

## 12)Xrcc4

# Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4), mRNA

- Référence NCBI : NM\_001006999
- **Taille 972 NT**
- Séquence NT :

```
a tggaaaggaa agtcagcaga atctctctgg
   61 cttctgaacc caatgtaacc tactttctac aagtgtcttg ggaggggacg ataggatctg
  121 gttttgttat tacacttaag gatggccatt cagcctggac tgcaaaagtt tctgaatcgg
  181 agattgcaca ggaagctgat gacatggcta tggagcagga aaaatacatg gatgagctga
  241 gacggggcact ggtgccagag tcgggagcag ctggtgcata caagtccatc ttttccaagg
  301 aacttcagca tttctccctg gagaaagaac tgaaagatgt ttctttcaga cttggttcct
  361 tcaacctaga caaagttaca aacccaactg aagtcacag agaactcatt tgctactgcc
  421 tggacaccat tgcggaaaaa caagccaaaa acgagcacct gcagaaggaa aacgaaaggc
  481 tcctgagaga ttggactgac gttcaaggcc gatttgagaa atgtgtgagt gacaaagaag
  541 ccttgagggc cgatttgtat caaagattta tcttggtgct gaatgagaag aaaacaaaaa
  601 tccgaagctt gttgagtga gtcacagcagc tggagaagag taccaaacct gaaagggaaa
  661 ctccgagttc tgacaaaata cctgaggagg atgggcttta tgatggcagc actgatgaag
  721 aaagcggagc ccctgtgctg ggcgcagata cccttgataa ggatgattcc ttattttcaa
  781 gtccagatgt cactgatatt gcaccaagta ggaagaggag acaccgaatg cagacaaatc
  841 ttgggacaga acctaaaatg gctccacagg agctgccact acaggagaag gaaaggcttg
  901 gctcttcacc gcctcagacc ttgaaagagg agggcacctc tgctgcaaag atgtccttag
  961 aaaccctgag aaacagcagc ccagaagacc tctttgacta g
```

- Séquence protéique :

NP\_001007000

```
MERKVSRLASEPNVTYFLQVSWEGTIGSGFVITLTDGHSWT
AKVSESEIAQEADDMAMEQEKYMDLRRALVPESGAAGAYKFIFSKDTQHFSLEKELK
DVSFRLGSFNLDKVTNPTEVIRELICyclDTIAEKQAKNEHLQKENERLLRDWTDVQG
RFEKCVSDKEALEADLYQRFILVLNEKTKIRSLLESEVQOLEKSTKPERETPSSDKIP
EEDGLYDGSTDEESGAPVLGADTLDKDLSLSPDVTDIAPSRKRRHRMQTNLGTEPK
MAPQELPLQEKERLGSSPPQTLKEEGTSAKMSLETLRNSSPEDLFD
```

- Amorces synthétisées :

Xrcc4\_AscI\_Fwd

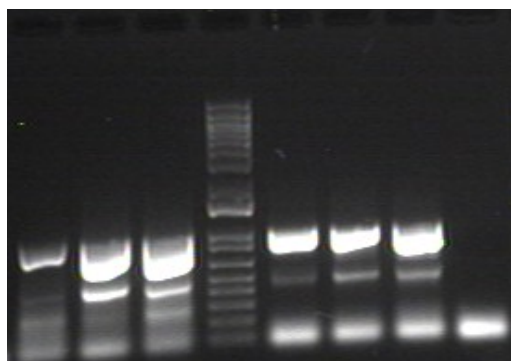
tataGGCGGCCa a tggaaaggaa agtcagcaga atc

Xrcc4\_NotI\_Rev

ttaaGCGGCCGCa ctagtcaaagaggtcttctgggc

- Expériences :

- PCR 10/07 : sur **les 7 conditions** cycle Q5-TM 56°C-Enhancer 5- 2min 30 d'élargation



|      |      |       |       |    |     |     |
|------|------|-------|-------|----|-----|-----|
| Rate | DiT0 | DiT24 | DiT48 | SP | CTX | Eau |
|------|------|-------|-------|----|-----|-----|

- Résultats séquençages

- FlagBirA Xrcc4 rate clone A

- B3Fwd rate 871NT

ATGGAAAGGAAAGTCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACTACTTTCTACAAGTGTCTTGGGA  
GGGTACGATAGGATCTGGTTTTGTTATTACACTTACGGATGGCCATTCGGCCTGGACTGCAAAAGTTTCTGAAT  
CGGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCA  
CTGGTGCCAGAGTCCGGAGCAGCTGGTGCATACAAGTTCATCTTTCCAAGGACACTCAGCATTTCTCCCTGGA  
GAAAGAACTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAAGTGAAGTCA  
TCAGAGAACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGA  
AAACGAAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGC  
TTTGGAGGCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAAACAAAATCCGAAGCTTGTTG  
AGTGAAGTCCAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGNAACTCCGAGTTCTGACAAAACACCTGAN  
GAGGATGGGCTTTATGATGGCAGCACTGATGAAGAAAGCAGAGCCCCTGTGCTGGGCGCANATACCTTGAT  
AANGATGANTCCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGTAGNAAGAGGANACACCGAATGC  
AGACAAATCTTGGGACAGAACTAAATGGCTCCNACAGGANCTGCNACTACNGGANANNAAGGNTTGG  
NTCNTCNNCNNNTCANNANNNNGNAAGNNNNGGCNNNNCTGCTGNA

- BGHRev rate 1096NT RESEQUENCAGE DU 25/11

ANNTNGNATNANCNGGGNATNGNCAGNNGGNNNNNGNTGCTGNNCNGNNGNATNATNANCCNNGNANGN  
NNNNANATCANNNNNNNGNNCNANNNNGGGGATNTNNNCCNNGNNNNNNNNNNCCAANGNAAAGNAA  
AGTCAGCAGAATCTNTNTGGCTTCTGAACCCAANGTANNNNACTTTCTNCAAGTNTCTTGGGAGGNTACGATA  
GGANNTNGTTTTNGTTATTACACTTACGGATGNCCNTTCGNNNTGGACTGCAAAAGTTTNTGAATCGGAGATTGC  
ACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGTGCCAGAg  
TCCGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACaTCAGCATTTCTCCCTGGAGAAAGAACTGAAA  
GATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAAGTGAAGTCATCAGAGAACTCATTT  
GCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACcTCAGAAGGAAAACGAAAGGCTCCT  
GAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTTGGAGGCCGATTTG  
TATCAAAGATTATCTTGGTGCTGAATGAGAAGAAAACAAAATCCGAAGCTTGTTGAGTGAAGTCCAGCAGCT  
GGAGAAGAGTACCAAACCTGAAAGGGAAAACCTCCGAGTTCTGACAAAACACCTGAGGAGGATGGGCTTTATGAT  
GGCAGCACTGATGAAGAAAGCAGAGCCCCTGTGCTGGGCGCAGATACCCTTGATAAGGATGATTCCTTATTTTCA  
AGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGAATGCAGACAAATCTTGGGACAGAACC  
TAAATGGCTCCACAGGAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTCTTACC GCCTCAGACCTTGAAA  
GAGGAGGGCACCTCTGCTGCAAACGTGTCCTTAGAAACCCTGAGAAACAGCAGCCCAGAGaCCTCTTTGACTA  
G

- Synthèse séquençage rate : 972NT

|                                                               |     |
|---------------------------------------------------------------|-----|
| ATGGAAAGGAAAGTCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACTACTT       | 56  |
| TCTACAAGTGTCTTTGGGAGGGTACGATAGGATCTGGTTTTGTTATTACACTTACGGATGG | 116 |
| CCATTTCGGCCTGGACTGCAAAAGTTTCTGAATCGGAGATTGCACAGGAAGCTGATGACAT | 176 |
| GGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCCGG  | 236 |
| AGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAA  | 296 |
| AGAACTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCC  | 356 |
| AACTGAAGTCATCAGAGAACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGC  | 416 |
| CAAAAACGAGCACCTGCAGAAGGAAAACGAAAGGCTCCTGAGAGATTGGACTGACGTTCA  | 476 |
| AGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTTGGAGGCCGATTTGTATCAAAG  | 536 |

ATTTATCTTGGTGCTGAATGAGAAGAAAAACAAAATCCGAAGCTTGTGAGTGAAGTCCA 596  
 GCAGCTGGAGAAGAGTACCAAACCTGAAAGGGAACTCCGAGTTCCTGACAAAACACCTGA 656  
 GGAGGATGGGCTTTATGATGGCAGCACTGATGAAGAAAGCAGAGCCCTGTGCTGGGCGC 716  
 AGATACCCCTTGATAAGGATGATTCCCTATTTTCAAGTCCAGATGTCAGTATGATATGCACC 776  
 AAGTAGGAAGAGGAGACACCGAATGCAGACAAATCTTGGGACAGAACCTAAAATGGCTCC 836  
 ACAGGAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTCTTCACCGCCTCAGACCTTGAA 896  
 AGAGGAGGGCACCTCTGCTGCAAACGTGTCTTAGAAACCTGAGAAACAGCAGCCCAGA 956  
 AGaCTCTTTGACTAG 972

