

INFORME DE BÚSQUEDA DE PATENTES PARA EL No de Radicación: 14-121983-00004-0000						
CRITERIOS PARA LA BÚSQUEDA (anexar pantallazo o reporte en PDF, junto con los boleanos utilizados)						
Palabras clave utilizadas		(HER3/ErbB3)				
CLASIFICACIONES INTERNACIONALES UTILIZADAS PARA LA BÚSQUEDA		C07K2317/565				
BASES DE DATOS CONSULTADAS.						
The lens		NCBI	Google Patents	Espacenet	GenomeQuest	
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	27/05/2014	WO2010127181	1-21	NI		X
		WO2011044311	1-21	NI		X
		WO 2011136911	1-21	NI	X	
		G. SALA ET AL, "An ErbB-3 antibody, MP-RM-1, inhibits tumor growth by blocking ligand-dependent and independent activation of ErbB-3/Akt signaling", ONCOGENE, 20110808, vol. 31, no. 10, doi:10.1038/onc.2011.322, ISSN 0950-9232, PAGE 1275 - 1286 1-23 p.	1-21	NI		X
		EDWARD HTUN VAN DER HORST ET AL, INTERNATIONAL JOURNAL OF CANCER, JOHN WILEY & SONS, INC, US, vol. 115, no. 4, doi: 10.1002/IJC.20867, ISSN 0020-7136, 20050701, PAGE 519 - 527 1-23 fig. 1d	1-23	NI		X
USPTO		US 2011171222				X
		US 2011033482				X
		US 2011280892				X
DOCUMENTOS ADICIONALES ENCONTRADOS POR EL EXAMINADOR DE ACUERDO A LOS CRITERIOS DE BÚSQUEDA.						
BÚSQUEDA DE SECUENCIAS						
Número de depósito / patente y N° de secuencia % de identidad						
SEQ ID NO	NCBI	The Lens	EMBL-EBI	DDJB	Genome Quest	

(de la solicitud)					
2		SEQ ID NO: 1273/ US7329737			
		92%			
3	GI:323432754	SEQ ID NO: 243/ US7947809			
	93%	93%			

CRITERIOS DE BÚSQUEDA / UNIDAD DE INVENCION (Pantallazos)

CDR 1 Cadena liviana

Percent Identity Matrix - created by Clustal2.1

```

1: WO2013078191_20 100.00  92.31  84.62
2: WO2013078191_18  92.31 100.00  92.31
3: WO2013078191_19  84.62  92.31 100.00

```

CLUSTAL O(1.2.1) multiple sequence alignment

```

WO2013078191_20  R G S S S N I G L N Y V S
WO2013078191_18  S G S S S N I G L N Y V S
WO2013078191_19  S G S L S N I G L N Y V S
                  ** *****

```

CDR 3 Cadena liviana

Percent Identity Matrix - created by Clustal2.1

```

1: WO2013078191_23 100.00  90.91  81.82  81.82  72.73  72.73  81.82  72.73  72.73
2: WO2013078191_24  90.91 100.00  90.91  90.91  63.64  81.82  72.73  72.73  72.73
3: WO2013078191_29  81.82  90.91 100.00  81.82  72.73  90.91  81.82  81.82  81.82
4: WO2013078191_28  81.82  90.91  81.82 100.00  72.73  90.91  81.82  81.82  81.82
5: WO2013078191_26  72.73  63.64  72.73  72.73 100.00  81.82  90.91  81.82  81.82
6: WO2013078191_22  72.73  81.82  90.91  90.91  81.82 100.00  90.91  90.91  90.91
7: WO2013078191_25  81.82  72.73  81.82  81.82  90.91  90.91 100.00  90.91  90.91
8: WO2013078191_27  72.73  72.73  81.82  81.82  81.82  90.91  90.91 100.00  90.91
9: WO2013078191_30  72.73  72.73  81.82  81.82  81.82  90.91  90.91  90.91 100.00

