

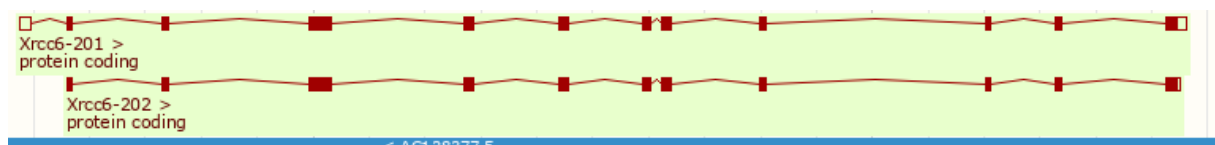
14)Xrcc6 (Ku70)

Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6), mRNA

Xrcc6 G22p1; Ku70; Kup70

- Référence NCBI : NM_139080
- Taille 1827 NT
- Séquence NT :

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- Séquence protéique :
- NP_620780

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- **Amorces synthétisées :**

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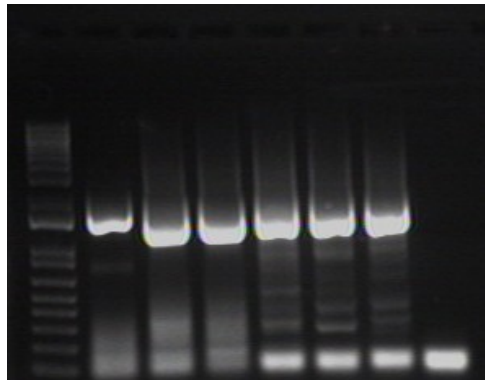
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Xrcc6_NotI_Rev

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- **Expériences :**

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



Rate DiT0 DiT24 DiT48 SP CTX Eau

- Sep/Oct : soucis clonage : Vecteur ? PCR mal digérée ?
- 08/09 : digestion et purification de 10ul rate, DiT0, DiT24h, 48h, SP et CTX
- 11/09 : mini rate ok
- 14/09 : ligation DiT0, 24, 48, SP et CTX
- 16/09 : mini DiT24h, 48h, SP et CTX **OK**
- 06/10 : religation dans nouv vecteur FB pour rate et DiT0
- 09/10 : miniprep **rate et DiT0 : rate OK**
- 16/10 : redigestion DiT0
- 22/10 : mini DiT0 **OK**
- 28/10 envoi au séquençage

➤ Résultats séquençages

○ FlagBirA Xrcc6 rate clone A

➤ B3Fwd rate 920NT

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➤ BGHRev 970NT

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➤ BGHRev 25/11

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➤ **Fwd2**

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➤ **Rev1**

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➤ **Synthèse séquençage rate : NT**

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 XXT

FlagBirA Xrcc6 rate (clone A) renvoyé au séquençage le 25/11
 mais manque toujours la fin de séquence : envoi d'un
 nouveau clone le 07/12

o FlagBirA Xrcc6 rate clone B

➤ B3Fwd rate 873NT

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➤ BGHRev 1071NT

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➤ Seq int Fwd1

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➤ Seq int Fwd2

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➤ Seq Int Rev1

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CTTTTCCAGTGAGGCTGTATCGAGAAACAAACGAACCAAGTGAAGAACTAAGACAAGGACTTTTAATGTAAACAC
AGGCAGTCTGCTCCTGCCAGTGATACCAAGCGGTCTCTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAA
GAGGAAACAGAGGAGCTGAAGCGGTTTGATGAGCCAGGT

➤ Synthèse séquençage rate : **NT**

ATGTCAGAGTGGGAATCCTACTACAAAAGT	31	
AGGGTGAGGAAGAGGAAGAGGAGGAGCAGCCCTGACACAAATGGAGAATATAAATATT		91
CAGGAAGAGATAGTTTGATTTTCTGGTTGACGCCTCCAGGGCTATGTTGAATCTCAGG		151
GTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGTGATCCAGAGTGTGTACACCA		211
GTAAGATCATAAGCAGCGATCGGGATCTCTTGGCAGTGGTGTCTATGGTACCGAGAAAG		271
ACAAAAATTCAGTGAACCTCAAAAGTATTTATGTCTTACAAGATCTGGATAACCCAGGAG		331

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CTAAACGAGTGTAGAGCTTGACCGCTTTAAGGGACAACAGGGGAAAAACATTTCCGAG 391
ACACAATTGGCCATGGGTCTGACTACTCTTTGAGTGAAGTGCTCTGGGTCTGTGCCAACC 451
TCTTCAGCGACGTCCAGTTCAAGATGAGTCATAAGAGGATCATGCTATTACCAATGAAG 511
ATGACCCCCATGGTAATGACAGTGCCAAAGCCAGCCGGGCCAGGACCAAAGCCAGCGATC 571
TGCGGGACACTGGGATCTTCCTCGACTTGATGCACCTGAAGAAGCGAGGGGGCTTTGACG 631
TGTCCTTGTCTACAGAGACATCATCAGCATCGCTGAGGATGAGGACCTCGGGGTTCACT 691
TTGAGGAGTCAAGCAAGCTGGAAGACCTGCTAAGGAAGGTTGAGCCAAAGGAGACCAAAA 751
AGCGAGTGCTGTCCAGGTTAAAGTTTAAGCTCGGCAAAGACGTAGCACTCATGGTGGGCG 811
TTTATAACTTGGTCCAGAAAGCTAACAAGCCTTTTCCAGTGAGGCTGTATCGAGAAACAA 871
ACGAACCAGTGAAACTAAGACAAGGACTTTTAATGTAACACAGGCAGTCTGCTCCTGC 931
CCAGTGATACCAAGCGGTCTCTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGG 991
AAACAGAGGAGCTGAAGCGGTTTGTATGAGCCAGGTTTGATTCTCATGGGCTTTAAGCCCA 1051
TGGTAATGCTGAAGAACCACCCTACCTGAGGCCCTCTCTGTTCTGTACCCAGAGGAGT 1111
CCTTGGTCAACGGGAGCTCAACCTTGTTCAGCGCCCTGCTCACCAAGTGTGTGGAGAAGG 1171
AGGTCATAGCAGTGTGTAGATACACAGCCGAAAGAAATGCTCCCTTATTTTGTGGCTT 1231
TGGTGCCACAGGAAGAGGAGCTAGATGATCAGAACATTCAGGTGACTCCCGCAGGCTTCC 1291
AGCTTGTCTTCCCTTACGCGGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGA 1351
TGGCCAACCCGGAACAGATAGACAAGATGAAGGCCATTGTTCAAAGCTCCGCTTTACAT 1411
ACAGGAGCGACAGTTTTCGAGAACCAGTGCTGCAGCAGCACTCCGGAACCTGGAGGCC 1471
TAGCTTTGGACATGATGGAGTCGGAGCAAGTGGTAGATCTGACACTGCCCAAGGTTGAAG 1531
CCATAAAGAAAAGACTGGGCTCCCTGGCAGATGAGTTTAAAGAACTTGCTACCTCCAG 1591
GTTATAATCCTGAGGGAAAAATTGCCAAGAGAAAAGCAGACAATGAAGGTTCTGCAAGTA 1651
AAAAGCCCAAGTAGAGTTATCAGAAGAGGAGCTGAAGGACCTTTTGGCCAAGGCGACAC 1711
TGGGCAAGCTCACTGTGCTGCACTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTG 1771
GACCGAAGAAGCAGGAACCTACTCGAGGCTCTCAGCAGACACTtGGAGAAgaactGA 1827

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MSEWESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDASRAMFESQGEDELTPFDMSIQCIQSVYTSKIISDR
DLLAVVFGYTEKDKNSVNFKSIYVLQDLNPGAKRVLELDRFKGQQGKKHFRDTIGHGSDYSLSEVLVWCANLFS
VQFKMSHKRIMLFTNEDDPHGNDASAKSRARTKASDLRDTGIFLDMHLKKRGGFDVSLFYRDIISIAEDEDLGVHF
EESSKLEDLLRKVRAKETKKRVLSRLKFKLGKDVALMVGVYNLVQKANKPFPVRLYRETNEPVKTKTRTFNVNTGSL
LPSDTKRSLTFGTRQIVLEKEETEELKRFDEPLILMGFKPMVMLKNHHYLRPSFLYPEESLVNGSSTLFSALLTKC
VEKEVAVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVMANPEQIDKMKAIVQ
KLRFTYRSDSFENPVLQQHFRNLEALALDMMMESEQVVDLTLPKVEAIKKRLGSLADEFKELVYPPGYNPEGKIAK
RKA DNEGSASKPKVELSEEELKDLFAKGTGKLTVPALRDICKAYGLKSGPKKQELLEALSRHLEKN-

➤ **Blast contre banque rat**

			Score	Score	Cover	value	ident	Len	
☒	Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6) mRNA	Rattus norvegicus	3374	3374	100%	0.0	100.00%	2070	NM_139080.2
☒	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 6 mRNA (cDNA clone ...	Rattus norvegicus	3374	3374	100%	0.0	100.00%	2098	BC078718.1
☒	Rattus norvegicus cDNA clone IMAGE:6918045, containing frame-shift errors	Rattus norvegicus	3363	3363	100%	0.0	99.89%	2056	BC061528.1
☒	Rattus norvegicus mRNA for G22p1, complete cds	Rattus norvegicus	3352	3352	100%	0.0	99.78%	1964	AB066102.1
☒	PREDICTED: Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6), transcript variant X1 mRNA	Rattus norvegicus	2076	3080	91%	0.0	100.00%	1919	XM_008765671.2