MERKVSRLASEPNVTYFLQVSWEGTIGSGFVITLTDGHSAWTAKVSESEIAQEADDMAMEQEYKYMDELRRALVP  
 ESGAAGAYKFIFSKDTQHFSLEKELKDVSFRLGSFNLDKVTNPTEVIRELICyclDTIAEKQAKNEHLQKENERLLRDW  
 TDVQGRFEKCVSDKEALEADLYQRFILVLNEKTKIRSLLEVVQLEKSTKPERETPSSDKTPEEDGLYDGSTDEESRA  
 PVLGADTLKDDSLFSPDVTDIAPSRKRRHRMQTNLGTPEPKMAPQELPLQEKERLGSSPPQTLKEEGTSAANVSL  
 TLRNSSPEDLFD-

### ➤ Blast contre banque rat :

|   |                                                                                                      | Name       | Score | Score | Cover | value | Ident  | Len  | Accession                      |
|---|------------------------------------------------------------------------------------------------------|------------|-------|-------|-------|-------|--------|------|--------------------------------|
| ✓ | PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4) .transcript variant X3 .mRNA | Norway rat | 1751  | 1751  | 100%  | 0.0   | 99.18% | 4325 | <a href="#">XM_006231751.2</a> |
| ✓ | Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4) .mRNA                                   | Norway rat | 1751  | 1751  | 100%  | 0.0   | 99.18% | 1497 | <a href="#">NM_001006999.1</a> |
| ✓ | PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4) .transcript variant X2 .mRNA | Norway rat | 1507  | 1754  | 100%  | 0.0   | 99.16% | 4358 | <a href="#">XM_008760637.2</a> |
| ✓ | PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4) .transcript variant X1 .mRNA | Norway rat | 1507  | 1754  | 100%  | 0.0   | 99.16% | 4292 | <a href="#">XM_008760636.1</a> |

### ➤ Différence Séquencage/CDS au niveau NT :

|           |                                                                                                                                 |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|---------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|           | 1                                                                                                                               | 10  | 20  | 30  | 40  | 50  | 60  | 70  | 80  | 90  | 100 | 110 | 120 | 130 |
| seq       | ATGGAAGGGAAGTCAGCAGAATCTCTG6CTTCTGAACCAATGTAACTACTTTCTACAGTGTCTTGGGAGGGTACGATAGGATCTGGTTTTGTATTACCTTACGGATGGCCATTCTGGCCTGGA     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | ATGGAAGGGAAGTCAGCAGAATCTCTG6CTTCTGAACCAATGTAACTACTTTCTACAGTGTCTTGGGAGGGTACGATAGGATCTGGTTTTGTATTACCTTACGGATGGCCATTCTGGCCTGGA     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | ATGGAAGGGAAGTCAGCAGAATCTCTG6CTTCTGAACCAATGTAACTACTTTCTACAGTGTCTTGGGAGGGTACGATAGGATCTGGTTTTGTATTACCTTACGGATGGCCATTCTGGCCTGGA     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 131                                                                                                                             | 140 | 150 | 160 | 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 | 250 | 260 |
| seq       | CTGCAAAAGTTTCTGAATCGGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAATACATGGATGAGCTGAGACGGGCCTGGTGCCAGAGTCTGGAGCAGCTGGTGATACAGTTTCAT |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTGCAAAAGTTTCTGAATCGGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAATACATGGATGAGCTGAGACGGGCCTGGTGCCAGAGTCTGGAGCAGCTGGTGATACAGTTTCAT |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTGCAAAAGTTTCTGAATCGGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAATACATGGATGAGCTGAGACGGGCCTGGTGCCAGAGTCTGGAGCAGCTGGTGATACAGTTTCAT |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 261                                                                                                                             | 270 | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | 360 | 370 | 380 | 390 |
| seq       | CTTTTCAAGGACACTCAGCATTCTCCCTGGAGAAAGACTGAAGATGTTTCTTTCAGACTTG6TTCTTCAACCTAGACAAAGTTACAAACCAACTGAAGTCATCAGAGAACTCATTTGCTACTGC    |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTTTTCAAGGACACTCAGCATTCTCCCTGGAGAAAGACTGAAGATGTTTCTTTCAGACTTG6TTCTTCAACCTAGACAAAGTTACAAACCAACTGAAGTCATCAGAGAACTCATTTGCTACTGC    |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTTTTCAAGGACACTCAGCATTCTCCCTGGAGAAAGACTGAAGATGTTTCTTTCAGACTTG6TTCTTCAACCTAGACAAAGTTACAAACCAACTGAAGTCATCAGAGAACTCATTTGCTACTGC    |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 391                                                                                                                             | 400 | 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 | 490 | 500 | 510 | 520 |
| seq       | CTGGACACCATTTGCGGAAACACAGCCAAACACGAGCACCTGCAGAGGAAACGAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTGAGAAATGTGTGAGTGACAAAGAGCTTTGGAGG   |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTGGACACCATTTGCGGAAACACAGCCAAACACGAGCACCTGCAGAGGAAACGAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTGAGAAATGTGTGAGTGACAAAGAGCTTTGGAGG   |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTGGACACCATTTGCGGAAACACAGCCAAACACGAGCACCTGCAGAGGAAACGAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTGAGAAATGTGTGAGTGACAAAGAGCTTTGGAGG   |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 521                                                                                                                             | 530 | 540 | 550 | 560 | 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 | 650 |
| seq       | CCGATTTGTATCAAGATTTATCTTGGTGTGAATGAGAGAAACAAAATCCGAGCTTGTGAGTGAGTCCAGCAGCTGGAGAGAGTACCAAACTGAAGGGAACTCCGAGTTCTGACAAAAC          |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CCGATTTGTATCAAGATTTATCTTGGTGTGAATGAGAGAAACAAAATCCGAGCTTGTGAGTGAGTCCAGCAGCTGGAGAGAGTACCAAACTGAAGGGAACTCCGAGTTCTGACAAAAC          |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CCGATTTGTATCAAGATTTATCTTGGTGTGAATGAGAGAAACAAAATCCGAGCTTGTGAGTGAGTCCAGCAGCTGGAGAGAGTACCAAACTGAAGGGAACTCCGAGTTCTGACAAAAC          |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 651                                                                                                                             | 660 | 670 | 680 | 690 | 700 | 710 | 720 | 730 | 740 | 750 | 760 | 770 | 780 |
| seq       | ACCTGAGGAGGATGGCTTTATGATGGCAGCAGCTGATGAGAAAGCAGAGCCCTGTGCTGGGCGCAGATACCTTGATAAGGATGATTCCTATTATTTCAAGTCCAGATGTCAGTATTTGACCAAGT   |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | ACCTGAGGAGGATGGCTTTATGATGGCAGCAGCTGATGAGAAAGCAGAGCCCTGTGCTGGGCGCAGATACCTTGATAAGGATGATTCCTATTATTTCAAGTCCAGATGTCAGTATTTGACCAAGT   |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | ACCTGAGGAGGATGGCTTTATGATGGCAGCAGCTGATGAGAAAGCAGAGCCCTGTGCTGGGCGCAGATACCTTGATAAGGATGATTCCTATTATTTCAAGTCCAGATGTCAGTATTTGACCAAGT   |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 781                                                                                                                             | 790 | 800 | 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 | 890 | 900 | 910 |
| seq       | AGGAAGAGGAGACACCGAATGCAGACAATCTTGGACAGAACCTAAATGGCTCCACAGGAGCTGCCACTACAGGAGAGGAAAGGCTTGGCTCTTACCGCCTCAGACCTTGAAGAGGAGGGACCT     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | AGGAAGAGGAGACACCGAATGCAGACAATCTTGGACAGAACCTAAATGGCTCCACAGGAGCTGCCACTACAGGAGAGGAAAGGCTTGGCTCTTACCGCCTCAGACCTTGAAGAGGAGGGACCT     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | AGGAAGAGGAGACACCGAATGCAGACAATCTTGGACAGAACCTAAATGGCTCCACAGGAGCTGCCACTACAGGAGAGGAAAGGCTTGGCTCTTACCGCCTCAGACCTTGAAGAGGAGGGACCT     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 911                                                                                                                             | 920 | 930 | 940 | 950 | 960 | 970 | 978 | 972 |     |     |     |     |     |
| seq       | CTGCTCAAAAGTGTCTTTAGAAACCTGAGAAACAGCAGCCAGAGAGCTCTTTGACTAG                                                                      |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTGCTCAAAAGTGTCTTTAGAAACCTGAGAAACAGCAGCCAGAGAGCTCTTTGACTAG                                                                      |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTGCTCAAAAGTGTCTTTAGAAACCTGAGAAACAGCAGCCAGAGAGCTCTTTGACTAG                                                                      |     |     |     |     |     |     |     |     |     |     |     |     |     |

Plusieurs mutations D'1NT

Mutations en 78, 123, 234,513,650,697, 921-922

➤ Différence au niveau PROT :

1102030405060708090100110120130

seqMERKYSRISLASEPNVTYFLQVSMEGTIGSGFVITLTDGHSANTAKVSESEIAQEADDMAHEQEKYMDLRRALVPESGAAGAYKFIKSKDTQHFSLKELKDVSFRLGGSFNLKVTNPTEVIRELICYC

refMERKYSRISLASEPNVTYFLQVSMEGTIGSGFVITLTDGHSANTAKVSESEIAQEADDMAHEQEKYMDLRRALVPESGAAGAYKFIKSKDTQHFSLKELKDVSFRLGGSFNLKVTNPTEVIRELICYC

ConsensusMERKYSRISLASEPNVTYFLQVSMEGTIGSGFVITLTDGHSANTAKVSESEIAQEADDMAHEQEKYMDLRRALVPESGAAGAYKFIKSKDTQHFSLKELKDVSFRLGGSFNLKVTNPTEVIRELICYC

