

INFORME DE BÚSQUEDA DE PATENTES PARA EL No de Radicación: 14-122453						
CRITERIOS PARA LA BÚSQUEDA (anexar pantallazo o reporte en PDF, junto con los boleanos utilizados)						
Palabras clave utilizadas		"anti CD3 biespecific antibodies" "anti-BCMA biespecific antibodies" "CD3 AND BCMA bispecific anditbod?"				
CLASIFICACIONES INTERNACIONALES UTILIZADAS PARA LA BÚSQUEDA		C07K168, A61 K39/G95, A61P35/02, A61 P37/00				
BASES DE DATOS CONSULTADAS.						
Google patents		Espacenet		WIPO		Siencie Direct
PubMed		NCBI		The lens		Patbase
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	20/Mayo/2014	RYAN MAUREEN C ET AL: "Antibody targeting of B-cell maturation antigen on malignant plasma cells MOLECULAR CANCER THERAPEUTICS, AMERICAN ASSOCIATION OF CANCER RESEARCH, US, vol. 6, no. 11, 1 November 2007 (2007-11-01), pages 3009-3018, XP002581270JSSN: 1535-7163 WO 2009/132058 A2	25 y 26	Novedad	X	
		WO 02/066516 A2 WO 2004/106383 A1	25 y 26	Novedad		X
USPTO	06/Octubre/2015	US9150664	A	NA	NA	NA
DOCUMENTOS ADICIONALES ENCONTRADOS POR EL EXAMINADOR DE ACUERDO A LOS CRITERIOS DE BÚSQUEDA.						
Ursula Reusch et al, "Anti-CD3 X Anti-Epidermal Growth Factor Receptor (EGFR) Bispecific Antibody Redirects T-Cell Cytolytic Activity to EGFR-Positive Cancers In vitro and in an Animal Model" Clin Cancer Res 12(1) January 1, 2006						
US 20110123532						
US 20090252683						
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	
317, 327, 347, 357, 367, 377, 387	NA: AAW67377.1	US 8575317/SEQ ID NO: 142				
	81%, 83%	82%, 84%				

318, 328, 338, 348, 358, 368, 378 y 388	NA: BAJ21230.1	US 8575317/SEQ ID NO: 156			
	94%, 95%	94%, 95%			

Pantallazos Búsqueda de Palabras Clave

Cadenas Pesadas

```
>SEQ_ID_NO_317
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYPGYHAYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDTDVLDYWGQGLTVTVSS

>SEQ_ID_NO_327
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYDGDWGDYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDADVDYWGQGLTVTVSS

>SEQ_ID_NO_337
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYPGYHAYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDTDVLDYWGQGLTVTVSS

>SEQ_ID_NO_347
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYDGDWGDYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDADVDYWGQGLTVTVSS

>SEQ_ID_NO_357
QVQLVQSGAKVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWMGYINPYPGYHAYNQKFQ
RVTMTRDKSTSTVYMELSSLTSEDVAVYYCARDGYRDTDVLDYWGQGLTVTVSS

>SEQ_ID_NO_367
QVQLVQSGAKVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWMGYINPYDGDWGDYNQKFQ
RVTMTRDKSTSTVYMELSSLTSEDVAVYYCARDGYRDADVDYWGQGLTVTVSS

>SEQ_ID_NO_377
QVQLVQSGAEVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWIGYINPYPGYHAYNQKFQ
KVTMTRDTSTSTVYMELSSLTSEDVAVYYCARDGYRDTDVLDYWGQGLTVTVSS

>SEQ_ID_NO_387
QVQLVQSGAEVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWIGYINPYDGDWGDYNQKFQ
KVTMTRDTSTSTVYMELSSLTSEDVAVYYCARDGYRDADVDYWGQGLTVTVSS

CLUSTAL multiple sequence alignment by MUSCLE (3.8)
```

```
SEQ_ID_NO_317      QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYPGYHAY
SEQ_ID_NO_337      QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYPGYHAY
SEQ_ID_NO_327      QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYDGDWGDY
SEQ_ID_NO_347      QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHHWVRQAPGQGLEWMGYINPYDGDWGDY
SEQ_ID_NO_367      QVQLVQSGAKVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWMGYINPYDGDWGDY
SEQ_ID_NO_387      QVQLVQSGAEVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWIGYINPYDGDWGDY
SEQ_ID_NO_357      QVQLVQSGAKVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWMGYINPYPGYHAY
SEQ_ID_NO_377      QVQLVQSGAEVIKPGASVKVSCKASGYTFTNHHHWVRQKPGQGLEWIGYINPYPGYHAY
*****: * *****:*****:*****: *
```

```
SEQ_ID_NO_317      NEKFQGRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDTDVLDYWGQGLTVTVS
SEQ_ID_NO_337      NEKFQGRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDTDVLDYWGQGLTVTVS
SEQ_ID_NO_327      NEKFQGRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDADVDYWGQGLTVTVS
SEQ_ID_NO_347      NEKFQGRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRDADVDYWGQGLTVTVS
SEQ_ID_NO_367      NQKFQGRVTMTRDKSTSTVYMELSSLTSEDVAVYYCARDGYRDADVDYWGQGLTVTVS
SEQ_ID_NO_387      NQKFQGRVTMTRDTSTSTVYMELSSLTSEDVAVYYCARDGYRDADVDYWGQGLTVTVS
SEQ_ID_NO_357      NQKFQGRVTMTRDKSTSTVYMELSSLTSEDVAVYYCARDGYRDTDVLDYWGQGLTVTVS
```