		1	10	20	30	40	50	60	70	80	90	100	110	120	130	
seq		ATGTCAGAGTGGGARTCTACTACAAACTGAGGGTGAGGAGAGGAGGAGGAGCAGAGCCCTGACACAAATGGAGARTATAAATATTCAGGAGAGATAGTTTGATTTTCTGGTGGTGCCTCC														
cds		ATGTCAGAGTGGGARTCTACTACAAACTGAGGGTGAGGAGAGGAGGAGGAGCAGAGCCCTGACACAAATGGAGARTATAAATATTCAGGAGAGATAGTTTGATTTTCTGGTGGTGCCTCC														
Consensus		ATGTCAGAGTGGGARTCTACTACAAACTGAGGGTGAGGAGAGGAGGAGGAGCAGAGCCCTGACACAAATGGAGARTATAAATATTCAGGAGAGATAGTTTGATTTTCTGGTGGTGCCTCC														
		131	140	150	160	170	180	190	200	210	220	230	240	250	260	
seq		GGGCTATGTTTGAATCTCAGGGTGAGAGCAGGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACAGTAGATCATAGCAGCGATCGGGATCTCTTGGCAGTGGTGTCTATGG														
cds		GGGCTATGTTTGAATCTCAGGGTGAGAGCAGGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACAGTAGATCATAGCAGCGATCGGGATCTCTTGGCAGTGGTGTCTATGG														
Consensus		GGGCTATGTTTGAATCTCAGGGTGAGAGCAGGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACAGTAGATCATAGCAGCGATCGGGATCTCTTGGCAGTGGTGTCTATGG														
		261	270	280	290	300	310	320	330	340	350	360	370	380	390	
seq		TACCAGAGAGACAAAATTCAGTGACCTTCAAAAGTATTTATGTCTTACAGATCTGGATACCCAGGAGCTARACGAGTGTAGAGCTTGACCCTTTAAGGGACACAGGGGAAAAAACATTTCGGA														
cds		TACCAGAGAGACAAAATTCAGTGACCTTCAAAAGTATTTATGTCTTACAGATCTGGATACCCAGGAGCTARACGAGTGTAGAGCTTGACCCTTTAAGGGACACAGGGGAAAAAACATTTCGGA														
Consensus		TACCAGAGAGACAAAATTCAGTGACCTTCAAAAGTATTTATGTCTTACAGATCTGGATACCCAGGAGCTARACGAGTGTAGAGCTTGACCCTTTAAGGGACACAGGGGAAAAAACATTTCGGA														
		391	400	410	420	430	440	450	460	470	480	490	500	510	520	
seq		GACACATTGGCCATGGGCTGACTACTCTTTGAGTGAAGTCTGGGCTGTGTCACAGCTCTTCAGCAGCTCCAGTTCAGATGAGTCTAAGAGGATCATGCTATTACCAATGAAGATGACCC														
cds		GACACATTGGCCATGGGCTGACTACTCTTTGAGTGAAGTCTGGGCTGTGTCACAGCTCTTCAGCAGCTCCAGTTCAGATGAGTCTAAGAGGATCATGCTATTACCAATGAAGATGACCC														
Consensus		GACACATTGGCCATGGGCTGACTACTCTTTGAGTGAAGTCTGGGCTGTGTCACAGCTCTTCAGCAGCTCCAGTTCAGATGAGTCTAAGAGGATCATGCTATTACCAATGAAGATGACCC														
		521	530	540	550	560	570	580	590	600	610	620	630	640	650	
seq		ATGGTARTGACAGTGCCAAAGCCAGCCGGGCCAGGACCAAGCCAGGCGATCTGCGGACACTGGGATCTTCCTGACCTTGATGCACCTGAAGAGGCGAGGGGGCTTTGACGTGCTCTTGTCTACAGAGA														
cds		ATGGTARTGACAGTGCCAAAGCCAGCCGGGCCAGGACCAAGCCAGGCGATCTGCGGACACTGGGATCTTCCTGACCTTGATGCACCTGAAGAGGCGAGGGGGCTTTGACGTGCTCTTGTCTACAGAGA														
Consensus		ATGGTARTGACAGTGCCAAAGCCAGCCGGGCCAGGACCAAGCCAGGCGATCTGCGGACACTGGGATCTTCCTGACCTTGATGCACCTGAAGAGGCGAGGGGGCTTTGACGTGCTCTTGTCTACAGAGA														
		651	660	670	680	690	700	710	720	730	740	750	760	770	780	
seq		CATCATCAGCATCGTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAGCAGCTGGAGACCTGCTACAGGAGGTTTCAGGCCAGGAGACCAAAAGCGAGTGTGTCAGGTTAAGATTAAAG														
cds		CATCATCAGCATCGTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAGCAGCTGGAGACCTGCTACAGGAGGTTTCAGGCCAGGAGACCAAAAGCGAGTGTGTCAGGTTAAGATTAAAG														
Consensus		CATCATCAGCATCGTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAGCAGCTGGAGACCTGCTACAGGAGGTTTCAGGCCAGGAGACCAAAAGCGAGTGTGTCAGGTTAAGATTAAAG														
		781	790	800	810	820	830	840	850	860	870	880	890	900	910	
seq		CTCGGCAAGAGCAGTACCTCATGGTGGGCGTTTATACCTTGGTCCGAAAGCTAACAGCCCTTTTCAGTGAGGCTGTATCGAGAAACAAACGACCTGAAACCTAAGACAGGACCTTTTATGTAA														
cds		CTCGGCAAGAGCAGTACCTCATGGTGGGCGTTTATACCTTGGTCCGAAAGCTAACAGCCCTTTTCAGTGAGGCTGTATCGAGAAACAAACGACCTGAAACCTAAGACAGGACCTTTTATGTAA														
Consensus		CTCGGCAAGAGCAGTACCTCATGGTGGGCGTTTATACCTTGGTCCGAAAGCTAACAGCCCTTTTCAGTGAGGCTGTATCGAGAAACAAACGACCTGAAACCTAAGACAGGACCTTTTATGTAA														
		911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	
seq		ACACAGGACAGTCTGCTCTGCCAGTGATACCAAGCGGCTCTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAACAGAGGAGCTGAGCGGTTTGATGAGCCAGGTTGATCTCATGGG														
cds		ACACAGGACAGTCTGCTCTGCCAGTGATACCAAGCGGCTCTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAACAGAGGAGCTGAGCGGTTTGATGAGCCAGGTTGATCTCATGGG														
Consensus		ACACAGGACAGTCTGCTCTGCCAGTGATACCAAGCGGCTCTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAACAGAGGAGCTGAGCGGTTTGATGAGCCAGGTTGATCTCATGGG														
		1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	
seq		CTTTAAGCCCATGGTAAATGCTGAAGACCAACCTACCTGAGGCCCTCTCTGTTCTGTACCCAGAGAGTCTTGGTCAACGGGAGCTCAACCTTGTTCAGCGCCCTGCTCAACAGTGTGTGGAGAG														
cds		CTTTAAGCCCATGGTAAATGCTGAAGACCAACCTACCTGAGGCCCTCTCTGTTCTGTACCCAGAGAGTCTTGGTCAACGGGAGCTCAACCTTGTTCAGCGCCCTGCTCAACAGTGTGTGGAGAG														
Consensus		CTTTAAGCCCATGGTAAATGCTGAAGACCAACCTACCTGAGGCCCTCTCTGTTCTGTACCCAGAGAGTCTTGGTCAACGGGAGCTCAACCTTGTTCAGCGCCCTGCTCAACAGTGTGTGGAGAG														
		1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	
seq		GAGGTCTATAGCAGTGTGTAGATACACAGCCGAAGATATGCTCCCTTATTTTGTGGCTTTGGTGCCACAGGAGAGGAGCTAGATGATCAGACATTCAAGGTGACTCCCGAGGCTTCCAGCTTGTCT														
cds		GAGGTCTATAGCAGTGTGTAGATACACAGCCGAAGATATGCTCCCTTATTTTGTGGCTTTGGTGCCACAGGAGAGGAGCTAGATGATCAGACATTCAAGGTGACTCCCGAGGCTTCCAGCTTGTCT														
Consensus		GAGGTCTATAGCAGTGTGTAGATACACAGCCGAAGATATGCTCCCTTATTTTGTGGCTTTGGTGCCACAGGAGAGGAGCTAGATGATCAGACATTCAAGGTGACTCCCGAGGCTTCCAGCTTGTCT														
		1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	
seq		TCTCCCTTACGCCGATGACAGCGGAGGTTGCCCTTTACGGAGAGGTGATGGCCARCCCGGACAGATAGACAGATGAGGCCATTGTTCAAAAGCTCCGCTTACATACAGGAGCGACAGTTTCGA														
cds		TCTCCCTTACGCCGATGACAGCGGAGGTTGCCCTTTACGGAGAGGTGATGGCCARCCCGGACAGATAGACAGATGAGGCCATTGTTCAAAAGCTCCGCTTACATACAGGAGCGACAGTTTCGA														
Consensus		TCTCCCTTACGCCGATGACAGCGGAGGTTGCCCTTTACGGAGAGGTGATGGCCARCCCGGACAGATAGACAGATGAGGCCATTGTTCAAAAGCTCCGCTTACATACAGGAGCGACAGTTTCGA														
		1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	
seq		GAACCCAGTGTCTGACGAGCAGCTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTGGGACAGTGGTAGATCTGACACTGCCAAGGTTGAAGCCATAAAGAAAGAGCTGGGCTCCCTGGCA														
cds		GAACCCAGTGTCTGACGAGCAGCTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTGGGACAGTGGTAGATCTGACACTGCCAAGGTTGAAGCCATAAAGAAAGAGCTGGGCTCCCTGGCA														
Consensus		GAACCCAGTGTCTGACGAGCAGCTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTGGGACAGTGGTAGATCTGACACTGCCAAGGTTGAAGCCATAAAGAAAGAGCTGGGCTCCCTGGCA														
		1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	
seq		GATGAGTTTAAAGAACTTGTCTACCTCCAGGTTATATCTCTGAGGGAAATTTGCCAAGAGAAAGCAGACATGAGGTTCTGCAGTAAAGAGCCAGGTAAGGTTATCAGAGAGGAGCTGAGGG														
cds		GATGAGTTTAAAGAACTTGTCTACCTCCAGGTTATATCTCTGAGGGAAATTTGCCAAGAGAAAGCAGACATGAGGTTCTGCAGTAAAGAGCCAGGTAAGGTTATCAGAGAGGAGCTGAGGG														
Consensus		GATGAGTTTAAAGAACTTGTCTACCTCCAGGTTATATCTCTGAGGGAAATTTGCCAAGAGAAAGCAGACATGAGGTTCTGCAGTAAAGAGCCAGGTAAGGTTATCAGAGAGGAGCTGAGGG														
		1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	
seq		ACCTTTTGGCAGGGGCACACTGGGCAAGCTCAGTGTGCTGCACTGAGGGACATCTGACAGGCTTATGGGCTAAGAGTGGACCGAAGAGCAGGAACTACTCGAGGCTCTCAGCAGACACTTGGAGAA														
cds		ACCTTTTGGCAGGGGCACACTGGGCAAGCTCAGTGTGCTGCACTGAGGGACATCTGACAGGCTTATGGGCTAAGAGTGGACCGAAGAGCAGGAACTACTCGAGGCTCTCAGCAGACACTTGGAGAA														
Consensus		ACCTTTTGGCAGGGGCACACTGGGCAAGCTCAGTGTGCTGCACTGAGGGACATCTGACAGGCTTATGGGCTAAGAGTGGACCGAAGAGCAGGAACTACTCGAGGCTCTCAGCAGACACTTGGAGAA														
		1821827														
seq		GAACCTGA														
cds		GAACCTGA														
Consensus		GAACCTGA														

Parfait

➤ **Différence au niveau PROT :**

		1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ref	MSMESYKTEGEEEEEEQSPDNTGEYKYSGRDSLIFLVDSARAMEFSQGEDELTPFDMSIQCIQSVYTSKIISSORDLLAVFYGTGTEKDKSNVFNKSIYVLQDLNPNPAKRVLELDRFKGQGGKKHFR													
Consensus		MSMESYKTEGEEEEEEQSPDNTGEYKYSGRDSLIFLVDSARAMEFSQGEDELTPFDMSIQCIQSVYTSKIISSORDLLAVFYGTGTEKDKSNVFNKSIYVLQDLNPNPAKRVLELDRFKGQGGKKHFR													
		131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	ref	DTIGHGSDYSLSEVLWYCRNLFSDVQFKSHSKRIHLFTNEODPHGNSAKSARRTKASOLDRTGFLDLHLKRRGGFDYSLFYRDTISIEDEDLGVHFEESKLEDLRKVRAKETKKRVLSRLKFK													
Consensus		DTIGHGSDYSLSEVLWYCRNLFSDVQFKSHSKRIHLFTNEODPHGNSAKSARRTKASOLDRTGFLDLHLKRRGGFDYSLFYRDTISIEDEDLGVHFEESKLEDLRKVRAKETKKRVLSRLKFK													
		261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	ref	LGKQVAYLVGYNMLVQKANKPPVYRLYRETNPEYKTKTRTFNVTGSLLPSTDKRSLTFGTRIVYLEKEETEELKRFDEPGLILMGKFPYHMLKNHHYLRPSLFLYPEESLVNGSSTLFSALLTKCKVEK													
Consensus		LGKQVAYLVGYNMLVQKANKPPVYRLYRETNPEYKTKTRTFNVTGSLLPSTDKRSLTFGTRIVYLEKEETEELKRFDEPGLILMGKFPYHMLKNHHYLRPSLFLYPEESLVNGSSTLFSALLTKCKVEK													
		391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	ref	EVIIVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFLQVFLPYADDKRVYFTEKYHNPPEQIDDKHAIYQKLRFTYRSDSFEMPVLQOHRNLEALALDHMESEQVVDLTLPKVEATKKRGLSLA													
Consensus		EVIIVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFLQVFLPYADDKRVYFTEKYHNPPEQIDDKHAIYQKLRFTYRSDSFEMPVLQOHRNLEALALDHMESEQVVDLTLPKVEATKKRGLSLA													
		521	530	540	550	560	570	580	590	600	608				
seq	ref	DEFELVYPYGPMPGEGIAKKRAKDNGSASKKPKVELSEELKOLFAGKGTGLKLYPALRDICKAYGLKSGPKQKQELLEASRLHLEKN													
Consensus		DEFELVYPYGPMPGEGIAKKRAKDNGSASKKPKVELSEELKOLFAGKGTGLKLYPALRDICKAYGLKSGPKQKQELLEASRLHLEKN													

✓	X-ray repair cross-complementing protein 6 [Rattus norvegicus]	Rattus norvegicus	1247	1247	100%	0.0	100.00%	608	NP_620780.2
✓	G22p1 [Rattus norvegicus]	Rattus norvegicus	1242	1242	100%	0.0	99.67%	609	BAB83858.1
✓	PREDICTED: X-ray repair cross-complementing protein 6 isoform X1 [Rattus norvegicus]	Rattus norvegicus	1094	1094	100%	0.0	90.30%	554	XP_008763893.1

o FlagBirA Xrcc6 DiT0 clone A

➤ B3Fwd DiT0

Fwd881

ATGTCAGAGTGGAATCCTACTACAAAAGTGGGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTCTGGTTGACGCCTCCAGGGCTATGTTTGAATCTC
AGGGTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAGTAAGATCATAA
GCAGCGATCGGGATCTCTTGGCAGTGGTGTCTATGGTACCGAGAAAGACAAAAATTCAGTGAACCTTCAAAAGT
ATTTATGTCTTACAAGATCTGGATAACCCAGGAGCTAAACGAGTGTAGAGCTTGACCGCTTTAAGGGACAACAG
GGGAAAAAACATTTCCGAGACACAATTGGCCATGGGTCTGACTACTCTTTGAGTGAAGTGCTCTGGGTCTGTGC
CAACCTCTTCAGCGACGTCCAGTTCAGATGAGTCATAAGAGGATCATGCTATTCACCAATGAAGATGACCCCAT
GGTAATGACAGTGCCAAAGCCAGCCGGGCCAGGACCAAAGCCAGCGATCTGCGGGACACTGGGATCTTCTCG
ACTTGATGCACCTGAAGAAGCGAGGGGGCTTTGACGTGTCCTTGTCTACAGAGACATCATCAGCATCGCTGAg
GATGAgGACCTCGGGGTTCACTTTGANGANTCAAGCAAGCTGGAAGANCTGCTANNNAGGNTCGAGCCNAGG
AGACCAAAAAGCGAGTGNTGTCCAGGTTAAAGTTTAAAGCTCGGCAAGACGTANCACTCATGGTGGGCGTTTATA
ACTTGGNCCANAAAGCTAACAAGCCTTTTNCAGTGAGGNTGTNTCGANAANNANCGAACNANTGAA

➤ BGHRev DiT0

Rev1044

ANGNTNANNTNGNCAANANGTANNNNCNNNNNGNNNTTATNNNTNNTNCAGNAAGNNNCANNNTTCCCA
GNGANGNTGTATCGAGNAACAACGAACCAAGTGAANTAAAGACAAGGANTTTAATGTAAACACAGNCAGTNTG
NTNCTGCCAGTGATNCCAAGCNNTCTNTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAAACAG
AGGAGCTGAAGCGTTTGTATGAGCCAGGTTTGAATCTCATGGGCTTTAAGCCCATGGTAATGCTGAAGAACCAC
CACTAcTGAGGCCCTCTCTGTTCTGTACCCAGAGGAGTCCCTGGTCAACGGGAGCTCAACCTTGTTAGCGCC
CTGCTACCAAGTGTGTGGAGAAGGAGGTCATAGCAGTGTGTAGATACACAGCCCCGAAAGAATGTCTCCCTTAT
TTTGTGGCTTTGGTGCCACAGGAAGAGGAGCTAGATGATCAGAACATTCAGGTGACTCCCGCAGGCTTCCAGCT
TGTCTTCTCCCTTACGCCGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGATGGCCAACCCGGAACAGA
TAGACAAGATGAAGGCCATTGTTCAAAAGCTCCGCTTTACATACAGGAGCGACAGTTTCGAGAACCCAGTGCTG
CAGCAGCACTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTCGGAGCAAGTGGTAGATCTGACACT
GCCCAAGGTTGAAGCCATAAAGAAAAGACTGGGCTCCCTGGCAGATGAGTTTAAAGAAGTGTCTACCCTCCAG
GTTATAATCCTGAGGGAAAAATTGCCAAGAGAAAAGCAGACAATGAAGGTTCTGCAAGTAAAAAGCCCAAGGT
AGAGTTATCAGAAGAGGAGCTGAAGGACCTTTTTGCCAAGGGCACACTGGGCAAGCTCACTGTGCCTGCACTG
AGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGACCGAAGAAGCAGGAAGTACTCGAGGCTCTCAGCAGAC
ACTTGGAGAAGAACTGA