131140150160170180190200210220230240250260

seqLDTIAEKQAKNEHLQKENERLLRDWTDVQGRFEKCVSDKEALEADLYQRFILVLNEKTKIRSLLEVVQQLKSTKPERETPSSDKTPEEDGLYDGSDEESAPVVGADTLKDQSLFSSPDVTDIAPS

refLDTIAEKQAKNEHLQKENERLLRDWTDVQGRFEKCVSDKEALEADLYQRFILVLNEKTKIRSLLEVVQQLKSTKPERETPSSDKTPEEDGLYDGSDEESAPVVGADTLKDQSLFSSPDVTDIAPS

ConsensusLDTIAEKQAKNEHLQKENERLLRDWTDVQGRFEKCVSDKEALEADLYQRFILVLNEKTKIRSLLEVVQQLKSTKPERETPSSDKTPEEDGLYDGSDEESAPVVGADTLKDQSLFSSPDVTDIAPS

261270280290300310320323

seqRKRRHRMQTNLGTPEKMAPQELPLQEKERLGSSPPQTLKEEGTSAANVSLETLRNSSPEDLFD

refRKRRHRMQTNLGTPEKMAPQELPLQEKERLGSSPPQTLKEEGTSAAKMSLETLRNSSPEDLFD

ConsensusRKRRHRMQTNLGTPEKMAPQELPLQEKERLGSSPPQTLKEEGTSAANVSLETLRNSSPEDLFD

3 differences : aa 217 ; 233, 307 et 308

| Description                         |                                                                    | Name       | Score | Score | Cover | value | Ident  | Len | Accession      |
|-------------------------------------|--------------------------------------------------------------------|------------|-------|-------|-------|-------|--------|-----|----------------|
| <input checked="" type="checkbox"/> | DNA repair protein XRCC4 [Rattus norvegicus]                       | Norway_rat | 653   | 653   | 100%  | 0.0   | 98.76% | 323 | NP_001007000.1 |
| <input checked="" type="checkbox"/> | PREDICTED: DNA repair protein XRCC4 isoform X1 [Rattus norvegicus] | Norway_rat | 644   | 644   | 100%  | 0.0   | 95.21% | 334 | XP_008758858.1 |

Flag BirA Xrcc4 rate (clone A) :OK avec qq mutations ,

o FlagBirA Xrcc4 DiT0 clone A

➤ B3Fwd DiT0 809NT REVOIR LE Fwd

ATGGAAAGGAAAGCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACCTACTTTCTACAAGTGTCTTGGGAGG  
GTACGATTGGATCTGGTTTTGTTATTACACTTACGGATGGCCATTCGGCCTGGACTGCAAAAGTTTCTGAATCGGA  
GATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGTG  
CCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTCTCCCTGGAGAAAGA  
ACTGAAAGATGTTTCTTTTCACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAAGTGAAGTCATCAGAGA  
ACTCATTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAAACGAA  
AGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTTGGAGG  
CCGATTTGTATCAAAGATTATCTTGGTGCTGAATGAGAAGAAAAACAAAAATCCGAAGCTTGTGAGTGAAGTCC  
AGCAGCTGGAGAAGAGTACCAAACCTGAAAGGNNNNNCCGAGTTCTGACAAAACACCTGAGGAGGNNNNNT  
TTATGATGGCAGCACTGATGAANAAAGCAGANCCCCTGTGCTGGGCGCANATNCCCTTGATAAGGATGANTCCT  
TATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGAANGCAGACAAATCT

➤ BGHRev DiT0 1057NT RESEQUENCAGE DU 25/11

ATNNAAAGGAAAGCAGCAGAATCTCTNTGGCTTCTGAACCCAATGTANNNTACTTTCTNCAAGTGTCTTGGGAG  
GGTACGATNGGATCTGGTTTTNGTTATTACACTTACGGATGNCCNTTCGGCCTGGACTGCAAAAGTTTCTGAATCG  
GAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGG  
TGCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTCTCCCTGGAGAAA  
GAACTGAAAGATGTTTCTTTTCACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAAGTGAAGTCATCAGA  
GAACTCATTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACcTGCAGAAGGAAAAACG  
AAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTTGGA  
GGCCGATTTGTATCAAAGATTATCTTGGTGCTGAATGAGAAGAAAAACAAAAATCCGAAGCTTGTGAGTGAAGT  
CCAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGGAACTCCGAGTTCTGACAAAACACCTGAGGAGGGTGG  
GCTTTATGATGGCAGCACTGATGAAGAAAGCAGAGCCCCTGTGCTGGGCGCAGATACCTTGATAAGGATGATTCC  
CTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGAATGCAGACAAATCTTGG  
GACAGAACCTAAAATGGCTCCACAGGAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTTTACCCGCTCAG  
ACCTTGAAAGAGGAGGGCACCTCTGCTGCAAACGTGTCTTAGAAACCCTGAGAAACAGCAGCCCAGAAANCC  
TCTTTGACTAG

➤ Synthèse séquençage DiT0 :

|                                                                |    |     |
|----------------------------------------------------------------|----|-----|
| ATGGAAAGGAAAG CAGCAGAATCTCTCTGGCTTC                            | 34 |     |
| TGAACCCAATGTAACCTACTTTCTACAAGTGTCTTGGGAGGGTACGATTGGATCTGGTTT   |    | 94  |
| TGTTATTACACTTACGGATGGCCATTCGGCCTGGACTGCAAAAGTTTCTGAATCGGAGAT   |    | 154 |
| TGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACG   |    | 214 |
| GGCACTGGTGCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACAC   |    | 274 |
| TCAGCATTCTCCCTGGAGAAAGAACTGAAAGATGTTTCTTTTCACTTGGTTCCTTCAA     |    | 334 |
| CCTAGACAAAGTTACAAACCCAAGTGAAGTCATCAGAGAACTCATTGCTACTGCCTGGA    |    | 394 |
| CACCATTTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAAACGAAAGGCTCCT |    | 454 |
| GAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTT   |    | 514 |
| GGAGGCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAAACAAAAATCCG  |    | 574 |
| AAGCTTGTGAGTGAAGTCCAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGGAACTCC     |    |     |
| GAGTTCTGACAAAAACCTGAGGAGGGTGGGCTTTATGATGGCAGCACTGATGAAGAAAG    |    |     |
| CAGAGCCCCTGTGCTGGGCGCAGATACCCCTTGATAAGGATGATTCTTATTTTCAAGTCC   |    |     |
| AGATGTCACATGATATTGCACCAAGTAGGAAGAGGAGACACCGAATGCAGACAAATCTTGG  |    |     |
| GACAGAACCTAAAATGGCTCCACAGGAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTC   |    |     |
| TTACCCGCTCAGACCTTGAAAGAGGAGGGCACCTCTGCTGCAAACGTGTCTTAGAAAC     |    |     |
| CCTGAGAAACAGCAGCCCAGAAANCTCTTTGACTAG                           |    |     |

Décalage d'1NT->pro avec stops

o FlagBirA Xrcc4 DiT24 clone ?

➤ B3Fwd DiT24 855NT

ATGGAAAGGAAAGTCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACTACTTTCTACAAGTGTCTTGGGAG  
GGTACGATAGGATCTGGTTTTGTTATTACACTTACGGATGGCCATTTCGGCTGGACTGCAAAAGTTTCTGAATCGG  
AGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGT  
GCCAGAGTCCGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAAAG  
AACTGAAAGATGTTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAAGTGAAGTCATCAGAG  
AACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAAACGA  
AAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTTGGAG  
GCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTGAGTGAAGTC  
CAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGGAACTCCGAGTTCTGACAAAACACCTGANGANGATGGG  
CTTTATGATGGCAGCACTGATGAAGAAAGCAGANCCCCTGTGCTGGGCGCANATACCCTTGATAAGGATGANNC  
CTTATTTTCAAGTCCAGATGTCACTGATATTGCACCNANTAGGAAGAGGAGACACCGAANGCAGACAANTCTTG  
GGACAGAAANTAAAATGGCTCCNCNGNANCTGNNNCTACNG

➤ BGHRev DiT24 970NT séquençage a du mal à démarrer

ATGNAAAGNAAAGTCAGCAGANTCTCTCTGGCTTCTGAACCCANTGTANNNTACTTTCTACAAGTGTCTTGGGA  
GGGTACGATAGGATCTGGTTTTGTTATTACACTTACGGATGGCCNTTCGNCNTGGACTGCAAAAGTTTNTGAATC  
GGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTG  
GTGCCAGAGTCCGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAAA  
GAACTGAAAGATGTTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAAGTGAAGTCATCAGA  
GAACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAACG  
AAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTTGGA  
GGCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTGAGTGAAGT  
CCAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGGAACTCCGAGTTCTGACAAAACACCTGAGGAGGATGG  
GCTTTATGATGGCAGCACTGATGAAGAAAGCAGAGCCCCTGTGCTGGGCGCAGATACCCTTGATAAGGATGATTC  
CTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGAATGCAGACAAATCTTGG  
GACAGAACCTAAAATGGCTCCACAGGAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTCTTACCCGCTCAG  
ACCTTGAAAGAGGAGGGCACCTCTGCTGCAAACGTGTCCTTAGAAACCTGAGAAACAGCAGCCCAGAAGaCC  
TCTTNNACTAG