SEQ_ID_NO_377 NQKFQGKVTMRDTSSTVYMESSLTSEDTAVYYCARDGYRDTDVLDYWGQGLVTVS
*:.*****.:*****

SEQ_ID_NO_317 S
SEQ_ID_NO_337 S
SEQ_ID_NO_327 S
SEQ_ID_NO_347 S
SEQ_ID_NO_367 S
SEQ_ID_NO_387 S
SEQ_ID_NO_357 S
SEQ_ID_NO_377 S

Percent Identity Matrix - created by Clustal2.1

#

1: SEQ_ID_NO_317	100.00	100.00	95.87	95.87	89.26	89.26	93.39
93.39 2: SEQ_ID_NO_337	100.00	100.00	95.87	95.87	89.26	89.26	93.39
93.39 3: SEQ_ID_NO_327	95.87	95.87	100.00	100.00	93.39	93.39	89.26
89.26 4: SEQ_ID_NO_347	95.87	95.87	100.00	100.00	93.39	93.39	89.26
89.26 5: SEQ_ID_NO_367	89.26	89.26	93.39	93.39	100.00	96.69	95.87
92.56 6: SEQ_ID_NO_387	89.26	89.26	93.39	93.39	96.69	100.00	92.56
95.87 7: SEQ_ID_NO_357	93.39	93.39	89.26	89.26	95.87	92.56	100.00
96.69 8: SEQ_ID_NO_377	93.39	93.39	89.26	89.26	92.56	95.87	96.69
100.00							

Cadenas Ligeras

>SEQ_ID_NO_318
DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRFSGSGS
GTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK
>SEQ_ID_NO_328
DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRFSGSGS
GTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK
>SEQ_ID_NO_338
DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRFSGSGS
GTDFTFTISSLEPEDIATYYCQQGNTLPWTFGQGTKVEIK
>SEQ_ID_NO_348
DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRFSGSGS
GTDFTFTISSLEPEDIATYYCQQGNTLPWTFGQGTKVEIK
>SEQ_ID_NO_358
DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQQKPGRAPKLLIYYTSRLHTGVPSRFSGSGS
GTDYSFTISSLQPEDIATYYCQQGNTLPWTFGQGTKVEIK
>SEQ_ID_NO_368
DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQQKPGRAPKLLIYYTSRLHTGVPSRFSGSGS
GTDYSFTISSLQPEDIATYYCQQGNTLPWTFGQGTKVEIK
>SEQ_ID_NO_378
DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRFSGSGS
GTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_388

DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRFSGSGS
GTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

