

INFORME DE BÚSQUEDA DE PATENTES PARA EL Radicado N° 14-42269-00000-0000						
CRITERIOS PARA LA BÚSQUEDA (anexar pantallazo o reporte en PDF, junto con los boleanos utilizados)						
Palabras clave utilizadas		H5 protein clade 1, H5N1 virus, infections H5N1, H5 protein (2), Newcastle disease virus, vaccine				
CLASIFICACIONES INTERNACIONALES UTILIZADAS PARA LA BÚSQUEDA		A61K 039/012.				
BASES DE DATOS CONSULTADAS.						
Patentscope		Google/patents				
NCBI		PatBase				
Espacenet		Sciencedirect				
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
PCT INTERNATIONAL SEARCH REPORT EPO	26/noviembre/2012	Hessel A. <i>et al.</i> , 2011. "Vectors Based on Modified Vaccinia Ankara Expressing Influenza H5N1 Hemagglutinin Induce Substantial Cross – Clade Protective Immunity"	1 - 40	Novedad/ Nivel inventivo	X	
		WO2008/052173	1 - 40	Nivel inventivo		X
		WO2007/053446	1 – 18, 24 - 40	Nivel inventivo		X
DOCUMENTOS ADICIONALES ENCONTRADOS POR EL EXAMINADOR DE ACUERDO A LOS CRITERIOS DE BÚSQUEDA.						
CN1781553						
US7981428						
US2008193471						
US2007184526						
US2005009008						
US2010278834						
US2009169505						
US2011305748						
WO15099609						
US2014234357						
US2014314777						
US2014199337						
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	
SEQ ID NO: 1	dbj BAE07201.1 Secuencia de	US2008193471 Secuencia de				

	aminoácidos presenta un 100% de identidad y cobertura	aminoácidos SEQ ID NO: 1, presenta un 98% de identidad y 100% cobertura			
SEQ ID NO: 2	gblAAR99628.1 Secuencia de aminoácidos presenta un 100% de identidad y cobertura				
SEQ ID NO: 5	US7981428 SEC ID NO: 7. Secuencia de aminoácidos presenta un 98% de identidad				
SEQ ID NO: 6	gblAAT39066.1 Secuencia de aminoácidos presenta un 100% de identidad y cobertura				
SEQ ID NO: 7	gblAAR99628.1 Secuencia de aminoácidos presenta un 100% de identidad y cobertura				
SEQ ID NO: 8	gblACA29672.1 Secuencia de aminoácidos presenta un 100% de identidad y cobertura				
SEQ ID NO: 9	US2007184526 SEC ID NO: 53. Secuencia de aminoácidos presenta un 97% de identidad y 100% y cobertura				
SEQ ID NO: 15	US2007184526 SEC ID NO: 34. Secuencia de aminoácidos presenta un 97% de identidad y 99% y cobertura				

Búsqueda en PatBase

2) Family number: 31460863 (US2005009008A)

Title: FUNCTIONAL INFLUENZA VIRUS-LIKE PARTICLES (VLPs)

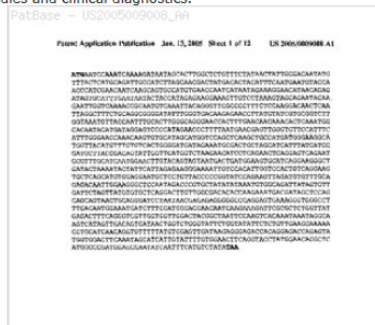
Abstract: Source: US2005009008A Recombinant influenza virus **proteins**, including influenza capsomers, subviral particles, virus-like particles (VLP), VLP complexes, and/or any portions of thereof, are provided as a vaccine for influenza viruses. The invention is based on the combination of two vaccine technologies: (1) intrinsically safe recombinant vaccine technology, and (2) highly immunogenic, self-assembled **protein** macromolecules embedded in plasma membranes and comprised of multiple copies of influenza virus structural **proteins** exhibiting neutralizing epitopes in native conformations. More specifically, this invention relates to the design and production of functional homotypic and heterotypic recombinant influenza virus-like particles (VLPs) comprised of recombinant structural **proteins** of human influenza virus type A/Sydney/5/94 (H3N2) and/or avian influenza virus type A/Hong Kong/1073/99 (H9N2) in baculovirus-infected insect cells and their application as a vaccine in the prevention of influenza infections and as a laboratory reagent for virus structural studies and clinical diagnostics.