➤ Synthèse séquençage DiT24 : 972NT

|                                                               |     |
|---------------------------------------------------------------|-----|
| ATGGAAAGGAAAGTCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACTACTTTCTA   | 60  |
| CAAGTGTCTTGGGAGGGTACGATAGGATCTGGTTTTGTTATTACACTTACGGATGGCCAT  | 120 |
| TCGGCTGGACTGCAAAAGTTTCTGAATCGGAGATTGCACAGGAAGCTGATGACATGGCT   | 180 |
| ATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCCGGAGCA  | 240 |
| GCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAAAGAA  | 300 |
| CTGAAAGATGTTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAAGT | 360 |
| GAAGTCATCAGAGAACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAA  | 420 |
| AACGAGCACCTGCAGAAGGAAAACGAAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGC  | 480 |
| CGATTTGAGAAATGTGTGAGTGACAAAGAAGCTTTGGAGGCCGATTTGTATCAAAGATTT  | 540 |
| ATCTTGGTGCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTGAGTGAAGTCCAGCAG   | 600 |
| CTGGAGAAGAGTACCAAACCTGAAAGGGAACTCCGAGTTCTGACAAAACACCTGAGGAG   | 660 |
| GATGGGCTTTATGATGGCAGCACTGATGAAGAAAGCAGAGCCCCTGTGCTGGGCGCAGAT  | 720 |
| ACCTTGATAAGGATGATTCCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGT   | 780 |
| AGGAAGAGGAGACACCGAATGCAGACAAATCTTGGGACAGAACCTAAAATGGCTCCACAG  | 840 |
| GAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTCTTACCCGCTCAGACCTTGAAAGAG   | 900 |
| GAGGGACCTCTGTGCAAACGTGTCCTTAGAAACCTGAGAAACAGCAGCCCAGAAGaC     | 960 |
| CTCTTNNACTAG                                                  | 972 |

MERKVSRI SLASEPNVTYFLQVSWEGTIGSGFVITLTDGHSAWTAKVSESEIAQEADDMAMEQEKYMDLRRALV  
PESGAAGAYKFIFSKDTQHFSLEKELKDVSFRLGFSFNLDKVTNPTEVIRELICyclDTIAEKQAKNEHLQKENER

LLRDWTDVQGRFEKCVSDKEALEADLYQRFIILVLNEKKTKIRSLLSEVQQLEKSTKPERETPSSDKTPEEDGLYD  
GSTDEESRAPVLGADTLDKDSSLFSSPDVTDIAPSRKRRHRMQTNLGTEPKMAPQELPLQEKERLGSSPPQTLKE  
EGTSAANVSLETLRNSSPEDLXX-

➤ **Blast contre banque rat :**

|                                     | Description                                                                                                         | Common Name                | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession                      |
|-------------------------------------|---------------------------------------------------------------------------------------------------------------------|----------------------------|-----------|-------------|-------------|---------|------------|----------|--------------------------------|
| <input checked="" type="checkbox"/> | <a href="#">PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4), transcript variant X3 mRNA</a> | <a href="#">Norway rat</a> | 1744      | 1744        | 100%        | 0.0     | 98.97%     | 4325     | <a href="#">XM_006231751.2</a> |
| <input checked="" type="checkbox"/> | <a href="#">Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4), mRNA</a>                                  | <a href="#">Norway rat</a> | 1744      | 1744        | 100%        | 0.0     | 98.97%     | 1497     | <a href="#">NM_001006999.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4), transcript variant X2 mRNA</a> | <a href="#">Norway rat</a> | 1500      | 1747        | 100%        | 0.0     | 98.93%     | 4358     | <a href="#">XM_008760637.2</a> |
| <input checked="" type="checkbox"/> | <a href="#">PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4), transcript variant X1 mRNA</a> | <a href="#">Norway rat</a> | 1500      | 1747        | 100%        | 0.0     | 98.93%     | 4292     | <a href="#">XM_008760636.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Rattus norvegicus TL0AFA7YM10 mRNA sequence</a>                                                         | <a href="#">Norway rat</a> | 1384      | 1384        | 81%         | 0.0     | 97.89%     | 1825     | <a href="#">FQ230968.1</a>     |

➤ **Différence Séquençage/CDS au niveau NT :**

|           | 1                                                                                                                                 | 10  | 20  | 30  | 40  | 50  | 60  | 70  | 80  | 90  | 100 | 110 | 120 | 130 |
|-----------|-----------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| seq       | ATGGAARAGGAAGTCAGCAGAAATCTCTG6GTTCTGACCCCAATGTAACTACTTTTACAAAGTGCTTGGGAGG6TACGATAGGATCGGTTTGTATTACACTTACGGATGGCCATTCTGGCCTTGGAA   |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | ATGGAARAGGAAGTCAGCAGAAATCTCTG6GTTCTGACCCCAATGTAACTACTTTTACAAAGTGCTTGGGAGG6TACGATAGGATCGGTTTGTATTACACTTACGGATGGCCATTCTAGCCTTGGAA   |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | ATGGAARAGGAAGTCAGCAGAAATCTCTG6GTTCTGACCCCAATGTAACTACTTTTACAAAGTGCTTGGGAGG6TACGATAGGATCGGTTTGTATTACACTTACGGATGGCCATTCTAGCCTTGGAA   |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 131                                                                                                                               | 140 | 150 | 160 | 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 | 250 | 260 |
| seq       | CTGCAAAAGTTTCTGAATCGAGAGTTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAATACATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCGGAGCAGCTGGTGCAATCAGAGTTTCA |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTGCAAAAGTTTCTGAATCGAGAGTTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAATACATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCGGAGCAGCTGGTGCAATCAGAGTTTCA |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTGCAAAAGTTTCTGAATCGAGAGTTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAATACATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCGGAGCAGCTGGTGCAATCAGAGTTTCA |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 261                                                                                                                               | 270 | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | 360 | 370 | 380 | 390 |
| seq       | CTTTTCCAGGACACTCAGCATTTCTCCCTGGGAAAGAACTGAAGAGATGTTTCTTCAGACTTGGTTCCTTCACTACGACAAGTTACAAACCCAACTGAGTGCATCAGAGAACTCATTTGTACTGCT    |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTTTTCCAGGACACTCAGCATTTCTCCCTGGGAAAGAACTGAAGAGATGTTTCTTCAGACTTGGTTCCTTCACTACGACAAGTTACAAACCCAACTGAGTGCATCAGAGAACTCATTTGTACTGCT    |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTTTTCCAGGACACTCAGCATTTCTCCCTGGGAAAGAACTGAAGAGATGTTTCTTCAGACTTGGTTCCTTCACTACGACAAGTTACAAACCCAACTGAGTGCATCAGAGAACTCATTTGTACTGCT    |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 391                                                                                                                               | 400 | 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 | 490 | 500 | 510 | 520 |
| seq       | CTGGACACCATTCGGGAAARACAGCCAAARACGAGCACCTGCAGAGGGAARACGAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTGAGAAATGTGTAGTGACAAAGAGCTTTGGAGG     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTGGACACCATTCGGGAAARACAGCCAAARACGAGCACCTGCAGAGGGAARACGAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTGAGAAATGTGTAGTGACAAAGAGCTTTGGAGG     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTGGACACCATTCGGGAAARACAGCCAAARACGAGCACCTGCAGAGGGAARACGAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTGAGAAATGTGTAGTGACAAAGAGCTTTGGAGG     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 521                                                                                                                               | 530 | 540 | 550 | 560 | 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 | 650 |
| seq       | CCGATTTGTATCAAGAGATTATCTTGGTGCTGAATGAGAGAAACAAAAATCCGAGCTTGTGTAGTGAGTCCAGCAGCTGGAGAGAGTACCAAACTTGAAGGGGAACCTCCGAGTTCTGACAAA       |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CCGATTTGTATCAAGAGATTATCTTGGTGCTGAATGAGAGAAACAAAAATCCGAGCTTGTGTAGTGAGTCCAGCAGCTGGAGAGAGTACCAAACTTGAAGGGGAACCTCCGAGTTCTGACAAA       |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CCGATTTGTATCAAGAGATTATCTTGGTGCTGAATGAGAGAAACAAAAATCCGAGCTTGTGTAGTGAGTCCAGCAGCTGGAGAGAGTACCAAACTTGAAGGGGAACCTCCGAGTTCTGACAAA       |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 651                                                                                                                               | 660 | 670 | 680 | 690 | 700 | 710 | 720 | 730 | 740 | 750 | 760 | 770 | 780 |
| seq       | ACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAGGAAGCAAGGCCCTGTGCTGGGCGAGATACCTTGATAGGATGATTCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGT      |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | ACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAGGAAGCAAGGCCCTGTGCTGGGCGAGATACCTTGATAGGATGATTCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGT      |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | ACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAGGAAGCAAGGCCCTGTGCTGGGCGAGATACCTTGATAGGATGATTCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGT      |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 781                                                                                                                               | 790 | 800 | 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 | 890 | 900 | 910 |
| seq       | AGGAAGAGGAGACCCGATGCAGACAATCTTGGGACAGACCTAAATGGCTCCACAGGAGCTGCCACTACAGGAGAGGAAAGGCTTGGCTCTTACCAGCCCTCAGACCTTGAAGAGGAGGGGACCT      |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | AGGAAGAGGAGACCCGATGCAGACAATCTTGGGACAGACCTAAATGGCTCCACAGGAGCTGCCACTACAGGAGAGGAAAGGCTTGGCTCTTACCAGCCCTCAGACCTTGAAGAGGAGGGGACCT      |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | AGGAAGAGGAGACCCGATGCAGACAATCTTGGGACAGACCTAAATGGCTCCACAGGAGCTGCCACTACAGGAGAGGAAAGGCTTGGCTCTTACCAGCCCTCAGACCTTGAAGAGGAGGGGACCT      |     |     |     |     |     |     |     |     |     |     |     |     |     |
|           | 911                                                                                                                               | 920 | 930 | 940 | 950 | 960 | 978 | 72  |     |     |     |     |     |     |
| seq       | CTGCTGCAACAGTGCTCTTAGAARACCTGAGAAACAGCAGCCGAGAGACCTCTTNNACTAG                                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cds       | CTGCTGCAACAGTGCTCTTAGAARACCTGAGAAACAGCAGCCGAGAGACCTCTTGGACTAG                                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Consensus | CTGCTGCAACaAGTGCTCTTAGAARACCTGAGAAACAGCAGCCGAGAGACCTCTTnnACTAG                                                                    |     |     |     |     |     |     |     |     |     |     |     |     |     |

