

INFORME DE BÚSQUEDA DE PATENTES PARA EL Radicado N° 14-115088-00000-0000						
CRITERIOS PARA LA BÚSQUEDA (anexar pantallazo o reporte en PDF, junto con los booleanos utilizados)						
Palabras clave utilizadas		Anticuerpo anti – TDP – 43, Anticuerpos anti – proteína de unión a ADN, proteinopatías de TDP – 43, agregados de TDP-43 .				
CLASIFICACIONES INTERNACIONALES UTILIZADAS PARA LA BÚSQUEDA		A61K 39/00, C07K 16/18.				
BASES DE DATOS CONSULTADAS.						
Patentscope		Google/patents				
NCBI		PatBase				
Espacenet		Sciencedirect				
Lens		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
EPO	12/12/2012	Biogen Idec and Neurimmune Announce Agreement on Three Neurodegenerative Disease Programs", , 20 December 2010 (2010-12-20), XP055064808, Retrieved from the Internet: URL:http://www.businesswire.com/news/home/20101220006526/en/Biogen-Idec-Neurimmune -Announce Agreement- Neurodegenerative - Disease [retrieved on 2013-05-31]	1, 7 – 25, 28 - 51	Nivel inventivo		X
		TARDBP (41-7.1): sc-100871", , 26 March 2009 (2009-03-26), XP055064934, Retrieved from the Internet: URL:http://datasheets.scbt.com/sc-100871.pdf [retrieved on 2013-06-03]	2, 4, 7 - 51	Nivel inventivo		X
		JOHNSON B S et al: "a yeast TDP-43 proteinopathy model: exploring the molecular determinants of TDP-43 aggregation and cellular toxicity", PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, NATIONAL ACADEMY OF SCIENCES, US, vol. 105, no. 17, 29 April 2008 (2008-04-29), pages 6439-6444, XP002534604, ISSN: 0027-8424,DOI: 10.1073/PNAS.0802082105	2, 4, 7 - 51	Nivel inventivo	X	
		YUKI SHIINA ET AL: "TDP-43 Dimerizes in Human Cells in Culture", CELLULAR AND MOLECULAR NEUROBIOLOGY, KLUWER ACADEMIC PUBLISHERS-PLENUM PUBLISHERS, NE, vol. 30, no. 4, 31 December 2009 (2009-12-31), pages 641-652, XP019815449, ISSN: 1573-6830	2, 4, 7 - 51	Nivel inventivo		X
		US5688511	2, 4, 7 - 51	Nivel inventivo		X
		WO2008081008	1, 7 – 25, 28 - 51	Documento tipo A		X

DOCUMENTOS ADICIONALES ENCONTRADOS POR EL EXAMINADOR DE ACUERDO A LOS CRITERIOS DE BÚSQUEDA.					
US2009263824A					
US2010136573A					
US2011287453A					
WO09044119A1					
CN101634656A					
Higashi S. <i>et al.</i> , 2007. Concurrence of TDP-43, tau and α -synuclein pathology in brains of Alzheimer's disease and dementia with Lewy bodies					
Hasegawa M. <i>et al.</i> , 2008. Phosphorylated TDP-43 in Frontotemporal Lobar Degeneration and Amyotrophic Lateral Sclerosis					
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	Genom e Quest
SEQ ID NO: 94	refINP_031401.1I				

Búsqueda de secuencias

QUERY: SEQ ID NO: 94

SBJCT: TAR DNA-binding protein 43 [Homo sapiens]

TAR DNA-binding protein 43 [Homo sapiens]

Sequence ID: [refINP_031401.1I](#) Length: 414 Number of Matches: 1

► [See 13 more title\(s\)](#)

Range 1: 1 to 414 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
1378 bits(3126)	0.0	414/414(100%)	414/414(100%)	0/414(0%)
Query 1	MSEYIRVTEDENDIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGI	60		
Sbjct 1	MSEYIRVTEDENDIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGI	60		
Query 61	LHAPDAGWGNLVYVVNYPKDNKRKMDDETASSAVKVKRAVQKTSDLIVLGLPWKTTEQDL	120		
Sbjct 61	LHAPDAGWGNLVYVVNYPKDNKRKMDDETASSAVKVKRAVQKTSDLIVLGLPWKTTEQDL	120		
Query 121	KEYFSTFGEVLMVQVKDLKTGHSGGFGFVRFTETQVKVMSQRHMIDGRWCDCKLPNS	180		
Sbjct 121	KEYFSTFGEVLMVQVKDLKTGHSGGFGFVRFTETQVKVMSQRHMIDGRWCDCKLPNS	180		
Query 181	KQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIKPFRAFAFVTFADDQIA	240		
Sbjct 181	KQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIKPFRAFAFVTFADDQIA	240		
Query 241	QSLCGEDLIIGISVHISNAEPKHNSNRQLERSGRFGGPNPGGFGNQGGFGNSRGGGAGLG	300		
Sbjct 241	QSLCGEDLIIGISVHISNAEPKHNSNRQLERSGRFGGPNPGGFGNQGGFGNSRGGGAGLG	300		
Query 301	NNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMGMMLASQQNQSGPSGNNQNGNMQ	360		
Sbjct 301	NNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMGMMLASQQNQSGPSGNNQNGNMQ	360		
Query 361	REPNAFSGGNSYSGNSGAAIGWGSASNAGSGSGFNNGFGSSMDSKSSGWGM	414		
Sbjct 361	REPNAFSGGNSYSGNSGAAIGWGSASNAGSGSGFNNGFGSSMDSKSSGWGM	414		

