

4) Artemis Dclre1c

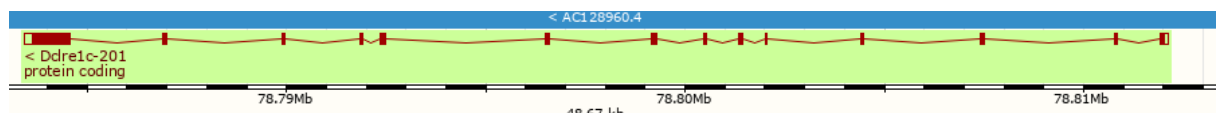
Rattus norvegicus DNA cross-link repair 1C (Dclre1c), mRNA

- **Référence NCBI** : NM_147145

Alias : Snm1l, SNM1-like protein; DNA cross-link repair 1C Protein

- **Taille** : 2097 NT
- **Séquence NT** :

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 61 ccattcccat tgaccgcttc gacagagaga acctgaaagc ccgtgcctac ttcctttcgc
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1021 gcccagtga tgcgtatcca aatgtcattc cgatcggcct cactgtggat aaggctcatgg
1081 acttttttaa gcctctgtgc cgctcttccc aatgtgctga accaaagtac aagcccctcg
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1981 cctctgactt tgaaatcccc tcaactccag aagctgagct tcccaagcca gagcatttac
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- Séquence prot :

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- Amorces synthétisées :

Dclre1c_AscI_Fwd

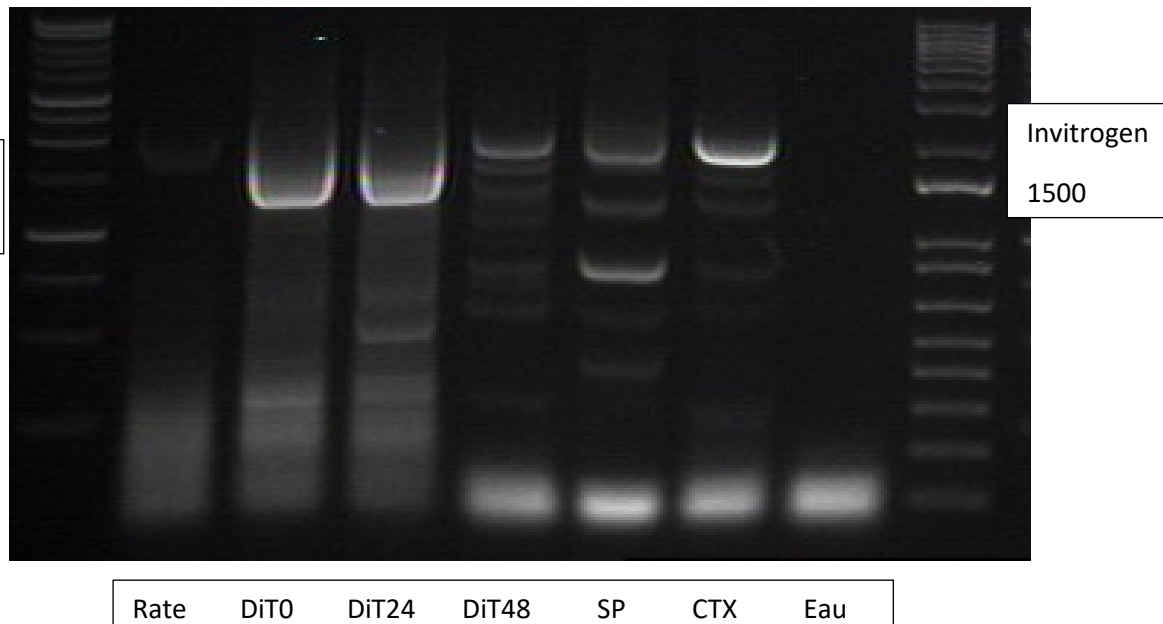
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Dclre1c_NotI_Rev

ttaaGCGGCGCa ttatttaaatactctgggagtgaac

- Expériences :

- PCR 20/07 : sur **les 7 conditions** cycle Q5-TM 60°C-Enhancer 0- 2min 30 d'élongation



- **15/10** essai de PCR Q5, 0 Enhancer à 62°C pour voir si moins de bandes non spe : on perd les bandes pour SP et CTX
- 23/10 extraction sur gel des PCR du 20/07 à 60°C
- 27/10 digestion/purification/ligation
- 28/10 transformation
- 30/10 miniprep
- 09/11 : envoi au séquençage
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- Résultats séquençages

- FlagBirA Dclre1c rate clone C

- B3Fwd rate 902NT

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GAT

- BGHRev rate 1039NT

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- Seq int Fwd1 du 25/11

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➤ Seq int Fwd2 du 25/11

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➤ Seq int Rev1 du 25/11

[illegible]

➤ Seq int Rev2 du 25/11

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➤ **Synthèse séquençage rate**

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 ENVHSQIFK-

➤ Blast contre banque rat :

	Description	Common Name	Max Score	Total Score	Query Cover	E-value	Ident	Len	Accession
✓	Rattus norvegicus DNA cross-link repair 1C (Dclre1c)_mRNA	Norway rat	3873	3873	100%	0.0	100.00%	2162	NM_147145.2
✓	Rattus norvegicus SNM1-like protein mRNA, complete cds	Norway rat	3845	3845	100%	0.0	99.76%	2182	AF395746.1
✓	PREDICTED: Rattus norvegicus DNA cross-link repair 1C (Dclre1c)_transcript variant X1_mRNA	Norway rat	3419	3874	100%	0.0	100.00%	4442	XM_017600460.1
✓	PREDICTED: Rattus norvegicus translation initiation factor IF-2-like (LOC108353135)_mRNA	Norway rat	135	135	3%	1e-29	100.00%	1222	XM_017600743.1

➤ Différence Séquencage/CDS au niveau NT :

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

261 270 280 290 300 310 320 330 340 350 360 370 380 390
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ref AEEYFQMNKLP CGMASHKT KT V L H T I S I K P S T M F G E R T R K T N V I V R T G E S S Y R A C F S F H S S Y S E I K D F L S Y I C P V N A Y P N V I P I G L T V D K V M D F L K P L C R S S Q C A E P K Y K P L G K L K R A R T V H L D S E E D D D
Consensus AEEYFQMNKLP CGMASHKT KT V L H T I S I K P S T M F G E R T R K T N V I V R T G E S S Y R A C F S F H S S Y S E I K D F L S Y I C P V N A Y P N V I P I G L T V D K V M D F L K P L C R S S Q C A E P K Y K P L G K L K R A R T V H L D S E E D D D

391 400 410 420 430 440 450 460 470 480 490 500 510 520
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ref L F D D P L L T H S R R K V P Y Q V T L H P E V F S M K A L P L D Q P E L G Q S P G C C K A E S M P S P L A N F V D C D E S N S D S E G E L E T P P S L Q G G L G P T T L P Q N A D P D V D V P R M E V F F K R K D E I T D E C L E N L P S S I E T G G S Q S P
Consensus L F D D P L L T H S R R K V P Y Q V T L H P E V F S M K A L P L D Q P E L G Q S P G C C K A E S M P S P L A N F V D C D E S N S D S E G E L E T P P S L Q G G L G P T T L P Q N A D P D V D V P R M E V F F K R K D E I T D E C L E N L P S S I E T G G S Q S P

521 530 540 550 560 570 580 590 600 610 620 630 640 650
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ref K R F S D S P K L G S D S G E S T H I S S Q N S S Q S T H I T D Q G S Q G W S Q C D T V L L S S Q E K S G G D S T S L N K D T Y K P K P K D S I S A S Q I E Q N A L C P Q D T H C L K S G A E V N G V P C I E E P D T V S G R K S S P E K T S L T S T Q A D S
Consensus K R F S D S P K L G S D S G E S T H I S S Q N S S Q S T H I T D Q G S Q G W S Q C D T V L L S S Q E K S G G D S T S L N K D T Y K P K P K D S I S A S Q I E Q N A L C P Q D T H C L K S G A E V N G V P C I E E P D T V S G R K S S P E K T S L T S T Q A D S

651 660 670 680 690 698
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ref Q S S D F E I P S T P E A E L P K P E H L Q F L Y G K L A T G E S I V L K K E N V H S Q I F K
Consensus Q S S D F E I P S T P E A E L P K P E H L Q F L Y G K L A T G E S I V L K K E N V H S Q I F K

	seq	cds	Consensus	Description	Common							Accession
					Name	Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	

- ☒ [protein artemis \[Rattus norvegicus\]](#) [Norway rat](#) 1449 1449 100% 0.0 100.00% 698 [NP_671486.2](#)
- ☒ [SNM1-like protein \[Rattus norvegicus\]](#) [Norway rat](#) 1421 1421 98% 0.0 99.42% 697 [AAM89124.1](#)
- ☒ [PREDICTED: protein artemis isoform X1 \[Rattus norvegicus\]](#) [Norway rat](#) 1275 1275 88% 0.0 100.00% 629 [XP_017455949.](#)
- ☒ [DNA cross-link repair 1C, PSO2 homolog \(S. cerevisiae\), isoform CRA_b \[Rattus norvegicus\]](#) [Norway rat](#) 1145 1145 79% 0.0 100.00% 552 [EDL78693.1](#)

1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
seq C T C T T T G A T G A C C C T A C T A C A C A T T C A G G C G C A A A G T T C C G T A C C A G T A C T C T T C A C C C T G A G G T A T T T C A R T G A G G C A C T A C C G T A G A T C A G C C T G A C T G G G A C A A G C C C G G A T G C T
cds C T C T T T G A T G A C C C T A C T A C A C A T T C A G G C G C A A A G T T C C G T A C C A G T A C T C T T C A C C C T G A G G T A T T T C A R T G A G G C A C T A C C G T A G A T C A G C C T G A C T G G G A C A A G C C C G G A T G C T
Consensus C T C T T T G A T G A C C C T A C T A C A C A T T C A G G C G C A A A G T T C C G T A C C A G T A C T C T T C A C C C T G A G G T A T T T C A R T G A G G C A C T A C C G T A G A T C A G C C T G A C T G G G A C A A G C C C G G A T G C T

1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
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cds G T A A A G C A G A G A T G C C G A G T C C T T C T T G G C A C A C T T T G T G G A C T G T G A C A G T C C A C A G T G A C A G T G A G G A G A G T T A G A G A C C C G C C T T C T C T G C A G G A G G T C T C G G C C C A C A C A C T C C C
Consensus G T A A A G C A G A G A T G C C G A G T C C T T C T T G G C A C A C T T T G T G G A C T G T G A C A G T C C A C A G T G A C A G T G A G G A G A G T T A G A G A C C C G C C T T C T C T G C A G G A G G T C T C G G C C C A C A C A C T C C C

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Consensus A C A C A A A A C G T G A T C C G A T G T G A T G T A C C T C G G T G G A A G T A T T C T C A A A G A A A A G A T G A A T C A C A G A T G A T G T T G G A A A A C T A C C T T C C T C C A T A G A G A C A G G G G A T C C A G T A C C A

