

7)Lig4

Rattus norvegicus DNA ligase 4 (Lig4), mRNA

DNA ligase (ATP) 4; ligase IV, DNA, ATP-dependent

- **Référence NCBI :** NM_001106095
- **Taille 2735 NT**
- **Séquences protéique** NP_001099565.1

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EMAPVIADLECRYSWDHSPLSMFRHYTVYLDLYAVINDLSSKIEATRLGVTALELRFR
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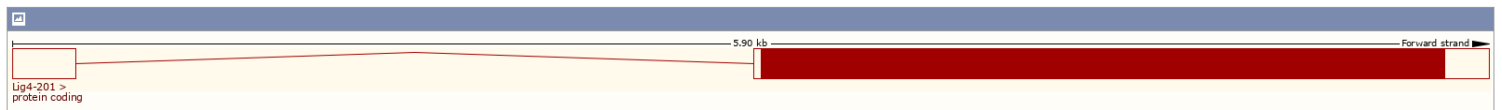
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601	cagaagctcc	tgaattaccg	aacccccagt	ggagctcgct	cagatgctgg	ggactttgcc
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1201	caggaaggct	ctctcaccoc	gtttattcac	aacgcattca	agacagatgt	gcaagtgtgc
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2641 cagactcctg aagaaatggc ccctgtgatt gctgacctag aatgtcgtta ttcttgggat
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2941 aaaatcctgc aggaacgttg ggtgatcgat tcagtagaca agtgtgaact gcaggaagaa
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ATTENTION : pas d'introns dans CDS

- **Amorces synthétisées :**

Lig4_AscI_Fwd

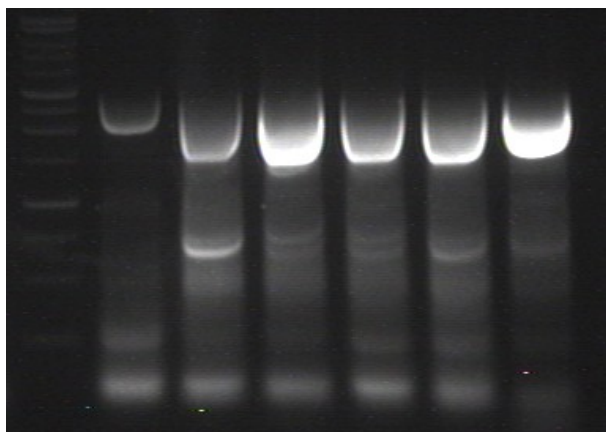
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Lig4_NotI_Rev

ttaaGCGGCCGCa ctaaagcaaatacaggtttttcttcc

- **Expériences :**

- 29/10 PCR pfu 60°C pfu 50ul 40 cycles
 - rate/DiTO/Di24hLPS : les miens de fevrier
 - 48h mix/SP/CTX faits le 28/10



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○ **FlagBirA Lig4 clone C**

➤ **B3Fwd 935NT**

ATGGCTTCCTACAAGCCTCACGAAGTGTGCGAGCTCATGTCCCCTTTGCAGACTTGTGCTCCACCTTAGAACGAA
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➤ **BGHRev 997NT**

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➤ **Int Fwd1**

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➤ **Int Fwd2**

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➤ **Int Rev1**

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➤ **Synthèse séquençage**

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➤ **Blast contre banque rat :**

✓	PREDICTED: Rattus norvegicus DNA ligase 4 (Lig4) transcript variant X2 mRNA	Rattus norvegicus	5053	5053	100%	0.0	100.00%	4882	XM_006253477.3
✓	PREDICTED: Rattus norvegicus DNA ligase 4 (Lig4) transcript variant X1 mRNA	Rattus norvegicus	5053	5053	100%	0.0	100.00%	7531	XM_017600050.1
✓	Rattus norvegicus DNA ligase 4 (Lig4) mRNA	Rattus norvegicus	5053	5053	100%	0.0	100.00%	3192	NM_001106095.1