SEQ ID NO: 1

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 118 from patent US 7807159	307	307	100%	2e-93	80%	ADS56889.1
☐	Sequence 77 from patent US 7807159	305	305	100%	1e-92	80%	ADS56868.1
☐	Sequence 335 from patent US 7982016	300	300	100%	6e-91	81%	AFL92862.1
☐	Sequence 262 from patent US 7285269	299	299	100%	3e-90	81%	ABX90443.1
☐	unnamed protein product [synthetic construct]	301	301	100%	3e-90	81%	CBX51231.1
☐	Sequence 30 from patent US 8551920	301	301	100%	7e-90	81%	AGY21032.1
☐	Sequence 326 from patent US 7485297	298	298	100%	1e-89	80%	ACN04887.1
☐	Sequence 115 from patent US 7807159	307	307	100%	2e-88	80%	ADS56887.1
☐	Sequence 1210 from patent US 7329737	297	297	100%	3e-88	78%	ACC02711.1
☐	Sequence 26 from patent US 7807159	305	305	100%	1e-87	80%	ADS56842.1

SEQ ID NO: 10

Sequences producing significant alignments:

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 473 from patent US 8703131	302	302	100%	2e-93	84%	AJL22747.1
☐	Sequence 111 from patent US 7368111	301	301	100%	1e-92	84%	ACE16217.1
☐	Sequence 781 from patent US 8703427	298	298	100%	2e-91	82%	AJL24910.1
☐	Sequence 37 from patent US 8748581	295	295	100%	2e-89	78%	AJM13125.1
☐	Sequence 60 from patent US 7193064	298	298	100%	2e-88	78%	ABP27425.1
☐	Sequence 69 from patent US 8748107	288	288	100%	8e-87	77%	AJM06246.1
☐	Sequence 8 from patent US 8197816	285	285	100%	5e-86	80%	AFN00072.1
☐	Sequence 39 from patent US 7736648	284	284	100%	2e-85	77%	ADR84017.1
☐	Sequence 84 from patent US 7132510	279	279	85%	3e-85	88%	ABL30459.1
☐	Sequence 61 from patent US 8030457	281	281	100%	1e-84	78%	AEQ82296.1

SEQ ID NO: 18

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Ig heavy chain variable region [Homo sapiens]	293	293	100%	2e-86	79%	AAC09134.1
☐	IgM heavy chain VH1 region precursor [Homo sapiens]	290	290	100%	7e-85	77%	AAC51715.1
☐	random intestinal-homing antibody heavy chain variable region [Homo sapiens]	287	287	100%	1e-83	74%	AAW67358.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	287	287	100%	4e-83	78%	AAC18175.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	284	284	96%	5e-81	79%	AAR32581.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	279	279	100%	5e-81	77%	ABF83225.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	279	279	100%	5e-81	79%	AFC97604.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	278	278	100%	1e-80	79%	ABF83408.1
☐	IGHM [Homo sapiens]	276	276	100%	4e-80	77%	AAA52825.1
☐	immunoglobulin mu heavy chain variable region [Homo sapiens]	280	280	100%	6e-80	78%	ACJ171703.1

SEQ ID NO: 26

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments

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Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	immunoglobulin variable region [Homo sapiens]	323	323	99%	1e-96	84%	ADX66209.1
☐	immunoglobulin A heavy chain variable region [Homo sapiens]	318	318	100%	4e-96	82%	AGP01437.1
☐	immunoglobulin variable region [Homo sapiens]	316	316	100%	1e-95	83%	ADU32618.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	315	315	100%	8e-95	82%	AAC51074.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	315	315	100%	9e-95	82%	ABF83379.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	317	317	100%	1e-94	80%	ACR16070.1
☐	immunoglobulin G heavy chain variable region [Homo sapiens]	314	314	100%	5e-94	80%	AEX29903.1
☐	immunoglobulin heavy chain variable region EV5-14-VH3-95 [Homo sapiens]	312	312	99%	6e-94	83%	ABC67015.1
☐	immunoglobulin G heavy chain variable region [Homo sapiens]	311	311	100%	2e-93	81%	AEX29899.1
☐	immunoglobulin heavy chain VHDJ region [Homo sapiens]	310	310	100%	3e-93	83%	BAC02134.1

SEQ ID NO: 35

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments

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Distance tree of results

Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	immunoglobulin heavy chain VHDJ region [Homo sapiens]	283	283	100%	2e-82	75%	BAC01867.1
☐	immunoglobulin heavy chain VHDJ region [Homo sapiens]	280	280	100%	8e-82	77%	BAC01337.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	281	281	100%	1e-81	76%	CAQ19629.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	279	279	100%	5e-81	74%	AAV23295.1
☐	immunoglobulin heavy chain variable region [Homo sapiens]	276	276	100%	4e-80	74%	ABM67212.1
☐	rotavirus-specific intestinal-homing antibody heavy chain variable region [Homo sapiens]	276	276	100%	5e-80	74%	AAW67388.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	275	275	100%	2e-79	73%	ABF83374.1
☐	Ig heavy chain V region - human (fragment)	278	278	100%	2e-79	73%	A32483
☐	IgM heavy chain VH1 region precursor [Homo sapiens]	277	277	100%	3e-79	74%	AAC51689.1
☐	circulating B cell antibody heavy chain variable region [Homo sapiens]	275	275	100%	3e-79	73%	ABF83354.1

