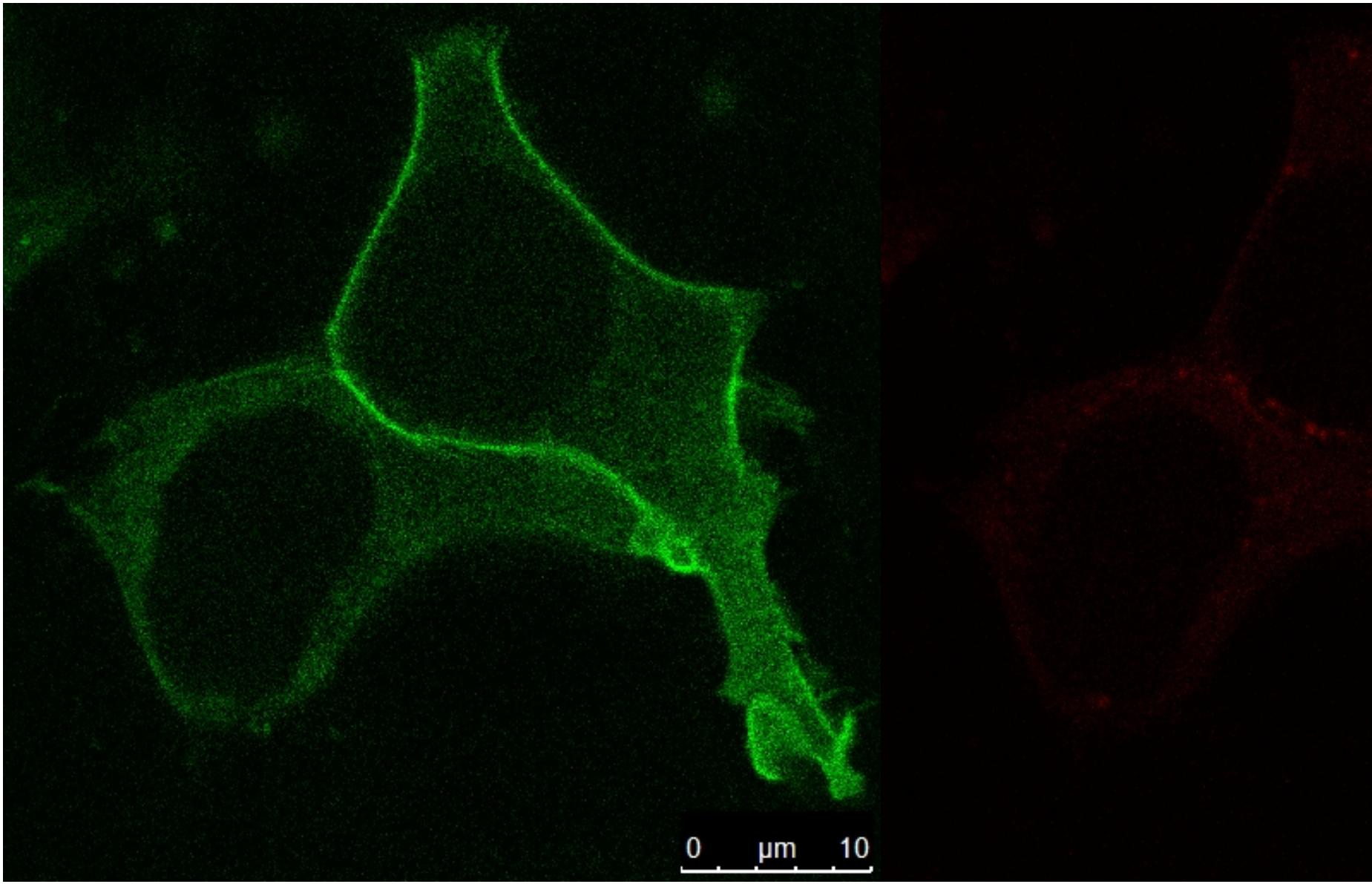
i solidarnie



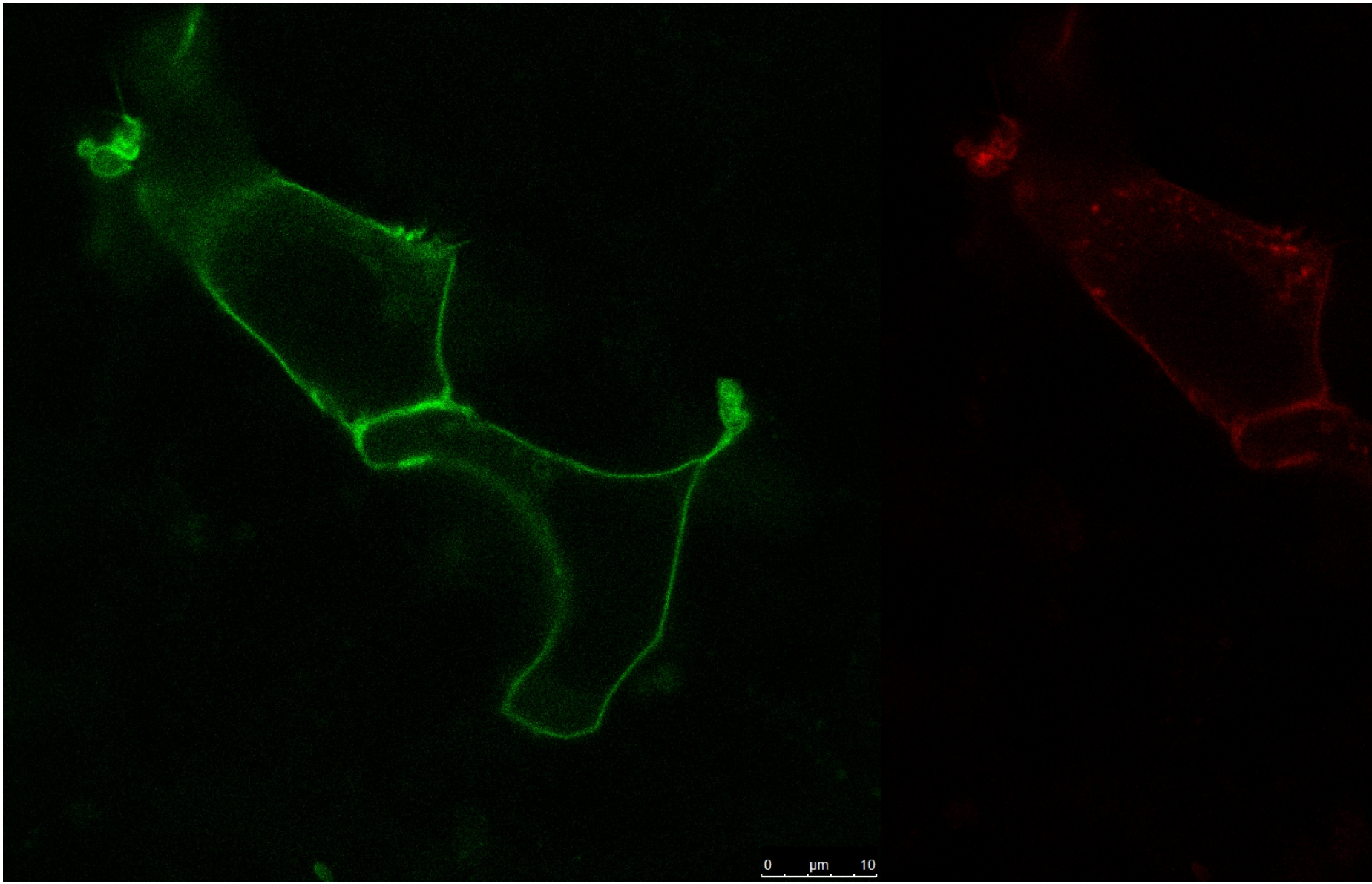
i wciąż



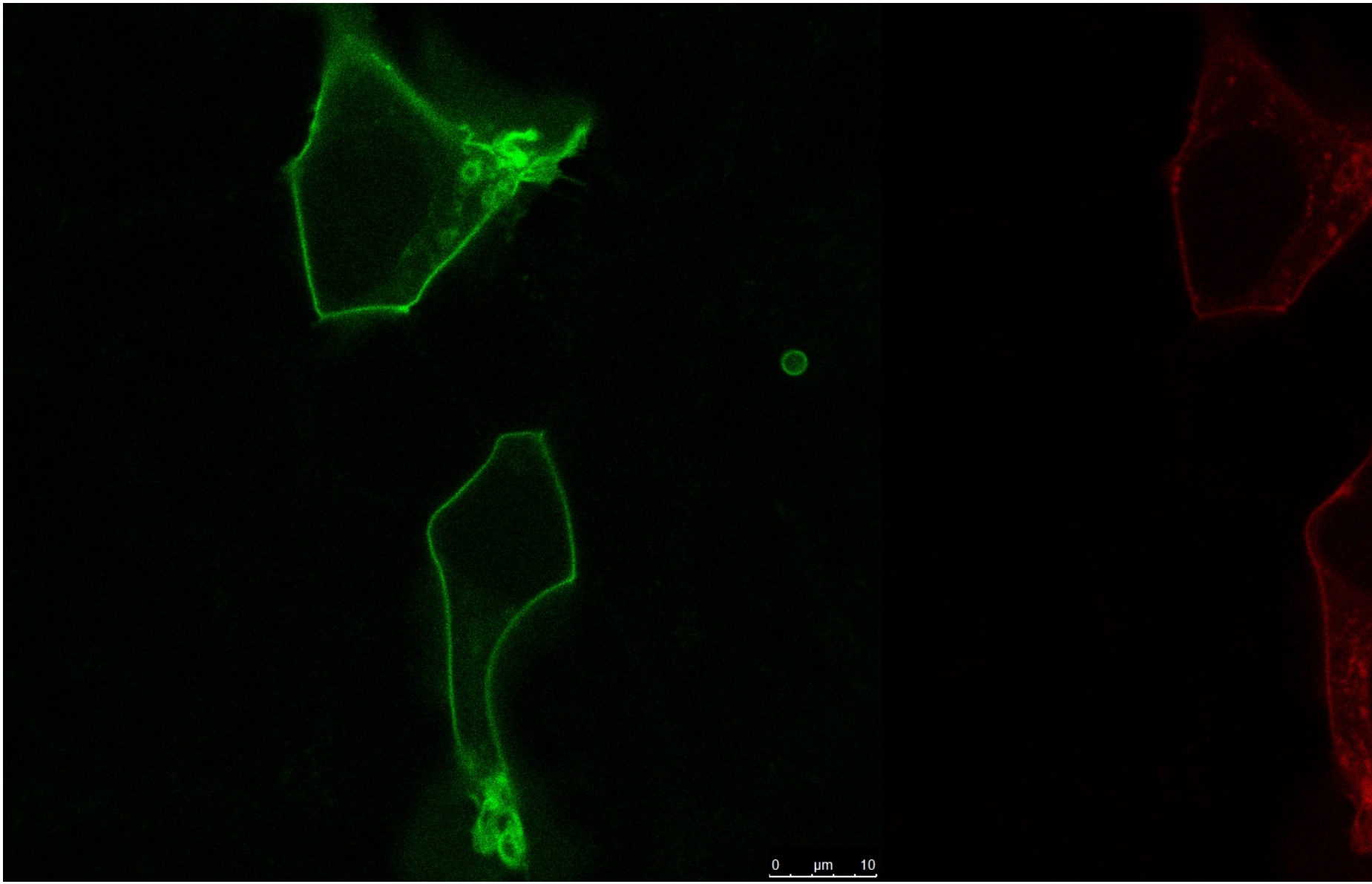
nie swiecilo należycie



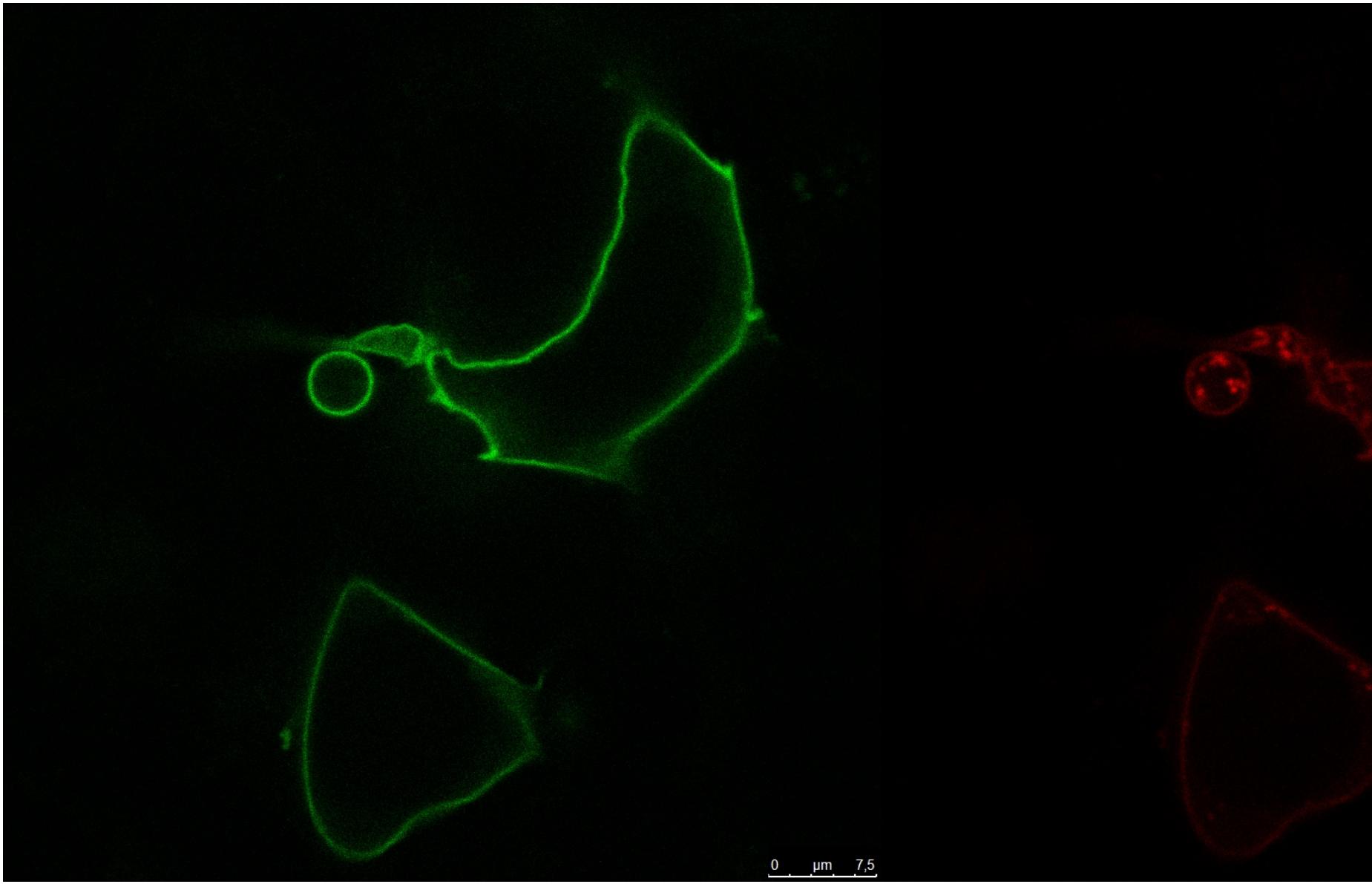
Z kolei beta-1 niosla nadzieję



i niosla



ku pokrzepieniu



Porównanie wyników (z akceptorem: beta-1-mCherry)

Dane dla pomiarów z beta-1-mCherry i gamma2:

```