➤ Fwd1

TTccTCGaCTTGATGCaCCTGAAGAAGCGAGGGGGCTTTGACGTGTCCTTGTCTACaGAGACATCATCNGCATCG
CTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAAGCAAGCTGGAAGACCTGCTAAGGAAGGTTTCGAG
CCAAGGAGACCAAAAAGCGAGTGCTGTCCAGGTTAAAGTTTAAAGCTCGGCAAAGACGTAGCACTCATGGTGGG
CGTTTATAACTTGGTCCAGAAAGCTAACAAGCCTTTTCCAGTGAGGCTGTATCGAGAAACAAACGAACCAAGTGA
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GGAGTCCCTGGTCAACGGGAGCTCAACCTTGTTAGCGCCCTGCTACCAAGTGTGTGGAGAAGGAGGTCATA
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AGATGATCAGAACATTCAGGTGACTCCCGCagGCTTCCAGCTTGTCTTCTCCCTTACGCCGATGACAAGCGGAA
GGTGCCCTTTACGGAGAAgGTGATGGCCAACCCGGAACAGATAGACAAGATGAAGGCCATTGTTCAAAAAGCTCC
GCTTTACATACAGGAGCGACAGTTTCGAGAACCCAGTGCTGCAGCAGCACTTCCGGAACCTGGaNGNCCTANCT
TTGGACATGATGGAGTCGGANCAAGTGGTANATCTGACACTGCCAANNNGAAGCCATAAANAANAANACTGGGC
TCCCTGGNANANGANTTTAAAGAACTTGTCTACCNTNCAGNTNNNATCCTGNNGGAAAANTGNNANNNNAAA
GCNNANANGNNNNNTGCNAGTAAAAGCCNNNNNNNNNTNTCANANAGNNNNNTNAGANNTTTG

➤ **Rev1**

CNCGANGGNNNGNNNNATCANNNNNNNNANNNNNANNANGGGGATNNGNCCNGNNNGNNNGNNNCNAA
NNTCAGANTNGGANTNNNNNTNNNAANTGNGGNGAGGAAGAGGAAGAGGAGGAGCAGAGCCNGANACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTNNGGTTGANGCCTNCAGGGNTATGTTTGANNNT
CAGGGTGAAGACGAGCTCACANNTTTTGATATGAGCATNCAGTGTATCCAGAGTGTGTACACCAGTAAGATCATA
AGCAGCGATNGGGANNTNTTGGCAGTGGTGTNTATGGTACCGAGAAAGACAAAAATTCAGTGAANTTCAAAA
GTATTTATNTCTTACAAGATNTGGATAACCCAGGAGNTAAACGAGTGTTAGAGCTTGACCGCTTTAAGGGACAAC
AGGGGAAAAAACATTTNNGAGACACAATTGGCCATGGGTCTGANTACTCTTTGAGTGAAGTGTNNNNNNNN
GTNNNNNNNNNTNNNNNNNNNNNCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAANCNNNNNNNANCAANN
CGNNNCNNCNCNNNNNNNNNCNNNTTNNNCNNCAANNNNNACNCGNCNNANNNNNNNNGANNCCNCN
GACNNTNNCATNNCNCNTNGCNNNCNNNCNNNNNANNCANNNAANGNCCTTNNCNCNNGTNNNNNNCTNNN
NCGNGANNTNCTCNANNCNNCCNNNNNNNNNANNNCNNNNGNCNNNNNNNNNNNNNNNNNNNNAAACNNN
CANCANNNGNTNNACNNCNTTNCNGNCNNNAACNNNAACNNNNNANCACNCNCNNNNNNNNNCNNCNCN
NCNNNNACCNNCCTNNNCNNNTCNNNCNGCNTNCNTNACTNCNNNNNNNNAAACNCCCAANNCTNANCC
NNNNNCNATGCNNANNNANNTCNCNNGANNNCANGNACACNNNNACNCCCCCTCGCNACNNNNNNNNNN
CANNNGNTCANGANCNCNGNTNCCCACNGATCTCTGNCTTTNGNCCNNNNCCNGCNCNNTGGCNNNN
NNNNNACCAGAGGAG

➤ **Synthèse séquençage DiT0 :**

ATGTCAGAGTGGGAATCCTACTACAAAACCTGAGGGTGAGGAAGAGGAAGAGGAGG	55
AGCAGAGCCCTGACACAAATGGAGAATATAAATATTAGGAAGAGATAGTTTGATTTTTC	115
TGGTTGACGCCTCCAGGGCTATGTTGAATCTCAGGGTGAAGACGAGCTCACACCTTTTG	175
ATATGAGCATCCAGTGTATCCAGAGTGTGTACACAGTAAGATCATAAGCAGCGATCGGG	235
ATCTCTTGGCAGTGGTGTCTATGGTACCGAGAAAGACAAAAATTCAGTGAACCTTCAAAA	295
GTATTTATGTCTTACAAGATCTGGATAACCCAGGAGCTAAACGAGTGTAGAGCTTGACC	355
GCTTTAAGGGACAACAGGGGAAAAAACATTTCCGAGACACAATTGGCCATGGGTCTGACT	415
ACTCTTTGAGTGAAGTGTCTGCGGTCTGTGCCAACCTCTTCAGCGACGTCCAGTTCAAGA	475
TGAGTCATAAGAGGATCATGCTATTACCAATGAAGATGACCCCATGGTAATGACAGTG	535
CCAAAGCCAGCCGGGCCAGGACCAAGCCAGCGATCTGCGGGACACTGGGATCTTCCTCG	595
ACTTGATGCACCTGAAGAAGCGAGGGGGCTTTGACGTGTCTTGTCTACAGAGACATCA	655
TCAGCATCGCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAAGCAAGCTGGAAG	715
ACCTGCTAAGGAAGGTTTCAGCCAAGGAGACCAAAAAGCGAGTGTCTGCCAGGTAAAG	774
TTTAAGCTCGGCAAGACGTAGCACTCATGGTGGGCGTTTATAACTTGGTCCAGAAAGCT	834
AACAAGCCTTTTCCAGTGAGGCTGTATCGAGAAACAACGAACCAAGTGAAGTAAAGACA	894
AGGACTTTTAATGTAAACACAGGCAGTCTGCTCCTGCCAGTGATACCAAGCGGTCTCTG	954
ACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAAACAGAGGAGCTGAAGCGGTTT	1014
GATGAGCCAGGTTTGATTCTCATGGGCTTTAAGCCCATGGTAATGCTGAAGAACCACCAC	1074
TACCTGAGGCCCTCTCTGTTCCTGTACCCAGAGGAGTCCCTGGTCAACGGGAGCTCAACC	1134
TTGTTACAGCGCCCTGCTACCAAGTGTGTGGAGAAGGAGGTCATAGCAGTGTGTAGATAC	1194
ACAGCCCGAAAGAATGCTCCCCCTATTTTGTGGCTTTGGTGCCACAGGAAGAGGAGCTA	1254
GATGATCAGAACATTCAGGTGACTCCCGCAGGCTTCCAGCTTGTCTTCTCCCTTACGCC	1314
GATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGATGGCCAACCCGGAACAGATAGAC	1374
AAGATGAAGGCCATTGTTCAAAAGCTCCGCTTTACATACAGGAGCGACAGTTTCGAGAAC	1434

CCAGTGCTGCAGCAGCACTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTCG	1494
GAGCAAGTGGTAGATCTGACACTGCCCCAAGGTTGAAGCCATAAAGAAAAGACTGGGCTCC	1554
CTGGCAGATGAGTTTAAAGAACTTGTCTACCTCCAGGTTATAATCCTGAGGGAAAAATT	1614
GCCAAGAGAAAAGCAGACAATGAAGGTTCTGCAAGTAAAAAGCCCAAGGTAGAGTTATCA	1674
GAAGAGGAGCTGAAGGACCTTTTTGCCAAGGGCACACTGGGCAAGCTCACTGTGCCTGCA	1734
CTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGACCGAAGAAGCAGGAACCTACTC	1794
GAGGCTCTCAGCAGACACTTGGAGAAGAACTGA	1827

MSEWESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDASRAMFESQGEDELTPFDMSIQCIQSVYTSKIISDR
 DLLAVVFGTEKDKNSVNFKSIYVLQDLNPGAKRVLELDRFKGQQGKKHFRDTIGHGSDYSLSEVLWVCANLFS
 VQFKMSHKRIMLFTNEDDPHGNSAKASRARTKASDLRDTGIFLDMHLKKRGGFDVSLFYRDIISIAEDEDLGVHF
 EESSKLEDLLRKVRAKETKKRVLSRLKFKLGKDVALMVGVYNLVQKANKPFPVRLYRETNEPVKTKTRTFNVNTGSLL
 LPSDTKRSLTFGTRQIVLEKEETEELKRFDEPGLILMGFKPMVMLKNHHYLRPSFLYPEESLVNGSSTLFSALLTKC
 KEVIAVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVMANPEQIDKMKAIVQ
 KLRFTYRSDSFENPVLQQHFRNLEALALDMMMESEQVVDLTLPKVEAIKKRLGSLADEFKELVYPGYNPEGKIAKRKA
 DNEGSASKPKVELSEEELKDLFAKGTLGKLTVPALRDICKAYGLKSGPKKQELLEALSRLHLEKN-

➤ **Blast contre banque rat :**

☒	Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6) mRNA	Norway rat	3369	3369	100%	0.0	99.95%	2070	NM_139080.2
☒	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 6 mRNA (cDNA clone MGC-93...	Norway rat	3369	3369	100%	0.0	99.95%	2098	BC078718.1
☒	Rattus norvegicus cDNA clone IMAGE:6918045 containing frame-shift errors	Norway rat	3369	3369	100%	0.0	99.95%	2056	BC061528.1
☒	Rattus norvegicus mRNA for G22p1 complete cds	Norway rat	3347	3347	100%	0.0	99.73%	1964	AB066102.1
☒	PREDICTED: Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6) transcript variant X1 mRNA	Norway rat	2071	3075	91%	0.0	99.91%	1919	XM_008765671.2

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

11012013014015016017018019020021022023024025026027028029030031032033034035036037038039040041042043044045046047048049050051052053054055056057058059060061062063064065066067068069070071072073074075076077078079080081082083084085086087088089090091092093094095096097098099010001010102010301040105010601070108010901100111011201130114011501160117011801190120012101220123012401250126012701280129013001310132013301340135013601370138013901400141014201430144014501460147014801490150015101520153015401550156015701580159016001610162016301640165016601670168016901700171017201730174017501760177017801790180018101820

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Mutation en 1114 C<T

➤ **Différence au niveau PROT :**

110120130

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MSEMESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDSRAMFESQGEDELTPTFDMSTQICIQSVYTSKIISDSDROLLAVVYFGTEKDKNSVNFKSIYVLQDLNPGAKRVLELDRFKGQGGKKHFR

MSEMESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDSRAMFESQGEDELTPTFDMSTQICIQSVYTSKIISDSDROLLAVVYFGTEKDKNSVNFKSIYVLQDLNPGAKRVLELDRFKGQGGKKHFR

MSEMESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDSRAMFESQGEDELTPTFDMSTQICIQSVYTSKIISDSDROLLAVVYFGTEKDKNSVNFKSIYVLQDLNPGAKRVLELDRFKGQGGKKHFR

131140150160170180190200210220230240250260

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Consensus

DTIGHGSDYSLSEVLHVCANLFSQVQFKMSHKRIHLFTNEDDPHGNDSAKASRARTKASDLRDTGIFLDLMLKKRG6FDVSLFYRDIISIAEDEDLGVHFEESKLEDLLRKVRAKETKKRVLSRLKFK

DTIGHGSDYSLSEVLHVCANLFSQVQFKMSHKRIHLFTNEDDPHGNDSAKASRARTKASDLRDTGIFLDLMLKKRG6FDVSLFYRDIISIAEDEDLGVHFEESKLEDLLRKVRAKETKKRVLSRLKFK

DTIGHGSDYSLSEVLHVCANLFSQVQFKMSHKRIHLFTNEDDPHGNDSAKASRARTKASDLRDTGIFLDLMLKKRG6FDVSLFYRDIISIAEDEDLGVHFEESKLEDLLRKVRAKETKKRVLSRLKFK

261270280290300310320330340350360370380390

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LKGDVALHVGYYNLVQKANKPFPVRLYRETNEPVKTKTRTFNVNTGSLLLPSDTKRSLTFGTRQIVLEKEETEELKRFDPEGLILMGFKPMVHMLKNHHYLRPSLFLYPEESLVNGSSTLFSALLTKCVEK

LKGDVALHVGYYNLVQKANKPFPVRLYRETNEPVKTKTRTFNVNTGSLLLPSDTKRSLTFGTRQIVLEKEETEELKRFDPEGLILMGFKPMVHMLKNHHYLRPSLFLYPEESLVNGSSTLFSALLTKCVEK

LKGDVALHVGYYNLVQKANKPFPVRLYRETNEPVKTKTRTFNVNTGSLLLPSDTKRSLTFGTRQIVLEKEETEELKRFDPEGLILMGFKPMVHMLKNHHYLRPSLFLYPEESLVNGSSTLFSALLTKCVEK

391400410420430440450460470480490500510520

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EVIACRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVHANPEQIDKMKAIYQKLRFITYRSDSFENPVLQQHFRNLEALALDMMHESEQVVDLTLPKVEAIKKRLGSLA

EVIACRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVHANPEQIDKMKAIYQKLRFITYRSDSFENPVLQQHFRNLEALALDMMHESEQVVDLTLPKVEAIKKRLGSLA

EVIACRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVHANPEQIDKMKAIYQKLRFITYRSDSFENPVLQQHFRNLEALALDMMHESEQVVDLTLPKVEAIKKRLGSLA

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DEFKELYYPGYNPEGKIAKRKADNEGSASKPKVELSEEELKDLFAKGTLGKLTYPALRDICKAYGLKSGPKKQELLEALSRHLEKN

DEFKELYYPGYNPEGKIAKRKADNEGSASKPKVELSEEELKDLFAKGTLGKLTYPALRDICKAYGLKSGPKKQELLEALSRHLEKN

DEFKELYYPGYNPEGKIAKRKADNEGSASKPKVELSEEELKDLFAKGTLGKLTYPALRDICKAYGLKSGPKKQELLEALSRHLEKN

pas de diff au niv prot

		Name	Score	Score	Cover	Value	Ident	Len	
☒	X-ray repair cross-complementing protein 6 [Rattus norvegicus]	Norway_rat	1247	1247	100%	0.0	100.00%	608	NP_620780.2
☒	G22p1 [Rattus norvegicus]	Norway_rat	1242	1242	100%	0.0	99.67%	609	BAB83858.1
☒	PREDICTED: X-ray repair cross-complementing protein 6 isoform X1 [Rattus norvegicus]	Norway_rat	1094	1094	100%	0.0	90.30%	554	XP_008763893.1

Flag BirA Xrcc6 DiT0 cloneA OK,

○ FlagBirA Xrcc6 DiT24hLPS clone A

➤ B3Fwd DiT24h

312NT

ATGTCAGAGTGGGAATCCTACTACAAAAGTGGGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTCTGGTTGACGCCTCCAGGGCTATGTTTGAATCTC
AGGGTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAGTAAGATCATAA
GCAGCGATCKGNNNNACNNNGNNNTNNTCNTCNANNTGATGCACCTGAANAANCNANGGGGCTTTGACNTG
TCCTTGNTCTNCNNANAC

➤ B3Fwd du 25/11

ATGTCAGAGTGGGAATCCTACTACAAAAGTGGGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTCTGGTTGACGCCTCCAGGGCTATGTTTGAATCTC
AGGGTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAGTAAGATCATAA
GCAGCGATCTGNNNGACNNNGNNATCTTCNTCNANNNGATGNANCNGAANAANCAGAGGGGGCTTTGACNT
GTCCTTGNTCTNCNNANNCNTNNNNNNNNNTCNNNGANGATNANGANNNNNNNNNNNNNTTTGANGANN
NNNNNNNNNNNGNNNNANNNNGNNNANGAANGNNCNANNNNNNNNGANNNNNNNNNNNTGCTGNCC
NNNNNNNNNTNNANNCTCGNNAANNACNTANNACTCNTGNNGGGCNNNNNTANNNTGNNNNNGANNNN
TNNCNNNNNTTTNNNNNNNNNGNNNNNNNNNNNAACGNNNNAGTGAAANNTNNNACNANNANT
TTTAATGNNNACNNNGNNANTCNGNTCCTNNNCNNTGNNNCCNANCNGNCTCTGACTTTNGGGACNNNN
NNANNGTGNTGGANAAAGANGAAACNNANNANCTNNAGCNNNTGATGANCNNGNTNNGATTCTNNNGN
NCTTTAAGCCNTGGANNTGCTGAAGANNNNNNNCTNCCNGNNGNCCTNTCTGTTNCTGNNCCCNAGNAN
NCNNTGNNCACGNNNCTCANCNNGTTCANNGNNCTNNNNANNNNTNNGTNNANNAGA

➤ BGHRev DiT24h

983NT

TTTTCCAGNGANGNTGTATNGAGAANCAAACGANCCAGTGAAANTAAGACAAGGACTTTAATGTAAACACAGG
CAGTCTGNTCCTGCCAGTGATNCCAAGCGGTNTNTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAG
GAAACAGAGGAGCTGaAGCGTTTGATGAGCCAGTTTGATTCTCATGGGCTTTAAGCCCATGGTAATGCTGAA
GAACCACTACTAcTGAGGCCCTCTGTTCCTGTACCCAGAGGAGTCCCTGGTCAACGGGAGCTCAACCTTGTT
CAGCGCCCTGCTCACCAAGTGTGTGGAGAAGGAGGTCATAGCAGTGTGTAGATACACAGCCCGAAAGAATGTCT
CCCCTTATTTGTGGCTTTGGTGCCACAGGAAGAGGAGCTAGATGATCAGAACATTCAGGTGACTCCCGCAGGC
TTCCAGCTTGCTTCCTCCCTTACGCCGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGATGGCCAACCC
GGAACAGATAGACAAGATGAAGGCCATTGTTCAAAGCTCCGCTTTACATACAGGAGCGACAGTTTCGAGAACC
CAGTGCTGCAGCAGCACTTCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTCGGAGCAAGTGGTAGA
TCTGACACTGCCAAGGTTGAAGCCATAAAGAAAAGACTGGGCTCCCTGGCAGATGAGTTTAAAGAACTTGCT
ACCCTCCAGGTTATAATCCTGAGGGAAAAATTGCCAAGAGAAAAGCAGACAATGAAGGTTCTGCAAGTAAAAAG
CCAAGGTAGAGTTATCAGAAGAGGAGCTGAAGGACCTTTTGGCCAAGGGCACACTGGGCAAGCTCACTGTGC
CTGCACTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGACCGAAGAAGCAGGAACACTCGAGGCTCT
CAGCAGACACTTGAGAGAAGAACTGA

312AA

DKDFNVNTGSLXLPDXKRXXTFGTRQIVLEKEETEELKRFDEPGLILMGFKPMVMLKNHHYLRPSLFLYPEESLVNG
SSTLFSALLTKVEKEVIAVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRVPFTEKVMAN
PEQIDKMKAIVQKLRFYRSDSFENPVQLQHFRNLEALALDMMESEQVVDLTLPKVEAIKKRLGSLADEFKELVYPP
GYNPEGKIAKRKADNEGSASKPKVELSEEELKDLFAKGTGLKLTVPALRDICKAYGLKSGPKKQELLEALSRLHLEKN-

➤ **Fwd2**

GaCTTGATGCaCCTGAAGAAGCGAGGGGGCTTTGACGNGTCNTTGNTCTACNgAGACATCATCNGCATCGCTGA
GGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAAGCNAAGCTGGAAGACCTGCTAAGGAAGGTTTCGAGCCAA
GGAGACCAAAAAGCGAGTGCTGTCCAGGTTAAAGTTTAAAGCTCGGCAAAGACGTAGCACTCATGGTGGGCGTT
TATAACTTGGNCCAGAAAGCTAACAAGCCTTTTCCNGTGAGGCTGTATCGAGAAACAAACGAACCAAGTGAAAAC
TAAGACAAGGACTTTTTAATGTAAACACAGGCNGTCTGCTCCTGCCAGTGATACCANGCGGTCTCTGACTTTTGG
GACGCGTCAGATTGTGCTGGAGAAAGAGGAAACAGAGGAGCTGAAGCGGTTTGATGAGCCAGGTNTGATTCTC
ATGGGCTTTAAGCCCATGGTAATGCTGAAGAACCACCACTACCTGAGGCCCTCTCTGTTCTGTNCNNNNAGGA
GTCCCTGGTCAACGGGAGCTCAACCTTGTTACGCGCCCTGCTCACCANGTGTGTGGAGAAGGAGGTCATAGCA
GTGTGTAGATACACAGNNNGNANGAATGTCTCCCTNATTTTGNNGCTTTGGTGCCACAGGAAGANGAGCTAG
ATGATCAGAACATTAGGTGACTCCCGCAGGCTTCCAGCTTGCTTCTCCTTACGCCGATGACAAGCGNAANG
TGCCCTTTACGGAGAANGTGATGGNCNNCCCCGGAACAGATAGACNAGATGAAGGNCATTGTTCAAAAGCTCCG
CTTTACNTACANGAGCGACAGTTTCGAGAACCCAGTGCTGCAGCAGCACTTCCGGNACCTGGNNGNCCTAGCT
TTGGACNTGATGGANTCGGAGCAGTGNTAGATCTGACNCTGCCNNNNNTGAAGCCNTNAANAAAAANACTGGG
CTCCCNNGCANATGANTTTAANAACCTGNCTANCCTCCNNNNNNNANCTGANGGAAAATTGCCANNNAAAAAN
NNNANNTGAAGGTNCTGCAANNNAANCCC

➤ **Séquençage mauvais**

➤ **Synthèse séquençage DiT24hLPS :**

ATGTCAGAGTGGAATCCTACTACAAAAGTGAAGGTGAGGAAGAGGAAGAGGAGGAGCAG	60
AGCCCTGACACAAATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTCTGGTT	120
GACGCTCCAGGGCTATGTTTGAATCTCAGGGTGAAGACGAGCTCACACCTTTTGATATG	180
AGCATCCAGTGTATCCAGAGTGTGTACACCAGTAAGATCATAAGCAGCGATCTGNNGAC	240
NNNGNNATCTTCNTCNANNGATGNANCNGAANAANC---AGGGGGCTTTGACNTGTCC	297
TTGNTCTNCNNANNCNTNNNNNNNNNTCNNNGANGATNANGANNNNN-----NNNNNNNCT	352
TTGANGANNNNNNNNNNNGNNNNANN--NGNNNANGAANGNNCNANNNNNNNNGANNNN	410
NNNNNNNT--GCTGNCCNNNNNNNNNTNNANNTCTCGNNAANNACNTANNACTCNTGNNG	468
GGCNNNNNTANN--TGNNNNNGANNNTNNCNNNNNTTTCNNNNNNNNNNNGNNNNNN	525
NNNNNNAACGNNNNAGTGAAANNTNNNACNANNANTTTAATGNNNACNNNGNNANTCNG	585
NTCCTNNNCNNTG-----NNCCNANCNGNCTCTGACTTT-----NGGGACNN	628
NNNN--ANNGTGN TGANAAGANGAAACNNANNANCTNNAGCNNNNTGATGANCNNGN	686
TNNGATTCTNNNGNNCTTTAAGCCNTGGANNTGCTGAAGANNNNNNNCTNCCNGNNGNC	746
GTTTAAGCTCGGCAAAGACGTAGCACTCATGGTGGGCGTTTATAACTTGGNCCAGAAAGC	833
TAACAAGCCTTTTCCNGTGAGGCTGTATCGAGAAACAAACGAACCAAGTGAAAACCTAAGAC	893
AAGGACTTTTAAATGTAAACACAGGCAGTCTGCTCCTGCCAGTGATACCAAGCGGTCTCT	953
GACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAAACAGAGGAGCTGAAGCGGTT	1013
TGATGAGCCAGGTTTGATTCTCATGGGCTTTAAGCCATGGTAATGCTGAAGAACCACCA	1073
CTACCTGAGGCCCTCTCTGTTCCGTACCCAGAGGAGTCCCTGGTCAACGGGAGCTCAAC	1133
CTTGTTCAGCGCCCTGCTCACCAGTGTGTGGAGAAGGAGGTATAGCAGTGTGTAGATA	1193
CACAGCCCGAAAGAATGTCTCCCTTATTTTGTGGCTTTGGTGCCACAGGAAGAGGAGCT	1253
AGATGATCAGAACATTCAGGTGACTCCCGCAGGCTTCCAGCTTGCTTCTCCTCCCTTACGC	1313
CGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGATGGCCAACCCGGAACAGATAGA	1373
CAAGATGAAGGCCATTGTTCAAAAGCTCCGCTTTACATACAGGAGCGACAGTTTCGAGAA	1433
CCCAGTGCTGCAGCAGCACTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTC	1493
GGAGCAAGTGGTAGATCTGACACTGCCCAAGGTTGAAGCCATAAAGAAAAGACTGGGCTC	1553
CCTGGCAGATGAGTTTAAAGAACTTGCTACCTCCAGGTTATAATCCTGAGGGAAAAAT	1613
TGCCAAGAGAAAAGCAGACAATGAAGGTTCTGCAAGTAAAAAGCCCAAGGTAGAGTTATC	1673
AGAAGAGGAGCTGAAGGACCTTTTTGCCAAGGGCACACTGGGCAAGCTCACTGTGCCTGC	1733
ACTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGACCGAAGAACGGAACCTACT	1793
CGAGGCTCTCAGCAGACACTTGGAGAAGAACTGA	

➤ **Blast contre banque rat :**

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

Séquençage Fwd pas très long, il manque des NT au milieu

➤ **Différence au niveau PROT :**

Flag BirA Xrcc6 DiT24hLPS (clone A) mauvais séquençage, pas
envoyé en interne (T0 OK)

○ pCR4Blunt Xrcc6 DiT48hMix clone C VOIR SEQUENCAGE JUL

➤ Fwd DiT48hMix 1052NT

ATGTCAGAGTGGGAATCCTACTACAAAAGTGGGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTCTGGTTGACGCCTCCAGGGCTATGTTTGAATCTC
AGGGTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAAGTAAGATCATAA
GCAGCGATCGGGATCTCTTGGCAGTGGTGTCTATGGTACCGAGAAAGACAAAAATTCAGTGAACCTTCAAAAGT
ATTTATGTCTTACAAGATCTGGATAACCCAGGAGCTAAACGAGTGTAGAGCTTGACCGCTTTAAGGGACAACAG
GGGAAAAAACATTTCCGAGACACAATTGGCCATGGGTCTGACTACTCTTTGAGTGAAGTGCTCTGGGTCTGTGC
CAACCTCTTCAGCGACGTCCAGTTCAAGATGAGTCATAAGAGGATCATGCTATTCACCAATGAAGATGACCCCAT
GGTAATGACAGTGCCAAAGCCAGCCGGGCCAGGACCAAAGCCAGCGATCTGCGGGACACTGGGATCTTCTCG
ACTTGATGCACCTGAAGAAGCGAGGGGGCTTTGACGTGTCCTTGTCTACAGAGACATCATCAGCATCGCTGAG
GATGAGGAcCTCGGGGTTCACTTTGAGGAGTCAAGCAAGCTGGAAGAcCTGCTAAgGAAgGTTTCGAGCCAAGG
AGANCAAAAAGCGAGTGCTGTCCAGGTTAAAGTTTAAAGCTCGGCAAAGACGTAGCACTCATGGTGGGCGTTTAT
AACTTGGTCCAGAAAGCTAACAAGCCTTTTCCAGTGAGGCTGTATCGAGAAACAAACGAACCAAGTGAAGTAA
NNCAAGGACTTTTAAATGTAAACACNGGCAGTCTGCTCCTGCCAGTGATNCNNNNNGGTCTCTGACTTTTNGG
NNNGTCANANNGTGCTNGNNAANNNAANCNNNNNNCTNANCNNNTNGATGANNNNGTTGATNTNATGG
GCTTNANCCANGGNNNTGCT