1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
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cds A A G C G T T C A G T A C T A C C A A A G C T G G G C A G T G A C T C T G A T G G A G A A T C C A C C A T A T C T C T C C A G A A T T C A T C A G T C A C C C A C A T A C C G A T C A G G A G C C A A G G C T G G G A C A G C A G T G T G
Consensus A A G C G T T C A G T A C T A C C A A A G C T G G G C A G T G A C T C T G A T G G A G A A T C C A C C A T A T C T C T C C A G A A T T C A T C A G T C A C C C A C A T A C C G A T C A G G A G C C A A G G C T G G G A C A G C A G T G T G

1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
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cds A T A C C G T T T G T A T C T C C C A G A G A A A G T G G T G G G A T A G C A C C T C T T G A C A G G A T A C C T A C A A C C A A A C C A A A G A T A G T A T T C T G C C T C C A A T A G A C A G A T G C A C T T T G T C C A C A
Consensus A T A C C G T T T G T A T C T C C C A G A G A A A G T G G T G G G A T A G C A C C T C T T G A C A G G A T A C C T A C A A C C A A A C C A A A G A T A G T A T T C T G C C T C C A A T A G A C A G A T G C A C T T T G T C C A C A

1821 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950
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cds G G A T A C T A C T G T A T T T G A A A G C G G A G C T G A G T A A A T G A G T C C C T T G A T T G A A A C C A G A C A C T G T A G T G G C A G A A A T C T C A C C T G A G A A A A C T C G T A C C A C A C A C A G G C A G A C T C A
Consensus G G A T A C T A C T G T A T T T G A A A G C G G A G C T G A G T A A A T G A G T C C C T T G A T T G A A A C C A G A C A C T G T A G T G G C A G A A A T C T C A C C T G A G A A A A C T C G T A C C A C A C A C A G G C A G A C T C A

1951 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080
seq C A G A G C T C C T C T A C T T T G A A A T C C C C T C A C T C C A G A G C T G A G C T C C C A G C C A G A G A T T A C A G T C T T A T A T G G A A G C T G G C A C A G G T G A G A G T A T A G T G T T G A A A A A G A A A T G T T C A C T
cds C A G A G C T C C T C T A C T T T G A A A T C C C C T C A C T C C A G A G C T G A G C T C C C A G C C A G A G A T T A C A G T C T T A T A T G G A A G C T G G C A C A G G T G A G A G T A T A G T G T T G A A A A A G A A A T G T T C A C T
Consensus C A G A G C T C C T C T A C T T T G A A A T C C C C T C A C T C C A G A G C T G A G C T C C C A G C C A G A G A T T A C A G T C T T A T A T G G A A G C T G G C A C A G G T G A G A G T A T A G T G T T G A A A A A G A A A T G T T C A C T

2081 2090 2097
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cds C C C A G A T A T T A A A T A A
Consensus C C C A G A T A T T A A A T A A

Flag BirA Dclre1c rate (clone C) parfait

○ **FlagBirA Dclre1c DiT0 clone A**

➤ **B3Fwd DiT0 861NT**

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➤ **BGHRev DiT0 994NT**

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➤ **Seq int Fwd1 du 25/11**

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➤ **Seq int Fwd2 du 25/11**

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➤ **Seq int Rev1 du 25/11**

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➤ **Seq int Rev2 du 25/11**

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➤ Synthèse séquençage DiT0

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PPSLQGGGLPPTLPQQNADPDVDVPRWEVFFKRKDEITDECLNLPSIETGGSQSPKRFSDSPKLGSDSDGESTHIS
SQNSSQSTHITDQGSQGWDSQCDTVLLSSQESGGDSTSLNKDITYPKPKDSISASQIEQNALCPQDTHCDLKSGA
EVNGVPCIEEPDVTSGRKSSPEKTSLTSTQADSQSSSDFEIPSTPEALPKPEHLQFLYGLKATGESIVLKKENVHSQIFK

➤ Blast DiT0 contre banque rat :

	Description	Name	Score	Score	Cover	value	Ident	Len	Accession
✓	Rattus norvegicus DNA cross-link repair 1C (Dclre1c). mRNA	Norway rat	3873	3873	100%	0.0	100.00%	2162	NM_147145.2
✓	Rattus norvegicus SNM1-like protein mRNA, complete cds	Norway rat	3845	3845	100%	0.0	99.76%	2182	AF395746.1
✓	PREDICTED: Rattus norvegicus DNA cross-link repair 1C (Dclre1c). transcript variant X1. mRNA	Norway rat	3419	3874	100%	0.0	100.00%	4442	XM_017600460.1

➤ **Différence Séquencage DiT0/CDS au niveau NT**

[illegible]

➤ **Différence Séquençage DiT0/CDS au niveau PROT :**

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MSSFQGGMEEYPTISIDRFQRENLRKARAYFLSHCHKDHNKGLRAPSHKRRECSLKVFLYCSPVTKELLLTSPKYKFMEENRIATIEIETPTQVSLVDEASGEKEEVVVTLLPAGHCPGSMFLFQGSNGT													
ref	MSSFQGGMEEYPTISIDRFQRENLRKARAYFLSHCHKDHNKGLRAPSHKRRECSLKVFLYCSPVTKELLLTSPKYKFMEENRIATIEIETPTQVSLVDEASGEKEEVVVTLLPAGHCPGSMFLFQGSNGT													
Consensus	MSSFQGGMEEYPTISIDRFQRENLRKARAYFLSHCHKDHNKGLRAPSHKRRECSLKVFLYCSPVTKELLLTSPKYKFMEENRIATIEIETPTQVSLVDEASGEKEEVVVTLLPAGHCPGSMFLFQGSNGT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	VLYTGDFRLAKGEVSRMELLHSGGGRYKDIQSVYLDITFCOPRFYQIPSRREECLRGVLELYRSWITRSPKHVYVNLCKAAYGYEYFTNLSEELGVQVHYVDKDMFKNMPDILHHLTTDRNTQIHACRHPK													
ref	VLYTGDFRLAKGEVSRMELLHSGGGRYKDIQSVYLDITFCOPRFYQIPSRREECLRGVLELYRSWITRSPKHVYVNLCKAAYGYEYFTNLSEELGVQVHYVDKDMFKNMPDILHHLTTDRNTQIHACRHPK													
Consensus	VLYTGDFRLAKGEVSRMELLHSGGGRYKDIQSVYLDITFCOPRFYQIPSRREECLRGVLELYRSWITRSPKHVYVNLCKAAYGYEYFTNLSEELGVQVHYVDKDMFKNMPDILHHLTTDRNTQIHACRHPK													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	AEEYFQNNKPCGNASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSFHSSYSEIKDFLSYICPNAYPNVPIGLTVDKVMDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEEDDD													
ref	AEEYFQNNKPCGNASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSFHSSYSEIKDFLSYICPNAYPNVPIGLTVDKVMDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEEDDD													
Consensus	AEEYFQNNKPCGNASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSFHSSYSEIKDFLSYICPNAYPNVPIGLTVDKVMDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEEDDD													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	LFDDPLLTHSRKVPYQVTLHPEVFSHKALPLDQPELGQSPGCCAKESHPSPSLANFYDCESNSDSEGELETPPSLQGGGLPTTLQQNADPDVDYPRHVEVFFKRKDEITDECLENLPSSETGGSQSP													
ref	LFDDPLLTHSRKVPYQVTLHPEVFSHKALPLDQPELGQSPGCCAKESHPSPSLANFYDCESNSDSEGELETPPSLQGGGLPTTLQQNADPDVDYPRHVEVFFKRKDEITDECLENLPSSETGGSQSP													
Consensus	LFDDPLLTHSRKVPYQVTLHPEVFSHKALPLDQPELGQSPGCCAKESHPSPSLANFYDCESNSDSEGELETPPSLQGGGLPTTLQQNADPDVDYPRHVEVFFKRKDEITDECLENLPSSETGGSQSP													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	KRFSDSPKLGSDSDGESTHISQNSQSTHTIDQGSQGNDSQCDTVLLSSQEKSGGDSTSLNKDTYKPKPKDSISASQIEQNALCPQDTHCDLKSQAEVNGVPCIEEPDVTYSGRKSSPEKTSLTSTQADS													
ref	KRFSDSPKLGSDSDGESTHISQNSQSTHTIDQGSQGNDSQCDTVLLSSQEKSGGDSTSLNKDTYKPKPKDSISASQIEQNALCPQDTHCDLKSQAEVNGVPCIEEPDVTYSGRKSSPEKTSLTSTQADS													
Consensus	KRFSDSPKLGSDSDGESTHISQNSQSTHTIDQGSQGNDSQCDTVLLSSQEKSGGDSTSLNKDTYKPKPKDSISASQIEQNALCPQDTHCDLKSQAEVNGVPCIEEPDVTYSGRKSSPEKTSLTSTQADS													
	651	660	670	680	690	698								
seq	QSSSDFEIPSTPERELPKPEHLQFLYGKLGATGESIVLKKENVHSQIFK													
ref	QSSSDFEIPSTPERELPKPEHLQFLYGKLGATGESIVLKKENVHSQIFK													
Consensus	QSSSDFEIPSTPERELPKPEHLQFLYGKLGATGESIVLKKENVHSQIFK													

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	protein artemis [Rattus norvegicus]	Norway rat	1449	1449	100%	0.0	100.00%	698	NP_671486.2
✓	SNM1-like protein [Rattus norvegicus]	Norway rat	1421	1421	98%	0.0	99.42%	697	AAM89124.1
✓	PREDICTED: protein artemis isoform X1 [Rattus norvegicus]	Norway rat	1275	1275	88%	0.0	100.00%	629	XP_017455949.1

Flag BirA Dclre1c DiT0 (clone A) parfait

o FlagBirA Dclre1c DiT24hLPS clone A

➤ B3Fwd DiT24h 873NT

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGACAGAGAGAACCTGAAA
GCCCCGTGCCTACTTCCTTTCGCACTGCCACAAGGATCACATGAAAGGATTAAGGGCTCCTTCCATGAAAAGAAGG
CTGGAATGCAGTTTGAAGGTCTTCCTGTACTGTTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCCAAAGTAC
AAGTTCTGGGAAAACCGAATTATAGCAATTGAAATTGAAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCGG
GTGAGAAGGAAGAAGTTGTTGTGACTCTCTTACCAGCTGGTCACTGCCAGGTTTCAGTTATGTTTCTATTTCAGG
GCAGTAATGGAAGTGTCTTATACACAGGAGACTTCAGACTGGCGAAAGGAGAAGTTTCCAGAATGGAGCTTCTG
CACTCTGGGGGCAGAGTAAAAGACATCCAAAGTGTATATTTAGACACCACTTTCTGTGACCCAAGGTTTATCAAA
TTCCAAGTCGTGAGGAGTGCTTGAGGGGGCGTTCTGGAGCTGGTTCGGAGCTGGATCACGAGGAGTCCGAAGCA
CGTCGTGTGGCTGAACTGCAAGGCCGCCTACGGCTATGAGTACTTATTCACCAACCTGAGTGAGGAGCTGGGAG
TCCAGGTTTCATGTGGACAAGCTGGACATGTTTAAAAACATGCCTGATATCCTGCACCATCTCACAACGGATCGAAA
CACCCAGATCCACGCCTGNCGCCACCCGAAGGNAGANANTATTTTCAGTGGAATAAGTTACCCTGTGGNATGG
NTTCCAAAATAAACTGNACTCCACACAATCAGCATCNAGCCATCTACC

