

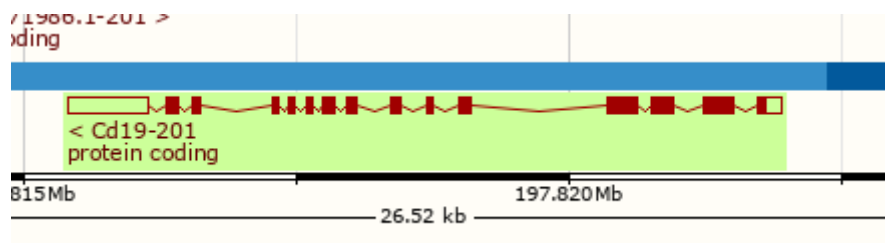
1)CD19

Rattus norvegicus **CD19** molecule, mRNA (cDNA clone IMAGE:7365041), complete cds

NM_001013237

Taille 1644NT

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atgcc a tctctctctcc ctgtctccct
    61 cctcctcttc cttaccttag taggaggcag gccccagaat tccttactgg tggaggtaga
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   181 gctggcttgg tatcgaggta accagtcaac acccttctctg gagctgagcc tcagggtccc
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   841 cgtgaaggtc attgcaagg cagcagtgtg gctctggctg ttgaggactg gtggatggat
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  1561 tgggtctgg cccagtcac aggaagatgc agactcttat gaaaacatgg ataaatctga
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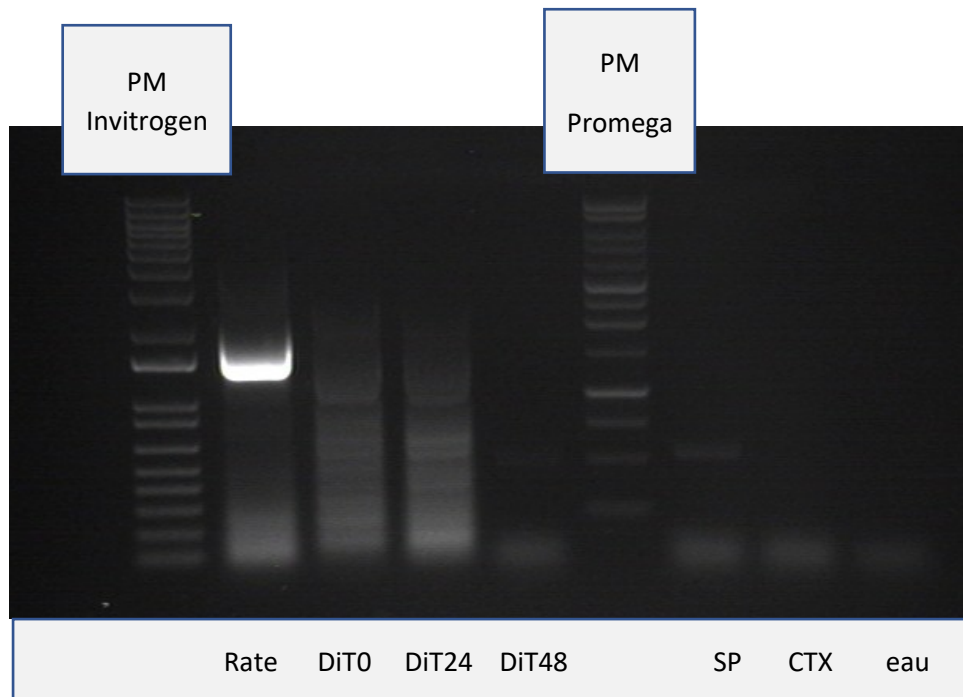


- **Séquence protéique :** NP_001013255

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WATDHPEVWKT KPVCAPREISLNQSLINQDLTVAPGSTLWLSGVPVPVPTKGSISWTHVHPKTLNVSLLSLGGE
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 EVQDAGAQRHETGLEEEGEAYEEDPDSEEGSEFYENDSNLEQDQLSQDGSYENPEDDPVGPEEEDSFSNAESYEN
 ADEELAQPVGRTMDFLSPHGS AWDP SREASSLGSQSYEDMRGILYAAPQLQSIRSGPSHEEDADSYENMDKSDDP
 EPAWAGEGHMGTWGAT-