SEQ_ID_NO_358
DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKPGRAPKLLIYYTSRLHTGVPS
SEQ_ID_NO_368
DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKPGRAPKLLIYYTSRLHTGVPS
SEQ_ID_NO_318
DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
SEQ_ID_NO_328
DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
SEQ_ID_NO_378
DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
SEQ_ID_NO_388
DIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
SEQ_ID_NO_338
DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
SEQ_ID_NO_348
DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS

*****:*****.*****

SEQ_ID_NO_358 RFSGSGSGTDYSFTISSLQPEDATYYCQQGNTLPWTFGQGTKVEIK
SEQ_ID_NO_368 RFSGSGSGTDYSFTISSLQPEDATYYCQQGNTLPWTFGQGTKVEIK
SEQ_ID_NO_318 RFSGSGSGTDFFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK
SEQ_ID_NO_328 RFSGSGSGTDFFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK
SEQ_ID_NO_378 RFSGSGSGTDFFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK
SEQ_ID_NO_388 RFSGSGSGTDFFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK
SEQ_ID_NO_338 RFSGSGSGTDFFTISLEPEDATYYCQQGNTLPWTFGQGTKVEIK
SEQ_ID_NO_348 RFSGSGSGTDFFTISLEPEDATYYCQQGNTLPWTFGQGTKVEIK
*****:*****:*****

Percent Identity Matrix - created by Clustal2.1

#

1: SEQ_ID_NO_358	100.00	100.00	95.33	95.33	95.33	95.33	96.26
96.26							
2: SEQ_ID_NO_368	100.00	100.00	95.33	95.33	95.33	95.33	96.26
96.26							
3: SEQ_ID_NO_318	95.33	95.33	100.00	100.00	100.00	100.00	97.20
97.20							
4: SEQ_ID_NO_328	95.33	95.33	100.00	100.00	100.00	100.00	97.20
97.20							
5: SEQ_ID_NO_378	95.33	95.33	100.00	100.00	100.00	100.00	97.20
97.20							
6: SEQ_ID_NO_388	95.33	95.33	100.00	100.00	100.00	100.00	97.20
97.20							
7: SEQ_ID_NO_338	96.26	96.26	97.20	97.20	97.20	97.20	100.00
100.00							
8: SEQ_ID_NO_348	96.26	96.26	97.20	97.20	97.20	97.20	100.00
100.00							

Secuencias completas de aminoácidos

>SEQ_ID_NO_319

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHWVRQAPGQGLEWMGYINPYPGYHAYNEKFQ
GRATMTSDTSTSTVYMESSLRSEDTAVYYCAR DGYRDTVDLYWGQGLTVTVSSGGGGSGGG

GSGGGGSDIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
RFSGSGSGTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_329

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHWVRQAPGQGLEWMGYINPYDGDWGDYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG
GSGGGGSDIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
RFSGSGSGTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_339

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHWVRQAPGQGLEWMGYINPYPGYHAYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG
GSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
RFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_340

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHWVRQAPGQGLEWMGYINPYPGYHAYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG
GSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
RFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQ
PGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKN
TAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQT
VTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWYQQKPGQAPRGLIGGTKFLAPGTPARFSGSL
GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

>SEQ_ID_NO_349

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHWVRQAPGQGLEWMGYINPYDGDWGDYNEKFQ
GRATMTSDTSTSTVYMELSSLRSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG
GSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPS
RFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_359

QVQLVQSGAKVIKPGASVKVSCKASGYTFTNHIIHWVRQKPGQGLEWMGYINPYPGYHAYNQKFQ
RVTMTRDKSTSTVYMELSSLTSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG
SGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGRAPKLLIYYTSRLHTGVPSR
FSGSGSGTDYSFTISSLQPEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_369

QVQLVQSGAKVIKPGASVKVSCKASGYTFTNHIIHWVRQKPGQGLEWMGYINPYDGDWGDYNQKFQ
GRVTMTRDKSTSTVYMELSSLTSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG
GSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGRAPKLLIYYTSRLHTGVPS
RFSGSGSGTDYSFTISSLQPEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_379