➤ BGHRev DiT24h 998NT

CCAAAGTNNNANCCCNTNGGGAAACNGAAGAGAGNTAGNNCAGTTCNNNTGANTCAGAGGAAGATGATGAT
NTCTTTGATGACCCTCTACTAACNCATTCAAGGCGCAAAGTTCGTAACCAAGTAACTCTTCACCNGAGGTATTTT
CAATGAAGGCACTACCGNTAGATCANCTGAACTGGGACAAAGCCCCGGATGCTGTAAAGCAGAGAGTATGCC
GAGTCNTTCTTTGGCCAACCTTTGTGGACTGTGACGAGTCCAACAGTGACAGTGAAGGAGAGTTAGAGACCCCGc
cTTCTCTGCAGGGAGGTCTCGGCCCCACAACACTCCACAGCAAAACGCTGATCCGGATGTGGATGTACCTCGGT
GGGAAGTATTCTTCAAAAGAAAAGATGAAATCACAGATGAATGTTTGAAAACCTTACCTTCTCCATAGAGACAG
GGGGATCGCAGTCACCAAAGCGTTTCAGTGACTACCAAAGCTGGGCAGTGACTCTGATGGAGAATCCACCCAT
ATCTCTTCCAGAATTCATCTCAGTCAACCCACATAACGGATCAAGGAAGCCAAGGCTGGGACAGCCAGTGTGAT
ACCGTTTTGTATCTTCCCAAGAGAAAAAGTGGTGGGGATAGCACCTCTTTGAACAAGGATACCTACAAACCAAAA
CCCAAAGATAGTATTTCTGCCTCCCAAATAGAACAGAATGCACCTTGTCCACAGGATACTCACTGTGATTTGAAAA
GCGGAGCTGAAGTAAATGGAGTCCCTTGTATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAG
AAAACATCGCTAACCAGCACACAGGCAGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCAACTCCAGAAGCT
GAGCTTCCCAAGCCAGAGCATTACAGTTCTTATATGGAAAGCTGGCAACAGGTGAGAGTATAGTGTGAAAAA
AGAAAATGTTCACTCCAGATATTTAAATAA

➤ Seq int Fwd1 du 25/11

GTGACCNNAGGTTTTATCAAATTCNAGTCGTGAGGAGTGCTTGAGGGGCGTTCTGGAGCTGGTTCGGAGCTG
GATCACGAGGAGTCCGAAGCACGTCGTGTGGCTGAACTGCAAGGCCGCCTACGGCTATGAGTACTTATTCACCA
ACCTGAGTGAGGAGCTGGGAGTCCAGGTTTCATGTGGACAAGCTGGACATGTTTAAAAACATGCCTGATATCCTG
CACCATCTCACAACGGATCGAAACACCCAGATCCACGCCTGCCGCCACCCGAAGGCAGAAGAGTATTTTCAGTG
GAATAAGTTACCCTGTGGCATGGCTTCCAAAATAAACTGTACTCCACACAATCAGCATCAAGCCATCTACCATG
TGGTTTGGAGAGAGGACCAGAAAAACAAACGTGATTGTGAGAACCGGAGAGAGCTCATACAGAGCTTGCTTCT
CTTTCCACTCCTCCTACAGTGAGATTAAAGATTTTTTGTAGCTACATCTGCCAGTGAATGCGTATCCAAATGTCATT
CCGATCGGCCTCACTGTGGATAAGGTCATGGACTTTTTAAAGCCTCTGTGCCGCTCTTCCCAATGTGCTGAACCA
AGTACAAGCCCCCTCGGGAAACTGAAGAGAGCTAGAACAGTTCACCTTGACTCAGAGGAAGATGATGATCTCTTT
GATGACCCTCTACTAACACATTCAAGGCGCAAAGTTCGTAACCAAGTAACTCTTCACCTGAGGTATTTTCAATGA
AGGCACTACCGCTAGATCAGCCTGAACTGGGACAAAGCCCCGGATGCTGTAAAGCAGANAGTATGCCGAGTCCT
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GCNNGNAGGTCTCGGCCCCACNACACTCCACAGCAAAACGCTGATCCGGATGTGGANGTACCNNNGTGGGAA
GTATTCTTCAAAGAAANANGAAATCNCNGATGAATGTTGGAAACTTACCTTCTNCNNNNNNNNNGGGGNTC

GCAGNNNNCNAAGCGTNNNNNGNNNNNNNCNANNCTNGGNANNGNNTCTNATGGANANCCNNCCNTATN
NNNTNC

➤ **Seq int Fwd2 du 25/11**

GCCNCCCGAAGGCAGAAGAGTATTTTCAGTGGAATAAGTTACCCTGTGGCATGGCTTCCAAAATAAACTGTAC
TCCACACAATCAGCATCAAGCCATCTACCATGTGGTTTGGAGAGAGGACCAGAAAAACAAACGTGATTGTGAGA
ACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTCCACTCCTCCTACAGTGAGATTAAAGATTTTTTGAGCTACA
TCTGCCAGTGAATGCGTATCCAAATGTCATTCCGATCGGCCTCACTGTGGATAAGGTCATGGACTTTTTAAAGCC
TCTGTGCCGCTCTCCCAATGTGCTGAACCAAAGTACAAGCCCTCGGGAAACTGAAGAGAGCTAGAACAGTTC
ACCTTGACTCAGAGGAAGATGATGATCTCTTTGATGACCCTCTACTAACACATTCAAGGCGCAAAGTTCGGTACCA
AGTAACTCTTCACCCTGAGGTATTTCAATGAAGGCACTACCGCTAGATCAGCCTGAACTGGGACAAAGCCCCGG
ATGCTGTAAAGCAGAGAGTATGCCGAGTCTTCTTTGGCCAACTTTGTGGACTGTGACGAGTCCAACAGTGACA
GTGAAGGAGAGTTAGAGACCCCGCTTCTCTGCAGGGAGGTCTCGGCCCCACAACACTCCCACAGCAAAACGC
TGATCCGGATGTGGATGTACCTCGGTGGGAAGTATTCTTCAAAGAAAAGATGAAATCACAGATGAATGTTTGGGA
AACTTACCTTCTCCATAGAGACAGGGGGaTCGCACTACCAAAGCGTTTCAGTGACTCACCNAAGCTGGGCA
GTGACTCTGATGGAGAATCCACCCATATCTTCCAGAATTCATCTCANTCAACCCACATAACGGATCAAGGAAG
CCAAGGNTGGGACAGCCAGTGTGATACCGTTTTGTTNTCTTCCCAAGAGAAANNGGTGGGNNNAGCACCTCTT
TGAACAAGGNTACCTACNAACNAAANCCAAGATAGNNNTTCTGCCNNCCAANTNNAANNNNANGCACTTNNN
NNNNGNNTANTCACT

➤ **Seq int Rev1 du 25/11**

CCAGAAAAACNNACGTGANNGNNNNNNNCNNGGAGNGAGCTCATACAGNGCTTGCTTCTCNNNNCNCNTNNNN
NNACANNGAGNNNNNNNGATTTTTNGAGNTNCNTCTNNNCAGTGAANNNGTATNCAAANGTCANTCCGATC
GGCCTCANNGNGGANAAGGTCATGGACTTTTTAAANCNTCTGTGCCGCTCTTCNCAATGTGNTGAANCNNNG
NNCAAGCCCCCTCGGGAAANTGAAGAGAGCTAGAACAGTTACCTTGACTCAGAGGAAGATGATGATNTCTTT
GATGNCCCTCTACTAACACATTCAAGGCGCAAAGTTCCGTACCAAGTAACTCTTACCCTGAGGTATTTTCAAT
GAAGGCNCTACCGNTAGATCAGCCTGAACTGGGACAAAGCCCCGGATGCTGTAAAGCAGAGAGTATNCCGA
GTCCTTNTTTGGCCAACTTTGTGGACTGTGACGAGTCCAACAGTGACAGNGAAGGAGAGTTAGAGACCCNC
CTTCTCTGCAGGGAGGTNTCGGCCCCACAACACTCCCACAGCAAAACGCTGATCCGGATGTGGATGTACCTCG
GTGGGAAGTATTCTTCAAAGAAAAGATGAAATCaCAGATGAANGTTTGGAAAACCTTACCTTCTCCATAGAG
ACAGGGGGATCGCAGTCACCAAAGCGTTTCAGTGACTACCAAAGCTGGGCAAGTACTCTGATGGAGAATCC
ACCCATATCTCTTCCAGAATTCATCTCAGTCAACCCACATAACGGATCAAGGAAGCCAAGGCTGGGACAGCCA
GTGTGATACCGTTTTGTTNTCTTCCCAAGAGAAAAG

➤ **Seq int Rev2 du 25/11**

CAGTAANGNANTNTNTNTNNNNNGNNNNNTTCAGACNGNGAAAGAGNAGTTTCCNGAANGGAGCTTNTGCA
NTNTGGGGCAGAGTAAAAGNCNTCAAAGTGTATTTAGACACCACTTTCTGTGACCCAAGTTTTATCAAA
TTCCAAGTCGTGAGGAGTGCTTGAGGGCGTTCNNGGAGCTGGTTNNGGAGCTGGATCACGAGGAGTCCGAAG
CACGTCGTGTGGCTGAACTGCAAGGCCGCNTACGGCTATGAGTACTTATTCACCAACtTGAGTGAGGAGCTGG
GAGTCCAGGTTTCATGTGGACAAGCTGGACATGTTTAAAAACATGCCTGATATCCTGCACCATCTCACAACGGAT
CGAAACACCCAGATCCACGCCTGCCGCCACCCGAAGGCAGAAGAGTATTTTCAGTGGAATAAGTTACCCTGTG
GCATGGCTTCCAAAATAAACTGTACTCCACACAATCAGCATCAAGCCATCTACCATGTGGTTTGGAGAGAG
GACCAGAAAAACAAACGTGATTGTGAGAACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTCCACTCCTCCT
ACAGTGAGATTAAAGATTTTTTGAGCTACATCTGCCAGTGAATGCGTATCCAAATGTCATTCCGATCGGCCTC
ACTGTGGATAAGGTCATGGACTTTTTAAAGCCTCTGTGCCGCTCTTCCCAATGTGCTGAACCAAAGTACAAGCC
CCTCGGGAAACTGAAGAGAGCTAGAACAGTTCACCTTGACTCAGAGGAAGATGATGATCTCTTTGATGACCCT
CTACTAACACATTCAAGGCGCAAAGTTCGGTACCAAGTAACTCTTACCCTGAGGTATTTTCAATGAAGGCACT

ACCGCTAGATCAGCCTGAACTGGGACAAAGCCCCGGATGCTGTAAAGCAGAGAGTATGCCGAGTCCTTCTTTG
 GCCAACTTTGTGGACTGTGACGAGTCCAACAGTGACAGTGAAGGAGAGTTAGAGACCCCGCCTTCTCTGCAGG
 GAGGTCTCGgCCCCNCAACACTCCCACA