```

CLUSTAL O(1.2.1) multiple sequence alignment

```
WO2013078191_23      AAWDDSPGGEA
WO2013078191_24      AAWDDSPSGEA
WO2013078191_29      AAWDDSPSGEV
WO2013078191_28      AAWDDSLSGEA
WO2013078191_26      AAWDDGLPGEV
WO2013078191_22      AAWDDSLSGEV
WO2013078191_25      AAWDDSLPGEV
WO2013078191_27      AAWDDSLIGEV
WO2013078191_30      AAWDDSLRGEV
                        *****
```

CDR 2 Cadena pesada

Percent Identity Matrix - created by Clustal2.1

1:	WO2013078191_32	100.00	94.12	94.12
2:	WO2013078191_33	94.12	100.00	94.12
3:	WO2013078191_34	94.12	94.12	100.00

CLUSTAL O(1.2.1) multiple sequence alignment

```
WO2013078191_32      YIGSSGGVTNYADSVKG
WO2013078191_33      IIGSSGGVTNYADSVKG
WO2013078191_34      VIGSSGGVTNYADSVKG
                        *****
```

Download

GenPept

Graphics

▼ Next ▲ Previous ▲ Descriptions

immunoglobulin lambda chain, partial [Homo sapiens]
Sequence ID: [dly|BAI04188.1](#) Length: 111 Number of Matches: 1

Range 1: 1 to 110

GenPept

Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
202 bits(474)	1e-61	Compositional matrix adjust.	98/110(89%)	100/110(90%)	0/110(0%)

Query 1

QSVLTQPPPSASGTPGQRVTISCSGSLNIGLNYSYVYQQLPGTAPKLLISRNNIQRPSGVP

60

Sbjct 1

QSVLTQPPPSASGTPGQRVTISCSGS SNIG N V IYQQLPGTAPKLLI NIQRPSGVP

60

Query 61

DRFSGSKSGTSASLAISGLRSEDEADYVYCAAWDDSPGGEAFGGGKLTVL

110

Sbjct 61

DRFSGSKSGTSASLAISGL+SEDEADYVYCA+HDDG G FGGGKLTVL

110

Related Information
[Map Viewer](#) - aligned genomic context

Sequences producing significant alignments:

Select: All None Selected 0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain L, Crystal Structure Of Serbb3-fab3379 Complex	234	234	100%	1e-71	100%	SCUS_L
☐	immunoglobulin light chain variable region [Homo sapiens]	208	208	100%	3e-64	92%	AKU38879.1
☐	immunoglobulin variable region VL lambda domain [Homo sapiens]	208	208	100%	3e-64	92%	AAT96531.1
☐	immunoglobulin variable region [Homo sapiens]	210	210	100%	5e-64	93%	ADJ65589.1
☐	immunoglobulin light chain variable region [Homo sapiens]	207	207	100%	2e-63	90%	AAK94795.1
☐	immunoglobulin light chain variable region [Homo sapiens]	205	205	100%	4e-63	90%	ABA26040.1
☐	immunoglobulin light chain variable region [Homo sapiens]	205	205	100%	7e-63	90%	ABA26059.1
☐	immunoglobulin light chain variable region [Homo sapiens]	204	204	100%	8e-63	90%	ABI74143.1
☐	anti-HPA-5b immunoglobulin light chain variable region [Homo sapiens]	204	204	100%	2e-62	89%	AAP31886.1
☐	immunoglobulin light chain variable region [Homo sapiens]	204	204	100%	3e-62	90%	ABI74165.1
☐	immunoglobulin light chain variable region [Homo sapiens]	203	203	100%	5e-62	89%	CAQ23542.1
☐	immunoglobulin G heavy chain variable region [Homo sapiens]	203	203	100%	5e-62	89%	AIT38787.1
☐	immunoglobulin light chain variable region [Homo sapiens]	202	202	100%	6e-62	89%	ABG38359.1
☐	immunoglobulin lambda light chain variable region [Homo sapiens]	202	202	97%	7e-62	92%	CAC28008.1
☐	immunoglobulin light chain variable region [Homo sapiens]	202	202	100%	9e-62	88%	ABI74144.1
☐	immunoglobulin variable region [Homo sapiens]	204	204	100%	1e-61	91%	ADJ65558.1
☐	immunoglobulin lambda chain [Homo sapiens]	202	202	100%	1e-61	89%	BAL04188.1
☐	variable immunoglobulin anti-Diquoxenin light chain [Homo sapiens]	202	202	97%	1e-61	91%	CAA67303.1
☐	immunoglobulin lambda light chain variable region [Homo sapiens]	201	201	99%	2e-61	89%	CAJ99556.1
☐	immunoglobulin light chain variable region YM2-PPS-14-L1-28 [Homo sapiens]	202	202	100%	2e-61	90%	ABC67025.1
☐	immunoglobulin lambda chain [Homo sapiens]	201	201	100%	3e-61	88%	BAL04186.1