QVQLVQSGAEVIKPGASVKVSCKASGYTFTNHIIHWVRQKPGQGLEWIGYINPYPGYHAYNQKFQ
KVTMTRDTSTSTVYMELSSLTSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG
GGGGSDIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRF
SGSGSGTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK

>SEQ_ID_NO_389

QVQLVQSGAEVIKPGASVKVSCKASGYTFTNHIIHWVRQKPGQGLEWIGYINPYDGDWGDYNQKFQ
KVTMTRDTSTSTVYMELSSLTSEDVAVYYCARDGYRRDADVDYWGQGLTVTVSSGGGGSGGG

GGGSDIQMTQSPSSLSASLGDRVITTCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGVPSRF
SGSGSGTDFTFTISSLQQEDIATYYCQQGNTLPWTFGQGTKVEIK

CDRs

>SEQ_ID_NO_311

NHIIH

>SEQ_ID_NO_312

YINPYPGYHAYNEKFQG

>SEQ_ID_NO_313

DGYRDTDVLDY

>SEQ_ID_NO_314

QASQDISNYLN

>SEQ_ID_NO_315

YTSRLHT

>SEQ_ID_NO_316

QQGNTLPWT

>SEQ_ID_NO_321

NHIIH

>SEQ_ID_NO_322

YINPYDGWGDYNEKFQG

>SEQ_ID_NO_323

DGYRDADVLDY

>SEQ_ID_NO_324

QASQDISNYLN

>SEQ_ID_NO_325

YTSRLHT

>SEQ_ID_NO_326

QQGNTLPWT

>SEQ_ID_NO_331

NHIIH

>SEQ_ID_NO_332

YINPYPGYHAYNEKFQG

>SEQ_ID_NO_333

DGYRDTDVLDY

>SEQ_ID_NO_334

QASQDISNYLN

>SEQ_ID_NO_335

YTSRLHT

>SEQ_ID_NO_336

QQGNTLPWT

>SEQ_ID_NO_341

NHIIH

>SEQ_ID_NO_342

YINPYDGWGDYNEKFQG

>SEQ_ID_NO_343

DGYRDADVLDY

>SEQ_ID_NO_344

QASQDISNYLN
>SEQ_ID_NO_345
YTSRLHT
>SEQ_ID_NO_346
QQGNTLPWT
>SEQ_ID_NO_351
NHIIH
>SEQ_ID_NO_353
DGYRDTDVLDY
>SEQ_ID_NO_354
QASQDISNYLN
>SEQ_ID_NO_355
YTSRLHT
>SEQ_ID_NO_356
QQGNTLPWT
>SEQ_ID_NO_361
NHIIH
>SEQ_ID_NO_362
YINPYDGWGDYNQKFQG
>SEQ_ID_NO_363
DGYRDADVLDY
>SEQ_ID_NO_364
QASQDISNYLN
>SEQ_ID_NO_365
YTSRLHT
>SEQ_ID_NO_366
QQGNTLPWT
>SEQ_ID_NO_371
NHIIH
>SEQ_ID_NO_372
YINPYPGYHAYNQKFQG
>SEQ_ID_NO_373
DGYRDTDVLDY
>SEQ_ID_NO_374
QASQDISNYLN
>SEQ_ID_NO_375
YTSRLHT
>SEQ_ID_NO_376
QQGNTLPWT
>SEQ_ID_NO_381
NHIIH
>SEQ_ID_NO_382
YINPYDGWGDYNQKFQG
>SEQ_ID_NO_383
DGYRDADVLDY
>SEQ_ID_NO_384
QASQDISNYLN

