

INFORME DE BÚSQUEDA DE PATENTES PARA EL No de Radicación:						
CRITERIOS PARA LA BÚSQUEDA (anexar pantallazo o reporte en PDF, junto con los boleanos utilizados)						
Palabras clave utilizadas		Anti-CD19, Chimeric antigen receptors, T lymphocyte, CD19 scFv				
CLASIFICACIONES INTERNACIONALES UTILIZADAS PARA LA BÚSQUEDA						
BASES DE DATOS CONSULTADAS.						
espacenet		Scholar google		Ncbi pubmed		Ncbi blast
				The Lens		
INFORMES DE EXÁMENES REALIZADOS EN OTRAS OFICINAS (documentos patentes, literatura no patente etc...)						
Oficina	Fecha del examen o de reporte de búsqueda de documentos	Anterioridades encontradas para el examen o reportados en el examen de búsqueda(relacionarlos todos)	Reiv. afectadas	RELEVANCIA (requisito que afecta)	FUERON TENIDOS EN CUENTA PARA EL EXAMEN EN LA OFICINA COLOMBIANA	
					SI	NO
EUROPEA	2/12/2014	US2004043401	1-38	Novedad		X (documento indicado para parental sin modificación)
		WO2009091826	1-38	Novedad		X (documento indicado para parental sin modificación)
		Tammana et al.Human Gene Therapy 21(2010)	1-38	Novedad		X (no disponible texto completo)
		Carpenito, et al. pNAS 106(9) 2009	1-38	Novedad		X (receptor mesotelina no relacionado con divisional)
WIPO		[A]WO2010025177 [A]US2004043401 [A]US2009297994 [A]US7319143 [A]US7265209 [A]US7448191 [A]US7446190 [A]US6410319 [A]US7514537 [A]WO2010085660	Ninguna			

USPTO	27/04/2015	Ninguno				
DOCUMENTOS ADICIONALES ENCONTRADOS POR EL EXAMINADOR DE ACUERDO A LOS CRITERIOS DE BÚSQUEDA.						
WO02077029						
WO2010025177						
J. Immunother. 32 (7), 689-702 (2009)						
Blood: 116 (20) 4099 - 4102						
BÚSQUEDA DE SECUENCIAS						
Número de depósito / patente y N° de secuencia % de identidad						
SEQ ID NO (de la solicitud)	NCBI	The Lens	EMBL-EBI	DDJB	Genome Quest	
14	número de acceso HM852952					
20 y 24	número de acceso ADM64594					

SEQ ID NO 14

WO_2012_079000_14

RID [4UPFHPU601R](#) (Expires on 11-20 12:11 pm)

Query ID lcl|Query_163923

Description WO_2012_079000_14

Molecule type nucleic acid

Query Length 726

Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.32+ [Citation](#)

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

Graphic Summary

Distribution of 111 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments

Color key for alignment scores

Score Range	Color
<40	Black
40-50	Blue
50-80	Green
80-200	Pink
>=200	Red

Query 1 100 200 300 400 500 600 700

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Synthetic construct FMC63-28Z receptor protein gene, complete cds	1155	1155	100%	0.0	95%	HM852952.1
☐	Mus musculus mRNA for immunoglobulin heavy chain variable region, subunits VH, DH and JH	660	660	49%	0.0	99%	Y14283.1
☐	Mus musculus mRNA for immunoglobulin light chain variable region, subunits VL and JL	571	571	44%	6e-159	99%	Y14284.1
☐	Mus musculus isolate B-N6 immunoglobulin light chain variable domain mRNA, partial cds	556	556	45%	2e-154	97%	AF434688.1
☐	Mus musculus clone iD3-02 immunoglobulin light chain variable region mRNA, partial cds	547	547	42%	1e-151	98%	JX492565.1
☐	Mouse Ig rearranged kappa-chain (V-IdCR J2) gene V10-J region, hybridoma KL2.29, partial cds	547	547	42%	1e-151	98%	M63611.1
☐	Mouse Ig active kappa-chain mRNA V-J5 region, clone 18C10	547	547	42%	1e-151	98%	M27793.1
☐	Mus musculus anti-idiotypic 4G9 monoclonal antibody light chain mRNA, partial cds	542	542	42%	4e-150	98%	DQ020030.1
☐	Mus musculus clone TL2.3 immunoglobulin light chain variable region mRNA, partial cds	536	536	42%	2e-148	98%	DQ279862.1
☐	Mus musculus clone 3F9 anti-alpha-2 integrin I-domain immunoglobulin light chain variable region mRNA, partial cds	536	536	43%	2e-148	97%	AY853693.1
☐	Mus musculus clone SPL23 immunoglobulin light chain variable region mRNA, partial cds	536	536	42%	2e-148	98%	AY648680.1
☐	Mus musculus mAb 8.5.1 immunoglobulin light chain variable region mRNA, partial cds	532	532	42%	3e-147	97%	AF163739.1
☐	Mus musculus clone FS3-05 immunoglobulin light chain variable region mRNA, partial cds	525	525	42%	4e-145	97%	JX492443.1
☐	Mus musculus clone aAPP-20 immunoglobulin light chain variable region mRNA, partial cds	525	525	42%	4e-145	97%	DQ321356.1
☐	Mouse Ig rearranged kappa-chain (V-IdCR J1) gene V10-J region, hybridoma KL2.18, partial cds	523	523	43%	2e-144	97%	M63608.1