##      amp_1              lft_1             amp_2              I
##  Min.   :  887.3   Min.   :1.645   Min.   : 1736   Min.
##  1st Qu.: 2568.2   1st Qu.:2.048   1st Qu.: 5856   1st (
##  Median : 6135.4   Median :2.540   Median :11468   Media
##  Mean   : 7535.9   Mean   :2.705   Mean   :10374   Mean
##  3rd Qu.:11775.0   3rd Qu.:3.219   3rd Qu.:13786   3rd (
##  Max.   :18814.9   Max.   :5.571   Max.   :23198   Max.
##     tau_amp
##  Min.   :2.630
##  1st Qu.:2.870
##  Median :2.890
##  Mean   :2.887
##  3rd Qu.:2.915
##  Max.   :3.030
```

Usunięcie danych odstających:

```
## The outliers for 99 % confidence interval are:
##  3.03 2.63
##  - - - - - - - - - - - - - - - - - - - - - - -

##
## The mean and median with outliers are respectively: 2.89
## The mean and median without outliers are respectively: 2
```

Test t Welcha na statystycznie istotną różnicą między srednimi czasami życia:

```
##
##  Welch Two Sample t-test
##
## data:  donor$tau_amp and FLIM$tau_amp
## t = 23.26, df = 58.544, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not
## 95 percent confidence interval:
##  0.1354953 0.1610069
## sample estimates:
## mean of x mean of y
##  3.038857  2.890606
```

```
##                        amp_1    lft_1    amp_2    lft_2  t
## donorout           10087.507 2.074023 54526.34 3.252000 3.
## akceptorbeta1out    7457.869 2.713727 10509.95 2.810727 2.
```

Transfer energii: 4.88%