● 29/09 : PCR 60°C Enhancer 5



- 16/10 : extraction CD19 rate en vue de clonage
- 23/10 purification / digestion / purification
- 26/10 : ligation dans FB
- 27/10 transformation
- 28/10 miniprep clone A FlagBirA CD19 rate à séquencer
- 03/11 : gel publi Alice avec le reste de PCR

- Résultats séquençages Nov9

- FlagBirA CD19 rate clone A

- B3Fwd 875NT

ATGCCATCTCCTCTCCCTGTCTCCCTCCTCCTCTTCTTACCTTAGTAGGAGGCAGGCCCCAGAATTCCTTACTGGT
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- BGHRev 1032NT

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TGN

- BGHRev RENVOYE le 25/11 959NT

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➤ **Int Fwd 974NT**

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CGANTCTTATGAAAATGCAGATGAGGAGCTGGCCCAACNNGNTGGCANGACGATGGACTTNCTGAGCCCCAC
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CCTGNATGC

➤ **Int Rev 687NT**

CTCTCNNTNTNNNTAGTNGAGGCAGNCCCCAGAANNNTTANTGGTGGAGGTAGAAGAGGGAGACAATGTT
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➤ **Synthèse séquençage**

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TTCTTGAGCTGAGCTCAGGTCCCCGGACCTGGGTCTGCACATCGGGCCCCTGGGCATC	240
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CTGTTCCGGTGGAATGCTTCAGACTTGGGGGACCTGGATTGTGACCTAGGAAACAGGTCC	420
TCAGGAGCCACAGGTCCACTTCTGGTTCCAGCTGTATGTGTGGGCTACAGATCATCCT	480
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 HPVREMWWVWGSLLLLPQAKASDEGTYYCLQGGLTIKMHVKVIASVALAVEDWWM
 DSPSCDFSICHLLYGFYGGFSLFSKSLHPEEEEEANDRPC-
 EILQSDASLRKRDPEPVWECALPSYIYLWPGPCALGC-PREWSCVLWKSTH-
 SPGCWSSET-NRTGRRRGGL-RARQRGGL-IL-E-LQP-AGSTFPGWQWL-EP-G-
 PRRSRGGRLLLQCRVL-KCR-
 GAGPTSWQDDGLPEPPRVCMPGPQGSILPWVPVLRRYERDPVCSSSAPINSVWSQS-
 GRCRL-KHG-I-RPRASMGRRGPHGDLGCHV

➤ Blast contre banque rat :

		Name	Score	Score	Cover	value	Ident	Len	Accession
2	PREDICTED: Rattus norvegicus CD19 molecule (Cd19)_transcript variant X1_mRNA	Norway rat	2992	2992	100%	0.0	99.63%	2687	XM_006230316.3
2	Rattus norvegicus CD19 molecule (Cd19)_mRNA	Norway rat	2979	2979	100%	0.0	99.45%	2404	NM_001013237.3
2	Rattus norvegicus CD19 molecule_mRNA (cDNA clone IMAGE:7365041)_complete cds	Norway rat	327	327	11%	2e-87	99.44%	1113	BC090026.1

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

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

Délétion de 3NT entre 825 et 827, qui entraine décalage cadre de lecture

➤ Différence au niveau PROT :