Sequences producing significant alignments:

Select: All None Selected 0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 57 from patent US 8926976	202	202	100%	3e-66	93%	AKV99400.1
☐	Sequence 44 from patent US 8926976	200	200	100%	2e-65	93%	AKV99387.1
☐	Sequence 25 from patent US 8357367	198	198	100%	8e-65	89%	AGD77694.1
☐	Sequence 12 from patent US 8492520	198	198	100%	8e-65	90%	AGU25563.1
☐	Sequence 68 from patent US 8967422	198	198	100%	8e-65	90%	AKX43339.1
☐	Sequence 243 from patent US 7947809	198	198	100%	1e-64	92%	AEH98708.1
☐	Sequence 45 from patent US 7867493	197	197	100%	3e-64	91%	AEC23431.1
☐	Sequence 1240 from patent US 7138501	201	240	100%	4e-64	89%	ABL53749.1
☐	Sequence 60 from patent US 8967422	200	200	100%	4e-64	90%	AKX43331.1
☐	Sequence 8 from patent US 8492529	200	200	100%	6e-64	90%	AGU25561.1
☐	Sequence 1255 from patent US 7138501	201	240	100%	6e-64	92%	ABL53755.1
☐	Sequence 346 from patent US 7612179	196	196	100%	8e-64	90%	ADA33961.1
☐	Sequence 5 from patent US 8216571	196	196	98%	1e-63	90%	AF003192.1
☒	Sequence 37 from patent US 8926976	196	196	100%	1e-63	91%	AKV99380.1
☐	Sequence 4 from patent US 8492529	200	200	100%	1e-63	90%	AGU25559.1
☐	Sequence 35 from patent US 8926976	195	195	100%	2e-63	91%	AKV99378.1
☐	Sequence 75 from patent US 8926976	194	194	100%	3e-63	91%	AKV99418.1
☐	Sequence 66 from patent US 8926976	194	194	100%	3e-63	90%	AKV99409.1
☐	Sequence 362 from patent US 7612179	194	194	100%	4e-63	89%	ADA33977.1
☐	Sequence 48 from patent US 8926976	194	194	100%	4e-63	90%	AKV99391.1
☐	Sequence 21 from patent US 8926976	194	194	100%	4e-63	90%	AKV99364.1
☐	Sequence 802 from patent US 7790862	194	194	100%	4e-63	88%	ADS38465.1
☐	Sequence 39 from patent US 7867493	194	194	100%	5e-63	89%	AEC23425.1
☐	Sequence 149 from patent US 8926976	193	193	100%	7e-63	90%	AKV99492.1
☐	Sequence 46 from patent US 7514534	194	194	100%	8e-63	89%	ACQ23221.1
☐	Sequence 29 from patent US 7767207	193	193	100%	8e-63	89%	ADS19808.1
☐	Sequence 43 from patent US 7867493	193	193	100%	8e-63	89%	AEC23429.1
☐	Sequence 40 from patent US 8926976	193	193	100%	9e-63	89%	AKV99383.1
☐	Sequence 1 from patent US 8131480	193	193	97%	9e-63	91%	AFD60128.1