Classifications:

International (IPC 8-9): A61K39/12 C12N15/33 A61K A61K35/56 A61K35/64 A61K36/06 A61K39/00 A61K39/145 A61K39/155 A61K39/245 A61K39/25 A61K39/295 A61K39/39 A61P31/12 A61P31/14 A61P31/16 A61P31/22 A61P37/04 C07H21/04 C07K14/005 C07K14/03 C07K14/04 C07K14/05 C07K14/11 C07K14/135 C07K14/165 C07K19/00 C12N1/15 C12N1/19 C12N15/00 C12N15/09 C12N15/11 C12N15/44 C12N15/86 C12N5/10 C12N7/00 C12N7/01 C12N7/04 C12N9/24 C12P21/00 C12P21/02 C12P21/06 C12Q1/68 C12Q1/70 C12R1/92 G01N33/569 (Advanced/Invention); C12R1/92 A61K39/00 A61K39/145 A61K39/245 A61K39/25 C07K14/04 C07K14/11 (Advanced/Non-invention); A61K39/00 A61K39/12 A61K39/145 A61K39/245 A61K39/39 A61P31/00 C07H21/00 C07K14/00 C07K14/005 C12N1/15 C12N1/19 C12N15/09 C12N5/10 C12N7/00 C12N7/01 C12N7/04 C12P21/06 C12Q1/68 C12Q1/70 G01N33/569 (Core/Invention); C07K14/005 (Core/Non-invention); A61K C07K C12N (Subclass/Invention)

International (IPC 1-7): A61K A61K0/00 A61K39 A61K39/12 A61K39/145 A61K39/25 C07H21/04 C07K1/00 C07K14/00 C07K17/00 C12N15/09 C12N15/63 C12N15/70 C12N15/74 C12N15/85 C12N15/87 C12N7/01 C12Q1/70

CPC: C12N2710/16723 C12N2760/16022 C12N2760/16023 C12N2760/16234 C12N2770/20034 C12N15/86 A61K39/155 C07K2319/735 C12N2760/18534 A61K2039/55561 A61K2039/58 A61K39/145 C07H21/04 C07K14/005 C12N7/00



5) Family number: 42164021 (US2010278834A)

Title: ANTIBODIES AGAINST H5N1 STRAINS OF INFLUENZA A VIRUS

Abstract: Source: US2010278834A Provided are human antibodies that can neutralize a H5N1 strain of influenza A virus. Also provided are antibodies that can neutralize a strain of influenza A virus in **clade** 2 of the H5 subtype, that can neutralize a H5N1 strain of influenza A virus and have a lambda light chain, and that are IgG antibodies (but not with a IgG1 heavy chain) that can neutralize a H5N1 strain of influenza A virus.

Classifications:

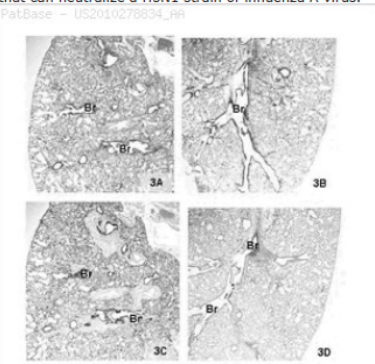
International (IPC 8-9): A61K39/395 A61K39/42 A61P31/16 C07H21/00 C07K16/00 C07K16/10 C07K16/46 C12N15/09 (Advanced/Invention); C12P21/08 (Advanced/Non-invention); A61K39/395 A61P31/00 C07K16/00 C07K16/08 C07K16/46 C12N15/09 (Core/Invention); C12P21/08 (Core/Non-invention)

International (IPC 1-7): C07K16/00

CPC: C07K16/1018 C07K2317/21 C07K2317/56 C07K2317/565

European: C07K16/10D M07K317/210 M07K317/560 M07K317/565

US: 424/133.1 424/135.1 424/142.1 424/142.100P 424/147.1 424/159.1 424/159.100P 530/387.1 530/387.100S 530/387.3 530/388.1 530/388.150S 530/388.3 530/389.4 530/389.400S 536/23.53 536/23.530S



6) Family number: 43358752 (US2009169505A)