		Score	Score	Cover	value	Ident	Len	Accession
CD19 antigen [Rattus norvegicus]	Norway rat	555	555	52%	0.0	98.92%	549	EDM17480.1
B-lymphocyte antigen CD19 precursor [Rattus norvegicus]	Norway rat	555	555	52%	0.0	98.92%	547	NP_001013255.2
PREDICTED: B-lymphocyte antigen CD19 isoform X1 [Rattus norvegicus]	Norway rat	553	553	51%	0.0	100.00%	546	XP_006230378.1
B-lymphocyte antigen CD19 isoform X1 [Rattus rattus]	black rat	514	514	52%	3e-175	94.60%	547	XP_032751521.1
B-lymphocyte antigen CD19 isoform X2 [Rattus rattus]	black rat	513	513	51%	1e-174	95.62%	546	XP_032751523.1
B-lymphocyte antigen CD19 isoform X1 [Mus caroli]	Ryukyu mouse	483	483	58%	8e-163	80.58%	546	XP_021024442.1
B-lymphocyte antigen CD19 isoform 1 precursor [Mus musculus]	house mouse	482	482	58%	2e-162	80.26%	547	NP_033974.2
B-lymphocyte antigen CD19 isoform X2 [Mus caroli]	Ryukyu mouse	482	482	51%	3e-162	88.69%	545	XP_021024443.1
unnamed protein product [Mus musculus]	house mouse	481	481	51%	5e-162	88.32%	546	BAE33595.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	-----													
refprot	-----													
Consensus	-----													
seq	MPSPLPVSLLLFLTLVGGRPQNSLLVEVEEGDNVYLSCLRDSSPVSEKLAHYRGNQSTPFLELSLRSPDLGLHIGPLGILLVIYVNSDHRGGFYLCQKRPSFKDTWQPAHTYVYEDSGELFRWNASDLG													
refprot	MPSPLPVSLLLFLTLVGGRPQNSLLVEVEEGDNVYLSCLRDSSPVSEKLAHYRGNQSTPFLELSLRSPDLGLHIGPLGILLVIYVNSDHRGGFYLCQKRPSFKDTWQPAHTYVYEDSGELFRWNASDLG													
Consensus	MPSPLPVSLLLFLTLVGGRPQNSLLVEVEEGDNVYLSCLRDSSPVSEKLAHYRGNQSTPFLELSLRSPDLGLHIGPLGILLVIYVNSDHRGGFYLCQKRPSFKDTWQPAHTYVYEDSGELFRWNASDLG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	-----													
refprot	-----													
Consensus	-----													
seq	DLDCDLGNRSSGSHRSTSGSQLYVWADHPVHKTTPYCAPREISLNQSLINQDLTVAPGSTLWLSGCVPPVPVTKGSIHSTHVPKTLNVSLLSLSLGGEHPVREHMYVMSLLLLPQAKASDEGTYYCL													
refprot	DLDCDLGNRSSGSHRSTSGSQLYVWADHPVHKTTPYCAPREISLNQSLINQDLTVAPGSTLWLSGCVPPVPVTKGSIHSTHVPKTLNVSLLSLSLGGEHPVREHMYVMSLLLLPQAKASDEGTYYCL													
Consensus	DLDCDLGNRSSGSHRSTSGSQLYVWADHPVHKTTPYCAPREISLNQSLINQDLTVAPGSTLWLSGCVPPVPVTKGSIHSTHVPKTLNVSLLSLSLGGEHPVREHMYVMSLLLLPQAKASDEGTYYCL													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	-----													
refprot	-----													
Consensus	-----													
seq	QGGLTIKMHVKVIASVALAVEDHMDSPSCDFSIHLLYGFYGGFSLFSKSLHPEEEEEANDRPEILQSDASLKRDPPEVMECALPSYIYLWPGPCALGCPREKSCVLKSTHSPGCHSSETNRTGR													
refprot	QGGLTIKMHVKVIASVALVEDHMDSPSCDFSIHLLYGFYGGFSLFSKSLHPEEEEEANDRPEILQSDASLKRDPPEVMECALPSYIYLWPGPCALGCPREKSCVLKSTHSPGCHSSETNRTGR													
Consensus	QGGLTIKMHVKVIASVALVEDHMDSPSCDFSIHLLYGFYGGFSLFSKSLHPEEEEEANDRPEILQSDASLKRDPPEVMECALPSYIYLWPGPCALGCPREKSCVLKSTHSPGCHSSETNRTGR													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	-----													
refprot	-----													
Consensus	-----													
seq	RRGGLRARQRGGLILELQPA-GSTFPGWQWLEPGPRRSRGGRLLLCQCVLKCAGAGPTSHQDDGLEPPRYVCMGPQPGSILPWVPLRRYERDPVCSAPINSVMSQSGRCRLCLKHGIRPRASMGRRGPR													
refprot	RRGGLRARQRGGLILELQPA-GSTFPGWQWLEPGPRRSRGGRLLLCQCVLKCAGAGPTSHQDDGLEPPRYVCMGPQPGSILPWVPLRRYERDPVCSAPINSVMSQSGRCRLCLKHGIRPRASMGRRGPR													
Consensus	RRGGLRARQRGGLILELQPA-GSTFPGWQWLEPGPRRSRGGRLLLCQCVLKCAGAGPTSHQDDGLEPPRYVCMGPQPGSILPWVPLRRYERDPVCSAPINSVMSQSGRCRLCLKHGIRPRASMGRRGPR													
	521	530	540	550	554									
seq	-----													
refprot	-----													
Consensus	-----													
seq	HGDLGCHV													
refprot	SHEEDADS YENMDKSDOPEPAWAGEGHMGTMGAT													
Consensus	hg#edads.....													