>SEQ_ID_NO_385

YTSRLHT

>SEQ_ID_NO_386

QQGNTLPWT

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 142 from patent US 8575317	203	203	100%	2e-66	82% AHE21564.1
☐	Sequence 112 from patent US 8575317	202	202	100%	7e-66	81% AHE21534.1
☐	Sequence 50 from patent US 8575317	202	202	100%	8e-66	81% AHE21492.1
☐	Sequence 140 from patent US 8575317	202	202	100%	9e-66	81% AHE21562.1
☐	Sequence 138 from patent US 8575317	201	201	100%	1e-65	81% AHE21560.1
☐	Sequence 143 from patent US 8575317	200	200	100%	3e-65	81% AHE21565.1
☐	Sequence 141 from patent US 8575317	200	200	100%	3e-65	80% AHE21563.1
☐	Sequence 154 from patent US 7332582	200	200	100%	3e-65	79% ACC07990.1
☐	Sequence 139 from patent US 8575317	200	200	100%	5e-65	80% AHE21561.1
☐	Sequence 167 from patent US 8575317	199	199	100%	1e-64	80% AHE21589.1
☐	Sequence 9 from patent US 8192736	199	199	100%	1e-64	80% AFL38337.1
☐	Sequence 137 from patent US 8575317	199	199	100%	1e-64	79% AHE21559.1
☐	Sequence 1 from patent US 7763250	199	199	99%	2e-64	82% ADS17955.1
☐	Sequence 93 from patent US 8101719	199	199	100%	2e-64	83% AFA83265.1
☐	Sequence 12 from patent US 7883705	199	199	100%	2e-64	81% AED38394.1
☐	Sequence 63 from patent US 6538111	199	199	100%	3e-64	80% AAP61010.1
☐	Sequence 23 from patent US 8460660	197	197	100%	4e-64	83% AGP15546.1
☐	Sequence 211 from patent US 8119340	197	197	99%	5e-64	81% AFB86385.1
☐	Sequence 6 from patent US 8314213	197	197	100%	6e-64	80% AGA36689.1
☐	Sequence 23 from patent US 9029510	197	197	100%	6e-64	80% AME89410.1
☐	Sequence 53 from patent US 5773218	197	197	100%	7e-64	82% AAC89656.1
☐	Sequence 5 from patent US 8314213	197	197	100%	8e-64	80% AGA36688.1
☐	Sequence 102 from patent US 8071730	196	196	100%	8e-64	81% AEW36199.1
☐	Sequence 21 from patent US 8460660	196	196	100%	1e-63	81% AGP15544.1
☐	Sequence 210 from patent US 8119340	196	196	99%	1e-63	82% AFB86384.1
☐	Sequence 82 from patent US 8491901	196	196	100%	1e-63	81% AGU21836.1
☐	Sequence 329 from patent US 7592429	196	196	100%	2e-63	79% ACW82126.1
☐	Sequence 204 from patent US 8575317	196	196	100%	2e-63	79% AHE21626.1
☐	Sequence 9 from patent US 8491901	196	196	100%	2e-63	82% AGU21791.1

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
☐	rotavirus-specific intestinal-homing antibody heavy chain variable region [Homo sapiens]	200	200	100%	3e-63	81% AAW67377.1
☐	rotavirus-specific intestinal-homing antibody heavy chain variable region [Homo sapiens]	200	200	100%	5e-63	80% AAW67376.1
☐	immunoglobulin alpha heavy chain [Homo sapiens]	200	200	100%	5e-63	80% AEB00258.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	198	198	100%	3e-62	82% ABM67149.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	197	197	100%	7e-62	80% ABM67154.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	197	197	100%	7e-62	78% AAD53821.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	197	197	100%	8e-62	83% ABM67163.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	196	196	100%	9e-62	80% ABF83234.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	196	196	100%	1e-61	81% AAA17971.1
☐	IgM heavy chain VH1 region precursor [Homo sapiens]	196	196	97%	2e-61	79% AAC51723.1
☐	immunoglobulin heavy chain V region [Homo sapiens]	196	196	100%	2e-61	80% AMK70091.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	196	196	100%	2e-61	79% AAY23293.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	196	196	100%	2e-61	81% ABM67212.1
☐	rotavirus-specific intestinal-homing antibody heavy chain variable region [Homo sapiens]	195	195	100%	3e-61	81% AAW67386.1
☐	rotavirus-specific intestinal-homing antibody heavy chain variable region [Homo sapiens]	195	195	100%	3e-61	81% AAW67388.1
☐	immunoglobulin heavy chain V region [Homo sapiens]	195	195	100%	4e-61	79% AMK70187.1
☐	immunoglobulin heavy chain V region [Homo sapiens]	195	195	100%	5e-61	81% AMK70551.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	195	195	98%	5e-61	80% CAD87740.1
☐	immunoglobulin heavy chain V region [Homo sapiens]	194	194	100%	7e-61	81% AMK70123.1
☐	immunoglobulin variable region [Homo sapiens]	194	194	99%	9e-61	81% ADX65198.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	194	194	100%	1e-60	79% ABF83225.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	194	194	100%	1e-60	80% ABM67232.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	194	194	100%	1e-60	78% AAC18196.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	193	193	100%	2e-60	80% ABM67155.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	193	193	100%	2e-60	80% ABF83374.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	193	193	100%	2e-60	78% AAY23316.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	193	193	100%	2e-60	80% ABM67110.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	193	193	100%	3e-60	79% ACN69999.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	192	192	100%	3e-60	79% AAY23310.1