SEQ ID NO: 45

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments

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Graphics

Distance tree of results

Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 22 from patent US 8460660	335	335	100%	6e-104	80%	AGP15545.1
☐	Sequence 23 from patent US 8460660	323	323	100%	3e-99	80%	AGP15546.1
☐	Sequence 109 from patent US 8852595	324	324	100%	3e-99	78%	AJN19225.1
☐	Sequence 86 from patent US 8900588	323	323	100%	3e-99	81%	AJN67543.1
☐	unnamed protein product (synthetic construct)	319	319	99%	2e-97	80%	CAF33420.1
☐	Sequence 1893 from patent US 7138501	332	332	100%	3e-97	80%	ABL54393.1
☐	Sequence 84 from patent US 8900588	317	317	100%	4e-97	80%	AJN67541.1
☐	Sequence 154 from patent US 7332582	319	319	100%	6e-97	77%	ACC07990.1
☐	Sequence 34 from patent US 7795411	319	319	100%	1e-96	79%	ADS45506.1
☐	Sequence 1299 from patent US 7138501	324	324	100%	1e-94	79%	ABL53799.1

SEQ ID NO: 53

Sequences producing significant alignments:

Select: All None Selected: 0

AlignmentsDownloadGenPeptGraphicsDistance tree of resultsMultiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 45 from patent US 7423128	367	367	100%	5e-116	89%	ADI54349.1
☐ Sequence 117 from patent US 7288251	363	363	100%	1e-114	88%	ABY17045.1
☐ Sequence 116 from patent US 7288251	361	361	100%	3e-114	88%	ABY17044.1
☐ Sequence 115 from patent US 7288251	360	360	100%	7e-114	87%	ABY17043.1
☐ Sequence 96 from patent US 8039597	361	361	100%	5e-113	87%	AEQ85193.1
☐ Sequence 20 from patent US 7521048	359	359	100%	7e-113	87%	ACR85125.1
☐ Sequence 18 from patent US 7972596	358	358	100%	9e-113	87%	AEK12809.1
☐ Sequence 184 from patent US 7521048	357	357	100%	1e-112	87%	ACR85190.1
☐ Sequence 22 from patent US 7521048	358	358	100%	2e-112	87%	ACR85126.1
☐ Sequence 48 from patent US 8039597	360	360	100%	3e-112	87%	AEQ85169.1

SEQ ID NO: 61

Sequences producing significant alignments:

Select: All None Selected: 0

AlignmentsDownloadGenPeptGraphicsDistance tree of resultsMultiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 51 from patent US 8398975	336	336	100%	2e-104	86%	AGO74067.1
☐ Sequence 6 from patent US 8398975	333	333	100%	4e-103	85%	AGO74043.1
☐ unnamed protein product [Homo sapiens]	332	332	100%	1e-102	85%	CAL63946.1
☐ Sequence 118 from patent US 7932372	331	331	100%	1e-102	84%	AEF65694.1
☐ Sequence 155 from patent US 8828382	332	332	100%	2e-102	83%	AJN01008.1
☐ Sequence 156 from patent US 8828382	329	329	100%	2e-101	85%	AJN01009.1
☐ Sequence 92 from patent US 8298533	329	329	100%	2e-101	84%	AFX16103.1
☐ Sequence 84 from patent US 6696550	328	328	100%	5e-101	83%	AAT14047.1
☐ Sequence 34 from patent US 7585500	326	326	100%	2e-100	83%	ACW50099.1
☐ Sequence 157 from patent US 8828382	322	322	100%	9e-99	83%	AJN01010.1

SEQ ID NO: 69

Sequences producing significant alignments:

Select: All None Selected: 0

AlignmentsDownloadGenPeptGraphicsDistance tree of resultsMultiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 575 from patent US 7973140	310	310	100%	2e-95	83%	AEK15289.1
☐ Sequence 88 from patent US 7754859	310	310	100%	8e-95	82%	ADS13425.1
☐ Sequence 89 from patent US 7608453	308	308	100%	2e-94	83%	ADA25248.1
☐ Sequence 44 from patent US 7579446	305	305	100%	2e-93	82%	ACW42392.1
☐ Sequence 18 from patent US 7608453	304	304	100%	4e-93	80%	ADA25177.1
☐ Sequence 89 from patent US 6903194	304	304	100%	5e-93	82%	AAY78242.1
☐ unnamed protein product [synthetic construct]	304	304	100%	7e-93	82%	CAL14836.1
☐ Sequence 22 from patent US 7608693	303	303	100%	1e-92	82%	ADA26355.1
☐ Sequence 273 from patent US 7973140	304	304	100%	1e-92	82%	AEK15129.1
☐ Sequence 574 from patent US 7973140	302	302	100%	1e-92	82%	AEK15288.1

SEQ ID NO: 77

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

AlignmentsDownloadGenPeptGraphicsDistance tree of resultsMultiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 545 from patent US 7973140	335	335	100%	3e-104	85%	AEK15265.1
☐ Sequence 58 from patent US 8207306	334	334	100%	5e-104	86%	AFQ19031.1
☐ Sequence 58 from patent US 8067544	333	333	100%	3e-103	84%	AEU59458.1
☐ Sequence 620 from patent US 7973140	331	331	100%	5e-103	85%	AEK15334.1
☐ Sequence 162 from patent US 8828382	330	330	100%	7e-103	83%	AJN01015.1
☐ Sequence 615 from patent US 7973140	330	330	100%	1e-102	85%	AEK15329.1
☐ Sequence 560 from patent US 7973140	330	330	100%	1e-102	84%	AEK15274.1
☐ Sequence 273 from patent US 7973140	330	330	100%	1e-102	85%	AEK15129.1
☐ Sequence 18 from patent US 8207306	330	330	100%	2e-102	86%	AFQ19011.1
☐ Sequence 175 from patent US 7973140	328	328	100%	4e-102	83%	AEK15080.1