➤ Rev DiT48hMix 748NT

Gaggccctctctgttctgtacccagaggagtccttggtcaacgggagctcaacctgttcagcgccctgctcaccaagtgtgtggagaaggaggtc
atagcagtgttagatacacagcccgaaagaatgtctcccttattttgtggctttggtgccacaggaagaggagctagatgatcagaacattcagg
tgactcccgaggcttcagctgtcttctccctacgccgatgacaagcggaaggtgccctttacggagaaggtgatggccaaccggaacagat
agacaagatgaaggccattgttcaaaagctccgctttacatacaggagcgacagtttcgagaaccagtgctgcagcagcacttccggaactgga
ggccctagctttggacatgatggagtcggagcaagtggttagatctgacactgcccaaggttgaagccataaagaaaagactgggctccctggcag
atgagtttaagaacttgtctaccctccaggttataatcctgagggaataatgccaagagaaaagcagacaatgaaggttctgcaagtaaaaag
cccaaggtagagttatcagaagaggagctgaaggaccttttgccaagggcacactgggcaagctcactgtgcctgactgagggacatctgcaa
ggcctatgggctaagagtggaaccaagaagcaggaactactcgaggctctcagcagacacttgagaagaactga

➤ B3Fwd 25/11

ATGTCAGAGTGGGAATCCTACTACAAAAGTGGGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTCTGGTTGACGCCTCCAGGGCTATGTTTGAATCTC
AGGGTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAAGTAAGATCATAA
GCAGCGATCTGCGGGACACTGGGATCTTCTCGACTTGATGCACCTGAAGAAGCGAGGGGGCTTTGACGTGTCC
TTGTTCTACAGAGACATCATCAGCATCGCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAAGCAAGCT
GGAAGACCTGCTAAGGAAGGTTTCGAGCCAAGGAGACCAAAAAGCGAGTGCTGTCCAGGTTAAAGTTTAAAGCTC
GGCAAAGACGTAGCACTCATGGTGGGCGTTTATAACTTGGTCCAGAAAGCTAACAAGCCTTTTCCAGTGAGGCT
GTATCGAGAAACAAACGAACCAAGTGAAGTAAAGCAAGGACTTTTAAATGTAAACACAGGCAGTCTGCTCCTGC
CCAGTGATACCAAGCGGTCTCTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAAACAGAGGAGCT
GAAGCGGTTTGATGAGCCAGGTTTGATTCTCATGGGCTTTAAGCCCATGGTAATGCTGAAGAACCACCACTACCT
GAGGNCCTCTCTGTTCTGTACCCAGAGGANTCCCTGGTCAACGGGAGCTCAACCTTGNTCAGCGCCCTGCTCA

CCAAGTGTGNGGAGAAGGNGGNCATANCANTGNGNANATNCNCAGCCCCGAAANAATGNCTNCCCTTANTTTG
NNNNTNNGNGNNNCNGNANNNNNNNNTANATGATCANANATTNNNGACTCCNNCNNNTNCNNCT

➤ BGHRev 25/11

CAANCNTTNCCAGNGNNNTGTATNGAGAANCAAANGANCCAGTGAAAAANTAAGNCAAGGACTNTTAANGT
AAACACAGNCAGTNTGNTNNTGCCAGTGATACCAAGCGGTCTNNGACTTTTGGGACGCGTCAGATTGTGNTG
GNGAAAGAGGAANCAGAGGAGCTGAAGCGGTTTGATGANNACAGGTTTGATTNTCATGGNCTTTAAGCNCANG
GTAATGCTGAAGAACCAcCAcTactGAGGCCCTcTcTGTTCcTGTACCCAGAGGAGTCcTGGTCAACGGGAGCTCA
ACcTTGTTCAGCGCCCTGCTCACCAAGTGTGTgGAGAAGGAGgTCATNGCANTGTGTAGATACACAGCCcGAAAG
AATGTCTCCCcTTATTTTGTGGCTTTGGTGCCACAGGAAGAGGAGCTAGATGATCAGAACATTACAGGTGACTCCC
GCAGGCTTCCAGCTTGTCTTCTCCCTTACGCCGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGATGGC
CAACCCGGAACAGATAGACAAGATGAAGGCCATTGTTCAAAAGCTCCGCTTTACATACAGGAGCGACAGTTTCG
AGAACCCAGTGCTGCAGCAGCACTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTCGGAGCAAGT
GGTAGATCTGACACTGCCCAAGGTTGAAGCCATAAAGAAAAGACTGGGCTCCNGNCAGATGAGTTTAAAGAA
CTTGTCTACCTCCAGGTTATAATCCTGAGGGAAAAATTGCCAAGAGAAAANCAGACAATGAAGGTTCTGCAAGT
AAAAAGCCCAAGGTAGAGTTATCAGAAGAGGAGCTGAAGGACCTTTTTGCCAAGGGCACACTGGGCAAGCTCA
CTGTGCCTGCACTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGNCCGAAGAAGCAGG



Rev1

CCCAGATNNTGATNGNNNCGNCATCANCATGGCATNNGNGNNNNGANANCGTGGTGNNCNNNGGNTGGAN
CNCNCGCNGGAGNCNGGCNTCAACNTGGACCGGAACNNNTGGCCGCCATGNTGATCCGGGAGNTGCGGGCC
GCCCTGGAGCTGTTTCGAGCAGGAGGNCCTGNCCCCNTNNNGAGCCGGTGGGAGAAGCTGGACAACCTTCATCA
ACCGGCCCGTGAAGCTGATCNTNGGCGACAAGGAGATNTTCGGCATCAGCCGGGGCATCGACAAGCAGGGCG
CCcTGCTGCTGGAGCAGGACGGCATCATCAAGCCCTGGATGGGCGGCGAGATCAGCcTGCGGAGCGCCGAGAA
GGGGGGATCTGGCCCCGGCGGCGGCCAATGTCAGAGTGGGAaTCcTACTACAAAACCTGAGGGTGAGGA
AGAGGAAGAGGAGGAGCAGAGCCCTGACACAAATGGAGAATATAAATATTAGGAAGAGATAGTTTTGATTTTTC
TGTTGACGCCTCCAGGGCTATGTTTGAATCTCAGGGTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGT
GTATCCAGAGTGTGTACACCAGTAAGATCATAAGCAGCGATCTGCGGGACACTGGGATCTTCTCGACTTGATGC
ACCTGAAGAAGCGAGGGGGCTTTGACGTGTCCTTGTCTACAGAGACATCATCAGCATCGCTGAGGATGAGGAC
CTCGGGGTTCACTTTGAGGAGTCAAGCAAGCTGGAAGACCTGCTAAGGAAGGTTGAGCCAAGGAGACCAAA
AAGCGAGTGCTGTCCAGGTTAAAGTTTAAAGCTCGGCAAGACGTCAGCACTCATGGTGGGCGTTTATAACTTGGT
CCAGAAAGCTAACAAGCCTTTTCCAGTGAGGCTGTATCGAGAAACAAACGAACCAAGTGAAGAACTAAGACAAGG
ACTTTTAATGTAAACACAGGCAGTCTGCTCCTGCCAGTGATACCAAGCGGTCTCTGACTTTTGGGACGCGTCAG
ATTGTGCTGGAGAAAGAGGAAACAGAGGAGCtGAAGCGGTTTGATGAGCCAGgttgAT

➤ Synthèse séquençage DiT48hMix :

ATGTCAGAGTGGGAATCCTACTACAAAACCTGAGGGTGAGGAAGAGGAAGAGGAGGAGCAG	60
AGCCCTGACACAAATGGAGAATATAAATATTTCAGGAAGAGATAGTTTGATTTTTCTGGTT	120
GACGCCTCCAGGGCTATGTTTGAATCTCAGGGTGAAGACGAGCTCACACCTTTTGATATG	180
AGCATCCAGTGATCCAGAGTGTGTACACCAGTAAGATCATAAGCAGCGATCGGGATCTC	240
TTGGCAGTGGTGTTCTATGGTACCGAGAAAGACAAAATTCAGTGAACCTCAAAAGTATT	300
TATGTCTTACAAGATCTGGATAACCCAGGAGCTAAACGAGTGTTAGAGCTTGACCGCTTT	360
AAGGGACAACAGGGGAAAAAACATTTCCGAGACACAATTGGCCATGGGTCTGACTACTCT	420
TTGAGTGAAGTGCTCTGGGTCTGTGCCAACCTCTTCAGCGACGTCCAGTTCAAGATGAGT	480
CATAAGAGGATCATGCTATTACCAATGAAGATGACCCCCATGGTAATGACAGTGCCAAA	540
GCCAGCCGGGCCAGGACCAAGCCAGCGATCTGCGGGACACTGGGATCTTCTCGACTTG	600

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ATGCACCTGAAGAAGCGAGGGGGCTTTGACGTGTCCTTGTCTACAGAGACATCATCAGC      660
ATCGCTGAGGATGAGGAcCTCGGGGTTCACCTTTGAGGAGTCAAGCAAGCTGGAAGAcCTG      720
CTAAgGAAgGTTTCGAGCCAAGGAGANCAAAAAGCGAGTGCTGTCCAGGTAAAGTTTAAAG      780
CTCGGCAAAAGACGTAGCACTCATGGTGGGCGTTTATAACTTGGTCCAGAAAGCTAACAAAG      840
CCTTTTCCAGTGAGGCTGTATCGAGAAAACAAACGAACCAAGTGAAGAACTAANNCAAGGACT      900
TTTAATGTAAACACNGGCAGTCTGCTCCTGCCAGTGATNCNNNNNGGTCTCTGACTTTT      960
NGGNNNNGTGANANNGTGCTNGNNAANNNAANCNNNNNNCTNANCNNNT----NGATGAN      1020
-----NNNGTTGATNTNATGGGCTTNANCCANGGNNNTGCTG      1080
aggccctctctgttccctgtacccagaggagtcctctggtcaacgggagctcaaccttggtc      1140
agcgcctctgtcaccaagtgtgtggagaaggaggtcatagcagtgtgtagatacacagcc      1200
cgaaaagaatgtctcccttattttgtggctttggtgccacaggaagaggagctagatgat      1260
cagaacattcaggtgactcccgaggtctccagcttcttctcctctacgccgatgac      1320
aagcggaaggtgccctttacggagaaggtgatggccaacccggaacagatagacaagatg      1380
aaggccattgttcaaaagctccgctttacatacaggagcgacagtttcgagaacccagtg      1440
ctgcagcagcacttccggaacctggaggccctagctttggacatgatggagtcggagcaa      1500
gtggttagatctgacactgccaaggttgaagccataaagaaaagactgggctccctggca      1560
gatgagtttaagaacttgtctaccctccaggttataatcctgagggaaaaattgccaaag      1620
agaaaagcagacaaatgaaggttctgcaagtaaaaagcccaaggtagagttatcagaagag      1680
gagctgaaggacctttttgccaagggcacactgggcaagctcactgtgcctgcactgagg      1740
gacatctgcaaggcctatgggctaaagagtggaccgaagaagcaggaactactcgaggct      1800
ctcagcagacacttggagaagaactga      1827

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MSEWESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDASRAMFESQGEDELTPFDMSIQCIQSVYTSKIISDR
DLLAVVFGTEKDKNSVNFKSIYVLQDLNPGAKRVLLEDRFKGQQGKKHFRDTIGHGSDYSLSEVLWVCANLFS
VQFKMSHKRIMLFTNEDDPHGNSAKASRARTKASDLRDTGIFLDMHLKKRGGFDVSLFYRDIISIAEDEDLGVHF
EESKLEDLLRKVRKEXKKRVLRLKFLGKDVALMVGVYLVQKANKPFPVRLYRETNEPVKTXRFTFNVNXGSL
LPDXXXSLTFXXXXVXXXXXXXXXXXXMXXLXXWAXXXXXLRPSLFYPEESLVNGSSTLFSALLTKCVEKIVAVCRY
TARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVMANPEQIDKMKAIQKLRFTYRSD
SFENPVLQQHFRNLEALALDMMESQVVDLTLPKVEAIKKRLGSLADEFKELVYPPGYNPEGKIAKRKADNEGSASK
KPKVELSEELKDLFAKGLTGLKLTVPALRDICKAYGLKSGPKKQELLEALSRLHLEKN-

➤ **Blast contre banque rat :**

	Description	max Score	total Score	query Cover	E- value	Per. Ident	Accession
☒	PREDICTED: Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6)_transcript variant X1_mRNA	1738	2825	86%	0.0	98.86%	XM_008765671.2
☒	Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6)_mRNA	1738	3119	95%	0.0	98.86%	NM_139080.2
☒	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 6_mRNA (cDNA clone MGC:93146 IMAGE:7115290)_	1738	3119	95%	0.0	98.86%	BC078718.1
☒	Rattus norvegicus mRNA for G22p1_complete cds	1738	3097	95%	0.0	98.86%	AB066102.1
☒	Rattus norvegicus cDNA clone IMAGE:6918045_containing frame-shift errors	1733	3119	95%	0.0	98.76%	BC061528.1