➤ Synthèse séquençage

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGAC 60
 AGAGAGAACCTGAAAGCCCGTGCCTACTTCTTTTCGCACTGCCACAAGGATCACATGAAA 120
 GGATTAAGGGCTCCTTCCATGAAAAGAAGGCTGGAATGCAGTTTGAAGGTCTTCTGTAC 180
 TGTCTCCAGTCACTAAGGAGCTGCTCTTAACCAAGCCAAAGTACAAGTCTTGGGAAAAAC 240
 CGAATTATAGCAATTGAAATTGAAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCG 300
 GGTGAGAAGGAAGAAGTTGTTGTGACTCTCTTACCAGCTGGTCACTGCCCAGGTTTCAGTT 360
 ATGTTTCTATTTTCAGGGCAGTAATGGAAGTGTCTTATACACAGGAGACTTCAGACTGGCG 420
 AAAGGAGAAGTTTCCAGAATGGAGCTTCTGCACTCTGGGGGCAGAGTAAAAGACATCCAA 480
 AGTGATATATTTAGACACCACTTTCTGTGACCCAAGGTTTTATCAAATTCCAAGTCGTGAG 540
 GAGTGCTTGAGGGGCGTTCTGGAGCTGGTTCGGAGCTGGATCACGAGGAGTCCGAAGCAC 600
 GTCGTGTGGCTGAACCTGCAAGGCCGCTACGGCTATGAGTACTTATTCACCAACCTGAGT 660
 GAGGAGCTGGGAGTCCAGGTTTCATGTGGACAAGCTGGACATGTTTAAAAACATGCCTGAT 720
 ATCCTGCACCATCTCACAACGGATCGAAACACCCAGATCCACGCCTGCCGCCACCCGAAG 780
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 GTACTCCACACAATCAGCATCAAGCCATCTACCATGTGGTTTGGAGAGAGGACCAGAAAA 900
 ACAACCGTGATTGTGAGAACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTTCCACTCC 960
 TCCTACAGTGAGATTAAAGATTTTTTGTGCTACATCTGCCAGTGAATGCGTATCCAAAT 1020
 GTCATTCGGCTGCGCCTCACTGTGGATAAGGTCATGGACTTTTTAAAGCCTCTGTGCCGC 1080
 TCTTCCCAATGTGCTGAACCAAGTACAAGCCCCCTCGGGAAGTGAAGAGAGCTAGAACA 1140
 GTTCACCTTGACTCAGAGGAAGATGATGATCTCTTTGATGACCCTCTACTAACACATTCA 1200
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 AGTCCTTCTTTGGCCAACCTTTGTGGACTGTGACGAGTCCAACAGTGACAGTGAAGGAGAG 1380
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 ACAGATGAATGTTTGGAAAACCTTACCTTCCATAGAGACAGGGGGATCGCAGTCACCA 1560
 AAGCGTTTCAGTGACTACCAAAGCTGGGCAGTGACTCTGATGGAGAATCCACCCATATC 1620
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 AGCCAGTGTGATACCGTTTGTATCTTCCCAAGAGAAAAGTGGTGGGGATAGCACCTCT 1740
 TTGAACAAGGATACCTACAAACCAAAACCCAAAGATAGTATTTCTGCCTCCCAAATAGAA 1800
 CAGAATGCACTTTGTCCACAGGATACTCACTGTGATTGAAAAGCGGAGCTGAAGTAAAT 1860
 GGAGTCCCTTGTATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAGAAA 1920
 ACATCGCTAACCAGCACACAGGCAGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCA 1980
 ACTCCAGAAGCTGAGCTTCCAAGCCAGAGCATTTACAGTTCTTATATGGAAGCTGGCA 2040
 ACAGGTGAGAGTATAGTGTGAAAAAAGAAAATGTTCACTCCAGATATTTAAATAA 2097

MSSFQGGQMEETYPTISIDRFDRENLKARAYFLSHCHKDHMKGLRAPSMKRRLECSLKVFLYCSPVTKELLTSPKYKF
 WENRIIAIEIETPTQVSLVDEASGEKEEVVVTLLPAGHCPGSVMFLFQGSNGTVLYTGDFRLAKGEVSRMELLHSGG
 RVKDIQSVYLDTTFCDFRPFYQIPSRREECLRGVLELVRSWITRSPKHVVWLNCKAAYGYEYLFNLSEELGVQVHVHDKL
 DMFKNMPDILHLLTDRNTQIHACRHPKAEFYQWNKLPCGMASKTKTVLHTISIKPSTMWFGERTRKTNVIVRT
 GESSYRACFSFHSSYSEIKDFLSYICPVNAYPNVPIGLTVDKVMDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEE
 DDDLFDPLLTHSRKVPYQVTLHPEVFSMKALPLDQPELGQSPGCCAESMPSPSLANFVDCDESNSDSEGELET
 PPSLQGGGLPTTLPPQNADPDVDVPRWEVFFKRKDEITDECLNLPSIETGGSQSPKRFSDSPKLGSDSDGESTHIS
 SQNSSQSTHITDQGSQGWDSQCDTVLLSSQEKSGGDSTSLNKDITYKPKPKDSISASQIEQNALCPQDTHCDLKSQA
 EVNGVPCIEEPDVTSGRKSSPEKTSLTSTQADSQSSDFEIPSTPEALPKPEHLQFLYGKLATGESIVLKKENVHSQIFK
 -

➤ Blast contre banque rat :

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Rattus norvegicus DNA cross-link repair 1C (Dclre1c). mRNA	Norway rat	3873	3873	100%	0.0	100.00%	2162	NM_147145.2
✓	Rattus norvegicus SNM1-like protein mRNA, complete cds	Norway rat	3845	3845	100%	0.0	99.76%	2182	AF395746.1
✓	PREDICTED: Rattus norvegicus DNA cross-link repair 1C (Dclre1c). transcript variant X1. mRNA	Norway rat	3419	3874	100%	0.0	100.00%	4442	XM_017600460.1
✓	PREDICTED: Rattus norvegicus translation initiation factor IF-2-like (LOC108353135). mRNA	Norway rat	135	135	3%	1e-29	100.00%	1222	XM_017600743.1

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

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGAGTCTCTTTCCAGGGACAGATGGAGGAATATCCACCATTCTCCATTGACCCTTCGACAGAGAGAACCTGAAGGCCGCTGCCCTACTTCTCTTCGCACTGCCACAGGATCACATGAAGGATTAAAGG													
cds	ATGAGTCTCTTTCCAGGGACAGATGGAGGAATATCCACCATTCTCCATTGACCCTTCGACAGAGAGAACCTGAAGGCCGCTGCCCTACTTCTCTTCGCACTGCCACAGGATCACATGAAGGATTAAAGG													
Consensus	ATGAGTCTCTTTCCAGGGACAGATGGAGGAATATCCACCATTCTCCATTGACCCTTCGACAGAGAGAACCTGAAGGCCGCTGCCCTACTTCTCTTCGCACTGCCACAGGATCACATGAAGGATTAAAGG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	CTCCTTCATGAAGAAGAGGCTGGAGTGCAGTTTGAAGGCTTCTGTACTGTCTCCAGTCACTAAGGAGCTGCTCTTACCAGGCCAAGATACAGTTCCTGGAAACCGCAATTATAGCAATTGAAT													
cds	CTCCTTCATGAAGAAGAGGCTGGAGTGCAGTTTGAAGGCTTCTGTACTGTCTCCAGTCACTAAGGAGCTGCTCTTACCAGGCCAAGATACAGTTCCTGGAAACCGCAATTATAGCAATTGAAT													
Consensus	CTCCTTCATGAAGAAGAGGCTGGAGTGCAGTTTGAAGGCTTCTGTACTGTCTCCAGTCACTAAGGAGCTGCTCTTACCAGGCCAAGATACAGTTCCTGGAAACCGCAATTATAGCAATTGAAT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	TGAARCTCTACCAGGTATCTTTAGTGTGATGAGGCATCGGGTGAGAGGAGAGAGTTGTGTGACTCTCTTACCAGCTGGTCACTGCCAGGTTCAAGTTATGTGTTCTATTTCAGGGCAGTATGGAACT													
cds	TGAARCTCTACCAGGTATCTTTAGTGTGATGAGGCATCGGGTGAGAGGAGAGAGTTGTGTGACTCTCTTACCAGCTGGTCACTGCCAGGTTCAAGTTATGTGTTCTATTTCAGGGCAGTATGGAACT													
Consensus	TGAARCTCTACCAGGTATCTTTAGTGTGATGAGGCATCGGGTGAGAGGAGAGAGTTGTGTGACTCTCTTACCAGCTGGTCACTGCCAGGTTCAAGTTATGTGTTCTATTTCAGGGCAGTATGGAACT													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	GTCTTATACACAGGAGACTTCAGACTGGCGAAGGAGAGATTTCCAGATGGAGCTTCTGCACTCTGGGGGCAGAGTAAAGACATCCAAAGTGATATTTAGACACCACCTTTCTGTACCCAGGTTTT													
cds	GTCTTATACACAGGAGACTTCAGACTGGCGAAGGAGAGATTTCCAGATGGAGCTTCTGCACTCTGGGGGCAGAGTAAAGACATCCAAAGTGATATTTAGACACCACCTTTCTGTACCCAGGTTTT													
Consensus	GTCTTATACACAGGAGACTTCAGACTGGCGAAGGAGAGATTTCCAGATGGAGCTTCTGCACTCTGGGGGCAGAGTAAAGACATCCAAAGTGATATTTAGACACCACCTTTCTGTACCCAGGTTTT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	ATCAAAATCCAAAGTCGTAGGAGTGCTTGAAGGGCGCTTCTGGAGCTGGTTCGGAGCTGGATCAGAGGAGTCCGAGACACGTCGTGTGGCTGAATCGAAGGCCGCTACGGCTATGAGTACTTATTCAC													
cds	ATCAAAATCCAAAGTCGTAGGAGTGCTTGAAGGGCGCTTCTGGAGCTGGTTCGGAGCTGGATCAGAGGAGTCCGAGACACGTCGTGTGGCTGAATCGAAGGCCGCTACGGCTATGAGTACTTATTCAC													
Consensus	ATCAAAATCCAAAGTCGTAGGAGTGCTTGAAGGGCGCTTCTGGAGCTGGTTCGGAGCTGGATCAGAGGAGTCCGAGACACGTCGTGTGGCTGAATCGAAGGCCGCTACGGCTATGAGTACTTATTCAC													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	CAACCTGAGTGAGGAGCTGGGAGTCCAGGTTTCTGTGGACAGCTGGACATGTTTAAARACATGCTGTATCTCTGACCATTCTCAGACGGATCGAARACCCAGATCCAGGCTGCCGCCACCCGAG													
cds	CAACCTGAGTGAGGAGCTGGGAGTCCAGGTTTCTGTGGACAGCTGGACATGTTTAAARACATGCTGTATCTCTGACCATTCTCAGACGGATCGAARACCCAGATCCAGGCTGCCGCCACCCGAG													
Consensus	CAACCTGAGTGAGGAGCTGGGAGTCCAGGTTTCTGTGGACAGCTGGACATGTTTAAARACATGCTGTATCTCTGACCATTCTCAGACGGATCGAARACCCAGATCCAGGCTGCCGCCACCCGAG													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	GCAGAGAGTATTTTCAGTGGATAGTTACCTGTGGCTGGCTTCCAAACTAARACTGTACTCCACACATCAGATCAGGCATCTCCATGTGGTTTGGAGAGGAGACCGAARACAAACGTGA													
cds	GCAGAGAGTATTTTCAGTGGATAGTTACCTGTGGCTGGCTTCCAAACTAARACTGTACTCCACACATCAGATCAGGCATCTCCATGTGGTTTGGAGAGGAGACCGAARACAAACGTGA													
Consensus	GCAGAGAGTATTTTCAGTGGATAGTTACCTGTGGCTGGCTTCCAAACTAARACTGTACTCCACACATCAGATCAGGCATCTCCATGTGGTTTGGAGAGGAGACCGAARACAAACGTGA													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	TTGTGAGACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTCCACTCTCTCAGCTGAGATTAAAGATTTTTAGCTACATCTGCCAGTGAATGCGTATCCAAATGTCAATTCGGATCGGCTCAC													
cds	TTGTGAGACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTCCACTCTCTCAGCTGAGATTAAAGATTTTTAGCTACATCTGCCAGTGAATGCGTATCCAAATGTCAATTCGGATCGGCTCAC													
Consensus	TTGTGAGACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTCCACTCTCTCAGCTGAGATTAAAGATTTTTAGCTACATCTGCCAGTGAATGCGTATCCAAATGTCAATTCGGATCGGCTCAC													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	TGTGGATAGGTGATGGACTTTTAAAGCCTCTGTGGCGCTCTCCCAATGTGCTGACACAAAGTACAGCCCCCTCGGAARCTGAAGAGAGCTAGACAGTTCACTTGACTCAGAGAGAGATGATGAT													
cds	TGTGGATAGGTGATGGACTTTTAAAGCCTCTGTGGCGCTCTCCCAATGTGCTGACACAAAGTACAGCCCCCTCGGAARCTGAAGAGAGCTAGACAGTTCACTTGACTCAGAGAGAGATGATGAT													
Consensus	TGTGGATAGGTGATGGACTTTTAAAGCCTCTGTGGCGCTCTCCCAATGTGCTGACACAAAGTACAGCCCCCTCGGAARCTGAAGAGAGCTAGACAGTTCACTTGACTCAGAGAGAGATGATGAT													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	CTCTTTGATGACCTCTACTAACACATTCAAGGCGCAAGTTCGGTACCAGTAACTCTTCACTCGAGGATTTTCATGAGGGACATACCCTAGATCAGCTGAACTGGGACAAAGCCCGATGTCT													
cds	CTCTTTGATGACCTCTACTAACACATTCAAGGCGCAAGTTCGGTACCAGTAACTCTTCACTCGAGGATTTTCATGAGGGACATACCCTAGATCAGCTGAACTGGGACAAAGCCCGATGTCT													
Consensus	CTCTTTGATGACCTCTACTAACACATTCAAGGCGCAAGTTCGGTACCAGTAACTCTTCACTCGAGGATTTTCATGAGGGACATACCCTAGATCAGCTGAACTGGGACAAAGCCCGATGTCT													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	GTAAAGCAGAGAGTATGCCAGTCTCTCTTTGGCCAACTTTGTGGACTGTGACAGTCCAAAGTGACAGTGAGAGTGAGGAGAGTTAGAGACCCCGCTTCTCTGCGGGAGGTTCTCGGCCCHACAACTCCC													
cds	GTAAAG													