Flag BirA CD19 (clone A) décalage du cadre de lecture :
mauvais

- Résultats séquençages Nov25

- FlagBirA CD19 rate clone C

- **B3Fwd 859NT**

ATGCCATCTCCTCTCCCTGTCTCCCTCCTCCTCTTCTTACCTTAGTAGGAGGCAGGCCCCAGAATTCCTTACTGGT
GGAGGTAGAAGAGGGAGACAATGTTGTGCTGTCATGCCTCCGGGACTCCTCACCTGTCTCTTCTGAGAAGCTGG
CTTGGTATCGAGGTAACCACTCAACACCCTTCTGGAGCTGAGCCTCAGGTCCCCGGACCTGGGTCTGCACATCG
GGCCCTGGGCATCTTGCTAGTGATTGTCAATGTCTCGGACCATAGGGGGGGCTTCTATCTGTGCCAAAAGAGGC
CCTCTTCAAGGACACCTGGCAGCCTGCCTGGACCGTAAACGTGGAGGATAGTGGGGAGCTGTTCCGGTGAAT
GCTTCAGACTTGGGGGACCTGGATTGTGACCTAGGAAACAGGTCTCAGGGAGCCACAGGTCCAATTCTGGTTC
CCAGCTGTATGTGTGGGCTACAGATCATCTGAGGTCTGGAACAAAGCCTGTATGTGCCCCACGGGAGATCAG
TCTGAATCAGAGTCTAATCAACCAAGATCTCACTGTGGCCCTGGCTCCACACTTTGGCTGTCCTGTGGCGTACCC
CCTGTCCCAGTGACCAAAGGCTCCATCTCCTGNACCCATGTGCATCCTAAGACGCTTAACGTTTCATTACTGAGCC
TAAGCCTTNGGGGAGAGCACCCAGTGAGAGAGANGTGGGNTTTGGGGGTNTCTTTTTGCTNCTGCCCCAAGC
CAAAGCTTCNGATGAANGNACNTATTATTGTCTCCANGNNNGNCTGACCATCNANATGCACNTGANNGTCATT
GCNNGGNCANCANTGTGGCTNTGGCTGNTNNNGACTGG