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 156 from patent US 8575317	209	209	100%	3e-69	94%	AHE21578.1					
☐	Sequence 35 from patent US 8716450	209	209	100%	3e-69	94%	AJL42743.1					
☐	Sequence 67 from patent US 5795965	209	209	100%	3e-69	94%	AAC94345.1					
☐	Sequence 71 from patent US 5795965	209	209	100%	7e-69	94%	AAC94347.1					
☐	Sequence 115 from patent US 7479543	208	208	100%	9e-69	93%	ACN02258.1					
☐	Sequence 2 from patent US 8398980	212	212	100%	1e-68	94%	AGO74258.1					
☐	Sequence 11 from patent US 8911732	208	208	100%	1e-68	93%	AJN78887.1					
☐	Sequence 52 from patent US 8475793	207	207	100%	4e-68	93%	AGU02717.1					
☐	Sequence 8 from patent US 8071072	207	207	100%	4e-68	93%	AEW31463.1					
☐	Sequence 119 from patent US 9035027	211	393	100%	4e-68	94%	AME95013.1					
☐	Sequence 117 from patent US 9035027	211	393	100%	4e-68	94%	AME95011.1					
☐	Sequence 54 from patent US 8475793	206	206	100%	4e-68	93%	AGU02719.1					
☐	Sequence 187 from patent US 9035027	210	352	100%	6e-68	94%	AME95081.1					
☐	Sequence 185 from patent US 9035027	210	352	100%	6e-68	94%	AME95079.1					
☐	Sequence 183 from patent US 9035027	210	352	100%	7e-68	94%	AME95077.1					
☐	Sequence 181 from patent US 9035027	210	352	100%	7e-68	94%	AME95075.1					
☐	Sequence 47 from patent US 8716450	210	409	100%	8e-68	94%	AJL42755.1					
☐	Sequence 45 from patent US 8716450	210	409	100%	8e-68	94%	AJL42753.1					
☐	Sequence 99 from patent US 8716450	210	385	100%	8e-68	94%	AJL42807.1					
☐	Sequence 97 from patent US 8716450	210	385	100%	8e-68	94%	AJL42805.1					
☐	Sequence 175 from patent US 8822645	210	336	100%	8e-68	94%	AJM98090.1					
☐	Sequence 173 from patent US 8822645	210	336	100%	8e-68	94%	AJM98088.1					
☐	Sequence 179 from patent US 9035027	209	408	100%	9e-68	94%	AME95073.1					
☐	Sequence 177 from patent US 9035027	209	408	100%	9e-68	94%	AME95071.1					
☐	Sequence 20 from patent US 8138313	206	206	100%	1e-67	92%	AFG81055.1					
☐	Sequence 17 from patent US 5821337	204	204	100%	4e-67	92%	AAE23186.1					
☐	unnamed protein product [synthetic construct]	204	204	100%	5e-67	91%	CAX46358.1					
☐	Sequence 26 from patent US 9085622	204	204	100%	7e-67	93%	AMF68738.1					