➤ Différence Séquençage/CDS au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	HSSFQGMEEYPTTISIDRFQRENLKARAYFLSHCHKDHMKGLRAPSHKRRLECSLKYFLYCSPTVKELLTSPKYKFENRIATIEIETPTQVSLVDEASGEKEEVYVTLTPAGHCPGSMVFLFQGSNGT													
ref	HSSFQGMEEYPTTISIDRFQRENLKARAYFLSHCHKDHMKGLRAPSHKRRLECSLKYFLYCSPTVKELLTSPKYKFENRIATIEIETPTQVSLVDEASGEKEEVYVTLTPAGHCPGSMVFLFQGSNGT													
Consensus	HSSFQGMEEYPTTISIDRFQRENLKARAYFLSHCHKDHMKGLRAPSHKRRLECSLKYFLYCSPTVKELLTSPKYKFENRIATIEIETPTQVSLVDEASGEKEEVYVTLTPAGHCPGSMVFLFQGSNGT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	VLYTGDFRLAKGEVSRMELLHSGGGRYKDIQSYYLDTTFCDPRFYQIPSRREELRGVLELVRSWITRSPKHVVLNCKARAYGYEYFTNLSEELGVQVHVVDKLDHFKNMPDILHHLTTDRNTQIHACRHPK													
ref	VLYTGDFRLAKGEVSRMELLHSGGGRYKDIQSYYLDTTFCDPRFYQIPSRREELRGVLELVRSWITRSPKHVVLNCKARAYGYEYFTNLSEELGVQVHVVDKLDHFKNMPDILHHLTTDRNTQIHACRHPK													
Consensus	VLYTGDFRLAKGEVSRMELLHSGGGRYKDIQSYYLDTTFCDPRFYQIPSRREELRGVLELVRSWITRSPKHVVLNCKARAYGYEYFTNLSEELGVQVHVVDKLDHFKNMPDILHHLTTDRNTQIHACRHPK													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	REEYFQMKLPCGHASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSFHSSYSEIKDFLSYICPNAYPNVPIGLTVDKYHDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEEDDD													
ref	REEYFQMKLPCGHASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSFHSSYSEIKDFLSYICPNAYPNVPIGLTVDKYHDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEEDDD													
Consensus	REEYFQMKLPCGHASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSFHSSYSEIKDFLSYICPNAYPNVPIGLTVDKYHDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEEDDD													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	LFDDPLLTHSRKVPYQVTLHPEVFSHKALPLDQPELGQSPGCKCAESHPSPSLANFYDCDESNSDSEGELETTPPSLQGGGLGPTTLQQNADPDVDPVPRNEVFFKRKDEITDECLENLPSSETGGSQSP													
ref	LFDDPLLTHSRKVPYQVTLHPEVFSHKALPLDQPELGQSPGCKCAESHPSPSLANFYDCDESNSDSEGELETTPPSLQGGGLGPTTLQQNADPDVDPVPRNEVFFKRKDEITDECLENLPSSETGGSQSP													
Consensus	LFDDPLLTHSRKVPYQVTLHPEVFSHKALPLDQPELGQSPGCKCAESHPSPSLANFYDCDESNSDSEGELETTPPSLQGGGLGPTTLQQNADPDVDPVPRNEVFFKRKDEITDECLENLPSSETGGSQSP													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	KRFSDSPKLGSDSGESTHISQSSQSTHITDQGSQGHDSQCDTVLLSSQEKSGGDSLSLNKDTYKPKPKDSSASQIEQNALCPQDTHCDLKSQAEVNGVPCIEEPDVTYSGRKSSEPKTSLTSTQADS													
ref	KRFSDSPKLGSDSGESTHISQSSQSTHITDQGSQGHDSQCDTVLLSSQEKSGGDSLSLNKDTYKPKPKDSSASQIEQNALCPQDTHCDLKSQAEVNGVPCIEEPDVTYSGRKSSEPKTSLTSTQADS													
Consensus	KRFSDSPKLGSDSGESTHISQSSQSTHITDQGSQGHDSQCDTVLLSSQEKSGGDSLSLNKDTYKPKPKDSSASQIEQNALCPQDTHCDLKSQAEVNGVPCIEEPDVTYSGRKSSEPKTSLTSTQADS													
	651	660	670	680	690	698								
seq	QSSSDFEIPSTPEALPKPEHLQFLYGKLATGESIVLKKENVHQSQIFK													
ref	QSSSDFEIPSTPEALPKPEHLQFLYGKLATGESIVLKKENVHQSQIFK													
Consensus	QSSSDFEIPSTPEALPKPEHLQFLYGKLATGESIVLKKENVHQSQIFK													

Flag BirA Dclre1c DiT24hLPS (cloneA) parfait

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	protein artemis [Rattus norvegicus]	Norway rat	1449	1449	100%	0.0	100.00%	698	NP_671486.2
✓	SNM1-like protein [Rattus norvegicus]	Norway rat	1421	1421	98%	0.0	99.42%	697	AAM89124.1
✓	PREDICTED: protein artemis isoform X1 [Rattus norvegicus]	Norway rat	1275	1275	88%	0.0	100.00%	629	XP_017455949.1
✓	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae), isoform CRA_b [Rattus norvegicus]	Norway rat	1145	1145	79%	0.0	100.00%	552	EDL78693.1
✓	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae), isoform CRA_a [Rattus norvegicus]	Norway rat	510	510	34%	1e-178	100.00%	257	EDL78692.1

- **FlagBirA Dclre1c 48h clone A NOUVEAU CLONE**

➤ B3Fwd 956NT

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGACA
GAGAGAACCTGAAAGCCCGTGCCTACTTCCTTTTCGCACTGCCACAAGGATCACATGAAAG
GATTAAGGGCTCCTTCCATGAAAAGAAGGCTGGAATGCAGTTGAAGGTCTTCCTGTACTG
TTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCCCAAAGTACAAGTTCTGGGAAAACCG
AATTATAGCAATTGAAATTGAAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCGGGTG
AGAAGGAAGAAGTTGTTGTGACTCTCTTACCAGCTGGTCACTGCCCAGGTTCAGTTATGAG
ACTTCAGACTGGCGAAAGGAGAAGTTTCCAGAATGGAGCTTCTGCACTCTGGGGGCAGAG
TAAAAGACATCCAAAGTGTATATTTAGACACCACTTTCTGTGACCCAAGGTTTTATCAAATT
CCAAGTCGTGAGGAGTGCTTGAGGGGCGTTCTGGAGCTGGTTCGGAGCTGGATCACGAGG
AGTCCGAAGCACGTCGTGTGGCTGAACTGCAAGGCCGCCTACGGCTATGAGTACTTATTCA
CCAACCTGAGTGAGGAGCTGGGAGTCCAGGTTTCATGTGGACAAGCTGGACATGTTTAAAA
ACATGCCTGATATCCTGCACCATCTCACAACGGATCGAAACACCCAGATCCACGCCTGCCG
CCACCCGAAGGCAGAAGAGTATTTTCAGTGGAATAAGTTACCCTGTGGCATGGCTTCCAAA
ACTAAAACTGtACTCCACACAATCAGCATCAAGCCATCTACCATGTGGNTTGGANANANGA
NCNGAAAACAAACGTGATTGNGANANCNNNNANNGCTCNNNCNNNNNTNNTNTCNTTCN
NNNCCNNCNACNNNNNANNTTAANATTTTNNAGCNCNNCTGCCCA

 BGHRev

CAGNGNNNNNNNNNANNTNNNNNGNNNNNNNNNANNNAGNNtcACCCATATCTCTTCCCA
GAATTCATCTCAGTCAACCCACATAACGGATCAAGGAAGCCAAGGCTGGGACAGCCAGTG
TGATACCGTTTTGTTATCTTCCCAAGAGAAAAGTGGTGGGGATAGCACCTCTTTGAACAAG
GATACCTACAAACCAAAACCCAAAGATAGTATTTCTGCCTCCCAAATAGAACAGAATGCAC
TTTGTCCACAGGATACTCACTGTGATTTGAAAAGCGGAGCTGAAGTAAATGGAGTCCCTTG
TATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAGAAAACATCGCTAAC
CAGCACACAGGCAGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCAACTCCAGAAGC
TGAGCTTCCCAAGCCAGAGCATTTACAGTTCTTATATGGAAAGCTGGCAACAGGTGAGAGT
ATAGTGTtGNAAAAAGAAAATGTTCACTCCCAGATATTTAAATAA