- **BGHRev 1033NT**

CCCANNGNCNAAGGCTNCNNNNNNNGNNNCCATNNGCANNNNNACGNNTTAANNNTTCATTANTGAGCCTA
NNNNNGGGGAGAGACCCAGTGAGAGAGANGNNGTTTGGGGGTCTCTTTTGCTANTGCCCAAGCCAAAGC
TTCAGATGAAGGTACCTATTATTGTNTCCAAGGAGNCNTGACCATCAAGATGCACGTGAAGGTCATTGCAAGGTC
AGCAGTGTGGCTCTGGCTGTTGAGGACTGGTGGATGGATAGTCCCAGTTGTGACTTTAGTATATGTCATCTTCTGT
ATGGTTTCTATGGCGGCTTTTCTCTATTTTCGAAGAGCCTTCATCCTGAGGAGGAAGAGGAAGCGAATGACCGAC
CCTGCTAGGAGATTCTTCAAAGTGACGCCTCCCTCAGGAAACGGGACCCAGAACCAGTATGGGAATGTGCTCTC
CCTTCTACATCTACCTCTGGCCAGGCCCATGCTCAGCGTTGGGCTGCTAGCCTAGGGAGTGGTCTGTGCTCTAT
GGAAATCCACGCATTGAAGTCCAGGATGCTGGAGCTCAGAGACATGAAACAGGACTGGAAGAAGAAGGGGAG
GCCTATGAAGAGCCAGACAGCGAGGAGGGCTCTGAATTCTATGAGAATGACTCCAACCTTGAGCAGGATCAACT
TTCCAGGATGGCAGTGGCTATGAGAACCCTGAGGATGACCCCGTAGGTCCAGAGGAGGAAGACTCCTTCTCCA
ATGCCGAGTCTTATGAAAATGCAGATGAGGAGCTGGCCCAACCAGTTGGCAGGACGATGGACTTCTGAGCCCC
CACGGGTCTGCATGGGACCCAGCCGGAAGCATCCTCCCTGGGTCCCAGTCTACGAAGATATGAGAGGGAT
CCTGTATGCAGCTCCTCAGCTCCAATCAATTCGGTCTGGTCCCAGTCATGAGGAAGATGCAGACTCTTATGAAAAC
ATGGATAAATCTGACGACCCAGAGCCAGCATGGGCAGGAGAGGGCCACATGGGGACTTGGGGTGCCACGTGA

- **Int Fwd 1007NT**

GTCTGAATCAGAGTCTAATCAACCAAGATCTCACTGTGGCCCTGGCTCCACACTTTGGCTGTCCTGTGGCGTACC
CCCTGTCCCAGTGACCAAAGGCTCCATCTCCTGGACCCATGTGCATCCTAAGACGCTTAACGTTTCATTACTGAGC
CTAAGCCTTGGGGGAGAGACCCAGTGAGAGAGATGTGGGTTTGGGGGTCTCTTTTGCTACTGCCCAAGCCA
AAGCTTCAGATGAAGGTACCTATTATTGTCTCCAAGGAGGCCTGACCATCAAGATGCACGTGAAGGTCATTGCAA
GGTCAGCAGTGTGGCTCTGGCTGTTGAGGACTGGTGGATGGATAGTCCCAGTTGTGACTTTAGTATATGTCATCTT
CTGTATGGTTTCTATGGCGGCTTTTCTCTATTTTCGAAGAGCCTTCATCCTGAGGAGGAAGAGGAAGCGAATGAC
CGACCCTGCTAGGAGATTCTTCAAAGTGACGCCTCCCTCAGGAAACGGGACCCAGAACCAGTATGGGAATGTGC
TCTCCCTTCTACATCTACCTCTGGCCAGGCCCATGCTCAGCGTTGGGCTGCTAGCCTAGGGAGTGGTCTGTGTC
CTATGGAAATCCACGCATTGAAGTCCAGGATGCTGGAGCTCAGAGACATGAAACAGGACTGGAAGAAGAAGGG
GAGGcCTATGAAGAGCCAGACAGCGAGGAGGGCTCTGAATTCTATGAGAATGACTCCaACCTTGAGCAGGATCA
ACTTTCCCAGGATGGCAGTGGCTATGAGAACCCTGANGATGACCCCGTANGTCCAGANGANGAAGANTCCTTC

TCNATGCCGAGTCTTATGAAAATGCANATGAGGAGCTGGNCCAACCAGTTGGCAGGACGATGGACTTCCTGAG
CCCCACGGGTCNGCATGGGACCCCAGCCGGAAGCATCCTCCNTTGGGTCCNAGTCCTACNAANANANGAN
AGGNNNNNNGNATGCAGCTCNTCANCTCNNTCNNTTCGGT