Mutations en 78, 123, 234, 513, 650, 697, 921-922 comme rate

➤ **Différence au niveau PROT :**

1 10 20 30 40 50 60 70 80 90 100 110 120 130

seq MERKYSRISLASEPNWYTFQLVSGHEGTIGSGFVITLDGHSANTAKYVSESEIAQEADDMHMEQEKYMDELRRALVPESGAAGAYKFIKSDTKQHFSLLEKLDKVSFRLGSFNLDKYTNPTVEVIRELICYC

ref MERKYSRISLASEPNWYTFQLVSGHEGTIGSGFVITLDGHSANTAKYVSESEIAQEADDMHMEQEKYMDELRRALVPESGAAGAYKFIKSDTKQHFSLLEKLDKVSFRLGSFNLDKYTNPTVEVIRELICYC

Consensus MERKYSRISLASEPNWYTFQLVSGHEGTIGSGFVITLDGHSANTAKYVSESEIAQEADDMHMEQEKYMDELRRALVPESGAAGAYKFIKSDTKQHFSLLEKLDKVSFRLGSFNLDKYTNPTVEVIRELICYC

131 140 150 160 170 180 190 200 210 220 230 240 250 260

seq LDTAEKQAKNEHLQKENERLLRDWTQVGRFEKCYSDKEALEADLQYRFILVLEKKTIRSLSEVQQLEKSTKPERETPSSDKTPEEDGLYDGSSTDEESRAPYVLGADTLDKDDSLFSSPDVDTIAPS

ref LDTAEKQAKNEHLQKENERLLRDWTQVGRFEKCYSDKEALEADLQYRFILVLEKKTIRSLSEVQQLEKSTKPERETPSSDKTPEEDGLYDGSSTDEESGAPYVLGADTLDKDDSLFSSPDVDTIAPS

Consensus LDTAEKQAKNEHLQKENERLLRDWTQVGRFEKCYSDKEALEADLQYRFILVLEKKTIRSLSEVQQLEKSTKPERETPSSDKTPEEDGLYDGSSTDEESRAPYVLGADTLDKDDSLFSSPDVDTIAPS

261 270 280 290 300 310 320323

seq RKKRRHRMTNLGTEPKHAPQELPLQEKERLGSSPPQTLKEEGTSAANVSLETLRNSSPEQLXX

ref RKKRRHRMTNLGTEPKHAPQELPLQEKERLGSSPPQTLKEEGTSAANKSLTETLRNSSPEQLFD

Consensus RKKRRHRMTNLGTEPKHAPQELPLQEKERLGSSPPQTLKEEGTSAANVSLETLRNSSPEQLfd

3 differences : aa 217 ; 233, 307 et 308

|                                     | Description                                                                        | Common Name                | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession                      |
|-------------------------------------|------------------------------------------------------------------------------------|----------------------------|-----------|-------------|-------------|---------|------------|----------|--------------------------------|
| <input checked="" type="checkbox"/> | <a href="#">DNA repair protein XRCC4 [Rattus norvegicus]</a>                       | <a href="#">Norway rat</a> | 649       | 649         | 99%         | 0.0     | 98.75%     | 323      | <a href="#">NP_001007000.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">PREDICTED: DNA repair protein XRCC4 isoform X1 [Rattus norvegicus]</a> | <a href="#">Norway rat</a> | 640       | 640         | 99%         | 0.0     | 95.18%     | 334      | <a href="#">XP_008758858.1</a> |

Flag BirA Xrcc4 DiT24hLPS (clone A) comme rate

o FlagBirA Xrcc4 DiT48hMix clone ?

➤ B3Fwd DiT48hMix 821NT

ATGGAAAGGAAAGTCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACCTACTTTCTACAAGTGTCTTGGGAG  
GGTACGATTGGATCTGGTTTTGTTATTACACTTACGGATGGCCATTTCGGCCTGGACTGCAAAAGTTTCTGAATCGG  
AGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGT  
GCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTCTCCCTGGAGAAAG  
AACTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAACCTGAAGTCATCAGAG  
AACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAACGA  
AAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCCTTGAG  
GCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTTGAGTGAAGTC  
CAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGGAACTCCGAGTTCTGACAAAATACCTGANGAGGANGGG  
CTTTATGATGGCAGCACTGATGAAGAAAGCGGANCCCCGTGTGCTGGGCGCAGATACCCCTTGATAAGGATGANTC  
CTTATTTTCNAGTCCANATGTCACTGATNTTGNACCNAGTAGGAAGAGGAGANACCGAANGNAGANAATCTTG  
GGACANAA

➤ BGHRev DiT48hMix 880NT

AGCNNCNANAAGGGGGGATCTGGCCCCGGCGGCGGCGCNAANNGAANGGAAAGTCAGCAGAATCTNTCT  
GGCTTCTGAACCCAANGTANCTACTTTNTACAAGTNTCTTGGNAGGGTACGATTGGATCTGGTTTTGTTATTAC  
ACTTACGGATGGCCNTTCGGCCTGGACTGCAAAAGTTTNTGAATCGGAGATTGCACAGGAAGCTGATGACATGG  
CTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCGGGAGCAGCTGGTGCATA  
CAAGTTCATCTTTTCCAAGGACACTCAGCATTCTCCCTGGAGAAAGAACTGAAAGATGTTTCTTTCAGACTTGG  
TTCCTTCAACCTAGACAAAGTTACAAACCCAACCTGAAGTCATCAGAGAACTCATTTGCTACTGCCTGGACACCATT  
GCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAACGAAAGGCTCCTGAGAGATTGGACTGACGTT  
CAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCCTTGAGGGCCGATTTGTATCAAAGATTTATCTTGGT  
GCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTTGAGTGAAAGTCCAGCAGCTGGAGAAGAGTACCAAACCT  
GAAAGGGAACTCCGAGTTCTGACAAAATACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAAGAAA  
GCGGAGCCCCTGTGCTGGGCGCAGATACCCTTGATAAGGATGATTCCTTATTTTCAAGTCCAGATGTCACTGATAT  
TGCACCAAGTAGGAAGAGGAGACACCGAATGCAGACAAATCTTGGGACAGAACCTAAAATGGCTCCACAGGAG  
CTGCCACTACAGGAGAAGGAAAGGCTTGCTCTTACCGCCTCAGACCTTGAAAGAGGAGGGCACCTCTGCTG  
CAAACGTGTCCTTAGAAACCCTGAGAAACAGCAGCCCAGAAGaCCTCTTTGACTAG

➤ Synthèse séquençage DiT48hMix :972 **NT**

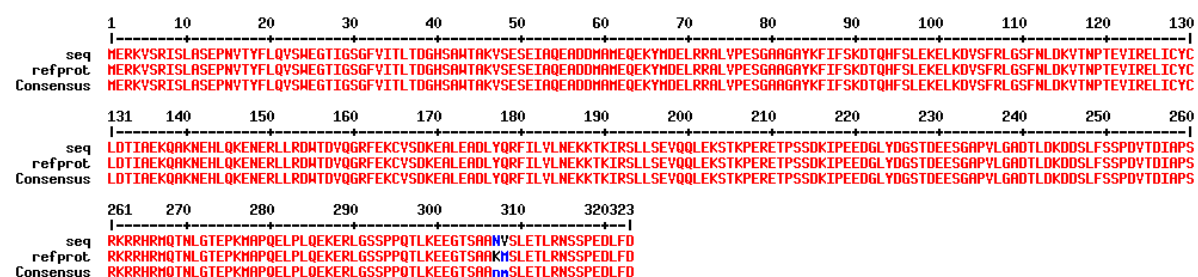
|                                                                |     |     |
|----------------------------------------------------------------|-----|-----|
| ATGGAAAGGAAAGTCAGC                                             | 18  |     |
| AGAATCTCTCTGGCTTCTGAACCCAATGTAACCTACTTTCTACAAGTGTCTTGGGAGGGT   |     | 78  |
| ACGATTGGATCTGGTTTTGTTATTACACTTACGGATGGCCATTTCGGCCTGGACTGCAAAA  |     | 138 |
| GTTTCTGAATCGGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATAC   |     | 198 |
| ATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTC   |     | 258 |
| ATCTTTTCCAAGGACACTCAGCATTCTCCCTGGAGAAAGAACTGAAAGATGTTTCTTTC    |     | 318 |
| AGACTTGGTTTCCTTCAACCTAGACAAAGTTACAAACCCAACCTGAAGTCATCAGAGAACTC |     | 378 |
| ATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAG   |     | 438 |
| GAAAAAGGAAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTG  |     | 498 |
| AGTGACAAAGAAGCCTTGAGAGCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAG   |     | 558 |
| AAGAAAACAAAAATCCGAAGCTTGTTGAGTGAAAGTCCAGCAGCTGGAGAAGAGTACCAAA  |     | 618 |
| CCTGAAAGGGAAACTCCGAGTTCTGACAAAATACCTGAGGAGGATGGGCTTTATGATGGC   |     | 720 |
| AGCACTGATGAAGAAAGCGGAGCCCCGTGTGCTGGGCGCAGATACCCTTGATAAGGATGAT  |     | 780 |
| TCCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGA   |     | 840 |
| ATGCAGACAAATCTTGGGACAGAACCTAAAATGGCTCCACAGGAGCTGCCACTACAGGAG   |     | 900 |
| AAGGAAAGGCTTGGCTCTTACCGCCTCAGACCTTGAAAGAGGAGGGCACCTCTGCTGCA    |     | 960 |
| AACGTGTCCTTAGAAACCCTGAGAAACAGCAGCCCAGAAGaCCTCTTTGACTAG         | 972 |     |