➤ Synthèse séquençage

[illegible]

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-----tcCACCCTATC 12
TCTTCCCAGAATTCATCTCAGTCAACCCACATAACGGATCAAGGAAGCCAAGGCTGGGAC 72
AGCCAGTGTGATACCGTTTGTATCTTCCAAGAGAAAAGTGGTGGGGATAGCACCTCT 132
TTGAACAAGGATACCTACAAACCAAAACCAAGATAGTATTTCTGCCTCCCAATAGAA 192
CAGAATGCACTTTGTCCACAGGATACTCACTGTGATTTGAAAAGCGGAGCTGAAGTAAAT 252
GGAGTCCCTTGTATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAGAAA 312
ACATCGCTAACCAGCACACAGGCAGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCA 372
ACTCCAGAAGCTGAGCTTCCAAGCCAGAGCATTACAGTTCTTATATGGAAAGCTGGCA 432
ACAGGTGAGAGTATAGTGTtGNAAAAAGAAAATGTTCACTCCCAGATATTTAAATAA 489
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Délétion en début de séquence

o **FlagBirA Dclre1c SP clone B NOUVEAU CLONE**

➤ **B3Fwd 917NT**

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGACAGAGAGAACCTGAAA
GCCCCGTGCCTACTTCCTTTTCGCACTGCCACAAGGATCACATGAAAGGATTAAGGGCTCCTTCCATGAAAAGAAGG
CTGGAATGCAGTTTGAAGGTCTTCTGTACTGTTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCCCAAAGTAC
AAGTTCTGGGAAAACCGAATTATAGCAATTGAAATTGAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCGG
GTGAGAAGGAAGAAGTTGTTGTGACTCTGATGGAGAATCCACCCATATCTTCTCCAGAATTCATCTCAGTCAAC
CCACATAACGGATCAAGGAAGCCAAGGCTGGGACAGCCAGTGTGATACCGTTTTGTTATCTTCCCAAGAGAAAA
GTGGTGGGGATAGCACCTCTTTGAACAAGGATACCTACAAACCAAACCCAAAGATAGTATTCTGCCTCCCAAA
TAGAACAGAATGCACTTTGTCCACAGGATACTCACTGTGATTTGAAAAGCGGAgCTGAAGTAAATGGAGTCCCTT
GTATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAGAAAACATCGCTNACCAGCACACAGGC
AGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCACTCCAGAAGCTGAGCTTCCCaAGCCAGAgCATTTACN
GTTCTTATATGGAAAGCTGGCAACAGGTGANAGTATAGTGTGAAAAANAAAATGTTCACTCCCANATATTTAAAT
AATGCNGCCGCTAACTCNAAGTCTANAGGGCCCGTTTAANNCCNCTGATCANCNTCNACTGTGCNTNCTANTTN
CNNNNNTCTNNNNNTNGCCC

➤ **BGHRev 1096NT**

ATGNTGANNNGNAGNTGNNGNNNNCCCNGAGCTGTTNGANCAGNNNGNNNNNNCCCCNACNGANNNGN
NNGNNNNNAGNNGGACNANTTCATCAACCGGCCCGNGAAGNTGATCNTNGGCGACAAGGAGNTNTTNGGCA
TCAGCCGGGGCATNGNCAAGCANGGCGCCCTGCTGCTGGAGCAGGACGGCNTCATCAAGCCCTGGATGGGC
GGCGAGATCAGCNTGCGGAGCGCCGAGAAGGGGGGATCTGGCCCCGGCGGCGGCGCGCCAATGAGTTCTTT
cCAGGGACAGATGGAGGAATATCCAACCcTCTCCATTGACCGCTTCGACAGAGAGAACcTGAAAGCCCCGTGCC
TACTTCCTTTTCGCACTGCCACAAGGATCACATGAAAGGATTAAGGGCTCCTTCCATGAAAAGAAGGCTGGAAT
GCAGTTTGAAGGTCTTCTGTACTGTTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCCCAAAGTACAAGTTC
TGGGAAAACCGAATTATAGCAATTGAAATTGAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCGGGTG
AGAAGGAAGAAGTTGTTGTGACTCTGATGGAGAATCCACCCATATCTTCTCCAGAATTCATCTCAGTCAACCC
ACATAACGGATCAAGGAAGCCAAGGCTGGGACAGCCAGTGTGATACCGTTTTGTTATCTTCCCAAGAGAAAAAG
TGGTGGGGATAGCACCTCTTTGAACAAGGATACCTACAAACCAAACCCAAAGATAGTATTTCTGCCTCCCAAA
TAGAACAGAATGCACTTTGTCCACAGGATACTCACTGTGATTTGAAAAGCGGAGCTGAAGTAAATGGAGTCCC
TTGTATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAGAAAACATCGCTAACCAGCACACAG
GCAGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCACTCCAGAAGCTGAGCTTCCCAAGCCAGAGCATTT
ACAGTTCTTATATGGAAAGCTGGCAACAGGTGAGAGTATAGTGTGAAAAAGAAAATGTTCACTCCCAGATA
TTTAAATAA

➤ **Synthèse séquençage**

Mauvais

o **FlagBirA Dclre1c CTX clone A NOUVEAU CLONE**

➤ **B3Fwd 868NT**

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGACA
GAGAGAACCTGAAAGCCCGTGCCTACTTCCTTTTCGCACTGCCACAAGGATCACATGAAAG
GATTAAGGGCTCCTTCCATGAAAAGAAGGCTGGAATGCAGTTTGAAGGTCTTCCTGTACTG
TTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCCAAAGTACAAGTTCTGGGAAAACCG
AATTATAGCAATTGAAATTGAAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCGGGTG
AGAAGGAAGAAGTTGTTGTGACTCTCTTACCAGCTGGTCACTGCCCAGGTTTCAGTTATGAG
ACTTCAGACTGGCGAAAGGAGAAGTTTCCAGAATGGAGCTTCTGCACTCTGGGGGCAGAG
TAAAAGACATCCAAAGTGTATATTTAGACACCACTTTCTGTGACCCAAGGTTTTATCAAATT
CCAAGTCGTGAGGAGTGCTTGAGGGGCGTTCTGGAGCTGGTTTCGGAGCTGGATCACGAGG
AGTCCGAAGCACGTCGTGTGGCTGAACTGCAAGGCCGCCTACGGCTATGAGTACTTATTCA
CCAACCTGAGTGAGGAGCTGGGAGTCCAGGTTTCATGTGGACAAGCTGGACATGTTTAAAA
ACATGCCTGATATCCTGCACCATCTCACAACGGATCGAAACACCCAGATCCACGCCTGCCG
CCACCCGAAGGcAGAAGAGTATTTTCAGTGGAATAAGTTACCCTGTGGCATGGCTTCCAAA
ACTAAaCTGTACTCCACACAATCAGCATCAAGCCATCTACCATGTGGTTTGGNNAGAGGAN
CAGAAAACNANNGTGAT

➤ **BGHRv 674NT**

GNCCCNANNNNNNNCCNNAGNNNNNCNNNGATNCNNANNNNNNNNGTANNNNGNTNNNN
AGTATTCTTCNNNGNAAANANNANANCNCAGNTNAATNNTTNNNAANCTTNCCNNCNCN
NCATANANNNCNNNNACACCAAAGNGNNNCNGNNNCTCACCAAANNTGGGCAGTGACTNN
GATGGAGAATCCACCCATATCTCTTCCAGAATTCATCTCAGTCAACCCACATAACGGATCA
AGGAAGCCAAGGCTGGGACAGCCAGTGTGATACCGTTTTGTTATCTTCCCAAGAGAAAAG
TGGTGGGGATAGCACCTCTTTGAACAAGGATACCTACAAACCAAACCCAAAGATAGTATT
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GCGGAGCTGAAGTAAATGGAGTCCCTTGTATTGAAGAACCAGACACTGTGAGTGGCAGGA
AATCTTCACCTGAGAAAACATCGCTAACCAGCACACAGGCAGACTCACAGAGCTCCTCTG
ACTTTGAAATCCCCTCAACTCCAGAAGCTGAGCTTCCCAAGCCAGAGCATTACAGTTCTT
ATATGGAAAGCTGGCAACAGGTGAGAGTATAGTGTGAAAAAAGAAAATGTTCACTCCCA
GATATTTAAATAA

➤ **Synthèse séquençage**

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGAC	60
AGAGAGAACCTGAAAGCCCGTGCCTACTTCCTTTTCGCACTGCCACAAGGATCACATGAAA	120
GGATTAAGGGCTCCTTCCATGAAAAGAAGGCTGGAATGCAGTTTGAAGGTCTTCCTGTAC	180
TGTTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCCAAAGTACAAGTTCTGGGAAAAC	240
CGAATTATAGCAATTGAAATTGAAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCG	300
GGTGAGAAGGAAGAAGTTGTTGTGACTCTCTTACCAGCTGGTCACTGCCAGGTTTCAGTT	360
ATG-----AGACTTCAGACTGGCG	379
AAAGGAGAAGTTTCCAGAATGGAGCTTCTGCACTCTGGGGGCAGAGTAAAAGACATCCAA	439
AGTGATATATTTAGACACCACTTTCTGTGACCCAAGGTTTATCAAATCCAAGTCGTGAG	499

Délétion en début de séquence

o **FlagBirA Dclre1c CTX clone B NOUVEAU CLONE**

➤ **B3Fwd 858NT**

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGACAGAGAGAACCTGA
AAGCCCGTGCCTACTTCTTTTGCAGTGCACAAAGGATCACATGAAAGGATTAAGGGCTCCTTCCATGAAAAGA
AGGCTGGAATGCAGTTTGAAGGTCTTCTGTACTGTTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCCGAA
GTACAAGTTCTGGGAAAACCGAATTATAGCAATTGAAATTGAAACTCCTACCCAGGTATCTTTAGTTGATGAGG
CATCGGGTGAGAAGGAAGAAGTTGTTGTGACTCTTACCAGCTGGTCACTGCCAGGTTCAATTATGTTTCTA
TTTCAGGGCAGTAATGGAAGTGTCTTATACACAGGAGACTTCAGACTGGCGAAAGGAGAAAGTTTCCAGAATG
GAGCTTCTGCACTCTGGGGGCAGAGTAAAAGACATCCAAAGTGTATATTTAGACACCACTTTCTGTGACCCAA
GGTTTTATCAAATTCGAAGTCGTGAGGAGTGCTTGAGGGGCGTTCTGGAGCTGGTTCGGAGCTGGATCACGA
GGAGTCCGAAGCACGTCGTGTGGCTGAACTGCAAGGCCGCCTACGGCTATGAGTACTTATTCACCAACCTGAG
TGAGGAGCTGGGAGTCCagGTTTCATGTGGACAAGCTGGACATGTTTAAAAACATGCCTGATATCCTGCACCAT
CTCACAACGGATCGAAACACCCAGATCCACGCCTGCCGCCACCCGAAGGcANAANAGTATTTTCAGTGGAATN
ANTTACCCTGTGGCATGGCTTCCAAACTAACTGTACTCNCACATCNGCATCA