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

ATCGCTTCGTCACCAAGCCTGCACCAAGTCTGCTCCGCTTTCCAGCGTTGTCTCTCCGCTTGCAAGCGATGCCAAGGCTTAAGCGAGCTTCCAGCGCTTGGCGAGTCTGCT

[illegible]

Séquençage interne :

Lig4_int_600Fwd : gtcagcacacgatattgtcc

Lig4_int_1191Fwd : aggtcgaatagagatagtgc

Lig4_int_1910Rev : gtgttcaatgattccaatgg

- FlagBirA Lig4 DiT0 clone A

Mauvais

- FlagBirA Lig4 DiT48 clone A

Mauvais

- FlagBirA Lig4 SP clone A

➤ B3Fwd 908NT

ATGGCTTCCTCACAAGCCTCACGAAGTGTGCGAGCTCATGTCCCCTTTGCAGACTTGTGCTCCACCTTAGAACGAA
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➤ BGHRev 984NT

CAGAGATGNNNANAGTNGCANGACTGTATGACGCTGGATGACCTGGAGCAGNTGAGGGGGAAAGCATNTGG
GAAGCTTGCCACAAAACaCCTTCACATAGGTGACGATGACGAACCCAGAGAAAAAAGGCGGAAACCCATCTCTA
AGACGAAGAAAACCATTTGGAATCATTGAaCACCTAAAAGCGCCTAcCCTTTCTAACATAAACAAGTTTCTAATGT
ATTTGAAGATGTTGAGTTTTGTGTCATGAGTGGATTAGATGGTTATCCAAAGCCTGACCTAGAGAACAAAATTGC
AGAATTTGGTGGTTATATAGTCCAGAATCCAGGCCAGATACATACTGTGTGATTGCAGGTTCTGAGAACATTAGG
GTCAGAAACATCATCTCTTCAGATAGGCATGATGTTGTCAAGCCCGAGTGGCTTTTAGAGTGTTTTAAACAAAA
ACATGTGTGCCATGGCAACCCCGCTTTATGATTACATGTGCCCATCAACAAAGCAGCATTGTGCCGTGAATATG
ACTGCTATGGTGATAGCTATTTCTGTTGATGCAGATTTGGATCAATTGAAAGAAGTGTTTTAAAGAATTAAACCCAG
TGAGCAGCAGACTCCTGAAGAAATGGCCCCTGTGATTGCTGACCTAGAATGTCGTTATTCCTGGGATCACTCTCCT
CTCAGTATGTTTCGACACTACACCGTTTATTTGGACTTGTATGCTGTTATTAATGACTTAAGTTCCAAAATCGAAGC
CACAAGGTTAGGTGTTACAGCACTTGAGCTGCGGTTTCGTGGAGCAAAGGTGGTTTCCCGCTTATCTGAAGGGG
TGTCTCACGTAATCATCGGGGAAGATCAGAGACGAGTCAGTGACTTTAAACGTTTCAAGAAGACGCTTAAGAAA
AAGTTTAAATCCTGCAGGAACGTTGGGTGATCGATTAGTACAGTGTGAAGTGCAGGAAGAAAACCTGTG
TTTGCTTTAG

[illegible]