SEQ ID NO: 87

Sequences producing significant alignments:

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AlignmentsDownloadGenPeptGraphicsDistance tree of resultsMultiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 571 from patent US 7973140	357	357	100%	1e-114	95%	AEK15285.1
☐ Sequence 63 from patent US 8067544	356	356	100%	2e-114	96%	AEU59463.1
☐ Sequence 113 from patent US 7326414	355	355	100%	1e-113	95%	ABZ64926.1
☐ unnamed protein product (synthetic construct)	349	349	100%	2e-111	92%	CAJ21102.1
☐ Sequence 24 from patent US 7498420	350	350	100%	3e-110	93%	ACP75690.1
☐ Sequence 606 from patent US 7973140	344	344	100%	2e-109	94%	AEK15320.1
☐ Sequence 587 from patent US 7973140	344	344	100%	2e-109	94%	AEK15301.1
☐ Sequence 296 from patent US 7285269	342	342	100%	4e-109	94%	ABX90476.1
☐ Sequence 7 from patent US 7960515	343	343	100%	1e-108	92%	AEI21318.1
☐ Sequence 29 from patent US 8420784	346	346	100%	3e-108	88%	AGM60648.1

SEQ ID NO: 130

Sequences producing significant alignments:

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AlignmentsDownloadGenPeptGraphicsDistance tree of resultsMultiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 9 from patent US 7452976	335	335	100%	2e-106	92%	ACK26206.1
☐ Sequence 62 from patent US 8067544	333	333	100%	3e-105	92%	AEU59462.1
☐ Sequence 127 from patent US 8025878	334	334	100%	3e-105	88%	AFQ60331.1
☐ Sequence 603 from patent US 7973140	332	332	100%	2e-104	90%	AEK15317.1
☐ Sequence 76 from patent US 8026344	332	332	100%	2e-104	88%	AFQ61995.1
☐ Sequence 63 from patent US 8030457	330	330	100%	5e-104	88%	AEQ82298.1
☐ Sequence 61 from patent US 8030457	330	330	100%	5e-104	88%	AEQ82296.1
☐ Sequence 602 from patent US 7973140	330	330	100%	6e-104	89%	AEK15316.1
☐ Sequence 229 from patent US 7973140	331	331	100%	7e-104	88%	AEK15107.1
☐ Sequence 7 from patent US 8609820	329	329	100%	2e-103	89%	AJQ52703.1

SEQ ID NO: 138

Sequences producing significant alignments:

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 196 from patent US 7488806	323	323	100%	3e-100	84%	ACN09183.1
☐	Sequence 559 from patent US 7973140	320	320	100%	2e-99	83%	AEK15273.1
☐	Sequence 212 from patent US 7488806	319	319	100%	6e-99	83%	ACN09190.1
☐	Sequence 14 from patent US 7771720	318	318	100%	1e-98	83%	ADS20603.1
☐	Sequence 148 from patent US 8314213	318	318	100%	2e-98	83%	AGA36831.1
☐	Sequence 28 from patent US 8822644	318	318	100%	3e-98	83%	AJM97905.1
☐	Sequence 582 from patent US 7973140	316	316	100%	2e-97	83%	AEK15296.1
☐	Sequence 58 from patent US 8309082	316	316	100%	3e-97	79%	AFX57166.1
☐	Sequence 142 from patent US 7378091	315	315	100%	3e-97	83%	ACE40658.1
☐	Sequence 237 from patent US 8048992	314	314	99%	4e-97	81%	AER81723.1

SEQ ID NO: 146

Sequences producing significant alignments:

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 40 from patent US 8221753	326	326	100%	3e-101	83%	AF006168.1
☐	Sequence 42 from patent US 7537762	327	327	100%	1e-100	83%	ACS07786.1
☐	Sequence 46 from patent US 7288253	326	326	100%	2e-100	83%	ABY17076.1
☐	Sequence 38 from patent US 7288253	325	325	100%	4e-100	83%	ABY17072.1
☐	Sequence 113 from patent US 8414893	324	324	100%	4e-100	83%	AGJ48310.1
☐	Sequence 66 from patent US 7288253	323	323	100%	6e-100	83%	ABY17086.1
☐	Sequence 39 from patent US 7973140	324	324	100%	7e-100	82%	AEK15012.1
☐	Sequence 624 from patent US 7973140	323	323	100%	9e-100	83%	AEK15338.1
☐	Sequence 55 from patent US 8133979	323	323	100%	1e-99	83%	AFD52448.1
☐	Sequence 78 from patent US 7537762	323	323	100%	1e-99	83%	ACS07804.1

SEQ ID NO: 155

Sequences producing significant alignments:

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 156 from patent US 8828382	297	297	100%	2e-89	79%	AJN01009.1
☐	Sequence 84 from patent US 6696550	297	297	100%	2e-89	81%	AAT14047.1
☐	Sequence 48 from patent US 8444981	296	296	100%	3e-89	81%	AGN08380.1
☐	Sequence 274 from patent US 8840894	295	295	100%	1e-88	79%	AJN09588.1
☐	unnamed protein product [Homo sapiens]	294	294	100%	2e-88	78%	CAL63950.1
☐	unnamed protein product [Homo sapiens]	294	294	100%	2e-88	79%	CAL63946.1
☐	Sequence 94 from patent US 7700098	294	294	100%	2e-88	81%	ADL81209.1
☐	Sequence 19 from patent US 8604174	294	294	100%	2e-88	80%	AJQ46678.1
☐	Sequence 77 from patent US 6696550	294	294	100%	3e-88	79%	AAT14040.1
☐	Sequence 6 from patent US 8398975	292	292	100%	8e-88	81%	AGO74043.1