Title: NOVEL VACCINES AGAINST MULTIPLE SUBTYPES OF INFLUENZA VIRUS

Abstract: Source: US2009169505A An aspect of the present invention is directed towards DNA plasmid vaccines capable of generating in a mammal an immune response against a plurality of influenza virus subtypes, comprising a DNA plasmid and a pharmaceutically acceptable excipient. The DNA plasmid is capable of expressing a consensus influenza antigen in a cell of the mammal in a quantity effective to elicit an immune response in the mammal, wherein the consensus influenza antigen comprises consensus hemagglutinin (HA), neuraminidase (NA), matrix **protein**, nucleoprotein, M2 ectodomain-nucleo-**protein** (M2e-NP), or a combination thereof. Preferably the consensus influenza antigen comprises HA, NA, M2e-NP, or a combination thereof. The DNA plasmid comprises a promoter operably linked to a coding sequence that encodes the consensus influenza antigen. Additionally, an aspect of the present invention includes methods of eliciting an immune response against a plurality of influenza virus subtypes in a mammal using the DNA plasmid vaccines provided.

Classifications:

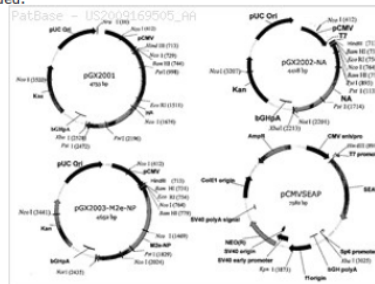
International (IPC 8-9): A01N43/04 A61K31/70 A61K31/7088 A61K31/711 A61K31/713 A61K35/76 A61K38/20 A61K39/00 A61K39/12 A61K39/145 A61K39/39 A61K39/395 A61K47/30 A61K47/34 A61K47/44 A61K48/00 A61P31/12 A61P31/16 A61P37/04 C07H21/02 C12N15/00 C12N15/09 C12N15/117 C12N15/44 C12N15/63 C12N15/85 C12P21/06 (Advanced/Invention); A61K39/12 A61K39/145 C12N15/44 C12N15/85 (Advanced/Non-invention); A01N43/02 A61K31/70 A61K38/20 A61K39/145 C12N15/00 (Core/Invention); C12N (Subclass/Invention)

International (IPC 1-7): A01N43/04

CPC: A61K9/0019 A61K38/2086 A61K39/145 A61K47/34 A61K2039/53 A61K2039/54 C07K14/005 C12N2760/16122 C12N2760/16134 A61K2039/70 C12N2760/16034 A61K39/12 A61K38/208 A61K2039/58

European: A61K38/20 A61K38/20M A61K38/20N A61K39/145 A61K39/295 A61K47/34 A61K9/00MS C07K14/005 K61K39/53 K61K39/54 M12N760/16122 M12N760/16134

US: 424/178.1 424/178.100S 424/199.1 424/199.100S 424/206.1 424/209.1 424/209.100S 424/85.2 424/85.200P 435/320.1 435/320.100S 435/69.1 435/77.1 536/23.1



10) Family number: 50951268 (US2013288338A)

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Title: RECOMBINANT VACCINIA VIRUS HAVING HEMAGGLUTININ **PROTEIN** GENES DERIVED FROM NOVEL INFLUENZA VIRUSES

Abstract: Source: US2013288338A Provided are a highly-safe recombinant vaccinia virus that is effective in preventing the onset of symptoms due to infection by novel influenza viruses, and a vaccine for the novel influenza viruses containing the recombinant vaccinia virus. This recombinant vaccinia virus is capable of expressing the hemagglutinin **protein** genes of the novel influenza virus. This novel influenza vaccine contains the recombinant vaccinia virus.

Classifications:

International (IPC 8-9): A61K31/711 A61K35/76 A61K39/145 A61K48/00 A61P31/16 C12N15/09 C12N15/44 C12N7/01 C12N7/04 (Advanced/Invention)

CPC: A61K2039/5256 A61K2039/545 C12N2710/24143 C12N2760/16134 A61K39/145 A61K31/711 A61K39/12 C07K14/005 C12N2760/16122

European: A61K31/711

US: 435/235.1



13) Family number: 57224005 (US2014234357A)

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Title: H5 **PROTEINS** OF H5N1 INFLUENZA VIRUS FOR USE AS A MEDICAMENT

Abstract: Source: US2014234357A The present invention is based on the surprising finding that H5 **protein** of **clade** 1 H5N1 induces, in particular by a single-shot vaccination, a cross-**clade** protective immune response to influenza viruses with H5N1 HA. In one aspect, the invention is thus directed to H5 **protein** of **clade** 1 H5N1 virus for use in a method of treating or preventing infections with H5N1 virus of a different **clade**, wherein the H5N1 virus of a different **clade** comprises a particular polynucleotide and/or H5 **protein**.