➤ **BGHRRev 668NT**

CACANCANNANNCTGATCNGNANNNNNNNNNNCCNNNNNNNGNNAGNATTNTTCANNNNNANANNNNNN
NANCNCAGATNAANNNNNNNNNNAACTTACCTTCTCCATAGAGNCAGGGGGATNNCNGTNNNNAAAGCGT
NNCAGTGANTCACNAAAGCTGGGCAGTGACNNNGATGGAGAATCCACCCATATCTTCCCAGAATTCATCTC
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AGAAAAAAGTGGTGGGGATAGCACCTCTTTGAACAAGGATACCTACAAACCAAAACCCAAAGATAGTATTTCT
GCCTCCCAATAGAACAGAATGCACTTTGTCCACAGGATACTCACTGTGATTTGAAAAGCGGAGCTGAAGTAA
ATGGAGTCTCTTGTATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAGAAAACATCGCTAAC
CAGCACACAGGCAGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCAACTCCAGAAGCTGAGCTTCCCAAGC
CAGAGCATTTACAGTTCTTATATGGAAAGCTGGCAACAGGTGAGAGTATAGTGTTGAAAAAGAAAATGTTCA
CTCCAGATATTTAAATAA

➤ **Int Fwd1 21/12**

TNCTGTGACCCNAGGTTTTATCNAATTCCAAGTCGTGAGGAGTGCTTGAGGGGCGTTCTGGAGCTGGTTCGGA
GCTGGATCACGAGGAGTCCGAAGCACGTCGTGTGGCTGAACTGCAAGGCCGCCTACGGCTATGAGTACTTATT
CACCACCTGAGTGAGGAGCTGGGAGTCCAGGTTTCATGTGGACAAGCTGGACATGTTTAAAAACATGCCTGAT
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TTCAGTGGAATAAGTTACCCTGTGGCATGGCTTCCAAACTAAACTGTACTCCACACAATCAGCATCAAGCCA
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GCTTGCTTCTCTTCCACTCCTACAGTGAGATTAAAGATTTTTTGAGCTACATCTGCCAGTGAATGCGTAT
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GAGGTATTTTCAATGAAGGCACTACCGCTAGATCAGCCTGAACTGGGACAAAGCCCCGGATGCTGTAAAGCA
GAGAGTATGCCGAGTCTTCTTNGGCCAACTTTGTGGACTGTGACGAGTCCNACAGTGACAGTGAANGANAG
TTAGAGACCCCGCCTTCTCTGCNGGAGGTCTTGGCCCCACNACACTCCCACAGCAAAACGCTGATCCGGANGT
GGANGTACCTCGGTGGGAAGTATTCTTCAAAGAAAAGANGAAATCNCAGATGAATGTTTGGAACTTACCTTC
CTCNTANANACNGGGGGNNCGCANNNNNNCNAANNNTTTCNNNGNNNNNNNCNAAGCTGGNNNNNGACT
CTNNTGGNNANCC

➤ Int Fwd2 21/12

GCCNCCCGAAGGNAGAAGAGTATTTTCAGTGGAATAAGTTACCCTGTGGCATGGCTTCCAAAACTAAAAGTGT
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AGAACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTTCCACTCCTCCTACAGTGAGATTAAAGATTTTTTGGAG
CTACATCTGCCAGTGAATGCGTATCCAAATGTCATTCCGATCGGCCTCACTGTGGATAAGGTCATGGACTTTT
TAAAGCCTCTGTGCCGCTCTTCCCAATGTGCTGAACCAAAGTACAAGCCCCTCGGGAAACTGAAGAGAGCTAG
AACAGTTTACCTTGACTCAGAGGAAGATGATGATCTCTTTGATGACCCTCTACTAACACATTCAAGGCGCAAAG
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CAAAGCCCCGGATGCTGTAAAGCAGAGAGTATGCCGAGTCCTTCTTTGGCCAACTTTGTGGACTGTGACGAGT
CCAACAGTGACAGTGAAGGAGAGTTAGAGACCCCGCCTTCTCTGCAGGGAGGTCTTGCCCCACAACACTCCC
ACAGCAAAACGCTGATCCGGATGTGGATGTACCTCGGTGGGAAGTATTCTTCAAAGAAAAAGATGAAATCACA
GATGAATGTTTGGAAAACCTTACCTTCTCCATAGAGACAGGGGGaTCGCAGTCACCAAAGCGTTTCAGTGACT
CACCAAAGCTGGGCAGTGACTCTGATGGAGAATCCACCCATATCTCTTCCAGAATTCATCTCANTCAACCCAC
ATAACGGATCAAGGAAGCCAAGGNTGGGACAGCCAGTGTGATACCNTTTTGNATCTTCCCAAGAAAAAGTG
GTGGGGANAGCACCTCTTTGAACAAGGATACCTACAACCAAACCNANATAGTATTTCTGCCTNCNNANTAN
AACANANGCACNTNNNCNNNGGATANTNNCTNNGATTTGAAANNGGNNCTNA

➤ Int Rev1 21/12

ATGTTNAANACANNNNGANNNCCTNCNNNTCTNNNNACGGNNCGNNACNCCNNNNNNNCNCCNNCNGC
NNNNNNNAAGNNNNNAGANNATTTCANNGGNATNNNNNCCNTNNGGCANNCTNCCAAAANTNAANNNGN
ACTCCACACAATCAGNNNCAAGCCANNTNCCATGTGGTNTGGAGAGAGGNCCAGAAAAACNNNCGNGATTG
TGAGNACCNNANNNANNTCATACAGAGCNTNNTTCTCTTTCCACTCNTCTACAGTGAGATTAAAGATTTNN
GANNTACATCTGCCAGTGAATGNGTATCCAAATGTCATTCCGATCGGCCTCNNTGNGGATAAGGTCATGGA
CTTTTAAAGCCTNTGTGCCGNTCTTCCCAATGNGCTGAACCAAAGTACAAGCCCCTNNGGAAACTGAAGAGA
GCTAGAACAGTTCACCTTGACTCAGAGGAAGATGATGATCTNNTTGTGNCCTCTACTAACACATTCAAGGCG
CAAAGTTCCGTACCAAGTAAGTCTTACCCTGAGGTATTTTCAATGAAGGCACTACCGNTAGATCAGCCTGAAC
TGGGACAAAGCCCCGGATGCTGTAAAGCAGAGAGTATGCCGAGTCCTTCTTTGGCCAACTTTGTGGACTGTGA
CGAGTCCAACAGTGACAGTGAAGGAGAGTTAGAGACCCNCCTTCTNTGCAGGGAGGTCTTGCCCCACAAC
ACTCCACAGCNAAACGNTGATCCGGATGTGGATGTACCTCGGTGGGAAGTATTCTTCAAAGAAAAAGATGA
AATCACAGATGAANGTTTGGAAAACCTTACCTTCTCCATAGAGACAGGGGGATCGCAGTCACCAAAGCGTTTC
AGTGACTACCAAAGNTGGGCAGTGACTCTGATGGAGAATCCACCCATATCTCTTCCAGAATTCATCTCAGTC
AACCACATAACGGATCAAGGAAGCCAAGGCTGGGACAGCCAGTGTGATACCGTTTTGTTNNNNNNNCANGA
AANAAG

➤ Int Rev2 21/12

TNTTNCAGCTGGTCNCNNNNANNNNANTNNNNNTNNNTTNNNGNCNGNAATGNAANTNTNTNATNCACA
GNNNANTTCANACTGGNGAAAGGAGAAGTTTNCAGAANGGAGNTTNTGCNNTNTGGGGCAGAGTAAAAGA
CATCCNAAGNGTATATTTAGACACCACTTTCTGTGACCCAAGGTTTNTCAAATTCANGTCGTGAGGAGTGCTT
GAGGGGCGTTNCGGAGCTGGTTNNGGAGCTGGATCACGAGGAGTCCGAAGCACGTCGTGTGGCTGAACTGCA
AGGCCGCTACGGCTATGAGTACTTATTCACCAACnGAGTGAGGAGCTGGGAGTCCAGGTTTCATGTGGACAA
GCTGGACATGTTTAAAAACATGCCTGATATCCTGCACCATCTCACAAACGGATCGAAACACCCAGATCCACGCCT
GCCGCCACCCGAAGGCAGAAGAGTATTTTCAGTGGAATAAGTTACCCTGTGGCATGGCTTCCAAAACTAAAAC
TGTAATCCACACAATCAGCATCAAGCCATCTACCATGTGGTTTGGAGAGAGGACCAGAAAAACAAACGTGATT
GTGAGAACCGGAGAGAGCTCATACAGAGCTTGCTTCTCTTTCCACTCCTCCTACAGTGAGATTAAAGATTTTTT
GAGCTACATCTGCCAGTGAATGCGTATCCAAATGTCATTCCGATCGGCCTCACTGTGGATAAGGTCATGGACT
TTTTAAAGCCTCTGTGCCGCTCTTCCCAATGTGCTGAACCAAAGTACAAGCCCCTCGGGAAACTGAAGAGAGCT
AGAACAGTTCACCTTGACTCAGAGGAAGATGATGATCTCTTTGATGACCCTCTACTAACACATTCAAGGCGCAA

AGTTCCGTACCAAGTAACTCTTCACCCTGAGGTATTTTCAATGAAGGCACTACCGCTAGATCAGCCTGAACTGG
GACAAAGCCCCGGATGCTGTAAAGCAGAGAGTATGCCGAGTCCTTCTTTGGCCAACTTTGTGGACTGTGACGA
GTCCAACAGTGACAGTGAAGGAGAGTTAGAGACCCCGCCTTCTCTGCAGGGAGGTCTNGGCCCCACANCACT
CCCACAG