SEQ ID NO: 163

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 625 from patent US 7973140	286	286	100%	6e-87	84% AEK15339.1
☐	Sequence 622 from patent US 7973140	286	286	100%	6e-87	84% AEK15336.1
☐	Sequence 96 from patent US 8182813	286	286	100%	1e-86	83% AFL43630.1
☐	Sequence 14 from patent US 8491907	286	286	100%	2e-86	81% AGU22075.1
☐	Sequence 39 from patent US 8293237	283	283	99%	6e-86	84% AFX07897.1
☐	Sequence 593 from patent US 7973140	284	284	100%	6e-86	82% AEK15007.1
☐	Sequence 145 from patent US 7973140	284	284	100%	7e-86	81% AEK15065.1
☐	Sequence 400 from patent US 8030457	283	283	100%	2e-85	81% AEQ82569.1
☐	Sequence 235 from patent US 7973140	283	283	100%	2e-85	82% AEK15110.1
☐	Sequence 127 from patent US 7378091	282	282	100%	4e-85	81% ACE40643.1

SEQ ID NO: 171

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 152 from patent US 7378091	286	286	100%	5e-86	78% ACE40668.1
☐	Sequence 222 from patent US 7705130	285	285	100%	1e-85	76% ADL89053.1
☐	Sequence 146 from patent US 8791244	285	285	100%	3e-85	76% AJM44648.1
☐	Sequence 51 from patent US 7423128	283	283	100%	3e-85	79% ADI54355.1
☐	Sequence 198 from patent US 7705130	283	283	100%	6e-85	77% ADL89041.1
☐	Sequence 120 from patent US 7705130	283	283	100%	6e-85	76% ADL89002.1
☐	Sequence 194 from patent US 7705130	283	283	100%	9e-85	76% ADL89039.1
☐	Sequence 10 from patent US 7767206	283	283	100%	1e-84	76% ADS19533.1
☐	Sequence 189 from patent US 7521048	282	282	100%	2e-84	78% ACR85195.1
☐	Sequence 170 from patent US 8309082	282	282	100%	2e-84	76% AFX57229.1

SEQ ID NO: 179

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 473 from patent US 8703131	275	275	100%	1e-82	79% AJL22747.1
☐	Sequence 781 from patent US 8703427	275	275	100%	2e-82	79% AJL24910.1
☐	Sequence 111 from patent US 7368111	273	273	100%	9e-82	78% ACE16217.1
☐	Sequence 37 from patent US 8748581	264	264	100%	6e-78	72% AJM13125.1
☐	Sequence 39 from patent US 7736648	257	257	100%	2e-75	74% ADR84017.1
☐	Sequence 3 from patent US 5891438	255	255	100%	3e-75	75% AAE23317.1
☐	Sequence 69 from patent US 8748107	254	254	100%	5e-74	70% AJM06246.1
☐	unnamed protein product (Homo sapiens)	253	253	100%	8e-74	73% CAL63908.1
☐	Sequence 33 from patent US 6881557	247	247	86%	9e-73	80% AAY12049.1
☐	Sequence 308 from patent US 8444976	244	244	85%	6e-72	80% AGN08189.1

SEQ ID NO: 187

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 58 from patent US 8207306	326	326	100%	1e-100	84%	AF019031.1
☐	Sequence 58 from patent US 8067544	323	323	100%	1e-99	83%	AEU59458.1
☐	Sequence 39 from patent US 8604174	322	322	100%	2e-99	83%	AJ046688.1
☐	Sequence 18 from patent US 8207306	321	321	100%	1e-98	83%	AF019011.1
☐	Sequence 560 from patent US 7973140	319	319	100%	3e-98	83%	AEK15274.1
☐	Sequence 393 from patent US 7973140	318	318	100%	3e-98	81%	AEK15189.1
☐	Sequence 14 from patent US 8207306	319	319	100%	3e-98	83%	AF019009.1
☐	Sequence 545 from patent US 7973140	319	319	100%	3e-98	82%	AEK15265.1
☐	Sequence 14 from patent US 8466263	319	319	100%	5e-98	82%	AGP24567.1
☐	Sequence 61 from patent US 8207306	319	319	100%	5e-98	83%	AF019033.1

SEQ ID NO: 195

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
☐	unnamed protein product (Homo sapiens)	323	323	100%	1e-99	84%	CAL63946.1
☐	Sequence 48 from patent US 8444981	322	322	100%	2e-99	84%	AGN08380.1
☐	Sequence 51 from patent US 8398975	319	319	100%	1e-98	82%	AGO74067.1
☐	unnamed protein product (Homo sapiens)	319	319	100%	2e-98	83%	CAL63950.1
☐	Sequence 572 from patent US 7973140	317	317	100%	4e-98	86%	AEK15286.1
☐	Sequence 16 from patent US 7618626	317	317	100%	1e-97	83%	ADA36206.1
☐	Sequence 357 from patent US 7982016	316	316	100%	2e-97	82%	AEL92873.1
☐	Sequence 98 from patent US 8784821	316	316	100%	2e-97	84%	AJM35866.1
☐	Sequence 118 from patent US 7932372	316	316	100%	4e-97	83%	AEF65694.1
☐	Sequence 77 from patent US 6696550	316	316	100%	5e-97	82%	AAT14040.1