Classifications:

International (IPC 8-9): A61K39/145 C07K14/005 (Advanced/Invention)

CPC: A61K39/145 C07K14/005 A61K2039/5256 A61K2039/55566 C12N2760/16134 A61K39/155 A61K2039/5252 A61K2039/55555 A61K2039/58 A61K2039/70 C12N2760/18134 A61K39/12

US: 424/186.1 530/350

Family:

Publication number	Publication date	Application number	Application date
US2014234357 AA	20140821	US20140184919	20140220
WO14127825 A1	20140828	WO2013EP53505	20130221

Priority:

WO2013EP53505 20130221

Probable Assignee: BOEHRINGER INGELHEIM VETMEDICA GMBH

Assignee(s): (std): BOEHRINGER INGELHEIM VETMED ; MUNDT EGBERT SIEGFRIED

Assignee(s): BOEHRINGER INGELHEIM VETMEDICA GMBH

Inventor(s): (std): MUNDT EGBERT ; MUNDT EGBERT SIEGFRIED

Agent(s): SIMON ELKE ET AL

Designated states: AE AG AL AM AO AT AU AZ BA BB BE BF BG BH BJ BN BR BW BY BZ CA CF CG CH CI CL CM CN CO CR CU CY CZ DE DK DM DO DZ EC EE EG ES FI FR GA GB GD GE GH GM GN GQ GR GT GW HN HR HU ID IE IL IN IS IT JP KE KG KM KN KP KR KZ LA LC LK LR LS LT LU LV LY MA MC MD ME MG MK ML MN MR MT MW MX MY MZ NA NE NG NI NL NO NZ OM PA PE PG PH PL PT QA RO RS RU RW SC SD SE SG SI SK SL SM SN ST SV SY SZ TD TG TH TJ TM TN TR TT TZ UA UG US UZ VC VN ZA ZM ZW

14) Family number: 59636088 (WO15099609A1)

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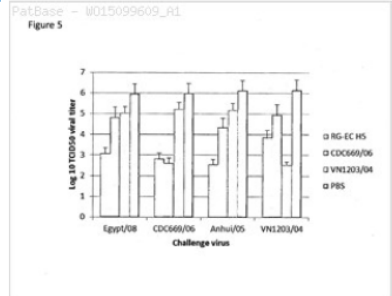
Title: MONOVALENT H5 VACCINE

Abstract: The present invention relates to a monovalent H5N1 vaccine. More specifically, the present invention relates to the development of a monovalent H5 vaccine strain using hemagglutinin (HA) engineering to elicit cross-**clade** protection. The present invention also relates to an epitope-chimeric H5 and to a reverse genetics (RG) influenza virus expressing the epitope-chimeric H5.

Classifications:

International (IPC 8-9): A61K39/145 A61P31/16 C07H21/04 C07K14/11 C12N15/44 C12N7/01 (Advanced/Invention)

CPC: A61K39/145 C07K14/11



Búsqueda de secuencias

SEQ ID NO: 1

hemagglutinin [Influenza A virus (A/Hong Kong/213/2003(H5N1))]

Sequence ID: [dbj|BAE07201.1](#) Length: 568 Number of Matches: 1

[► See 1 more title\(s\)](#)

Range 1: 17 to 568 [GenPept](#) [Graphics](#) [▼](#) Next Match [▲](#) Previous Match