➤ **Int Rev 622NT**

CTTANTNGTGGAGGTAGAAGANGGAGACAATGNTGTGNTGTCATNCNTNNGGGANTNNTCNCCNNTNTNTT
NNGAGAAGNNGGNTTGGTATNGAGGTAACCANTCAACANCCTTNCNGGANNTGANCNTCAGNTCCCNGGAC
CTGGGTNTGCACATCGGGCCCCCTGGGCATCTTGNTAGTGATTGTCAATGTCTCGGACCATAGGGGGGGCTTCTAT
CTGTGCCAAAAGAGGCCCTCTTTCAAGGACACCTGGCAGCCTGCCTGGACNGTAAACGTGGAGGATAGTGGGG
AGCTGTTCCGGTGGAATGCTTCAGACTTGGGGGACCTGGATTGTGACCTAGGAAACAGTCCCTCAGGGAGCCA
CAGGTCCACTTCTGGTTCCCAGCTGTATGTGTGGGCTACAGATCATCCTGAGGTCTGGAACAAAGCCTGTATG
TGCCCCACGGGAGATCAGTCTGAATCAGAGTCTAATCAACCAAGATCTCACTGTGGCCCCCTGGCTCCACACTTTG
GCTGTCTGTGGCGTACCCCCTGTCCCAGTGACCAAAGGCTCCATCTCCTGGACCCATGTGCATCCTAAGACGCTT
AACGTTTCATTNNNTTNNNNNNNNNAAGGGGA

➤ **Synthèse séquençage**

ATGCCATCTCCTCTCCCTGTCTCCCTCCTCCTCTTCCCTTACCTTAGTAGGAGGCAGGCCC	60
CAGAATTCCCTTACTGGTGGAGGTAGAAGAGGGAGACAATGTTGTGCTGTCATGCCTCCGG	120
GACTCCTCACCTGTCTCTTCTGAGAAGCTGGCTTGGTATCGAGGTAACCAGTCAACACCC	180
TTCTTGAGAGCTGAGCCTCAGGTCCCCGGACCTGGGTCTGCACATCGGGCCCCCTGGGCATC	240
TTGCTAGTGATTGTCAATGTCTCGGACCATAGGGGGGGCTTCTATCTGTGCCAAAAGAGG	300
CCCTCTTTCAAGGACACCTGGCAGCCTGCCTGGACCGTAAACGTGGAGGATAGTGGGGAG	360
CTGTTCCGGTGGAATGCTTCAGACTTGGGGGACCTGGATTGTGACCTAGGAAACAGGTCC	420
TCAGGGAGCCACAGGTCCACTTCTGGTTCCCAGCTGTATGTGTGGGCTACAGATCATCCT	480
GAGGTCTGGAACAAAGCCTGTATGTGCCCCACGGGAGATCAGTCTGAATCAGAGTCTA	540
ATCAACCAAGATCTCACTGTGGCCCCCTGGCTCCACACTTTGGCTGTCTGTGGCGTACCC	600
CCTGTCCCAGTGACCAAAGGCTCCATCTCCTGGACCCATGTGCATCCTAAGACGCTTAAC	660
GTTTCATTACTAGCCCTAAGCCTTGGGGGAGAGCACCCAGTGAGAGAGATGTGGGTTTGG	720
GGGTCTCTTTTGCTACTGCCCCAAGCCAAAGCTTCAGATGAAGGTACCTATTATTGTC	778
TCCAAGGAGGCCTGACCATCAAGATGCACGTGAAGGTCATTGCAAGGTCAGCAGTGTGGC	838
TCTGGCTGTTGAGGACTGGTGGATGGATAGTCCCAGTTGTGACTTTAGTATATGTCATCT	898
TCTGTATGGTTTCTATGGCGGCTTTTCTCTATTTTCAAGAGCCTTCATCCTGAGGAGGA	958
AGAGGAAGCGAATGACCGACCCTGCTAGGAGATTCTTCAAAGTGACGCCTCCCTCAGGAA	1018
ACGGGACCCAGAACCAGTATGGGAATGTGCTCTCCCTTCCCTACATCTACCTCTGGCCAGG	1078
CCCATGCTCAGCGTTGGGCTGCTAGCCTAGGGAGTGGTCTGTGTCTATGGAAATCCAC	1138
GCATTGAAGTCCAGGATGCTGGAGCTCAGAGACATGAACAGGACTGGAAGAAGAAGGGG	1198
AGGCCTATGAAGAGCCAGACAGCGAGGAGGGCTCTGAATTCTATGAGAATGACTCCAACC	1258
TTGAGCAGGATCAACTTTCCAGGATGGCAGTGGCTATGAGAACCCTGAGGATGACCCCG	1318
TAGTCCAGAGGAGGAAGACTCCTTCCAATGCCAGTCTTATGAAAATGCAGATGAGG	1378
AGCTGGCCCCAACAGTTGGCAGGACGATGGACTTCTGAGCCCCACGGGTCTGCATGGG	1438
ACCCCAGCCGGGAAGCATCCTCCCTTGGGTCCCAGTCCACGAAGATATGAGAGGGATCC	1498
TGTATGCAGCTCCTCAGCTCCAATCAATTTCGGTCTGGTCCCAGTCATAGGAAGATGCAG	1558
ACTCTTATGAAAACATGGATAAATCTGACGACCCAGAGCCAGCATGGGCAGGAGAGGGCC	1618
ACATGGGGACTTGGGGTGCCACGTGA	1644