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

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	ATGTCAGAGTGGGAATCCTACTACAAACTGAGGGTGAGGAGAGGAGAGGAGGAGCAGAGCCCTGACACAAATGGAGATATAAATATTCTAGGAGAGATAGTTGATTTTCTGGTTGACGCTCCCA													
CDS	ATGTCAGAGTGGGAATCCTACTACAAACTGAGGGTGAGGAGAGGAGAGGAGGAGCAGAGCCCTGACACAAATGGAGATATAAATATTCTAGGAGAGATAGTTGATTTTCTGGTTGACGCTCCCA													
Consensus	ATGTCAGAGTGGGAATCCTACTACAAACTGAGGGTGAGGAGAGGAGAGGAGGAGCAGAGCCCTGACACAAATGGAGATATAAATATTCTAGGAGAGATAGTTGATTTTCTGGTTGACGCTCCCA													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	GGGCTATGTTTGAAATCTCAGGGTGAGGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAGTAGATCATAGGACGCGATCGGGATCTCTGGCAGTGGTGTCTATGG													
CDS	GGGCTATGTTTGAAATCTCAGGGTGAGGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAGTAGATCATAGGACGCGATCGGGATCTCTGGCAGTGGTGTCTATGG													
Consensus	GGGCTATGTTTGAAATCTCAGGGTGAGGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAGTAGATCATAGGACGCGATCGGGATCTCTGGCAGTGGTGTCTATGG													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	TACCAGAAAGCAAAATTCAGTGAACTTCAAAGATATTTATGTCTTACAGATCTGGATACCCAGGAGCTAAACGAGTGTAGAGCTTGACCGCTTTAAGGGACACAGGGGAAAAACATTTCCGA													
CDS	TACCAGAAAGCAAAATTCAGTGAACTTCAAAGATATTTATGTCTTACAGATCTGGATACCCAGGAGCTAAACGAGTGTAGAGCTTGACCGCTTTAAGGGACACAGGGGAAAAACATTTCCGA													
Consensus	TACCAGAAAGCAAAATTCAGTGAACTTCAAAGATATTTATGTCTTACAGATCTGGATACCCAGGAGCTAAACGAGTGTAGAGCTTGACCGCTTTAAGGGACACAGGGGAAAAACATTTCCGA													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequence	GACACAAATGGGCTATGGGTGACACTCTTTGAGTGAAGTGCTCTGGGTCTGTGCCAGCTCTTCAGGCAGCTCCAGTTCAGATGAGTCATAGAGGATCATGCTATTACCAATGAAGATGACCCCC													
CDS	GACACAAATGGGCTATGGGTGACACTCTTTGAGTGAAGTGCTCTGGGTCTGTGCCAGCTCTTCAGGCAGCTCCAGTTCAGATGAGTCATAGAGGATCATGCTATTACCAATGAAGATGACCCCC													
Consensus	GACACAAATGGGCTATGGGTGACACTCTTTGAGTGAAGTGCTCTGGGTCTGTGCCAGCTCTTCAGGCAGCTCCAGTTCAGATGAGTCATAGAGGATCATGCTATTACCAATGAAGATGACCCCC													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequence	ATGGTATGACGTGCCAAGCCAGCCGGGCCAGGCCAAGGCCAGCGATCTCGGGGACCTGGGATCTTCTCGACTTGATGCACCTGAGAGAGCGAGGGGGCTTGACGTGTCTTGTCTACAGAGA													
CDS	ATGGTATGACGTGCCAAGCCAGCCGGGCCAGGCCAAGGCCAGCGATCTCGGGGACCTGGGATCTTCTCGACTTGATGCACCTGAGAGAGCGAGGGGGCTTGACGTGTCTTGTCTACAGAGA													
Consensus	ATGGTATGACGTGCCAAGCCAGCCGGGCCAGGCCAAGGCCAGCGATCTCGGGGACCTGGGATCTTCTCGACTTGATGCACCTGAGAGAGCGAGGGGGCTTGACGTGTCTTGTCTACAGAGA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequence	CATCATCAGATCGCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAGCAGCTGGAGACCTGCTAGGAGAGGTTGAGCCAGGGAGACAAAGAGCGAGTGTCTGTCAGGTTAAGGTTTAAAG													
CDS	CATCATCAGATCGCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAGCAGCTGGAGACCTGCTAGGAGAGGTTGAGCCAGGGAGACAAAGAGCGAGTGTCTGTCAGGTTAAGGTTTAAAG													
Consensus	CATCATCAGATCGCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAGCAGCTGGAGACCTGCTAGGAGAGGTTGAGCCAGGGAGACAAAGAGCGAGTGTCTGTCAGGTTAAGGTTTAAAG													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
sequence	CTCGGCAAGAGCTAGCACTCATGCTGGGCGTTTATACCTTGGTCCGAAAGCTAACAAGCCTTTCCAGTGAGGCTGTATCGAAGAACACAGACACAGTGAAGAACTAACCAAGGACCTTTATATGTA													
CDS	CTCGGCAAGAGCTAGCACTCATGCTGGGCGTTTATACCTTGGTCCGAAAGCTAACAAGCCTTTCCAGTGAGGCTGTATCGAAGAACACAGACACAGTGAAGAACTAACCAAGGACCTTTATATGTA													
Consensus	CTCGGCAAGAGCTAGCACTCATGCTGGGCGTTTATACCTTGGTCCGAAAGCTAACAAGCCTTTCCAGTGAGGCTGTATCGAAGAACACAGACACAGTGAAGAACTAACCAAGGACCTTTATATGTA													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
sequence	ACACNGGAGCTGCTCCTGCCCAGTGATNCNNNNNGGCTCTGACTTTTNGGNNNGTCANANNGTGCTGNNA---NNNARNCNNNNCTNA-NCNNNTGATGANNNG--TTGATN-TNATGGG													
CDS	ACACNGGAGCTGCTCCTGCCCAGTGATNCNNNNNGGCTCTGACTTTTNGGNNNGTCANANNGTGCTGNNA---NNNARNCNNNNCTNA-NCNNNTGATGANNNG--TTGATN-TNATGGG													
Consensus	ACACaGGAGCTGCTCCTGCCCAGTGATaCnaannGGTCTCTGACTTTTnGGannnGTCAnAnnnGTGCTGanAR...nnaARnanannanCTnA,nCnnnTnGATGannnaG...TTGATn,TnATGGG													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
sequence	CTTNAN---CCAGNGNNNGCTGA---GGCCCTCTCTGTTCTGTACCCAGAGGATCCCTGGTTCACGGGGAGCTCAGCTTGTTCAGCGCCCTGCTACCAAGTGTGTGGAGAG													
CDS	CTTNAN---CCAGNGNNNGCTGA---GGCCCTCTCTGTTCTGTACCCAGAGGATCCCTGGTTCACGGGGAGCTCAGCTTGTTCAGCGCCCTGCTACCAAGTGTGTGGAGAG													
Consensus	CTTnAR...CCAGnGnaaTGCTGA.....GGCCCTCTCTGTTCTGTACCCAGAGGATCCCTGGTTCACGGGGAGCTCAGCTTGTTCAGCGCCCTGCTACCAAGTGTGTGGAGAG													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
sequence	GAGGTCATGACGTGTGTAGATACACAGCCCAAGAGATGTCTCCCTTATTTTGTGGCTTTGGTGCCACAGGAGAGGAGCTAGATGATCAGACATTCAGGTGACTCCCGAGGCTTCAGCTTGTCT													
CDS	GAGGTCATGACGTGTGTAGATACACAGCCCAAGAGATGTCTCCCTTATTTTGTGGCTTTGGTGCCACAGGAGAGGAGCTAGATGATCAGACATTCAGGTGACTCCCGAGGCTTCAGCTTGTCT													
Consensus	GAGGTCATGACGTGTGTAGATACACAGCCCAAGAGATGTCTCCCTTATTTTGTGGCTTTGGTGCCACAGGAGAGGAGCTAGATGATCAGACATTCAGGTGACTCCCGAGGCTTCAGCTTGTCT													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
sequence	TCTTCCCTTACGCCGATGACACAGCGGAGGTTGCCCTTACGGAGAGGTTGATGGCCACCCGGACACAGATAGACAGATGAGGCCATTGTTCAAAGCTCCGCTTTACATACAGGAGCGACGTTTCGA													
CDS	TCTTCCCTTACGCCGATGACACAGCGGAGGTTGCCCTTACGGAGAGGTTGATGGCCACCCGGACACAGATAGACAGATGAGGCCATTGTTCAAAGCTCCGCTTTACATACAGGAGCGACGTTTCGA													
Consensus	TCTTCCCTTACGCCGATGACACAGCGGAGGTTGCCCTTACGGAGAGGTTGATGGCCACCCGGACACAGATAGACAGATGAGGCCATTGTTCAAAGCTCCGCTTTACATACAGGAGCGACGTTTCGA													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
sequence	GAACCCAGTGTGCAGCAGCACTTCCGGACCTGGAGGCCCTAGCTTTGGACATGATGGATCGGAGCAGTGGTAGATCTGACACTGCCAAGGTTGAGCCATTAAGAAAGAGCTGGGCTCCCTGGCA													
CDS	GAACCCAGTGTGCAGCAGCACTTCCGGACCTGGAGGCCCTAGCTTTGGACATGATGGATCGGAGCAGTGGTAGATCTGACACTGCCAAGGTTGAGCCATTAAGAAAGAGCTGGGCTCCCTGGCA													
Consensus	GAACCCAGTGTGCAGCAGCACTTCCGGACCTGGAGGCCCTAGCTTTGGACATGATGGATCGGAGCAGTGGTAGATCTGACACTGCCAAGGTTGAGCCATTAAGAAAGAGCTGGGCTCCCTGGCA													
	1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
sequence	GATGAGTTTAAAGACTTGTCTACCTCCAGGTTATATCTTGAGGGAARATTCAGAGAGAAAGCGACATGAGGTTCTGCAAGTAAAGGCCAAGGTAGAGTTATCAGAGAGGAGCTGAGGG													
CDS	GATGAGTTTAAAGACTTGTCTACCTCCAGGTTATATCTTGAGGGAARATTCAGAGAGAAAGCGACATGAGGTTCTGCAAGTAAAGGCCAAGGTAGAGTTATCAGAGAGGAGCTGAGGG													
Consensus	GATGAGTTTAAAGACTTGTCTACCTCCAGGTTATATCTTGAGGGAARATTCAGAGAGAAAGCGACATGAGGTTCTGCAAGTAAAGGCCAAGGTAGAGTTATCAGAGAGGAGCTGAGGG													
	1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820
sequence	ACCTTTTTGCCAAGGGCACACTGGGCAGCTCACTGTGCTGCACCTGAGGGACATCTGCAGGCCATRTGGCTAAAGAGTGGACCGAGAGCAGGAGCTACTCGAGGCTCTCAGCAGCACTTGGAGAA													
CDS	ACCTTTTTGCCAAGGGCACACTGGGCAGCTCACTGTGCTGCACCTGAGGGACATCTGCAGGCCATRTGGCTAAAGAGTGGACCGAGAGCAGGAGCTACTCGAGGCTCTCAGCAGCACTTGGAGAA													
Consensus	ACCTTTTTGCCAAGGGCACACTGGGCAGCTCACTGTGCTGCACCTGAGGGACATCTGCAGGCCATRTGGCTAAAGAGTGGACCGAGAGCAGGAGCTACTCGAGGCTCTCAGCAGCACTTGGAGAA													
	1821	1827												
sequence	GAACTGA													
CDS	GAACTGA													
Consensus	GAACTGA													

➤ Différence au niveau PROT :

sequence	MSEMEYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDSRAMFESQGEDELTPFDMISIQCIQSVYTSKIISDSDRLAVVYFYGTEKDKNSVNFKSIYVLQDLONPGAKRYLELDRFKGQGGKKHFR													
refprot	MSEMEYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDSRAMFESQGEDELTPFDMISIQCIQSVYTSKIISDSDRLAVVYFYGTEKDKNSVNFKSIYVLQDLONPGAKRYLELDRFKGQGGKKHFR													
Consensus	MSEMEYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDSRAMFESQGEDELTPFDMISIQCIQSVYTSKIISDSDRLAVVYFYGTEKDKNSVNFKSIYVLQDLONPGAKRYLELDRFKGQGGKKHFR													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	DTIGHGSDYSLSEVLAVCANLFSQYQFKMSHKRIHLFTNEDDPHGNDASAKSRARTKASDLRDTGIFLDLHMLKKRGGFDVSLFYRDIISIADEEDLGVHFEESKLEDLLRKVRAKEKKRYLSRLKFK													
refprot	DTIGHGSDYSLSEVLAVCANLFSQYQFKMSHKRIHLFTNEDDPHGNDASAKSRARTKASDLRDTGIFLDLHMLKKRGGFDVSLFYRDIISIADEEDLGVHFEESKLEDLLRKVRAKEKKRYLSRLKFK													
Consensus	DTIGHGSDYSLSEVLAVCANLFSQYQFKMSHKRIHLFTNEDDPHGNDASAKSRARTKASDLRDTGIFLDLHMLKKRGGFDVSLFYRDIISIADEEDLGVHFEESKLEDLLRKVRAKEKKRYLSRLKFK													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	LGKQVALMVGYYNLVQKANKPFPVRLYRETNEPVKTXRTFNVNXXGSLLLPSDXXXSLTFXXXXXVXXXXXXXXXXXXXX--LXXMXXXXXRPFLYPEESLVNGSSTLFSALLTKCYEK													
refprot	LGKQVALMVGYYNLVQKANKPFPVRLYRETNEPVKTXRTFNVNXXGSLLLPSDXXXSLTFXXXXXVXXXXXXXXXXXXXX--LXXMXXXXXRPFLYPEESLVNGSSTLFSALLTKCYEK													
Consensus	LGKQVALMVGYYNLVQKANKPFPVRLYRETNEPVKTXRTFNVNXXGSLLLPSDXXXSLTFXXXXXVXXXXXXXXXXXXXX--LXXMXXXXXRPFLYPEESLVNGSSTLFSALLTKCYEK													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequence	EVIIVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFEKVMANPEQIDKMKRIYQKLRTYRSDSFENPVLQQHFRNLALALDHMESEQVVDLTLPKVEAIKKRLGSLA													
refprot	EVIIVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFEKVMANPEQIDKMKRIYQKLRTYRSDSFENPVLQQHFRNLALALDHMESEQVVDLTLPKVEAIKKRLGSLA													
Consensus	EVIIVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFEKVMANPEQIDKMKRIYQKLRTYRSDSFENPVLQQHFRNLALALDHMESEQVVDLTLPKVEAIKKRLGSLA													
	521	530	540	550	560	570	580	590	600	608				
sequence	DEFKELVYPPGYNPEGKIAKRKADNEGSASKPKVELSEELKDLFAKGTGLGLTVPALRDICKAYGLKSGPKKQELLEALSRHLEKN													
refprot	DEFKELVYPPGYNPEGKIAKRKADNEGSASKPKVELSEELKDLFAKGTGLGLTVPALRDICKAYGLKSGPKKQELLEALSRHLEKN													
Consensus	DEFKELVYPPGYNPEGKIAKRKADNEGSASKPKVELSEELKDLFAKGTGLGLTVPALRDICKAYGLKSGPKKQELLEALSRHLEKN													