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					
☐	anti-IL6 receptor antibody [synthetic construct]	209	209	100%	2e-67	94%	BAJ21230.1					
☐	immunoglobulin VL region=humanized bispecific antibody [human, Peptide Recombinant, 107 aa]	204	204	100%	4e-65	92%	AAB24132.1					
☐	Chain L, X-ray Structures Of Fragments From Binding And Nonbinding Versions Of A Humanized Anti-cd18 Antibody: Structural Indications Of Th	202	202	100%	5e-63	91%	2FGW L					
☐	Chain L, Nerve Growth Factor In Complex With Fab From Humanized Version Of Mouse Mab 911 (tanezumab)	201	201	100%	2e-62	90%	4EDW L					
☐	anti-CD22 single chain variable region [synthetic construct]	201	201	100%	3e-62	91%	A1S76185.1					
☐	Chain L, Vascular Endothelial Growth Factor In Complex With A Neutralizing Antibody	200	200	100%	3e-62	89%	1BJ1 L					
☐	anti-rabies virus immunoglobulin light chain variable region [Homo sapiens]	196	196	100%	4e-62	90%	AAY33393.1					
☐	immunoglobulin G heavy chain variable region [Homo sapiens]	196	196	100%	6e-62	91%	A1T38746.1					
☐	Chain A, Structure Of The Germline Vk1 O18O8 LIGHT CHAIN VARIABLE Domain Homodimer	196	196	100%	8e-62	90%	2Q2Q A					
☐	immunoglobulin kappa light chain variable domain ki O18O8 [synthetic construct]	195	195	100%	1e-61	90%	ABR37293.1					
☐	Chain L, X-ray Structures Of Fragments From Binding And Nonbinding Versions Of A Humanized Anti-cd18 Antibody: Structural Indications Of Th	195	195	100%	1e-61	89%	1FGV L					
☐	Chain L, Vascular Endothelial Growth Factor In Complex With An Affinity Matured Antibody	199	199	100%	1e-61	88%	1CZ8 L					
☐	Chain A, Solution Structure Of The Ki O18O8 Y87H IMMUNOGLOBULIN LIGHT Variable Domain	194	194	100%	3e-61	89%	2KOM A					
☐	Chain A, Ki O18O8 Y87H IMMUNOGLOBULIN LIGHT CHAIN VARIABLE DOMAIN	194	194	100%	3e-61	89%	3CDF A					
☐	immunoglobulin kappa light chain variable region [Homo sapiens]	194	194	100%	5e-61	90%	CAG27369.1					
☐	anti-rabies virus immunoglobulin light chain variable region [Homo sapiens]	193	193	100%	6e-61	89%	AAY33403.1					
☐	anti-rabies virus immunoglobulin light chain variable region [Homo sapiens]	193	193	100%	6e-61	88%	AAY33370.1					
☐	immunoglobulin light chain variable region [Homo sapiens]	193	193	100%	9e-61	90%	AAK94808.1					
☐	Chain C, Idiopathic Antibody D1.3 Fv Fragment-Antidiopathic Antibody E5.2 Fv Fragment Complex	192	192	100%	1e-60	85%	1DVF C					
☐	anti-human-CD3-anti-human-HMWG bi-scFv antibody fragment precursor [synthetic construct]	205	390	100%	1e-60	92%	CAH69219.1					
☐	Anti-ava1 [synthetic construct]	198	198	100%	1e-60	89%	ALB08477.1					
☐	immunoglobulin kappa light chain variable region [Homo sapiens]	191	191	100%	3e-60	89%	ACY78416.1					
☐	anti-IL6 receptor antibody [synthetic construct]	191	191	100%	4e-60	86%	BAJ21232.1					
☐	immunoglobulin kappa light chain variable region [Homo sapiens]	191	191	100%	6e-60	89%	AAZ09046.1					
☐	immunoglobulin kappa light chain variable region VK1 [Homo sapiens]	191	191	100%	7e-60	87%	AAV40720.1					
☐	Chain L, Crystal Structure Of Human IL-1beta In Complex With Therapeutic Antibody Binding Fragment Of Gevokizumab	194	194	100%	7e-60	86%	4G6M L					
☐	immunoglobulin light chain variable region [Homo sapiens]	191	191	100%	7e-60	89%	AAK94823.1					
☐	Chain L, Crystal Structure Of The Therapeutic Antibody Binding Fragment Of Gevokizumab In Its Unbound State	194	194	100%	8e-60	86%	4G6K L					
☐	immunoglobulin light chain variable region [Mus musculus]	190	190	100%	8e-60	84%	ABC55327.1					

anti CD3 bispecific antibodies

WebImágenesNoticiasVideosMás ▾Herramientas de búsqueda

Cerca de 67,700 resultados (0.47 segundos)