Synthetic construct FMC63-28Z receptor protein gene, complete cds

Sequence ID: [gb|HM852952.1|](#) Length: 1470 Number of Matches: 1

Range 1: 67 to 801 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1155 bits(625)	0.0	701/736(95%)	11/736(1%)	Plus/Plus
Query 1	GACATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC	60		
Sbjct 67	GACATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC	126		
Query 61	ATCAGTTGCAGGGCAAGTCAGGACATTAGTAAATATTTAAATTGGTATCAGCAGAAACCA	120		
Sbjct 127	ATCAGTTGCAGGGCAAGTCAGGACATTAGTAAATATTTAAATTGGTATCAGCAGAAACCA	186		
Query 121	GATGGAAC TGTTAAACTCCTGATCTACCATACATCAAGATTACACTCAGGAGTCCCATCA	180		
Sbjct 187	GATGGAAC TGTTAAACTCCTGATCTACCATACATCAAGATTACACTCAGGAGTCCCATCA	246		
Query 181	AGGTTCA GTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA	240		
Sbjct 247	AGGTTCA GTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA	306		
Query 241	GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTACACGTTGCGAGGG	300		
Sbjct 307	GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTACACGTTGCGAGGG	366		
Query 301	GGGACCAAGCTGGAGATCACAGG-T--GGCGGTGGCT-CGG---G--CGGTGGTGGGTCTG	351		
Sbjct 367	GGGACTAAGTTGGAAATAACAGGCTCCACCTCTGGATCCGGCAAGCCCGGATCTGGCGAG	426		
Query 352	GGTGGCGGC-GGATCTGAGGTGAAACTGCAGGAGTCAGGACCTGGCCTGGTGGCGCCCTC	410		
Sbjct 427	GGATCCACCAAGGGC-GAGGTGAAACTGCAGGAGTCAGGACCTGGCCTGGTGGCGCCCTC	485		
Query 411	ACAGAGCCTGTCCGTACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGTGTAAAG	470		
Sbjct 486	ACAGAGCCTGTCCGTACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGTGTAAAG	545		
Query 471	CTGGATTGCCAGCCTCCACGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGTAGTGA	530		
Sbjct 546	CTGGATTGCCAGCCTCCACGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGTAGTGA	605		
Query 531	AACCACATACTATAATTAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACCTCAA	590		
Sbjct 606	AACCACATACTATAATTAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACCTCAA	665		

```

Query 591 GAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAAGTATGACACAGCCATTTACTACTG 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 666 GAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAAGTATGACACAGCCATTTACTACTG 725

Query 651 TGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGACTACTGGGGCCAAGGAACCTC 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 726 TGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGACTACTGGGGTCAAGGAACCTC 785

Query 711 AGTCACCGTCTCCTCA 726
          ||||||||||||||
Sbjct 786 AGTCACCGTCTCCTCA 801

```

Synthetic construct FMC63-28Z receptor protein gene, complete cds

GenBank: HM852952.1

[FASTA](#) [Graphics](#)