SEQ ID NO: 203

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 130 from patent US 8357780	319	319	100%	9e-99	85%	AGD78985.1
☐	Sequence 191 from patent US 8895010	317	317	100%	6e-98	83%	AJN62356.1
☐	Sequence 187 from patent US 8679496	317	317	100%	9e-98	82%	AJL00204.1
☐	Sequence 572 from patent US 7973140	316	316	100%	1e-97	84%	AEK15286.1
☐	Sequence 41 from patent US 8580263	315	315	100%	6e-97	82%	AHD62224.1
☐	Sequence 17 from patent US 8580263	315	315	100%	6e-97	82%	AHD62203.1
☐	Sequence 26 from patent US 7563443	314	314	100%	7e-97	84%	ACW22367.1
☐	Sequence 63 from patent US 8414893	313	313	100%	3e-96	84%	AGJ48270.1
☐	Sequence 34 from patent US 8735331	313	313	100%	3e-96	83%	AJL57114.1
☐	Sequence 130 from patent US 8222377	312	312	100%	3e-96	83%	AFQ08491.1

SEQ ID NO: 211

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 63 from patent US 8414893	337	337	100%	2e-105	90% AGJ48270.1
☐	Sequence 335 from patent US 7982016	335	335	100%	6e-105	88% AEL92862.1
☐	Sequence 592 from patent US 7973140	333	333	100%	4e-104	88% AEK15308.1
☐	Sequence 183 from patent US 8273351	332	332	100%	4e-104	87% AFT60760.1
☐	Sequence 87 from patent US 6696550	334	334	100%	1e-103	86% AAT14050.1
☐	Sequence 101 from patent US 7780963	333	333	100%	1e-103	87% ADS27061.1
☐	unnamed protein product [synthetic construct]	335	335	100%	1e-103	90% CBX51231.1
☐	Sequence 30 from patent US 8551920	335	335	100%	3e-103	90% AGY21032.1
☐	Sequence 13 from patent US 7452537	330	330	100%	4e-103	89% ACK23911.1
☐	Sequence 30 from patent US 8460660	329	329	100%	2e-102	88% AGP15553.1

SEQ ID NO: 219

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 1255 from patent US 7329737	328	328	100%	3e-101	88% ACC02756.1
☐	Sequence 133 from patent US 8119130	323	323	100%	2e-100	87% AFB84287.1
☐	Sequence 114 from patent US 8119130	323	323	100%	2e-100	87% AFB84268.1
☐	Sequence 34 from patent US 8735331	321	321	100%	1e-99	85% AJL57114.1
☐	Sequence 69 from patent US 8802089	321	321	100%	2e-99	87% AJM49569.1
☐	Sequence 23 from patent US 8323647	321	321	100%	2e-99	86% AGA40596.1
☐	unnamed protein product [synthetic construct]	321	321	100%	3e-99	86% CAF32933.1
☐	unnamed protein product [synthetic construct]	319	319	100%	4e-99	87% CAF32932.1
☐	Sequence 70 from patent US 8030457	319	319	100%	5e-99	88% AEQ82305.1
☐	Sequence 634 from patent US 7485297	319	319	100%	5e-99	87% ACN05041.1

SEQ ID NO: 6

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 8 from patent US 7192582	320	320	100%	1e-100	90% ABP23449.1
☐	Sequence 94 from patent US 8258266	314	314	100%	2e-98	89% AFS93708.1
☐	Sequence 16 from patent US 8540987	313	313	100%	4e-98	89% AGX45849.1
☐	unnamed protein product [Homo sapiens]	313	313	100%	6e-98	89% CAT03449.1
☐	Sequence 131 from patent US 7601818	312	312	100%	8e-98	89% ADA08642.1
☐	Sequence 14 from patent US 8685402	312	312	100%	2e-97	89% AJL06397.1
☐	Sequence 49 from patent US 8652469	311	311	100%	4e-97	88% AHL59206.1
☐	unnamed protein product [Homo sapiens]	309	309	100%	1e-96	88% CAD23777.1
☐	Sequence 63 from patent US 8563694	313	313	100%	2e-96	89% AHD030373.1
☐	Sequence 27 from patent US 7115717	313	313	100%	2e-96	89% ABJ48585.1

SEQ ID NO: 14

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
☐	Sequence 56 from patent US 7566772	279	279	99%	1e-84	83%
☐	Sequence 444 from patent US 7485297	279	279	99%	3e-84	84%
☐	unnamed protein product [Homo sapiens]	278	278	99%	4e-84	83%
☐	Sequence 366 from patent US 8916160	277	277	99%	1e-83	83%
☐	Sequence 1923 from patent US 8114968	276	276	99%	2e-83	84%
☐	Sequence 1919 from patent US 8114968	276	276	99%	4e-83	83%
☐	Sequence 60 from patent US 7566772	274	274	99%	1e-82	83%
☐	Sequence 172 from patent US 8216581	274	274	99%	2e-82	83%
☐	Sequence 233 from patent US 7988971	272	272	99%	8e-82	83%
☐	Sequence 1069 from patent US 7329737	273	273	96%	1e-81	84%

SEQ ID NO: 22

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
☐	Sequence 2 from patent US 7718774	309	309	100%	1e-96	90%
☐	Sequence 28 from patent US 7423128	309	309	100%	1e-96	90%
☐	Sequence 343 from patent US 7973140	308	308	100%	2e-96	90%
☐	Sequence 119 from patent US 8182813	306	306	100%	1e-95	90%
☐	Sequence 135 from patent US 8828382	305	305	100%	3e-95	89%
☐	Sequence 26 from patent US 6924360	305	305	100%	6e-95	89%
☐	Sequence 8 from patent US 8597648	304	304	100%	1e-94	88%
☐	Sequence 134 from patent US 8828382	303	303	100%	2e-94	88%
☐	Sequence 140 from patent US 7790862	303	303	100%	2e-94	89%
☐	Sequence 29 from patent US 7423128	303	303	100%	2e-94	89%