Paula Moreno Anticuerpos ▾

[Nucleotide Sequences](#)

Paste or Choose your query.

```
>WQ2013078191_2
EVQLLESGGGLVQPGGSLRLCAASGFTFSYYYMQWRQAPGKGLHWISYIGSGGGVTNYADSVKGRFTISRDNISNTLYLQMNSLRAEDTAVYYCARVGLGDAFDIWGGQTMVTSS
>WQ2013078191_3
OSVLTOPPSASGTPGQORTVTSISGSLNIGLNYVSYYOOLPGTAPKLLISRNINORPSGVPDRFSGSKSGTSAISLGLRSEDAEDYYCAHWDSPPGFEAFGGGKTLTVL
```

Type of Search ☐ Patents Databases Only
☒ Patents and Public Reference Databases

Result Name IP 2015-07-31 17:19:39 ☐ Send E-mail on completion

☐ Compare to both nucleotide and protein databases * Please note by selecting to search both nucleotide and protein databases your account will be billed for double the amount of sequences searched.

[GenePAST](#) [Blast](#) [Fragment Search](#) [Motif](#)

Percent identity 80

Over the length of

Additional Strategy Parameters

Limit subject length from 100 to 1000 residues

Keep a maximum of results (per query)

Subject Databases

▶ Apply filters to subject databases

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Patents

 Reference Data

Proteins

Patents

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20,000 Results

Query % Id	Subj. Id	Align % Id	No. Diff	Query Identifier	Patent Assignee	Patent Title	Patent Sequence Location	Identifier	Extended Legal Status	Publication Date	PDF Link	
WO2013078191_3 1-3 of 10,000 [View all 10,000 Results]												
☐	100	100	100	0	WO2013078191_3	REBELLETTO, MARLON	empty	TBD (information not in GQ-Pat)	JP2015506912-0003	PENDING	05-Mar-2015	PDF
☐	100	100	100	0	WO2013078191_3	MEDHIMUNE LLC	BINDING MOLECULES SPECIFIC FOR HER3 AND USES THEREOF	claim: 3; 23; 26; 28; 42; 43	US20140363429-0003	PENDING	11-Dec-2014	PDF
☐	100	100	100	0	WO2013078191_3	CHOWDHURY, PARTHA S.; TICE, DAVID J.; XIAO, ZHAN; STEINER, PHILIPP J.; KINNEER, KRISTA J.; REBELLETTO, MARLON	BINDING MOLECULES SPECIFIC FOR HER3 AND USES THEREOF	TBD (information not in GQ-Pat)	CA2856287-0003	PENDING	30-May-2013	PDF
seq_1 1-3 of 10,000 [View all 10,000 Results]												
☐	98.33	100	100	0	seq_1	MEDHIMUNE LLC; CHOWDHURY, PARTHA S.; TICE, DAVID J.; XIAO, ZHAN; STEINER, PHILIPP J.; KINNEER, KRISTA J.; REBELLETTO, MARLON	BINDING MOLECULES SPECIFIC FOR HER3 AND USES THEREOF	TBD (information not in GQ-Pat)	CA2856287-0002	PENDING	30-May-2013	PDF
☐	98.33	100	100	0	seq_1	MEDHIMUNE LLC [US];	BINDING MOLECULES SPECIFIC FOR HER3 AND USES THEREOF	TBD (information not in GQ-Pat)	EP2797857-0002	PENDING	05-Nov-2014	PDF
☐	98.33	100	100	0	seq_1	MEDHIMUNE LLC	BINDING MOLECULES SPECIFIC FOR HER3 AND USES THEREOF	probable disclosure (not found by automated parsing)	KR1020140113912-0002	UNKNOWN	25-Sep-2014	PDF

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