	Description	Score	Score	Cover	value	Ident	Accession
✓	X-ray repair cross-complementing protein 6 [Rattus norvegicus]	1132	1132	100%	0.0	92.60%	NP_620780.2
✓	G22p1 [Rattus norvegicus]	1127	1127	100%	0.0	92.27%	BAB83858.1
✓	PREDICTED: X-ray repair cross-complementing protein 6 isoform X1 [Rattus norvegicus]	979	979	100%	0.0	82.89%	XP_008763893.1

pcR4Blunt Xrcc6 DiT48hMix C semble OK mais pas
envoyé en séquençage interne

- FlagBirA Xrcc6 DiT48hMix clone B

➤ B3Fwd 25/11 950NT

ATGTCAGAGTGGGAATCCTACTACAAAAGTGGGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTTCTGGTTGACGCCTCCAGGGCTATGTTTGAATCTC
AGGGTGAAGACGAGCTCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAAGTAAAGATCATAA
GCAGCGATCTGCGGGACACTGGGATCTTCCTCGACTTGATGCACCTGAAGAAGCGAGGGGGCTTTGACGTGTCC
TTGTTCTACAGAGACATCATCAGCATCGCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAAGCAAGCT
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GGCAAAGACGTAGCACTCATGGTGGGCGTTTATAACTTGGTCCAGAAAGCTAACAAGCCTTTTCCAGTGAGGCT
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GAAGCGGTTTGATGAGCCAGGTTTGATTCTCATGGGCTTTAAGCCCATGGTAATGCTGAAGAACCACCACTACCT
GAgGNCCTCTCTGTTCTGTACCCAGAGGANTCCCTGGTCAACGGGAGCTCAACCTTGNTCAGCGCCCTGCTCA
CCAAGTGTGNGGAGAAGGNGGNCATANCANTGNGNANATNCNCAGCCGAAANAATGNCTNCCCTTANTTTG
NNNTNNGNGNNNNCNGNANNNNNNTANATGATCANANATTNNNGACTCCNNCNNNTNCNNCT

➤ BGHRev 25/11 948NT pas la fin de séquence

CAANCNTTNCAGNGNNNNNTGTATNGAGAANCAANGANCCAGTGAAAANTAAGNCAAGGACTNTTAANGT
AAACACAGNCAGTNTGNTNNTGCCAGTGATACCAAGCGGTCTNNGACTTTTGGGACGCGTCAGATTGTGNTG
GNGAAAGAGGAANCAGAGGAGCTGAAGCGGTTTGATGANNACAGTTTGATTNTCATGGNCTTTAAGCNCANG
GTAATGCTGAAGAACCACaCacTactGAGGCCCTcTcTGTTCcTGATCCAGAGGAGTCcTGGTCAACGGGAGCTCA

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AATGTCTCCCcTTATTTTGTGGCTTTGGTGCCACAGGAAGAGGAGCTAGATGATCAGAACATTcAGGTGACTCCC
GCAGGCTTCCAGCTTGTCTTCTCCCTTACGCCGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGATGGC
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CTTGTCTACCCCTCCAGGTTATAATCCTGAGGGAAAAATTGCCAAGAGAAAAANCAGACAATGAAGGTTCTGCAAGT
AAAAAGCCCAAGGTAGAGTTATCAGAAGAGGAGCTGAAGGACCTTTTTGCCAAGGGCACACTGGGCAAGCTCA
CTGTGCCTGCACTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGNCCGAAGAAGCAGG



Rev1

CCCAGATNNTGATNGNNNCGNcATCANCATGGCATNNGNGNNNNGANANCGTGGTGNNcNNNGG
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GAGNTGCGGGCCGCCCTGGAGCTGTTcGAGCAGGAGGNCCTGNCCCCNTNNNGAGCCGGTGGGAG
AAGCTGGACAaTTCATCAACCGGCCCGTGAAGCTGATCNTNGGCGACAAGGAGATNTTCGGCATCA
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ttgaT

○ FlagBirA Xrcc6 SP clone A

➤ B3Fwd SP 864NT

ATGTCAGAGTGGGAATCCTACTACAAAAGTGAAGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
AATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTCTGGTTGACGCCTCCAGGGCTATGTTTGAATCTC
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NAGANCAAAAAGCGAGTGCTGTCCAGGTTAAAGTTAAGCTCGGCAANACGTANCACTCATGGTGGGCGTTTAT
AACTTGGNCCANAANGCTAACAAGCCTTTTNCAGTGNNNTGNATCGANA

➤ BGHRev SP 981NT

TNCCAGTGANGNTGTATCGAGNANCAACGAACCAGTGAAANTAAGACAAGGACTTTTAATGTAAACACAGNC
AGTNTGNTNCTGCCAGTGATNCCAAGCGNTNTNTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAG
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GCTCACTGTGCCTGCACTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGACCGAAGAAGCAGGAAC
ACTCGAGGCTCTCAGCAGACACTtGGAGAAGAACTGA

➤ Fwd2

CTTNNTCGANTTGATGCNCCTGAAGAAGCGAGGGGGCTTTGACGTGTCCTTGTCTACNGAGACATCATCNGC
ATCGCTGAGGATGAGGACCTCGGGGTTCACCTTTGAGGAGTCAAGCAAGCTGGAAGACCTGCTAAGGAAGGTT
CGAGCCAAGGAGACCAAAAAGCGAGTGCTGTCCAGGTTAAAGTTAAGCTCGGCAAAGACGTAGCACTCATG
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NATAAANAAAAGACTGGGNTCCCTNGNANATGANTTTAAAGAACTTGNCTACCCTCCNNNNATNATCCTGAN
GNAAAAANNNGNNNANANAAAANCNNNNNNNGNANNNTGCAGTAAAGCNCNANNANANTATNNNANANNNC
TNAGANNTTTGNCNAGG

➤ Rev1

ANGGGGNTNNGNNCNGNNNNNNNGCGCGCCAATNTCNGANTGGGANNNNNNNTNCAAAAANTGAGGGTGAG
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AGGAGNTAAACGAGTGTTAGAGCTTGACCGCTTTAAGGGACAACAGGGGAAAAAACATTTCCGAGACACAA
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➤ Synthèse séquençage SP:

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CCAGTGATACCAAGCGGTCTCTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGG	991
AAACAGAGGAGCTGAAGCGGTTTGTATGAGCCAGGTTTGATTCTCATGGGCTTTAAGCCCA	1051
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CCTTGGTCAACGGGAGCTCAACCTTGTTCAGCGCCCTGCTCACCAGTGTGTGGAGAAGG	1171
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VEKEVIAVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVMANPEQIDKMKAIVQ

KLRFTYRSDSFENPVLQQHFRNLEALALDMMESQVVDLTLPKVEAIKKRLGSLADEFKELVYPPGGYNPEGKIAKRKA
DNEGSASKKPKVELSEEELKDLFAKGTLGKLTVPALRDICKAYGLKSGPKKQELLEALSRHLEKN-

➤ **Blast contre banque rat :**

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6)_mRNA	Norway rat	3374	3374	100%	0.0	100.00%	2070	NM_139080.2
✓	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 6_mRNA (cDNA clone MGC:9...	Norway rat	3374	3374	100%	0.0	100.00%	2098	BC078718.1
✓	Rattus norvegicus cDNA clone IMAGE:6918045 containing frame-shift errors	Norway rat	3363	3363	100%	0.0	99.89%	2056	BC061528.1
✓	Rattus norvegicus mRNA for G22p1 complete cds	Norway rat	3352	3352	100%	0.0	99.78%	1964	AB066102.1
✓	PREDICTED: Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6)_transcript variant X1_mRNA	Norway rat	2076	3080	91%	0.0	100.00%	1919	XM_008765671.2

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

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	X-ray repair cross-complementing protein 6 [Rattus norvegicus]	Norway rat	1247	1247	100%	0.0	100.00%	608	NP_620780.2
☒	G22p1 [Rattus norvegicus]	Norway rat	1242	1242	100%	0.0	99.67%	609	BAB83858.1
☒	PREDICTED: X-ray repair cross-complementing protein 6 isoform X1 [Rattus norvegicus]	Norway rat	1094	1094	100%	0.0	90.30%	554	XP_008763893.

Flag BirA Xrcc6 SP clone A parfait

○ FlagBirA Xrcc6 CTX clone A

➤ B3Fwd CTX 852NT

ATGTCAGAGTGGGAATCCTACTACAAAAGTGGGGTGAGGAAGAGGAAGAGGAGGAGCAGAGCCCTGACACA
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GATGAGGAcCTCGGGGTTCACTTTGAGGAGTCAAGCAAGCTGGAAGNNCTGCTAANGAANGNTCGAGCCAAG
GAGANCAAAAAGCGAGTGCTGNCCAGGTTAAAGTTTAAAGCTCNGCAAAGACGTANCACTCATGGTGGGCGTTN
ANAACTTGGNCCANAAAGCTAACAAGCCTTTTCCAGTG

➤ BGHRev CTX 985NT

AGCCTTTCCAGNGANGNNGTATCGAGAAACAACGAACCAAGTGAANTAAAGACAAGGACTTTAATGTAAACACA
GGCAGTNTGNTNCNNCCAGTGATNCCAAGCGGTNTNTGACTTTTGGGACGCGTCAGATTGTGCTGGAGAAA
GAGGAAACAGAGGAGCTGAAGCGGTTTGATGAGCCAGGTTTGATTCTCATGGGCTTTAAGCCCATGGTAATGCT
GAAGAACCACCACTACcTGAGgCCCTCTCTGTTCTGTACCCAGAGGAGtCCCTGgTCAACGGGAGCTCAACCTT
GTTGAGCGCCCTGCTCACCAAGTGTGTGGAGAAGGAGGTCATAGCAGTGTGTAGATACACAGCCCGAAAGAATG
TCTCCCCTATTTTGTGGCTTTGGTGCCACAGGAAGAGGAGCTAGATGATCAGAACATTGAGGTGACTCCCGCAG
GCTTCCAGCTTGTCTTCTCCCTTACGCCGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGGTGATGGCCAAC
CCGGAACAGATAGACAAGATGAAGGCCATTGTTCAAAAGCTCCGCTTTACATACAGGAGCGACAGTTTCGAGAA
CCCAGTGCTGCAGCAGCACTTCCGGAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTCGGAGCAAGTGGTA
GATCTGACACTGCCCAAGGTTGAAGCCATAAAGAAAAGACTGGGCTCCCTGGCAGATGAGTTTAAAGAACTTGT
CTACCCTCCAGGTTATAATCCTGAGGGAAAAATTGCCAAGAGAAAAAGCAGACAATGAAGGTTCTGCAAGTAAAA
AGCCCAAGGTAGAGTTATCAGAAGAGGAGCTGAAGGACCTTTTGGCCAAGGGCACACTGGGCAAGCTCACTGT
GCCTGCACTGAGGGACATCTGCAAGGCCTATGGGCTAAAGAGTGGAACCGAAGAAGCAGGAACCTACTCGAGGCT
CTCAGCAGACACTtGGAGAAGAACTGA

➤ Int Fwd

TTcCTCGACTTGaTGCACTGAAGAAGCGAGGGGGCTTTGaCGTGTCTTGTCTACaGAGACATCATCNGCATC
GCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCAAGCNAGCTGGAAGACCTGCTAAGGAAGGTTCTGA
GCCAAGGAGACCAAAAAGCGAGTGCTGTCCAGGTTAAAGTTTAAAGCTCGGCAAAGACGTAGCACTCATGGTGG
GCGTTTATAACTTGGNCCAGAAAAGCTAACAAGCCTTTTCCAGTGAGGCTGTATCGAGAAACAACGAACCAAGTG
AAAATAAGACAAGGACTTTTAAATGTAAACACAGGCAGTCTGCTCCTGCCAGTGATACCAAGCGGTCTCTGACT
TTTGGGACGCGTCAGATTGTGCTGGAGAAAGAGGAAACAGAGGAGCTGAAGCGGTTTGATGAGCCAGGTTTG
ATTCTCATGGGCTTTAAGCCCATGGTAATGCTGAAGAACCACCACTACCTGAGGCCCTCTCTGTTCTGTACCCag
AGGAGTCCCTGGTCAACGGGAGCTCAACCTTGTTGAGCGCCCTGCTACCAAGTGTGTGGAGAAGGAGGTCAT
AGCAGTGTGTAGATACACAGCCNGAAAGAATGTCTCCCCTATTTTGTGGCTTTGGTGCCACAGGAAGAGGAGC
TAGATGATCAGAACATTGAGGTGACTCCCGCagGCTTCCAGCTTGCTTCTCCTTACGCCGATGACAAGCGGA
AGGTGCCCTTTACGGAGAAgGtGATGGCCAACCCGGAACAGATAGACAAGATGAAGGcCATTGTTCAAAAGCTC
CGCTTTACATACAGGAGCGACAGTTTCGAGAACCCAGTGCTGCAGCAgCACTTCCGGAACCTGGAGGcCCTAGC