Score	Expect	Identities	Positives	Gaps
1879 bits(4265)	0.0	552/552(100%)	552/552(100%)	0/552(0%)
Query 1	DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDCSVAGW			60
Sbjct 17	DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDCSVAGW			76
Query 61	LLGNPNCDEFINVPWESIYEKANPANDLCYPGDPNDYEELKHLISRINHFEKIQIIPKN			120
Sbjct 77	LLGNPNCDEFINVPWESIYEKANPANDLCYPGDPNDYEELKHLISRINHFEKIQIIPKN			136
Query 121	SWSSHEASLGVSACPYQGSFFRNVMWLKKNNAYPTIKRSYNNNTQEDLLVLWGIHH			180
Sbjct 137	SWSSHEASLGVSACPYQGSFFRNVMWLKKNNAYPTIKRSYNNNTQEDLLVLWGIHH			196
Query 181	PNDAAEQTRLYQNPTTYSVGTSTLNQRLVPKIATRISKVNGQNGRMEFFWTILKPNDAIN			240
Sbjct 197	PNDAAEQTRLYQNPTTYSVGTSTLNQRLVPKIATRISKVNGQNGRMEFFWTILKPNDAIN			256
Query 241	FESNGNFIAPYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSSMPFHNIHPLTIG			300
Sbjct 257	FESNGNFIAPYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSSMPFHNIHPLTIG			316
Query 301	ECPKYVKSRLVLATGLRNSPQRERRRRKGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQ			360
Sbjct 317	ECPKYVKSRLVLATGLRNSPQRERRRRKGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQ			376
Query 361	GSYAADKSTQKIDGVTNKVNSIIDKMNTQFEAVGREFNLERRIENLNKKMEDGFLD			420
Sbjct 377	GSYAADKSTQKIDGVTNKVNSIIDKMNTQFEAVGREFNLERRIENLNKKMEDGFLD			436
Query 421	WVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEYHKCDNECME			480
Sbjct 437	WVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEYHKCDNECME			496
Query 481	SVRNGTYDYPQYSEEARLKREEISGVKLESIGTYQILSIYSTVASSLALAIMVAGLSLWM			540
Sbjct 497	SVRNGTYDYPQYSEEARLKREEISGVKLESIGTYQILSIYSTVASSLALAIMVAGLSLWM			556
Query 541	CNGLSLQCRICI 552			
Sbjct 557	CNGLSLQCRICI 568			

SEQ ID NO: 2

hemagglutinin subtype H5 [Influenza A virus (A/duck/China/E319-2/03(H5N1))]

Sequence ID: [gb|AAR99628.1](#) Length: 567 Number of Matches: 1

Range 1: 17 to 567 [GenPept](#) [Graphics](#) [▼](#) Next Match [▲](#) Previous Match

Score	Expect	Identities	Positives	Gaps
1874 bits(4253)	0.0	551/551(100%)	551/551(100%)	0/551(0%)
Query 1	DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDCSVAGW			60
Sbjct 17	DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDCSVAGW			76
Query 61	LLGNPNCDEFINVPWESIYEKANPANDLCYPGDPNDYEELKHLISRINHFEKIQIIPKS			120
Sbjct 77	LLGNPNCDEFINVPWESIYEKANPANDLCYPGDPNDYEELKHLISRINHFEKIQIIPKS			136
Query 121	SWSDHEASSGVSSACPYQGSFFRNVMWLKKNDAYPTIKRSYNNNTQEDLLVLWGIHH			180
Sbjct 137	SWSDHEASSGVSSACPYQGSFFRNVMWLKKNDAYPTIKRSYNNNTQEDLLVLWGIHH			196
Query 181	PNDAAEQTRLYQNPTTYSVGTSTLNQRLVPKIATRISKVNGQSGRMDFFWTILKPNDAIN			240
Sbjct 197	PNDAAEQTRLYQNPTTYSVGTSTLNQRLVPKIATRISKVNGQSGRMDFFWTILKPNDAIN			256
Query 241	FESNGNFIAPYAYKIVKKGDSAIMKSEVEYGNCTKCQTPMGAINSSMPFHNIHPLTIG			300
Sbjct 257	FESNGNFIAPYAYKIVKKGDSAIMKSEVEYGNCTKCQTPMGAINSSMPFHNIHPLTIG			316
Query 301	ECPKYVKSRLVLATGLRNSPQRERRRRKGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQ			360
Sbjct 317	ECPKYVKSRLVLATGLRNSPQRERRRRKGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQ			376
Query 361	SGYAADKSTQKIDGVTNKVNSIIDKMNTQFEAVGREFNLERRIENLNKKMEDGFLDV			420
Sbjct 377	SGYAADKSTQKIDGVTNKVNSIIDKMNTQFEAVGREFNLERRIENLNKKMEDGFLDV			436
Query 421	WVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEYHKCDNECMES			480
Sbjct 437	WVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEYHKCDNECMES			496
Query 481	VRNGTYDYPQYSEEARLKREEISGVKLESIGTYQILSIYSTVASSLALAIMVAGLSLWMC			540
Sbjct 497	VRNGTYDYPQYSEEARLKREEISGVKLESIGTYQILSIYSTVASSLALAIMVAGLSLWMC			556
Query 541	SNGLSLQCRICI 551			
Sbjct 557	SNGLSLQCRICI 567			