Se muestran resultados de anti CD3 *bispecific* antibodies
Buscar, en cambio, anti CD3 bispecific antibodies

Artículos académicos para anti CD3 bispecific antibodies
... coated with anti-glioma× anti-CD3 bispecific antibody ... - Nitta - Mencionado por 43
... by a trifunctional anti-EpCAM× anti-CD3 antibody: a ... - Burges - Mencionado por 166
... of an anti-PSA x anti-CD3 bispecific antibody for the ... - Katzenwadel - Mencionado por 28

Anti-CD3-based bispecific antibody designed for therapy of ...
www.ncbi.nlm.nih.gov/pubmed/9650561 ▾ Traducir esta página
por BK Link - 1998 - Mencionado por 24 - Artículos relacionados
Anti-CD3-based bispecific antibody designed for therapy of human B-cell malignancy can induce T-cell activation by antigen-dependent and ...

T cells armed with anti-CD3 x anti-CD20 bispecific antibody ...
www.ncbi.nlm.nih.gov/pubmed/15781336 ▾ Traducir esta página
por JM Gall - 2005 - Mencionado por 37 - Artículos relacionados
T cells armed with anti-CD3 x anti-CD20 bispecific antibody enhance killing of CD20+ malignant B cells and bypass complement-mediated rituximab resistance ...

Bispecific T-Cell Engaging Antibodies for Cancer Therapy
cancerres.aacrjournals.org/content/69/.../4941.full.ht... ▾ Traducir esta página
por PA Baeuerle - 2009 - Mencionado por 199 - Artículos relacionados
15 jun. 2009 - Here, we review the principle of a new class of bispecific antibodies ...
The anti-CD3 specific single-chain antibody (green) is shared by all BiTE ...

anti BCMA bispecific antibodies

WebImágenesNoticiasVideosMás ▾Herramientas de búsqueda

Cerca de 35,200 resultados (0.75 segundos)

Se muestran resultados de anti BCMA *bispecific* antibodies
Buscar, en cambio, anti BCMA bispecific antibodies

Artículos académicos para anti BCMA bispecific antibodies
... engineering and design of therapeutic antibodies - Presta - Mencionado por 168
... cell, and, via the Fc portion of the bispecific antibody - Lindhofer - Mencionado por 57
Antibody-based therapies in multiple myeloma - Tai - Mencionado por 27

An anti-B cell maturation antigen bispecific antibody for ...
www.ncbi.nlm.nih.gov/pubmed/25826669 - Traducir esta página
por NS Ramadoss - 2015 - Artículos relacionados
15 abr. 2015 - We report a bispecific antibody against B cell maturation antigen (BiFab-BCMA), which potently and specifically redirects T cells to lyse ...

Patent EP2762497A1 - Bispecific antibodies ... - Google
www.google.com/patents/EP2762497A1?cl=en ▾ Traducir esta página
6 ago. 2014 - A bispecific antibody specifically binding to the two targets human ...
The use of anti-BCMA antibodies for the treatment of lymphomas and ...

BCMA-BASED STRATIFICATION AND THERAPY FOR ...
www.fqs.org/patents/app/20130101599 ▾ Traducir esta página
25 abr. 2013 - The method of claim 10, wherein said anti-BCMA antibody is a monoclonal antibody, a chimeric antibody a humanized antibody, or a bispecific ...

Patent EP2762497A1 - Bispecific antibodies ... - Google
www.google.com.ar/patents/EP2762497A1?cl=pt... ▾ Traducir esta página



Menu ▾ Search ▾ History ▾ Session ▾ Folder ▾ Order Help ▾ Logoff

#	Search query	Results	Options
1	TAC=(CD3~ AND BCMA~ BISPECIFIC~ ANTIBOD?~)	3	View Browse Hits Optimise more...