On dirait une forme tronquée qui débute plus loin dans la séquence

○ FlagBirA Lig4 SP clone B

➤ B3Fwd 869NT

ATGGCTTCCTCACAAGCCTCACGAACTGTCGCAGCTCATGTCCCCTTTGCAGACTTGTGCTCCACCTTAGAACGAA
TACAGAAAGGCCAATGCTAGCTGCTGTAGCAGATGTGGAGCGTGTGGAGAAGGACATGAAGCAGCAGAGTTTC
TACATCGAAACTAAGCTCGATGGCGAGCGCATGCAGATGCACAAGGATGGCGCCCTGTACCGGTACTTCTCCAGA
AATGGTTACAACCTACACCGATCAGTTCGGCGAATCTCCACAGGAAGGCTCTCTACCCCGTTTATTCACAACGCAT
TCAAGACAGATGTGCAAGTGTGCATCCTTGATGGCGAGATGATGGCCTACAACCCAACGACACAGACTTTTCATGC
AGAAGGGGGTCAAGTTTGATATCAAAAGGATGGTGAAGATTCTGACCTACAGACATGCTACTGTGTTTTCGATG
TGCTGATGGTTAATAATAAGAAGCTAGGGCGTGAGACTCTCAGGAAGAGGTATGATATCCTTAGTAGCACTTTTAC
ACCCATACAAGGTGAATAGAGATAGTGCAGAAAACTCAAGCTCAGACAAAGCAGGAAGTAGTGGATGCATTAA
ATGATGCCATAGACAAGAGAGAAGAGGGGATCATGGTTAAACACCCTCTGTCCATTTACAAGCCAGACAAAAGA
gGTGAAgGGTGGCTAAAGATTAAACCAGAGTATGTCACTGGATTGATGGATGAATTAGANCTCTTAATTGTTGGG
GGCTACTGGGGTAAAGGNTCTCGAGGTGGNATGATGTCTCACTTTCTGTGTGCAGTGGCAGANACNCNNNTCC
TGNNANAGCCNTCTGNGTNCNACACTCTGNNNNNTGNNNGNNNNNGGN

➤ BGHRev 972NT

GAGNGGCATGACTGTANGACGCTGGATGACCTGGAGCAGCTGAGGGGGAAAGCATCTGGGAAGCTTGCCACA
AAACACCTTCACATAGGTGACGATGACGAACCCAGAGAAAAAAGCGGAAACCCATCTcTAAGACGAAGAAAA
CCATtGGAATCATTGAACACCTAAAAGCGCCTAaCCTTTCTAACATAAAACAAAGTTTCTAATGTATTTGAAGATGT
TGAGTTTTGTGTCATGAGTGGATTAGATGGTTATCCAAAGCCTGACCTAGAGAACAAAATTGCAGAATTTGGTG
GTTATATAGTCCAGAATCCAGGCCAGATACATACTGTGTGATTGCAGGTTCTGAGAACATTAGGGTCAGAAAC
ATCATCTCTTCAGATAGGCATGATGTTGTCAAGCCCGAGTGGCTTTTAGAGTGTTTTAAACAAAAACATGTGTG
CCATGGCAACCCCGCTTTATGATTCACATGTGCCCATCAACAAAGCAGCATTTTGCCCGTGAATATGACTGCTAT
GGTGATAGCTATTTGTTGATGCAGATTTGGATCAATTGAAAGAAGTGTTTTTAAGAATTAAACCCAGTGAGCA
GCAGACTCCTGAAGAAATGGCCCCTGTGATTGCTGACCTAGAATGTCGTTATTCCTGGGATCACTCTCCTCTCAG
TATGTTTCGACACTACACCGTTTATTTGGACTTGATGCTGTTATTAATGACTTAAGTTCCAAAATCGAAGCCACA
AGGTTAGGTGTTACAGCACTTGAGCTGCGGTTTCGTGGAGCAAAGGTGGTTTCCCGCTTATCTGAAGGGGTGTC
TCACGTAATCATCGGGGAAGATCAGAGACGAGTCAGTGACTTTAAACGTTTCAAGAAGCGCTTAAGAAAAAG
TTAAAATCCTGCAGGAACGTTGGGTGATCGATTCAGTAGACAAGTGTGAAGTGCAGGAAGAAAACCTGTATTT
GCTTTAG

Idem clone A

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
fud														
BGHRev														
cds														
Consensus														
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
fud														
BGHRev														
cds														
Consensus														
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
fud														
BGHRev														
cds														
Consensus														
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
fud														
BGHRev														
cds														
Consensus														
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
fud														
BGHRev														
cds														
Consensus														
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
fud														
BGHRev														
cds														
Consensus														
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
fud														
BGHRev														
cds														
Consensus														
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
fud														
BGHRev														
cds														
Consensus														
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
fud														
BGHRev														
cds														
Consensus														
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
fud														
BGHRev														
cds														
Consensus														
	1301	1310	1320	1330	1340	1350	1360	1370	138					