Go to: ☐

LOCUS HM852952 1470 bp DNA linear SYN 11-JUN-2012
 DEFINITION Synthetic construct FMC63-28Z receptor protein gene, complete cds.
 ACCESSION HM852952
 VERSION HM852952.1 GI:305690546
 KEYWORDS .
 SOURCE synthetic construct
 ORGANISM [synthetic construct](#)
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 1470)
 AUTHORS Kochenderfer,J.N., Feldman,S.A., Zhao,Y., Xu,H., Black,M.A.,
 Morgan,R.A., Wilson,W.H. and Rosenberg,S.A.
 TITLE Construction and preclinical evaluation of an anti-CD19 chimeric
 antigen receptor
 JOURNAL J. Immunother. 32 (7), 689-702 (2009)
 PUBMED [19561539](#)
 REFERENCE 2 (bases 1 to 1470)
 AUTHORS Kochenderfer,J.N., Wilson,W.H., Janik,J.E., Dudley,M.E.,
 Stetler-Stevenson,M., Feldman,S.A., Maric,I., Raffeld,M.,
 Nathan,D.A., Lanier,B.J., Morgan,R.A. and Rosenberg,S.A.

TITLE Eradication of B-lineage cells and regression of lymphoma in a
 patient treated with autologous T cells genetically engineered to
 recognize CD19
 JOURNAL Blood 116 (20), 4099-4102 (2010)
 PUBMED [20668228](#)
 REFERENCE 3 (bases 1 to 1470)
 AUTHORS Kochenderfer,J.N.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUL-2010) Surgery Branch, NCI, NIH 10 Center Drive
 Bldg 10 CRC Room 3-3888, Bethesda, MD 20892, USA

CLUSTAL O(1.2.1) multiple sequence alignment

```

WO_2012_079000_14 -----
-----
WO_2012_079000_18 -----
-----

```


gi|305690546|gb|HM852952.1|
GGCGAGGGATCCACCAAGGGCGAGGTGAAACTGCAGGAGTCAGGACCTGGCCTGGTGGCG

WO_2012_079000_14
CCCTCACAGAGCCTGTCCGTCACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGT
WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
CCCTCACAGAGCCTGTCCGTCACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGT

WO_2012_079000_14
GTAAGCTGGATTGCGCCAGCCTCCACGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGT
WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
GTAAGCTGGATTGCGCCAGCCTCCACGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGT

WO_2012_079000_14
AGTGAAACCACATACTATAATTCAGCTCTCAAATCCAGACTGACCATCATCAAGGACAAC
WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
AGTGAAACCACATACTATAATTCAGCTCTCAAATCCAGACTGACCATCATCAAGGACAAC

WO_2012_079000_14
TCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACCTGATGACACAGCCATTTAC
WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
TCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACCTGATGACACAGCCATTTAC

WO_2012_079000_14
TACTGTGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGACTACTGGGGCCAAGGA
WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
TACTGTGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGACTACTGGGGTCAAGGA

WO_2012_079000_14 ACCTCAGTCACCGTCTCCTCA-----

WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
ACCTCAGTCACCGTCTCCTCAGCGGCCGCAATTGAAGTTATGTATCCTCCTCCTTACCTA

WO_2012_079000_14 -----

WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
GACAATGAGAAGAGCAATGGAACCATTATCCATGTGAAAGGGAAACACCTTTGTCCAAGT

WO_2012_079000_14 -----

WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
CCCCCTATTTCCCGGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTTGGGGGAGTCCTG

WO_2012_079000_14 -----

WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
GCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTTTCTGGGTGAGGAGTAAGAGG

WO_2012_079000_14 -----

WO_2012_079000_18 -----

gi|305690546|gb|HM852952.1|
AGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCCCGCCGCCCGGGCCCCACCCGC

WO_2012_079000_14 -----

WO_2012_079000_18 -----
-----AGAGTGAAG

gi|305690546|gb|HM852952.1|
AAGCATTACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCAGAGTGAAG

WO_2012_079000_14 -----

WO_2012_079000_18
TTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAG
gi|305690546|gb|HM852952.1|
TTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAG

WO_2012_079000_14 -----

WO_2012_079000_18
CTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCT
gi|305690546|gb|HM852952.1|
CTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCT

WO_2012_079000_14 -----

WO_2012_079000_18
GAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAG

gi|305690546|gb|HM852952.1|
GAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAG

WO_2012_079000_14 -----

WO_2012_079000_18
AAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGC
gi|305690546|gb|HM852952.1|
AAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGC

WO_2012_079000_14 -----

WO_2012_079000_18
AAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCC
gi|305690546|gb|HM852952.1|
AAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCC

WO_2012_079000_14 -----
WO_2012_079000_18 CTTACATGCAGGCCCTGCCCCCTCGC---
gi|305690546|gb|HM852952.1| CTTACATGCAGGCCCTGCCCCCTCGCTAA

SEQ ID NO 20

>WO_2012_079000_20
DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPS
RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEITGGGSGGGGSGGG
GSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTY
YNSALKSRLTI IKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQTSVTV
SS
>WO_2012_079000_24
RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN
ELQKDKMAEAYSEIGMKGERRRGKGHGGLYQGLSTATKDTYDALHMQALPPR
>WO_2012_079000_12
MALPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK
PDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFG
GGTKLEITGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWI
RQPPRKGLEWLGVIWGSETTYNSALKSRLTI IKDNSKSQVFLKMNSLQTDDTAIYYCAK
HYYYGGSYAMDYWGQTSVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT
RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGC
SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG
GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHGGLYQGLSTATKDTYDALHM
QALPPR
>WO_2012_079000_21
TTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIY
>gi|305690547|gb|ADM64594.1| FMC63-28Z receptor protein [synthetic
construct]
MLLLVTSLLLCELPHPAFLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQ
KPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTF
GGGKLEITGSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG
VSWIRQPPRKGLEWLGVIWGSETTYNSALKSRLTI IKDNSKSQVFLKMNSLQTDDTAIY
YCAKHYYYGGSYAMDYWGQTSVTVSSAAAIEVMYPPPYLDNEKSNGTIIHVKGKHLCP

PLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTR
 KHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP
 EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDA
 LHMQUALPPR

SEQ ID NO 12

Percent Identity Matrix - created by Clustal2.1

1: WO_2012_079000_12	100.00	77.22
2: gi 305690547 gb ADM64594.1	77.22	100.00

CLUSTAL O(1.2.1) multiple sequence alignment

WO_2012_079000_12 gi 305690547 gb ADM64594.1	MALPVTAL-LLPLALLLHAARPDIMTQTSSLSASLGDRVTISCRASQDISKYLNWYQQ MLLLVTSLLLCELPHPAFLIPDIQMTQTSSLSASLGDRVTISCRASQDISKYLNWYQQ * * * * * . *****
WO_2012_079000_12 gi 305690547 gb ADM64594.1	KPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTF KPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTF *****
WO_2012_079000_12 gi 305690547 gb ADM64594.1	GGGTKLEITGGG---GSGGGGSGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG GGGTKLEITGSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG ***** . * . * . *****
WO_2012_079000_12 gi 305690547 gb ADM64594.1	VSWIRQPPRKGLEWLGVIWGSETTYNSALKSRLTIKDNSKSKVFLKMNSLQTDTAIY VSWIRQPPRKGLEWLGVIWGSETTYNSALKSRLTIKDNSKSKVFLKMNSLQTDTAIY *****
WO_2012_079000_12 gi 305690547 gb ADM64594.1	YCAKHYYYGGSYAMDYWGQGTSVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG YCAKHYYYGGSYAMDYWGQGTSVTVSSAAIEVMYPPPYLD--N-----EKSNGT *****::: * * . : *
WO_2012_079000_12 gi 305690547 gb ADM64594.1	AVHTRGLDFACD-----IYIWAP--LAG--TCGVLLLSLVITLYCKRGRKLLYIFKQ IIHVKGKHLCPSPLPFGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDY :.*.* :. . :.* :.* :* **: : : :.*. * .
WO_2012_079000_12 gi 305690547 gb ADM64594.1	PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE MNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE * * : . . . * :. . . *****
WO_2012_079000_12 gi 305690547 gb ADM64594.1	YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQ YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQ *****
WO_2012_079000_12 gi 305690547 gb ADM64594.1	GLSTATKDTYDALHMQALPPR GLSTATKDTYDALHMQALPPR *****