➤ **Blast contre banque rat :**

➤ **Différence Séquençage/CDS au niveau NT :**



➤ **Différence au niveau PROT :**



Mutations en 307-308

Flag BirA Xrcc4 DiT48hMix (clone ?) OK qq mutations

## FlagBirA Xrcc4 SP clone ?

### ➤ B3Fwd SP 871NT

ATGGAAAGGAAAGTCAGCAGAATCTCTTTGGCTTCTGAACCAATGTAACCTACTTTCTACAAGTGTCTTGGGAG  
GGTACGATTGGATCTGGTTTTGTTATTACACTTACGGATGGCCATTCGGCCTGGACTGCAAAAGTTTCTGAATCGG  
AGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGT  
GCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAAAG  
AACTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCAACTGAAGTCATCAGAG  
AACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAACGA  
AAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCCTTGAG  
GCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTTGAGTGAAGTC  
CAGCAGCTGGAGAAGAGTACCAAAcCTGAAAGGGAAACTCCGAGTTCTGACNAAATACCTGANGAGGANGGG  
CTTTATGATGGCAGCACTGATGAAGAAAGCGGANCCCCCTGTGCTGGGCGCANATNCCCTTGATAAGGATGANTC  
CTTATTTTCAAGTCCAGATGTCACTGATATTGCACCNAGTAGGAAGAGGAGACACCGAATGCAGANAANTCTTN  
NNCAGAACCTAAATGGCTCCNCNNGAGCTGCNNCTACNGGANAAGGAAAGGNTTGG

### ➤ BGHRev SP 970NT

AAGGGGGGATNTGGCCNNGCGGCGGCNCCANNGGAANGGAAAGTCAGCAGANTNTCTTTGGCTTCTGAA  
CCCAANGTANCNTACTTTCTNCAAGTNTCTTGGGAGGGTACGATTGGATCTGGTTTTGTTATTACACTTACGGAT  
GNCCNTTCGGCNTGGACTGCAAAAGTTTNTGAATCGGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGC  
AGGNNNNNNNCATGGATGAGCTGAGACGGGCACTGGTGCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCA  
TCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAAAGAACTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAA  
CCTAGACAAAGTTACAAACCAACTGAAGTCATCAGAGAACTCATTGCTACTGCCTGGACACCATTGCGGAAAA  
ACAAGCCAAAAACGAGCACCTGCAGAAGGAAAACGAAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCG  
ATTTGAGAAATGTGTGAGTGACAAAGAAGCCTTGGAGGCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGA  
GAAGAAAACAAAATCCGAAGCTTGTTGAGTGAAGTCCAGCAGCTGGAGAAGAGTACCAAACTGAAAGGGA  
AACTCCGAGTTCTGACAAAATACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAAGAAAGCGGAGCCC  
CTGTGCTGGGCGCAGATACCCTTGATAAGGATGATTCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGT  
AGGAAGAGGAGACACCGAATGCAGACAAATCTTGGGACAGAACCTAAAATGGCTCCACAGGAGCTGCCACTAC  
AGGAGAAGGAAAGGCTTGGCTCTTACCGCCTCAGACCTTGAAAGAGGAGGGCACCTCTGCTGCAAACGTGTC  
CTTAGAAACCCTGAGAAACAGCAGCCCAGAAGACCTCTTTGACTAG

### ➤ Synthèse séquençage SP: 972NT

ATGGAAAGGAAAGTCAGCAGAATCTCTT 28  
TGGCTTCTGAACCAATGTAACCTACTTTCTACAAGTGTCTTGGGAGGGTACGATTGGAT 88  
CTGGTTTTGTTATTACACTTACGGATGGCCATTCGGCCTGGACTGCAAAAGTTTCTGAAT 148  
CGGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGC 208  
TGAGACGGGCACTGGTGCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCA 268  
AGGACACTCAGCATTTCTCCCTGGAGAAAGAACTGAAAGATGTTTCTTTCAGACTTGGTT 328  
CCTTCAACCTAGACAAAGTTACAAACCAACTGAAGTCATCAGAGAACTCATTGCTACT 388  
GCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAACGAAA 448  
GGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAG 508  
AAGCCTTGGAGGCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAACAA 568  
AAATCCGAAGCTTGTGAGTGAAGTCCAGCAGCTGGAGAAGAGTACCAAAcCTGAAAGGG 628  
AAACTCCGAGTTCTGACAAAATACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATG 688  
AAGAAAGCGGAGCCCTGTGCTGGGCGCAGATACCCTTGATAAGGATGATTCTTATTTT  
CAAGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGAATGCAGACAA  
ATCTTGGGACAGAACTTAAAATGGCTCCACAGGAGCTGCCACTACAGGAGAAGGAAAGGC  
TTGGCTCTTACCGCCTCAGACCTTGAAAGAGGAGGGCACCTCTGCTGCAAACGTGTCCT  
TAGAAACCCTGAGAAACAGCAGCCCAGAAGACCTCTTTGACTAG

MERKVSRI SLASEPNVTYF LQVSWEGTIGSGFVITLTDGHSAAWTAKVSESEIAQEADDMAMEQEKYMDLRRALV  
PESGAAGAYKFIFSKDTQHFSLEKELKDVSFRLGSLNLDKVTNPTEVIRELICCYCLDTIAEKQAKNEHLQKENER  
LLRDWTDVQGRFEKCVSDKEALEADLYQRFILVLNEKKTIRSLLEVVQQLKSTKPERETPSSDKIPEEDGLYD  
GSTDEESGAPVLGADTLDDKSDLSFSSPDVTDIAPSRKRHRMQLTNLGTEPKMAPQELPLQEKERLGSSPPQTLKE  
EGTSAANVSLETLRNSSPEDLF-

➤ **Blast contre banque rat :**

|   | Name                                                                                                               | Score                      | Score | Cover | value | Ident | Len    | Accession                           |
|---|--------------------------------------------------------------------------------------------------------------------|----------------------------|-------|-------|-------|-------|--------|-------------------------------------|
| ✓ | <a href="#">PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4)_transcript variant X3_mRNA</a> | <a href="#">Norway rat</a> | 1762  | 1762  | 100%  | 0.0   | 99.38% | 4325 <a href="#">XM_006231751.2</a> |
| ✓ | <a href="#">Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4)_mRNA</a>                                  | <a href="#">Norway rat</a> | 1762  | 1762  | 100%  | 0.0   | 99.38% | 1497 <a href="#">NM_001006999.1</a> |
| ✓ | <a href="#">PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4)_transcript variant X2_mRNA</a> | <a href="#">Norway rat</a> | 1530  | 1765  | 100%  | 0.0   | 99.64% | 4358 <a href="#">XM_008760637.2</a> |
| ✓ | <a href="#">PREDICTED: Rattus norvegicus X-ray repair cross complementing 4 (Xrcc4)_transcript variant X1_mRNA</a> | <a href="#">Norway rat</a> | 1530  | 1765  | 100%  | 0.0   | 99.64% | 4292 <a href="#">XM_008760636.1</a> |
| ✓ | <a href="#">Rattus norvegicus TL0AEA7YM10 mRNA sequence</a>                                                        | <a href="#">Norway rat</a> | 1400  | 1400  | 81%   | 0.0   | 98.26% | 1825 <a href="#">FQ230968.1</a>     |