MPSPPLVSLLLFLTLVGGRPQNSLLVEVEEGDNVVLSCLRDSSPVSSEKLAWYRGNQSTPFLELSLRSPDLGLHIGPLG
ILLVIVNVSDHRGGFYLCQKRPSFKDTWQPAWTVNVEDSGELFRWNASDLGDLDCDLGNRSSGSHRSTSGSGLYV
WATDHPEVWTKPVCAPREISLNQSLINQDLTVAPGSTLWLSCGVPPVPVTKGSISWTHVHPKTLNVSLLSLGLGE
HPVREMWWVWSLLLLPQAKASDEGTYCYLQGGTLIKMHVKVIARS AVLWLLRTGGWIVPVVTLVYVIFCMVSM
AAFLYFRRFILRRKRKRMTPARRFFKVTPPSGNGTQNNQYGNVLSLPTSTSGQAHAQRWAASLGS GPVSYGNPRI
EVQDAGAQRHETGLEEEGEAYEEP DSEEGSEFYENDSNLEQDQLSQDGS GYENPEDDPVGPEEEDSFSNAESYEN
ADEELAQPVGRTMDFLSPHGS AWDP SREASSLSQSYEDMRGILYAAPQLQSIRSGPSHEEDADSYENMDKSDDP
EPAWAGEGHMGTWGAT-