➤ **Synthèse séquençage**

ATGAGTTCTTTCCAGGGACAGATGGAGGAATATCCAACCATCTCCATTGACCGCTTCGAC	60
AGAGAGAACCTGAAAGCCCGTGCCCTACTTCCTTTTCGCACTGCCACAAGGATCACATGAAA	120
GGATTAAGGGCTCCTTCCATGAAAAGAAGGCTGGAATGCAGTTTGAAGGTCTTCCTGTAC	180
TGTTCTCCAGTCACTAAGGAGCTGCTCTTAACCAGCCGAAGTACAAGTCTGGGAAAAC	240
CGAATTATAGCAATTGAAATTGAAACTCCTACCCAGGTATCTTTAGTTGATGAGGCATCG	300
GGTGAGAAGGAAGAGTTGTTGTGACTCTCTTACCAGCTGGTCACTGCCAGGTTCAGTT	360
ATGTTTTCTATTTTCAGGGCAGTAATGGAAGTGTCTTATACACAGGAGACTTCAGACTGGCG	420
AAAGGAGAAGTTTCCAGAAATGGAGCTTCTGCACCTCTGGGGGCAGAGTAAAAGACATCCAA	480
AGTGATATATTTAGACACCACTTTCTGTGACCCAGGTTTATCAAATCCAAGTCGTGAG	540
GAGTGCTTGAGGGGCGTTCTGGAGCTGGTTCGGAGCTGGATCACGAGGAGTCCGAAGCAC	600
GTCGTGTGGCTGAATGCAAGGCGCCTACGGCTATGAGTACTTATTCACCAACCTGAGT	660
GAGGAGCTGGGAGTCCagGTTTCATGTGGACAAGCTGGACATGTTTAAAAACATGCCTGAT	720
ATCCTGCACCATCTCACACGGATCGAAACACCCAGATCCACGCCTGCCGCCACCCGAAG	780
GCAGAAGAGTATTTTCAGTGAATAAGTTACCCTGTGGCATGGCTTCCAAAACATAAACT	840
GTACTCCACACAATCAGCATCAAGCCATCTACCATGTGGTTTGGAGAGAGGACCAGAAAA	900
ACAAACGTGATTGTGAGAACCGGAGAGAGCTCATAAGAGCTTGCTTCTCTTTCCACTCC	960
TCTACAGTGAGATTAAAGATTTTTTGGAGCTACATCTGCCAGTGAATGCGTATCCAAAT	1020
GTCAATCCGATCGGCCTCACTGTGGATAAGGTCATGGACTTTTTAAAGCCTCTGTGCCGC	1080
TCTTCCCAATGTGCTGAACCAAGTACAAGCCCTCGGGAAACTGAAGAGAGCTAGAACA	1140
GTTACCTTGACTCAGAGGAAGATGATGATCTCTTTGATGACCTCTACTAACACATTCA	1200
AGGCGCAAAGTTCCGTACCAAGTAACTCTTACCCCTGAGGTATTTTCAATGAAGGCACCTA	1260
CCGCTAGATCAGCCTGAACTGGGACAAAGCCCGGATGCTGTAAAGCAGAGAGTATGCCG	1320
AGTCCTTCTTTGGCCAACTTTGTGGACTGTGACGAGTCCAACAGTGACAGTGAAGGAGAG	1380
TTAGAGACCCCGCCTTCTCTGCAGGGAGGTCTTGGCCCCACAACACTCCACAGCAAAAC	1440
GCTGATCCGGATGTGGATGTACCTCGGTGGGAAGTATTTCTCAAAGAAAAGATGAAATC	1500
ACAGATGAATGTTTGGAAAACCTACCTTCTCCATAGAGACAGGGGATCGCAGTCACCA	1560
AAGCGTTTCAGTGACTCACCAGCTGGGCAGTGACTCTGATGGAGAAATCCACCCATATC	1620
TCTTCCAGAAATTCATCTCAGTCAACCCACATAACGGATCAAGGAAGCCAAGGCTGGGAC	1680
AGCCAGTGTGATACCGTTTGTGTATCTTCCCAAGAAAAAGTGGTGGGGATAGACCTCT	1740
TTGAACAAGGATACCTACAAACCAAAACCCAAAGATAGTATTTCTGCCTCCCAATAGAA	1800
CAGAATGCACCTTGTCCACAGGATACTCACTGTGATTTGAAAAGCGGAGCTGAAGTAAAT	1860
GGAGTCTCTTGTATTGAAGAACCAGACACTGTGAGTGGCAGGAAATCTTCACCTGAGAAA	1920
ACATCGCTAACACAGCACAGGCAGACTCACAGAGCTCCTCTGACTTTGAAATCCCCTCA	1980
ACTCCAGAAGCTGAGCTTCCCAAGCCAGAGCATTTACAGTCTTATATGGAAGCTGGCA	2040
ACAGGTGAGAGTATAGTGTGAAAAAGAAAAATGTTCACTCCAGATATTTAAATAA	2097

MSSFQGMEEYPTISIDRFDRENLKARAYFLSHCHKDHMKGLRAPSMKRRLECSLKVFLYCSPVTKEILLTSPKYKF
WENRIIAIEIETPTQVSLVDEASGEKEEVVVTLLPAGHCPGSMFLFQGSNGTVLYTGDFRLAKGEVSRMELLHSGG
RVKDIQSVYLDTTFCDFRIFYQIPSRREELRGVLELVRSWITRSPKHVVWLNCKAAYGYEYLFNTLSEELGVQVHVDKL
DMFKNMPDILHHLTDRNTQIHACRHPKAEFFQWNKLPCGMASKTKTVLHTISIKPSTMWFGERTRTKNVIVRT
GESSYRACFSFHSYSEIKDFLSYICPVNAYPNVPIGLTVDKVMDFLKPLCRSSQCAEPKYKPLGKLRARTVHLDSEE
DDDLFDDPLLTHSRKVPYQVTLHPEVFSMKALPLDQPELGQSPGCCAESMPSPSLANFVDCDESNSDSEGELET
PPSLQGGGLPPTLLPQQNADPDVDVPRWEVFFKRKDEITDECLNLPSSIETGGSQSPKRFSDSPKLGSDSDGESTHIS
SQNSSQSTHITDQGSQGWDSQCDTVLLSSQESGGDSTSLNKDITYKPKPKDSISASQIEQNALCPQDTHCDLKSQA
EVNGVSCIEEPDVTVSGRKSSPEKTSLTSTQADSQSSSDFEIPSTPEAELPKPEHLQFLYGLKATGESIVLKKENVHSQIFK

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➤ Différence Séquençage/CDS au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MSFQGMEEYPTISIDRFDRENLKARAYFLSHCHKDHMKGLRAPSMMKRLKSLKVFVLYCSPYTKELLTSPKYKFHENRTIAIEIETPTQVSLYDEASGEKEEYVYLLPAGHCPG6SVHFLFQ6SNGT													
ref	MSFQGMEEYPTISIDRFDRENLKARAYFLSHCHKDHMKGLRAPSMMKRLKSLKVFVLYCSPYTKELLTSPKYKFHENRTIAIEIETPTQVSLYDEASGEKEEYVYLLPAGHCPG6SVHFLFQ6SNGT													
Consensus	MSFQGMEEYPTISIDRFDRENLKARAYFLSHCHKDHMKGLRAPSMMKRLKSLKVFVLYCSPYTKELLTSPKYKFHENRTIAIEIETPTQVSLYDEASGEKEEYVYLLPAGHCPG6SVHFLFQ6SNGT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	VLYTGDFRLAKGEYSRHELLHSGGRVKDIQSYVLOTTFCOPRFYQIPSRREECLRGVLELVRSHITRSPKHVYVHLNCKARYGYEYLTNLSEELGVQVHVOKLDMFKNMPDILHLLTDRNTQIHACRHPK													
ref	VLYTGDFRLAKGEYSRHELLHSGGRVKDIQSYVLOTTFCOPRFYQIPSRREECLRGVLELVRSHITRSPKHVYVHLNCKARYGYEYLTNLSEELGVQVHVOKLDMFKNMPDILHLLTDRNTQIHACRHPK													
Consensus	VLYTGDFRLAKGEYSRHELLHSGGRVKDIQSYVLOTTFCOPRFYQIPSRREECLRGVLELVRSHITRSPKHVYVHLNCKARYGYEYLTNLSEELGVQVHVOKLDMFKNMPDILHLLTDRNTQIHACRHPK													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	AEEYFQANKLPCGASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSHSSYSEIKDFLSYICPNRAYPNYIPIGLTVDKYHDFLKPLCRSSQCAEPKYKPLGKLKRARTVHLDSEEDDD													
ref	AEEYFQANKLPCGASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSHSSYSEIKDFLSYICPNRAYPNYIPIGLTVDKYHDFLKPLCRSSQCAEPKYKPLGKLKRARTVHLDSEEDDD													
Consensus	AEEYFQANKLPCGASKTKTVLHTISIKPSTHMFGERTRKTNVIVRTGESSYRACFSHSSYSEIKDFLSYICPNRAYPNYIPIGLTVDKYHDFLKPLCRSSQCAEPKYKPLGKLKRARTVHLDSEEDDD													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	LFDDPLLTHSRKYPYQVTLHPEVFSMKALPLDQPELGSPGCKRAESHPSPSLANFVDCDESNSDSEGELETTPPSLQGGGPTTL PQNADPDVDVPRNEVFFKRKDEITDECLNLPSSEITG6GSQP													
ref	LFDDPLLTHSRKYPYQVTLHPEVFSMKALPLDQPELGSPGCKRAESHPSPSLANFVDCDESNSDSEGELETTPPSLQGGGPTTL PQNADPDVDVPRNEVFFKRKDEITDECLNLPSSEITG6GSQP													
Consensus	LFDDPLLTHSRKYPYQVTLHPEVFSMKALPLDQPELGSPGCKRAESHPSPSLANFVDCDESNSDSEGELETTPPSLQGGGPTTL PQNADPDVDVPRNEVFFKRKDEITDECLNLPSSEITG6GSQP													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	KRFSOSPKLGSOSDGESTHISQNSQSTHITDQGSQGHOSQCDTVLLSSQEKSGGDSTSLNKDITYPKPKDSISASQIEQNALCPQDTHCDLKSRAEVNGVSCIEEPDITYSGRKSPEKTSLSSTQADS													
ref	KRFSOSPKLGSOSDGESTHISQNSQSTHITDQGSQGHOSQCDTVLLSSQEKSGGDSTSLNKDITYPKPKDSISASQIEQNALCPQDTHCDLKSRAEVNGVSCIEEPDITYSGRKSPEKTSLSSTQADS													
Consensus	KRFSOSPKLGSOSDGESTHISQNSQSTHITDQGSQGHOSQCDTVLLSSQEKSGGDSTSLNKDITYPKPKDSISASQIEQNALCPQDTHCDLKSRAEVNGVSCIEEPDITYSGRKSPEKTSLSSTQADS													
	651	660	670	680	690	698								
seq	QSSSDFEIPSTPEALPKPEHLQFLYGKLATGESIVLKKENVHSQIFK													
ref	QSSSDFEIPSTPEALPKPEHLQFLYGKLATGESIVLKKENVHSQIFK													
Consensus	QSSSDFEIPSTPEALPKPEHLQFLYGKLATGESIVLKKENVHSQIFK													

Une mutation en 623 S>P

	Description	Scientific name	Score	Score	Cover	value	Ident	Len	Accession
✓	protein artemis [Rattus norvegicus]	Rattus norvegicus	1446	1446	100%	0.0	99.86%	698	NP_671486.2
✓	SNM1-like protein [Rattus norvegicus]	Rattus norvegicus	1422	1422	98%	0.0	99.56%	697	AAM89124.1
✓	PREDICTED: protein artemis isoform X1 [Rattus norvegicus]	Rattus norvegicus	1273	1273	88%	0.0	99.84%	629	XP_017455949.1
✓	DNA cross-link repair 1C, PSQ2 homolog (S. cerevisiae) isoform CRA_b [Rattus norvegicus]	Rattus norvegicus	1142	1142	79%	0.0	99.82%	552	EDL78693.1
✓	DNA cross-link repair 1C, PSQ2 homolog (S. cerevisiae) isoform CRA_a [Rattus norvegicus]	Rattus norvegicus	510	510	34%	9e-179	100.00%	257	EDL78692.1

Pour rate/T0/T24h :

Dclre1c_SeqInt_Fwd_1

~460NT pour démarrer vers 610NT

GGGCAGAGTAAAAGACATCC

Dclre1c_SeqInt_Fwd_2

~720 pour démarrer vers 870

TCCTGCACCATCTCACAACG

Dclre1c_SeqInt_Rev_1

~1750 pour démarrer vers 1600

GGGTTTTGGTTTGTAGGTAT

Dclre1c_SeqInt_Rev_2

~1480 pour démarrer vers 1330

AGAATACTTCCCACCGAGG

Dclre1c_SeqInt_Fwd_3

Vers 210 pour un démarrage vers 360

TAACCAGCCCAAAGTACAAG