SEQ ID NO: 5

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 4 from patent US 8202967						1929	1929	100%	0.0	100%	AFN93795.1
☐ Sequence 2 from patent US 8202967						1912	1912	100%	0.0	99%	AFN93793.1
☐ Sequence 3 from patent US 8202967						1893	1893	100%	0.0	98%	AFN93794.1
☐ unnamed protein product (synthetic construct)						1892	1892	100%	0.0	98%	CDI30189.1
☐ Sequence 7 from patent US 7981428						1887	1887	100%	0.0	98%	AEL90875.1
☐ Sequence 34 from patent US 8815522						1883	1883	100%	0.0	98%	AJM65712.1
☐ Sequence 24 from patent US 7910112						1883	1883	100%	0.0	98%	AED70851.1
☐ Sequence 112 from patent US 8192927						1882	1882	99%	0.0	98%	AFL38733.1
☐ Sequence 1 from patent US 8900585						1879	1879	100%	0.0	98%	AJN67426.1
☐ Sequence 5 from patent US 7981428						1876	1876	100%	0.0	98%	AEL90874.1

US_7981428_B2_7

Sequence ID: 1cd|Query_163363 Length: 568 Number of Matches: 1

Range 1: 1 to 568						Graphics	Next Match	Previous Match
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1170 bits(3026)	0.0	Compositional matrix adjust.	557/568(98%)	563/568(99%)	0/568(0%)			
Query 1	MEKTVLLLAIVSLVKS	DQICIGYHANNSTEQVDTIMEKNVTVT	HAQDILEKTHNGKLC	DL	60			
Sbjct 1	MEK VLLLAIVSLVKS	DQICIG HANNSTEQVDTIMEKNVTVT	HAQDILEKTHNGKLC	DL	60			
Query 61	DGVKPLILRDCSVAGWLLGNP	MCDEFINVPWESIYVEKANPANDLCY	PGNFNDYEELKHL	120				
Sbjct 61	DGVKPLILRDCSVAGWLLGNP	MCDEFINVPWESIYVEKANPANDLCY	PGNFNDYEELKHL	120				
Query 121	LSRINHFEKIQIIPKNSWSD	HEASSGVSSACPYQGSSSFFRN	VVWLKKNAYPTIKRSY	180				
Sbjct 121	LSRINHFEKIQIIPKNSWSD	HEASSGVSSACPYQG SSFFRN	VVWLKKN+ YPTIKRSY	180				
Query 181	NNINQEDLLVLWGIHHPNDA	AEEQTRLYQNPTTYISVGTSTLN	QRLVPKIATRSKVN	GQNG	240			
Sbjct 181	NNINQEDLLVLWGIHHPNDA	AEEQTRLYQNPTTYISVGTSTLN	QRLVPKIATRSKVN	GQNG+G	240			
Query 241	RMDFFWTILKPNDAINFES	NGNFIAPYAYKIVKKGDS	SAIMKSEVEYGN	CNCKQTPMGA	300			
Sbjct 241	RMDFFWTILKPNDAINFES	NGNFIAPYAYKIVKKGDS	IMKSE+EYGN	CNCKQTPMGA	300			
Query 301	INSSMPFHNIHPLTIGEC	PKYVKS	NKLVLATGLRNSPQ	RERRRRKRG	LFGAIGFIEGGW	360		
Sbjct 301	INSSMPFHNIHPLTIGEC	PKYVKS	NKLVLATGLRNSPQ	RERRRRKRG	LFGAIGFIEGGW	360		
Query 361	QGMVDGWYGYHHSNEQ	SGSYAADKESTQK	AIDGVTNKVNSI	IDKMNTQFE	AVGREFPNNLE	420		
Sbjct 361	QGMVDGWYGYHHSNEQ	SGSYAADKESTQK	AIDGVTNKVNSI	IDKMNTQFE	AVGREFPNNLE	420		
Query 421	RRIENLNKKMEDGFLDV	WTYNAELLVLMENERTL	DFHDSNVKNLYDK	VRLQLRDN	AKELG	480		
Sbjct 421	RRIENLNKKMEDGFLDV	WTYNAELLVLMENERTL	DFHDSNVKNLYDK	VRLQLRDN	AKELG	480		
Query 481	NGCFEFYHKCDNECMES	VRNGTYDYPQYSE	EARLKREEISGV	KLESIGTYQIL	SIYSTVA	540		
Sbjct 481	NGCFEFYHKCDNECMES	VRNGTYDYPQYSE	EARLKREEISGV	KLESIGTYQIL	SIYSTVA	540		
Query 541	SSLALAIMVAGLSLW	MCSNGSLQCRICI	568					
Sbjct 541	SSLALAIMVAGLSLW	MCSNGSLQCRICI	568					