TTTGGACNTGATGGAGTCNGANCAAGTGGTAGATCTGANACTGCCANNNTGAAGCCATAANAAANACTGGG
CTCCCTNNNNATGAGTTTAAANAACCTGNCTACCTNCNGTNANANNNTGANGNAAAANTGNANANAAAAGC

➤ Int rev

GGNATCATCAAGNCNNGANGGNNNNNNNATCANNNNNNGGANNNNNNNNNNNGGGGNTNNGNCNNNGNG
GNGNNNGNNAANNTCANNTNGNNATNTNNTANAAAANTGAGGGTGAGGANGAGGAAGAGGAGGAGC
AGAGNNNGANNNAATGGAGAATATAAATATTCAGGAAGAGATAGTTTGATTTTTNTGGTTGANGCNTNCAGG
GNTATGTTTGANTNTCAGGGTGAAGANGAGCTCACACNTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTAC
ANCAGTAAGATCATAAGCAGCGATNGGGANNTNTTGGCAGTGGTGTNTATGGTACCGAGAAAGACAAAAATT
CAGTGAACCTTCAAAGTATTTATGTNTTACAAGATNNGGATAACCCAGGAGCTAAACGAGTGTAGAGCTTGACC
GCTTTAAGGGACAACAGGGGAAAAAACATTTCCGAGACACAATTGGCCATGGGTCTGACTACTCTTTGAGTGAA
GTGCTNNNNNNNNNGNNNNNNNNNTNNNNNNNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAC
CNNNNNNANNAANNCGCNNCAGCNCNNNNNTNCNNNTTCNNCANCNNAANCNNACGCGTCCCAAAN
NNCNGATNCCGCNGANNNTNNCNTNCCNNNGCNCNNCNGCCNNNNNANNCANNNNAANGNCCTTNTCNG
NGTNNNNNTNCCGNGNNNTTCTCNCNNCNCNNCNCNNNNNANNCNNNNNNCNCNNNNNNNNNNNN
NNNNNNCAACNCCCACCANNGNNNNACNNCNTTCCGNGCNCNNNAACNNNAACNNNNNNNCACNCNCN
NNNNNNCNCNNNNCNCNNNACCNNCCTANNCNNNTCNCNCNGCNTNCNTNACTNCNNNNAGNNAAACNC
NANNCCNNANCC

➤ Synthèse séquençage CTX: **NT**

ATGTCAGAGTGGGAATCCTACTACAAAACCTGAGGGTGAGGAAG	43	
AGGAAGAGGAGGAGCAGAGCCCTGACACAAATGGAGAATATAAATATTCAGGAAGAGATA		103
GTTTGATTTTTCTGGTTGACGCCTCCAGGGCTATGTTGAATCTCAGGGTGAAGACGAGC		163
TCACACCTTTTGATATGAGCATCCAGTGTATCCAGAGTGTGTACACCAGTAAGATCATAA		223
GCAGCGATCGGGATCTCTTGGCAGTGGTGTCTATGGTACCGAGAAAGACAAAAATTCAG		283
TGAACTTCAAAAGTATTTATGTCTTACAAGATCTGGATAACCCAGGAGCTAAACGAGTGT		343
TAGAGCTTGACCGCTTTAAGGGACAACAGGGGAAAAACATTTCCGAGACACAATTGGCC		403
ATGGGTCTGACTACTCTTTGAGTGAAGTGTCTCTGGGTCTGTGCCAACCTCTTCAGCGACG		463
TCCAGTTCAAGATGAGTCATAAGAGGATCATGCTATTACCAATGAAGATGACCCCATG		523
GTAATGACAGTGCCAAAGCCAGCCGGGCCAGGACCAAGCCAGCGATCTGCGGGACACTG		583
GGATCTTCTCGACTTGATGCACCTGAAGAAGCGAGGGGGCTTTGACGTGTCTTGTCT		643
ACAGAGACATCATCAGCATCGCTGAGGATGAGGACCTCGGGGTTCACTTTGAGGAGTCA	702	
AGCAAGCTGGAAGACCTGCTAAGGAAGGTTTCGAGCCAAGGAGACCAAAAGCGAGTGTG		762
TCCAGGTTAAAGTTTAAAGCTCGGCAAGAGCGTAGCACTCATGGTGGGCGTTTATAA	230	
CTTGGNCCAGAAAGCTAACAAGCCTTTTCCAGTGAGGCTGTATCGAGAAACAAACGAACC		290
AGTGAAGAACTAAGACAAGGACTTTTAAATGTAAACACAGGCAGTCTGCTCCTGCCAGTGA		350
TACCAAGCGGTCTCTGACTTTTGGGACCGCTCAGATTGTGCTGGAGAAAAGAGGAAACAGA		410
GGAGCTGAAGCGGTTTGATGAGCCAGGTTTGATTCATGGGCTTTAAGCCCATGGTAAT		470
GCTGAAGAACCACCACTACCTGAGGCCCTCTCTGTCTGTACCCagAGGAGTCCCTGGT		530
CAACGGGAGCTCAACCTTGTTACGCGCCCTGCTCACCAAGTGTGTGGAGAAGGAGGTCAT		590
AGCAGTGTGTAGATACACAGCCCGAAAGAATGTCTCCCTTATTTTGTGGCTTTGGTGCC		396
ACAGGAAGAGGAGCTAGATGATCAGAACATTCAGGTGACTCCCGCAgGCTTCAGCTTGT		710
CTTCTCCCTTACGCCGATGACAAGCGGAAGGTGCCCTTTACGGAGAAGtGATGGCCAA		770
CCCGGAACAGATAGACAAGATGAAGGcCATTGTTCAAAGCTCCGCTTTACATACAGGAG		830
CGACAGTTTCGAGAACCCAGTGTGTCAGCAGCACTTCCGGAACCTGGAGGCCCTAGCTTT		636
GGACATGATGGAGTCGGAGCAAGTGGTAGATCTGACACTGCCAAGGTTGAAGCCATAAA		696
GAAAAGACTGGGCTCCCTGGCAGATGAGTTTAAAGAACTTGTCTACCTCCAGGTTATAA		756
TCCTGAGGGAAAAATTGCCAAGAGAAAAGCAGACAATGAAGGTTCTGCAAGTAAAAAGCC		816
CAAGGTAGAGTTATCAGAAGAGGAGCTGAAGGACCTTTTGGCAAGGGCACACTGGGCAA		876
GCTCACTGTGCCTGCACTGAGGGACATCTGCAAGGCCATGGGCTAAAGAGTGGACCGAA		936
GAAGCAGGAACCTACTCGAGGCTCTCAGCAGACACTtGGAGAAGAACTGA	985	

MSEWESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVDASRAMFESQGEDELTPFDMSIQCIQSVYTSKIISDR
DLLAVVFYGTEDKNSVNFYSIYVLQDLNPGAKRVLELDRFKGQQGKKHFRDTIGHGSDYSLSEVLWVCANLFS
VQFKMSHKRIMLFTNEDDPHGNSAKASRARTKASDLRDTGIFLDMHLKKRGGFVSLFYRDIISIAEDEDLGVHF
EESSKLEDLLRKVRACKETKKRVLSRLKFLGKDVALMVGVYNLXQKANKPFPVRLYRETNEPVKTKTRTFNVNTGSL

LPSDTKRSLTFGTRQIVLEKEETEELKRFDPEGLILMGFKPMVMLKNHHYLRPSLFLYPEESLVNGSSTLFSALLTKCVE
 KEVIAVCRYTARKNVSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKVMANPEQIDKMKAIVQ
 KLRFTYRSDSFENPVLQQHFRNLEALALDMMESEQVVDLTLPKVEAIKKRLGSLADEFKELVYPPGYNPEGKIAKRKA
 DNEGSASKPKPKVELSEELKDLFAKGTLGKLTVPALRDICKAYGLKSGPKKQELLEALSRLHLEKN-

➤ **Blast contre banque rat :**

	Description	Common Name	Score	Score	Cover	value	Ident	Len	Accession
☒	Rattus norvegicus X-ray repair cross complementing 6 (Xrcc6) mRNA	Norway rat	3365	3365	100%	0.0	99.89%	2070	NM_139080.2
☒	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 6 mRNA (cDNA clone M...	Norway rat	3365	3365	100%	0.0	99.89%	2098	BC078718.1
☒	Rattus norvegicus cDNA clone IMAGE:6918045 containing frame-shift errors	Norway rat	3365	3365	100%	0.0	99.89%	2056	BC061528.1
☒	Rattus norvegicus mRNA for G22p1 complete cds	Norway rat	3343	3343	100%	0.0	99.67%	1964	AB066102.1
☒	PREDICTED: Rattus rattus X-ray repair cross complementing 6 (Xrcc6) mRNA	black rat	3277	3277	100%	0.0	99.01%	2228	XM_032918413.1

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

➤ **Différence au niveau PROT :**

☒ [X-ray repair cross-complementing protein 6 \[Rattus norvegicus\]](#)
[Norway rat](#)
1244 1244 100% 0.0 99.84% 608
[NP_620780.2](#)

☒ [G22f](#)
[BAB93858.1](#)

☒ [PREI](#)
[XP_008763893.1](#)

seq	ref	Consensus
MSEWESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVQASRAMFESQGEDELTPFDHSIQCIQSYVYTKIISDRDLLAVVFGYTEKDKNSVNFKSIYVLQDLNMPGAKRVLEDRFGQGQGGKHF	MSEWESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVQASRAMFESQGEDELTPFDHSIQCIQSYVYTKIISDRDLLAVVFGYTEKDKNSVNFKSIYVLQDLNMPGAKRVLEDRFGQGQGGKHF	MSEWESYYKTEGEEEEEEQSPDTNGEYKYSGRDSLIFLVQASRAMFESQGEDELTPFDHSIQCIQSYVYTKIISDRDLLAVVFGYTEKDKNSVNFKSIYVLQDLNMPGAKRVLEDRFGQGQGGKHF
131	140	150
160	170	180
190	200	210
220	230	240
250	260	
DTTGHGSDYSLSEVLVACNRLFSDVQFKSHKRIALFTNEDDPHGNSAKASRARTKASDLRTGTGIFDLMLHKKRGGFQVSLFYRDIISAEDELGVHFEESKLEDLRKVRAKETKKRVLSRLFK	DTTGHGSDYSLSEVLVACNRLFSDVQFKSHKRIALFTNEDDPHGNSAKASRARTKASDLRTGTGIFDLMLHKKRGGFQVSLFYRDIISAEDELGVHFEESKLEDLRKVRAKETKKRVLSRLFK	DTTGHGSDYSLSEVLVACNRLFSDVQFKSHKRIALFTNEDDPHGNSAKASRARTKASDLRTGTGIFDLMLHKKRGGFQVSLFYRDIISAEDELGVHFEESKLEDLRKVRAKETKKRVLSRLFK
261	270	280
290	300	310
320	330	340
350	360	370
380	390	
LGKQVALHVGVYNLVQKANKPPFVRLYRETNPEYKTKRTRFNVTGSLLLPSDTKRSLTFGRITQIVLEKEETEELKRFDEPGLILHGFKPMVHLKNIHLYRPSLFLYPEESLVNGSSTLFSALLTKCKVEK	LGKQVALHVGVYNLVQKANKPPFVRLYRETNPEYKTKRTRFNVTGSLLLPSDTKRSLTFGRITQIVLEKEETEELKRFDEPGLILHGFKPMVHLKNIHLYRPSLFLYPEESLVNGSSTLFSALLTKCKVEK	LGKQVALHVGVYNLVQKANKPPFVRLYRETNPEYKTKRTRFNVTGSLLLPSDTKRSLTFGRITQIVLEKEETEELKRFDEPGLILHGFKPMVHLKNIHLYRPSLFLYPEESLVNGSSTLFSALLTKCKVEK
391	400	410
420	430	440
450	460	470
480	490	500
510	520	
EVYAVCRYTARKNSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKYHNPQEIQKNKAIYQKLRFTYRSDSFENPVLQQHFRNLALALDHMESEGVYDILTPKYEIRIKKRLGSLA	EVYAVCRYTARKNSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKYHNPQEIQKNKAIYQKLRFTYRSDSFENPVLQQHFRNLALALDHMESEGVYDILTPKYEIRIKKRLGSLA	EVYAVCRYTARKNSPYFVALVPQEEELDDQNIQVTPAGFQLVFLPYADDKRKVPFTEKYHNPQEIQKNKAIYQKLRFTYRSDSFENPVLQQHFRNLALALDHMESEGVYDILTPKYEIRIKKRLGSLA
521	530	540
550	560	570
580	590	600
608		
DEFKELVYPPGYNPEGKIKRKRDMESGASKPKVELSEELKDLFAKGTLGKLTVPALRDICKAYGLKSGPKQDLEALSRHLEKN	DEFKELVYPPGYNPEGKIKRKRDMESGASKPKVELSEELKDLFAKGTLGKLTVPALRDICKAYGLKSGPKQDLEALSRHLEKN	DEFKELVYPPGYNPEGKIKRKRDMESGASKPKVELSEELKDLFAKGTLGKLTVPALRDICKAYGLKSGPKQDLEALSRHLEKN
seq	ref	Consensus

Flag BirA Xrcc6 CTX (clone A) OK

Conclusion séquencages :

- FlagBirA Xrcc6 DiT0, T24LPS, SP et CTX ok
- pCR4Blunt Xrcc6 DiT48hMix OK
- Il manque au séquençage le milieu de la séquence (cf longue séquence), primers internes pour le séquençage commandés 10/11
- Pour la **rate** : en attente des résultats de séquençage

Séquencage int

Xrcc6_IntSeqFwd_1

ATAGTTTGATTTTCTGG

à 100 pour un séquençage ~250NT

Xrcc6_IntSeqFwd_2

GCCAGCCGGGCCAGGACCAAAGC

A 541, pour un séquençage ~690NT

Xrcc6_IntSeqRev_1

CAGGTAGTGGTGGTTCTTCAGC

A 1058 pour un démarrage ~908NT en reverse