➤ **Différence Séquençage/CDS au niveau NT :**

|           | 1                                                                                                                              | 10  | 20  | 30  | 40  | 50  | 60    | 70  | 80  | 90  | 100 | 110 | 120 | 130 |
|-----------|--------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-----|-----|-----|
| seq       | ATGGAAGGGAAGTCAAGCAATCTCTTGGCTCTGAAACCAATGATGACCTACTTCTTCACAGTGTCTTGGGAGGAGACGATTGGATCTGGTTTGGTATTACACTTACGGATGGCAATCGGCTGGA   |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | ATGGAAGGGAAGTCAAGCAATCTCTTGGCTCTGAAACCAATGATGACCTACTTCTTCACAGTGTCTTGGGAGGAGACGATTGGATCTGGTTTGGTATTACACTTACGGATGGCAATCGGCTGGA   |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | ATGGAAGGGAAGTCAAGCAATCTCTTGGCTCTGAAACCAATGATGACCTACTTCTTCACAGTGTCTTGGGAGGAGACGATTGGATCTGGTTTGGTATTACACTTACGGATGGCAATCGGCTGGA   |     |     |     |     |     |       |     |     |     |     |     |     |     |
|           | 131                                                                                                                            | 140 | 150 | 160 | 170 | 180 | 190   | 200 | 210 | 220 | 230 | 240 | 250 | 260 |
| seq       | CTGCAAAAGTTTCTGAATCGAGATTGCAACAGGAGCTGATGACATGGCTATGGAGCGGAAATACATGGATGAGCTGAGACGGGACTGGTGCCAGAGTCGGGAGCAGCTGGTGATACAGTTTCA    |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | CTGCAAAAGTTTCTGAATCGAGATTGCAACAGGAGCTGATGACATGGCTATGGAGCGGAAATACATGGATGAGCTGAGACGGGACTGGTGCCAGAGTCGGGAGCAGCTGGTGATACAGTTTCA    |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | CTGCAAAAGTTTCTGAATCGAGATTGCAACAGGAGCTGATGACATGGCTATGGAGCGGAAATACATGGATGAGCTGAGACGGGACTGGTGCCAGAGTCGGGAGCAGCTGGTGATACAGTTTCA    |     |     |     |     |     |       |     |     |     |     |     |     |     |
|           | 261                                                                                                                            | 270 | 280 | 290 | 300 | 310 | 320   | 330 | 340 | 350 | 360 | 370 | 380 | 390 |
| seq       | CTTTTCCAGGAGCACTCAGCATTTCTCCCTGGAGAAAGAACTGAAGATGTTTCTTCAGACTTGGTTCTTCACCTAGACAAAGTTACAAACCCAACTGAAGTCATCAGAGAACTCATTTGCTACTGC |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | CTTTTCCAGGAGCACTCAGCATTTCTCCCTGGAGAAAGAACTGAAGATGTTTCTTCAGACTTGGTTCTTCACCTAGACAAAGTTACAAACCCAACTGAAGTCATCAGAGAACTCATTTGCTACTGC |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | CTTTTCCAGGAGCACTCAGCATTTCTCCCTGGAGAAAGAACTGAAGATGTTTCTTCAGACTTGGTTCTTCACCTAGACAAAGTTACAAACCCAACTGAAGTCATCAGAGAACTCATTTGCTACTGC |     |     |     |     |     |       |     |     |     |     |     |     |     |
|           | 391                                                                                                                            | 400 | 410 | 420 | 430 | 440 | 450   | 460 | 470 | 480 | 490 | 500 | 510 | 520 |
| seq       | CTGGACACCATTGCGGAATAACAGCCAAACAGGACCTGCAAGAGGAACCAAGAGGCTCCTGAGAGATTGGATGACGCTTCAGGCGCGATTGAGAAATGTGTAGTGACAAAGAGCCTTGGGG      |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | CTGGACACCATTGCGGAATAACAGCCAAACAGGACCTGCAAGAGGAACCAAGAGGCTCCTGAGAGATTGGATGACGCTTCAGGCGCGATTGAGAAATGTGTAGTGACAAAGAGCCTTGGGG      |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | CTGGACACCATTGCGGAATAACAGCCAAACAGGACCTGCAAGAGGAACCAAGAGGCTCCTGAGAGATTGGATGACGCTTCAGGCGCGATTGAGAAATGTGTAGTGACAAAGAGCCTTGGGG      |     |     |     |     |     |       |     |     |     |     |     |     |     |
|           | 521                                                                                                                            | 530 | 540 | 550 | 560 | 570 | 580   | 590 | 600 | 610 | 620 | 630 | 640 | 650 |
| seq       | CCGATTTGTATCAAGATTATCTTGGTGCTGAATGAGAGAAACAAAAATCCGAGCTTGTGAGTGAGTCCAGCAGCTGGAGAGAGTACCAACCTGAAAGGGAACTCCGAGTCTGACAAAT         |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | CCGATTTGTATCAAGATTATCTTGGTGCTGAATGAGAGAAACAAAAATCCGAGCTTGTGAGTGAGTCCAGCAGCTGGAGAGAGTACCAACCTGAAAGGGAACTCCGAGTCTGACAAAT         |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | CCGATTTGTATCAAGATTATCTTGGTGCTGAATGAGAGAAACAAAAATCCGAGCTTGTGAGTGAGTCCAGCAGCTGGAGAGAGTACCAACCTGAAAGGGAACTCCGAGTCTGACAAAT         |     |     |     |     |     |       |     |     |     |     |     |     |     |
|           | 651                                                                                                                            | 660 | 670 | 680 | 690 | 700 | 710   | 720 | 730 | 740 | 750 | 760 | 770 | 780 |
| seq       | ACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAAGAAGCGAGCCCTGTGCTGGGCGCAGATACCCTGATAGAGATGATTCCTATTATTCAAGTCCAGATGCTACTGATATTGCACCAAGT |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | ACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAAGAAGCGAGCCCTGTGCTGGGCGCAGATACCCTGATAGAGATGATTCCTATTATTCAAGTCCAGATGCTACTGATATTGCACCAAGT |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | ACCTGAGGAGGATGGGCTTTATGATGGCAGCACTGATGAAGAAGCGAGCCCTGTGCTGGGCGCAGATACCCTGATAGAGATGATTCCTATTATTCAAGTCCAGATGCTACTGATATTGCACCAAGT |     |     |     |     |     |       |     |     |     |     |     |     |     |
|           | 781                                                                                                                            | 790 | 800 | 810 | 820 | 830 | 840   | 850 | 860 | 870 | 880 | 890 | 900 | 910 |
| seq       | AGGAAGAGGAGACCCGATTGACAGCAATCTTGGGACAGAACCTAAATGGCTCCACAGAGCTGCCACTACAGGAGAGGAAGAGCTTGGCTCTTCACGCTCAGACCTGAAAGAGGAGGGGACCT     |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | AGGAAGAGGAGACCCGATTGACAGCAATCTTGGGACAGAACCTAAATGGCTCCACAGAGCTGCCACTACAGGAGAGGAAGAGCTTGGCTCTTCACGCTCAGACCTGAAAGAGGAGGGGACCT     |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | AGGAAGAGGAGACCCGATTGACAGCAATCTTGGGACAGAACCTAAATGGCTCCACAGAGCTGCCACTACAGGAGAGGAAGAGCTTGGCTCTTCACGCTCAGACCTGAAAGAGGAGGGGACCT     |     |     |     |     |     |       |     |     |     |     |     |     |     |
|           | 911                                                                                                                            | 920 | 930 | 940 | 950 | 960 | 97872 |     |     |     |     |     |     |     |
| seq       | CTGCTGCAAACTGTCTCTTGAARACCTGAGAAACAGCAGCCAGAGACCTCTTGTACTAG                                                                    |     |     |     |     |     |       |     |     |     |     |     |     |     |
| cds       | CTGCTGCAAACTGTCTCTTGAARACCTGAGAAACAGCAGCCAGAGACCTCTTGTACTAG                                                                    |     |     |     |     |     |       |     |     |     |     |     |     |     |
| Consensus | CTGCTGCAAACTGTCTCTTGAARACCTGAGAAACAGCAGCCAGAGACCTCTTGTACTAG                                                                    |     |     |     |     |     |       |     |     |     |     |     |     |     |

Mutations en 28, 78, 84, 123, 921-922

➤ **Différence au niveau PROT :**

seq  
 refprot  
 Consensus

1 10 20 30 40 50 60 70 80 90 100 110 120 130  
 MERKYSRISLASEPNVITYFLQVSWEGTIGSGFVITLDGHSANTAKYSESEIAQEADDMAMEQEKYMDLRRALVPESGAAGAYKFIKSDTQHFSLLEKLDKYSFRLGSFNLKDYTNPTVEIRELTCYC  
 MERKYSRISLASEPNVITYFLQVSWEGTIGSGFVITLDGHSANTAKYSESEIAQEADDMAMEQEKYMDLRRALVPESGAAGAYKFIKSDTQHFSLLEKLDKYSFRLGSFNLKDYTNPTVEIRELTCYC  
 MERKYSRISLASEPNVITYFLQVSWEGTIGSGFVITLDGHSANTAKYSESEIAQEADDMAMEQEKYMDLRRALVPESGAAGAYKFIKSDTQHFSLLEKLDKYSFRLGSFNLKDYTNPTVEIRELTCYC

131 140 150 160 170 180 190 200 210 220 230 240 250 260  
 LDTAEQKQKNEHLQKEMERLLRDWTDVQGRFEKCVSDKEALEADLYQRFILVLEKKTIRKSLSEVQLEKSTKPERETPSSDKIPEEDGLYDGSDEESGAPVLGADTLDKDSDLSSPDVTDAPS  
 LDTAEQKQKNEHLQKEMERLLRDWTDVQGRFEKCVSDKEALEADLYQRFILVLEKKTIRKSLSEVQLEKSTKPERETPSSDKIPEEDGLYDGSDEESGAPVLGADTLDKDSDLSSPDVTDAPS  
 LDTAEQKQKNEHLQKEMERLLRDWTDVQGRFEKCVSDKEALEADLYQRFILVLEKKTIRKSLSEVQLEKSTKPERETPSSDKIPEEDGLYDGSDEESGAPVLGADTLDKDSDLSSPDVTDAPS

261 270 280 290 300 310 320323  
 RRRRHRHQTLNLTGTEPKMAPQELPLQEKERLGSSPPQTLKEEGTSAAKNSLETLRNNSPEOLFQ  
 RRRRHRHQTLNLTGTEPKMAPQELPLQEKERLGSSPPQTLKEEGTSAAKNSLETLRNNSPEOLFQ  
 RRRRHRHQTLNLTGTEPKMAPQELPLQEKERLGSSPPQTLKEEGTSAAKNSLETLRNNSPEOLFQ

Mutation AA 307-308

|                                     | Description                                                        | Common Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession      |
|-------------------------------------|--------------------------------------------------------------------|-------------|-----------|-------------|-------------|---------|------------|----------|----------------|
| <input checked="" type="checkbox"/> | DNA repair protein XRCC4 [Rattus norvegicus]                       | Norway_rat  | 659       | 659         | 100%        | 0.0     | 99.38%     | 323      | NP_001007000.1 |
| <input checked="" type="checkbox"/> | PREDICTED: DNA repair protein XRCC4 isoform X1 [Rattus norvegicus] | Norway_rat  | 649       | 649         | 100%        | 0.0     | 95.81%     | 334      | XP_008758858.1 |

Flag BirA Xrcc4 SP (clone ?) OK, qq mutations les même que DiT48h

o FlagBirA Xrcc4 CTX clone ?