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 7 from patent US 883123	899	899	100%	0.0	100%	AJN51992.1				
☐	Sequence 5 from patent US 8202967	899	899	100%	0.0	100%	AFN93796.1				
☐	Sequence 668 from patent US 8287859	891	891	100%	0.0	99%	AGB59029.1				
☐	Sequence 667 from patent US 8287859	891	891	100%	0.0	99%	AGB59028.1				
☐	Sequence 3 from patent US 8202967	891	891	100%	0.0	99%	AFN93794.1				
☐	Sequence 35 from patent US 8080255	891	891	100%	0.0	99%	AEX16632.1				
☐	Sequence 34 from patent US 8080255	891	891	100%	0.0	99%	AEX16631.1				
☐	Sequence 13 from patent US 7981428	891	891	100%	0.0	99%	AEL90880.1				
☐	Sequence 13 from patent US 7504109	891	891	100%	0.0	99%	ACP82361.1				
☐	Sequence 111 from patent US 8512711	867	867	100%	0.0	97%	AGV94261.1				

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hemagglutinin, partial [Influenza A virus (A/Hong Kong/213/2003(H5N1))]
Sequence ID: [gb|AAT39066.1](#) Length: 531 Number of Matches: 1

Range 1: 1 to 263 [GenPept](#) [Graphics](#) [▼](#) Next Match [▲](#) Previous Match

Score	Expect	Identities	Positives	Gaps
899 bits(2037)	0.0	263/263(100%)	263/263(100%)	0/263(0%)
Query 1	HANNWTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDCSVAGWLLGNPMC	60		
Sbjct 1	HANNWTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDCSVAGWLLGNPMC	60		
Query 61	DEFINVPWSYIVEKANPANDLCYPGDFNDYEELKHLISRINHFEKIQIIPKNSWSHEA	120		
Sbjct 61	DEFINVPWSYIVEKANPANDLCYPGDFNDYEELKHLISRINHFEKIQIIPKNSWSHEA	120		
Query 121	SLGVSSACPYQKSSFFRNVVWLKKNNAIPTIKRSYNNNTQEDLLVLWGIHHPNDAAEQ	180		
Sbjct 121	SLGVSSACPYQKSSFFRNVVWLKKNNAIPTIKRSYNNNTQEDLLVLWGIHHPNDAAEQ	180		
Query 181	TRLQNPTTYSVGTSTLNQRLVPKIATRISKVNGQNGRMEFFWTILKPDAINFESNGNF	240		
Sbjct 181	TRLQNPTTYSVGTSTLNQRLVPKIATRISKVNGQNGRMEFFWTILKPDAINFESNGNF	240		
Query 241	IAPEYAYKIVKKGDSAIMKSELE 263			
Sbjct 241	IAPEYAYKIVKKGDSAIMKSELE 263			

SEQ ID NO: 7

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hemagglutinin subtype H5 [Influenza A virus (A/duck/China/E319-2/03(H5N1))]
Sequence ID: [gb|AAR99628.1](#) Length: 567 Number of Matches: 1

Range 1: 1 to 286 GenPept Graphics

Score	Expect	Identities	Positives	Gaps
970 bits(2199)	0.0	286/286(100%)	286/286(100%)	0/286(0%)
Query 5	MEKTVLLLAIVSLVKSQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDL	64		
Sbjct 1	MEKTVLLLAIVSLVKSQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDL	60		
Query 65	DGVKPLILRDCSVAGWLLGNPMCDEFINVPWSYIVEKANPANDLCYPGNFNDYEELKHL	124		
Sbjct 61	DGVKPLILRDCSVAGWLLGNPMCDEFINVPWSYIVEKANPANDLCYPGNFNDYEELKHL	120		
Query 125	LSRINHFEKIQIIPKSSWSDEASSGVSSACPYQGSSTFFRNVVWLKKNDAIPTIKRSY	184		
Sbjct 121	LSRINHFEKIQIIPKSSWSDEASSGVSSACPYQGSSTFFRNVVWLKKNDAIPTIKRSY	180		
Query 185	NNTNQEDLLVLWGIHHPNDAAEQTRLQNPTTYSVGTSTLNQRLVPKIATRISKVNGQSG	244		
Sbjct 181	NNTNQEDLLVLWGIHHPNDAAEQTRLQNPTTYSVGTSTLNQRLVPKIATRISKVNGQSG	240		
Query 245	RMDFFWTILKPDAINFESNGNFIAPAYKIVKKGDSAIMKSEVE 290			
Sbjct 241	RMDFFWTILKPDAINFESNGNFIAPAYKIVKKGDSAIMKSEVE 286			