➤ **Blast contre banque rat :**

OK, sauf en 1485 $T < C$

➤ Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
ref	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
Consensus	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
seq	MPSPLPYSLLFLTLVGGRPQNSLLVEVEEGDNVVLSCLRDSSPVSEKLAWYRGNQSTPFLELSLRSPDLGLHIGPLGILLVIYVNSDHRGGFYLCQKRPSFKDTHQPAWTVNVEDSGELFRWNASDLG													
ref	MPSPLPYSLLFLTLVGGRPQNSLLVEVEEGDNVVLSCLRDSSPVSEKLAWYRGNQSTPFLELSLRSPDLGLHIGPLGILLVIYVNSDHRGGFYLCQKRPSFKDTHQPAWTVNVEDSGELFRWNASDLG													
Consensus	MPSPLPYSLLFLTLVGGRPQNSLLVEVEEGDNVVLSCLRDSSPVSEKLAWYRGNQSTPFLELSLRSPDLGLHIGPLGILLVIYVNSDHRGGFYLCQKRPSFKDTHQPAWTVNVEDSGELFRWNASDLG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
ref	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
Consensus	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
seq	DLDCDLGNRSSGSHRSTSGSQLYVWATHDPEVWTKPVCAPREISLNQSLINQDLTVAPGSTLMLSCGVPPVPVTKGSIWTHVHPKTLNYSLLSLSLGGEHPVREHNVGSLLLLPOAKASDEGTYYCL													
ref	DLDCDLGNRSSGSHRSTSGSQLYVWATHDPEVWTKPVCAPREISLNQSLINQDLTVAPGSTLMLSCGVPPVPVTKGSIWTHVHPKTLNYSLLSLSLGGEHPVREHNVGSLLLLPOAKASDEGTYYCL													
Consensus	DLDCDLGNRSSGSHRSTSGSQLYVWATHDPEVWTKPVCAPREISLNQSLINQDLTVAPGSTLMLSCGVPPVPVTKGSIWTHVHPKTLNYSLLSLSLGGEHPVREHNVGSLLLLPOAKASDEGTYYCL													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
ref	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
Consensus	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
seq	QGGLTIKMHVKVIARSAVWLMLLRTGGHIVPVYTLVYVIFCHVSHAFLYFRRAFILRRKRKRMTDPARRFFKVTPPSGNGTQNYGNYLSLPTSTSGQAHAQRHAASLGSGPVSYGNPRIEVQDAGAQR													
ref	QGGLTIKMHVKVIARSAVWLMLLRTGGHIVPVYTLVYVIFCHVSHAFLYFRRAFILRRKRKRMTDPARRFFKVTPPSGNGTQNYGNYLSLPTSTSGQAHAQRHAASLGSGPVSYGNPRIEVQDAGAQR													
Consensus	QGGLTIKMHVKVIARSAVWLMLLRTGGHIVPVYTLVYVIFCHVSHAFLYFRRAFILRRKRKRMTDPARRFFKVTPPSGNGTQNYGNYLSLPTSTSGQAHAQRHAASLGSGPVSYGNPRIEVQDAGAQR													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
ref	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
Consensus	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
seq	HETGLEEEGEAYEEDPSEEGSEFYENDSNLEQDQLSQDGSYENPEDDPVGPPEEEDSFSAESYENADEELAQPVGRTDHLSPHGSAMDPSREASSLGSSQSYEDMRGILYAAPQLQSIIRSGPSHEEDAD													
ref	HETGLEEEGEAYEEDPSEEGSEFYENDSNLEQDQLSQDGSYENPEDDPVGPPEEEDSFSAESYENADEELAQPVGRTDHLSPHGSAMDPSREASSLGSSQSYEDMRGILYAAPQLQSIIRSGPSHEEDAD													
Consensus	HETGLEEEGEAYEEDPSEEGSEFYENDSNLEQDQLSQDGSYENPEDDPVGPPEEEDSFSAESYENADEELAQPVGRTDHLSPHGSAMDPSREASSLGSSQSYEDMRGILYAAPQLQSIIRSGPSHEEDAD													
	521	530	540	547										
seq	-----													
ref	-----													
Consensus	-----													
seq	SYENMDKSDDPEPAWAGEGHMGTMGAT													
ref	SYENMDKSDDPEPAWAGEGHMGTMGAT													
Consensus	SYENMDKSDDPEPAWAGEGHMGTMGAT													

		Name	Score	Score	Cover	value	Ident	Len	Accession
☒	B-lymphocyte antigen CD19 precursor [Rattus norvegicus]	Norway rat	1122	1122	100%	0.0	100.00%	547	NP_001013255.2
☒	CD19 antigen [Rattus norvegicus]	Norway rat	1116	1116	100%	0.0	99.64%	549	EDM17480.1
☒	PREDICTED: B-lymphocyte antigen CD19 isoform X1 [Rattus norvegicus]	Norway rat	1114	1114	100%	0.0	99.82%	546	XP_006230378.1
☒	Cd19 protein [Rattus norvegicus]	Norway rat	111	111	9%	2e-29	100.00%	52	AAH90026.1

Pas de diff au niv prot

Flag BirA CD19 (clone C) OK : substitution d'un NT qui ne change pas la prot

Séquençage interne :

- CD19_SeqInt_Fwd

En 470 pour un démarrage ~620NT

CAGATCATCCTGAGGTCTGG

- CD19_SeqInt_Rev

Aux ~1070 pour un démarrage ~920NT

TAGATGTAGGAAGGGAGAGC