SEQ ID NO: 31

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
☐	Sequence 203 from patent US 7582298	285	285	100%	1e-87	85%
☐	Sequence 55 from patent US 8609816	283	283	100%	1e-86	86%
☐	unnamed protein product [Homo sapiens]	282	282	100%	4e-86	85%
☐	Sequence 40 from patent US 8039596	281	281	100%	6e-86	85%
☐	Sequence 16 from patent US 7868141	279	279	99%	2e-85	86%
☐	Sequence 8 from patent US 7947811	279	279	100%	3e-85	84%
☐	Sequence 349 from patent US 8124093	279	279	100%	5e-85	82%
☐	unnamed protein product [Homo sapiens]	279	279	100%	5e-85	85%
☐	Sequence 377 from patent US 7988971	279	279	100%	6e-85	85%
☐	Sequence 5 from patent US 8394378	278	278	100%	1e-84	84%

SEQ ID NO: 40

Sequences producing significant alignments:

Select AllNoneSelected0

AlignmentsDownloadGenPeptGraphicsDistance tree of resultsMultiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	immunoglobulin kappa light chain variable region [Homo sapiens]	325	325	100%	3e-100	89%	AAQ02698.1
☐	anti-GM2 ganglioside IgM monoclonal kappa light chain variable region [Homo sapiens]	323	323	100%	3e-99	89%	AAC26480.1
☐	immunoglobulin G heavy chain variable region [Homo sapiens]	323	323	100%	3e-99	89%	AIT38107.1
☐	immunoglobulin light chain variable region YM2-PPS-14-K4-30 [Homo sapiens]	324	324	99%	1e-98	89%	ABC67024.1
☐	immunoglobulin G heavy chain variable region [Homo sapiens]	321	321	100%	1e-98	89%	AIT38682.1
☐	immunoglobulin variable kappa chain [Homo sapiens]	321	321	100%	1e-98	89%	CAJ57195.1
☐	immunoglobulin light chain variable region [Homo sapiens]	321	321	100%	2e-98	89%	ABG38394.1
☐	immunoglobulin light chain variable region [Homo sapiens]	320	320	100%	3e-98	87%	AAK94840.1
☐	immunoglobulin kappa light chain variable region [Homo sapiens]	319	319	97%	3e-98	90%	AAZ09160.1
☐	immunoglobulin kappa light chain variable region [Homo sapiens]	319	319	100%	2e-97	89%	ACJ71709.1

PatBase

2) Family number: 41695167 (US2009263824A)PatBase

Title: DETECTION OF NEURODEGENERATIVE DISEASE

Abstract: Source: US2009263824A Provided are methods of assessing the absence or presence of a neurodegenerative disease in a subject comprising characterizing TDP-43 in a tissue sample of the subject. Also disclosed are methods for diagnosing a neurodegenerative disease in a subject, and methods for determining the efficacy of a drug against a neurodegenerative disease. Novel **antibodies** that bind to TDP-43 are also provided.

Classifications:
International (IPC 8-9): C07K16/00 C07K16/18 G01N33/53 G01N33/566 G01N33/567 (Advanced/Invention);
C07K16/00 G01N33/53 (Core/Invention)
CPC: C07K16/18 G01N33/6896 G01N2800/2821 G01N2800/52
European: G01N33/68V2 S01N800/28B1 S01N800/52
US: 435/7.1 435/7.100P 435/7.21 435/7.9 435/7.92 436/501 436/503 530/387.1 530/387.100S 530/389.1

PatBase - US2009263824_A#1

Patent Application Publication Oct. 22, 2009 Sheet 1 of 9 US 2009/0263824 A1

FIG. 1

4) Family number: 42798129 (US2011287453A)PatBase

Title: ANTIBODY BINDING SPECIFICALLY TO TDP-43 AGGREGATE

Abstract: Source: US2011287453A The present invention provides an **antibody** that specifically binds to an abnormal TDP-43 protein aggregate, an agent comprising the **antibody** for detecting a TDP-43 proteinopathy lesion, and a method for detecting or diagnosing a TDP-43 proteinopathy lesion by using the **antibody**.

Classifications:
International (IPC 8-9): A61K39/395 A61P21/04 A61P25/16 C07K16/00 C07K16/18 C12N15/09 C12N5/10 C12N5/16 C12P21/08 G01N33/53 G01N33/68 (Advanced/Invention);
A61K39/395 A61P21/04 A61P25/16 C12P21/08 (Advanced/Non-invention);
A61K39/395 A61P21/00 A61P25/00 C07K16/18 C12N15/09 C12N5/10 C12P21/08 G01N33/53 (Core/Invention);
C12P21/08 (Core/Non-invention)
CPC: C07K16/18 G01N33/6875
European: C07K16/18 G01N33/68H
US: 435/326 435/326S 435/331 435/331S 435/7.92 435/7.920P 436/501 436/501S 530/387.3 530/387.300S 530/387.9 530/387.900S 530/388.85 530/389.1

PatBase - US2011287453_A#1

Patent Application Publication Nov. 24, 2011 Sheet 1 of 8 US 2011/027453 A1

Fig.1

Title: Preparation method of human TDP-43 monoclonal antibody coating ELISA plate and ELISA detection kit

Abstract: Source: CN101634656A The invention relates to a preparation method of a new human TDP-43 monoclonal antibody coating ELISA plate and ELISA detection kit. The key technology mainly lies in that: genetic engineering method is utilized to prepare a specific mouse anti-human monoclonal antibody, and the ELISA plate by which the antibody is purified and then coated is taken as important component of the kit, and then the ELISA plate, TDP-43 polyclonal antibody and horseradish peroxidase labelled second antibody, TDP-43 standard substance, TDP-43 positive control, sample diluent, cleaning solution, development solution and stop solution are assembled into a humanized TDP-43 ELISA detection kit; a sensitive and rapid method for detecting concentration of TDP-43 in ELISA antibody capturing human serum or cell and tissue culture is established, and the method has high specificity and high stability. The kit is mainly used in general laboratory or neuropathology clinical research.