➤ B3Fwd CTX 834NT

ATGGAAAGGAAAGTCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACCTACTTTCTACAAGTGTCTTGGGAG  
GGTACGATTGGATCTGGTTTTGTTATTACACTTACGGATGGCCATTTCGGCCTGGACTGCAAAAGTTTCTGAATCGG  
AGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGT  
GCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAAAG  
AACTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAACCTGAAGTCATCAGAG  
AACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAAACGA  
AAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCCTTGGAG  
GCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTGAGTGAAGTC  
CAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGGGAACTCCGAGTTCTGACAAAATACCTGANGAGGATGGG  
CTTTATGATGGCAGCACTGATGAAGAAAGCGGANCCCCTGTGCTGGGCGCANATACCCTTGATAAGGATGANTC  
CTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGAANGCANACAAATCTNN  
NNCAGAACCTAAAAATGGCTC

➤ BGHRev CTX 977NT RENVOYE 25/11

ATGNAAAGGAAANTCAGCAGANTCTNTNTGGCTTNTGAACCCAATGTANCCTACTTTCTACAAGTGTCTTGGGA  
GGGTACGATNNGATCTGGTTTTGTTATTACACTTACGGATGGCCNTTCGGCCTGGACTGCAAAAGTTTNTGAATC  
GGAGATTGCACAGGAAGCTGATGACATGGCTATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTG  
GTGCCAGAGTCGGGAGCAGCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAA  
AGAACTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAACCTGAAGTCATCAG  
AGAACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAAAACGAGCACCTGCAGAAGGAAAAAC  
GAAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGCCGATTTGAGAAATGTGTGAGTGACAAAGAAGCCTTGG  
AGGCCGATTTGTATCAAAGATTTATCTTGGTGCTGAATGAGAAGAAAACAAAAATCCGAAGCTTGTGAGTGAA  
GTCCAGCAGCTGGAGAAGAGTACCAAACCTGAAAGGGGAACTCCGAGTTCTGACAAAATACCTGAGGAGGATG  
GGCTTTATGATGGCAGCACTGATGAAGAAAGCGGAGCCCCTGTGCTGGGCGCAGATACCCTTGATAAGGATGAT  
TCCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGTAGGAAGAGGAGACACCGAATGCAGACAAATCTT  
GGGACAGAACCTAAAATGGCTCCACAGGAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTCTTACCCGCCCTC  
AGACCTTGAAAGAGGAGGGCACCTCTGCTGCAAACGTGTCTTAGAAACCCTGAGAAACAGCAGCCCAGAAGa  
CCTCTTTGACTAGTGCGG

➤ Synthèse séquençage CTX: 972NT

|                                                               |     |
|---------------------------------------------------------------|-----|
| ATGGAAAGGAAAGTCAGCAGAATCTCTCTGGCTTCTGAACCCAATGTAACCTACTTTCTA  | 60  |
| CAAGTGTCTTGGGAGGGTACGATTGGATCTGGTTTTGTTATTACACTTACGGATGGCCAT  | 120 |
| TCGGCCTGGACTGCAAAAGTTTCTGAATCGGAGATTGCACAGGAAGCTGATGACATGGCT  | 180 |
| ATGGAGCAGGAAAAATACATGGATGAGCTGAGACGGGCACTGGTCCAGAGTCGGGAGCA   | 240 |
| GCTGGTGCATACAAGTTCATCTTTTCCAAGGACACTCAGCATTTCTCCCTGGAGAAAGAA  | 300 |
| CTGAAAGATGTTTCTTTCAGACTTGGTTCCTTCAACCTAGACAAAGTTACAAACCCAACCT | 360 |
| GAAGTCATCAGAGAACTCATTTGCTACTGCCTGGACACCATTGCGGAAAAACAAGCCAAA  | 420 |
| AACGAGCACCTGCAGAAGGAAAAACGAAAGGCTCCTGAGAGATTGGACTGACGTTCAAGGC | 480 |
| CGATTTGAGAAATGTGTGAGTGACAAAGAAGCCTTGGAGGCCGATTTGTATCAAAGATTT  | 540 |
| ATCTTGGTGCTGAATGAGAAGAAAAACAAAAATCCGAAGCTTGTGAGTGAAGTCCAGCAG  | 600 |
| CTGGAGAAGAGTACCAAACCTGAAAGGGGAACTCCGAGTTCTGACAAAATACCTGAGGAG  | 660 |
| GATGGGCTTTATGATGGCAGCACTGATGAAGAAAGCGGAGCCCCTGTGCTGGGCGCAGAT  | 720 |
| ACCTTGATAAGGATGATTCTTATTTTCAAGTCCAGATGTCACTGATATTGCACCAAGT    | 780 |
| AGGAAGAGGAGACACCGAATGCAGACAAATCTTGGGACAGAACCTAAAATGGCTCCACAG  | 840 |
| GAGCTGCCACTACAGGAGAAGGAAAGGCTTGGCTCTTACCCGCCCTCAGACCTTGAAAGAG | 900 |
| GAGGACACCTCTGCTGCAAACGTGTCTTAGAAACCCTGAGAAACAGCAGCCCAGAAGaC   | 960 |
| CTCTTTGACTAG                                                  | 972 |

➤ **Blast contre banque rat :**

➤ **Différence Séquençage/CDS au niveau NT :**

Mutations en 78, 84, 123, 921-922

➤ **Différence au niveau PROT :**

1 10 20 30 40 50 60 70 80 90 100 110 120 130  
seq ref MERKYSRISLASEPNVYTFLLQVSMEGTIGSGFYITLDGHSANTAKYSESEIAQEQADDNAMEQEKYMDLRRALVPESGAGAYKFFSKDTQHFSLKELKDYSFRLGSGFNLKDYVNPTEVIRELICYC  
Consensus MERKYSRISLASEPNVYTFLLQVSMEGTIGSGFYITLDGHSANTAKYSESEIAQEQADDNAMEQEKYMDLRRALVPESGAGAYKFFSKDTQHFSLKELKDYSFRLGSGFNLKDYVNPTEVIRELICYC

131 140 150 160 170 180 190 200 210 220 230 240 250 260  
seq ref LDTAEKQAKNEHLQKENERLLRDHDTVQGRFEKCYSDKEALEADLYQRFILVLNEKKTIKIRSLSEVQLEKSTKPERETPSSDKIPEEDGLYDGDSTDEESGAPVLAGDTLDKDDSLFSSPDVTDIAPS  
Consensus LDTAEKQAKNEHLQKENERLLRDHDTVQGRFEKCYSDKEALEADLYQRFILVLNEKKTIKIRSLSEVQLEKSTKPERETPSSDKIPEEDGLYDGDSTDEESGAPVLAGDTLDKDDSLFSSPDVTDIAPS

261 270 280 290 300 310 320323  
seq RKKRRHRMQLTGTEPKMAPQELPLQEKERLGSSPPQTLKEEGTSAAKNSLETLRNSSPEDLFD  
ref RKKRRHRMQLTGTEPKMAPQELPLQEKERLGSSPPQTLKEEGTSAAKNSLETLRNSSPEDLFD  
Consensus RKKRRHRMQLTGTEPKMAPQELPLQEKERLGSSPPQTLKEEGTSAAKNSLETLRNSSPEDLFD

mutations en 307-308

|                                     | Description                                                                        | Common Name                | Max Score | Total Score | Coverage | E-value | Per. Ident | Rec. Len | Accession                      |
|-------------------------------------|------------------------------------------------------------------------------------|----------------------------|-----------|-------------|----------|---------|------------|----------|--------------------------------|
| <input checked="" type="checkbox"/> | <a href="#">DNA repair protein XRCC4 [Rattus norvegicus]</a>                       | <a href="#">Norway rat</a> | 659       | 659         | 100%     | 0.0     | 99.38%     | 323      | <a href="#">NP_001007000.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">PREDICTED: DNA repair protein XRCC4 isoform X1 [Rattus norvegicus]</a> | <a href="#">Norway rat</a> | 649       | 649         | 100%     | 0.0     | 95.81%     | 334      | <a href="#">XP_008758858.1</a> |

Flag BirA Xrcc4 CTX (clone ?) OK comme DiT48h et SP