Classifications:
International (IPC 8-9): G01N33/535 G01N33/543 G01N33/577 (Advanced/Invention);
G01N33/577 (Core/Invention)

Family:

Publication number	Publication date	Application number	Application date
CN101634656 A	20100127	CN200910063674	20090821

Priority:

CN200910063674 20090821

Probable Assignee: WUHAN SANYING BIO TECHNOLOGY C

Assignee(s): (std): WUHAN SANYING BIO TECHNOLOGY C

Assignee(s): WUHAN SANYING BIO TECHNOLOGY CO

Inventor(s): (std): JINHONG PENG ; PING LAN

Inventor(s): LAN PING ; PENG JINHONG

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IP Search

Mario Forero Anticuerpos

Query

Nucleotide Sequences

Protein Sequences

Paste or Choose your query.

>H02013061163_10
EVQLVESGGGLVQPGGSLRLISCTTSGFIFSDYWHWRQAPGKGLTWVSRINLDGSDTIYADSVKGRFTISRNDKNTLYLQWNSLRVEDAIYYCARSRKSVWGQTMVTYSS
>H02013061163_14
QSALTQPASVSGSPGQSITISCTGNTDVGAYDYVSN5QLPGKAPKFVIFDQVVRPSGISDRFSGSKSGNTASLTISGLQAEDEADYYCSYTKSGTLVFGGGTKRVTYV

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.

Search Strategy

GenePAST

Blast

Fragment Search

Motif

Percent identity

80

Over the length of

my query

Additional Strategy Parameters

Limit subject length from

100

to

500

residues

Keep a maximum of

500

results (per query)

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Apply filters to subject databases

Nucleotides

Patents

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1,000 Results

#	Query %	Seq %	Seq %	Seq %	Seq %	Query Identifier	Patient Assignments	Patient Title	Patient Sequence Location	Identifier	Extended Legal Status	Publication Date	PDF Link	
W0201306163.10	100	100	100	100	100	100	UNIVERSITY OF ZURICH BIOGEN IDEC INTERNATIONAL, NEUROSCIENCE GMBH ROGER, WITSCHE, HOCK, CHRISTOPH BARENCI MONTRASSO, MARIA GRAZIA MONTRASSO, FABIO GRIMM, RAY BARBERIS, BEATRICE WITNER, PAUL QUINTERO-MONZON, OMAR COOPERMAN, JIMMY BIOGEN IDEC INTERNATIONAL NEUROSCIENCE GMBH CHN UNIV ZURICH CHN	TOP-13 SPECIFIC BINDING MOLECULES	TBD (information not available)	CA2853142-0010	PENDING	02-May-2013	PDF	
	100	100	100	100	100	100	UNIVERSITY OF ZURICH BIOGEN IDEC INTERNATIONAL, NEUROSCIENCE GMBH ROGER, WITSCHE, HOCK, CHRISTOPH BARENCI MONTRASSO, MARIA GRAZIA MONTRASSO, FABIO GRIMM, RAY BARBERIS, BEATRICE WITNER, PAUL QUINTERO-MONZON, OMAR COOPERMAN, JIMMY BIOGEN IDEC INTERNATIONAL NEUROSCIENCE GMBH CHN UNIV ZURICH CHN	TOP-13 SPECIFIC BINDING MOLECULES	claim 1	W0201306163-0014	PENDING	02-May-2013	PDF	
	100	100	100	100	100	100	UNIVERSITY OF ZURICH BIOGEN IDEC INTERNATIONAL, NEUROSCIENCE GMBH ROGER, WITSCHE, HOCK, CHRISTOPH BARENCI MONTRASSO, MARIA GRAZIA MONTRASSO, FABIO GRIMM, RAY BARBERIS, BEATRICE WITNER, PAUL QUINTERO-MONZON, OMAR COOPERMAN, JIMMY BIOGEN IDEC INTERNATIONAL NEUROSCIENCE GMBH CHN UNIV ZURICH CHN	TOP-13 SPECIFIC BINDING MOLECULES	empty	TBD (information not available)	CA2853142-0010	PENDING	26-Feb-2015	PDF
	100	100	100	100	100	100	UNIVERSITY OF ZURICH BIOGEN IDEC INTERNATIONAL, NEUROSCIENCE GMBH ROGER, WITSCHE, HOCK, CHRISTOPH BARENCI MONTRASSO, MARIA GRAZIA MONTRASSO, FABIO GRIMM, RAY BARBERIS, BEATRICE WITNER, PAUL QUINTERO-MONZON, OMAR COOPERMAN, JIMMY BIOGEN IDEC INTERNATIONAL NEUROSCIENCE GMBH CHN UNIV ZURICH CHN	TOP-13 SPECIFIC BINDING MOLECULES	empty	TBD (information not available)	CA2853142-0014	PENDING	02-May-2013	PDF
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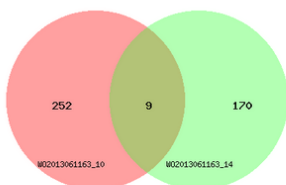
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