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 6 from patent US 8202967		981	981	100%	0.0	100%	AFN93797.1
☐ Sequence 2 from patent US 8202967		970	970	98%	0.0	100%	AFN93793.1
☐ Sequence 4 from patent US 8202967		962	962	98%	0.0	99%	AFN93795.1
☐ unnamed protein product [synthetic construct]		950	950	98%	0.0	98%	CDI30189.1
☐ Sequence 114 from patent US 8192927		947	947	98%	0.0	98%	AFL38735.1
☐ Sequence 112 from patent US 8192927		947	947	98%	0.0	98%	AFL38733.1
☐ Sequence 18 from patent US 7981428		946	946	96%	0.0	100%	AEL90885.1
☐ Sequence 44 from patent US 8658354		942	942	98%	0.0	97%	AHL65190.1
☐ Sequence 24 from patent US 7910112		940	940	98%	0.0	98%	AED70851.1
☐ unnamed protein product [synthetic construct]		940	940	98%	0.0	98%	CBX55726.1

SEQ ID NO: 8

hemagglutinin [Influenza A virus (A/chicken/Egypt/07202-NLQP/2007(H5N1))]

Sequence ID: [gb|ACA29672.1](#) Length: 568 Number of Matches: 1

[See 7 more title\(s\)](#)

Range 1: 1 to 562 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Positives	Gaps	
1904 bits(4322)	0.0	562/562(100%)	562/562(100%)	0/562(0%)	
Query 1	MEKIVLLLAIVSLVKS	DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLC	DL	60	
Sbjct 1	MEKIVLLLAIVSLVKS	DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLC	DL	60	
Query 61	DGVKPLILRDCSVAG	LLGNPMCDFLNVSEWSYIVEKINPANDLCYPGNFN	NYEELKHL	120	
Sbjct 61	DGVKPLILRDCSVAG	LLGNPMCDFLNVSEWSYIVEKINPANDLCYPGNFN	NYEELKHL	120	
Query 121	LSRINRFEDIQIIPK	SSWPDHEASSGVSSACPYQGGPSFYRNVVWL	IKKDNAYPTIKKSY	180	
Sbjct 121	LSRINRFEDIQIIPK	SSWPDHEASSGVSSACPYQGGPSFYRNVVWL	IKKDNAYPTIKKSY	180	
Query 181	HNTNQEDLLVLWGI	HHPNDEAEQTRLYQNPTTYSVGTSTLNQRLVPKIATRSK	VNGQSG	240	
Sbjct 181	HNTNQEDLLVLWGI	HHPNDEAEQTRLYQNPTTYSVGTSTLNQRLVPKIATRSK	VNGQSG	240	
Query 241	RVEFFWTILKSNDA	INFESNGFIAPENAYKIVKKGDSIMKSELEYGNCNTK	KCQTPIGA	300	
Sbjct 241	RVEFFWTILKSNDA	INFESNGFIAPENAYKIVKKGDSIMKSELEYGNCNTK	KCQTPIGA	300	
Query 301	INSSMPFHHIHPLT	IGCEPKYVKS	NRLVLATGLRNSPQGERRRKRGLGAIAGFIEGGW	360	
Sbjct 301	INSSMPFHHIHPLT	IGCEPKYVKS	NRLVLATGLRNSPQGERRRKRGLGAIAGFIEGGW	360	
Query 361	QGMVDGWYGYHHS	NEQSGGYAADKESTQKALDGVTNKVNSIIDKMNTQ	FEAVGREFN	420	
Sbjct 361	QGMVDGWYGYHHS	NEQSGGYAADKESTQKALDGVTNKVNSIIDKMNTQ	FEAVGREFN	420	
Query 421	RRIENLNKMKMED	GFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQ	LRD	NAKELG	480
Sbjct 421	RRIENLNKMKMED	GFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQ	LRD	NAKELG	480
Query 481	NGCFEFYHRCDNE	CMSVRNGTYDYPQYSEEARLKREEISGVKLESIGTYQILSI	YSTVA	540	
Sbjct 481	NGCFEFYHRCDNE	CMSVRNGTYDYPQYSEEARLKREEISGVKLESIGTYQILSI	YSTVA	540	
Query 541	SSLALAIMVAGLFL	WMCSNGSL	562		
Sbjct 541	SSLALAIMVAGLFL	WMCSNGSL	562		

SEQ ID NO: 9

SEQ ID NO: 53 de US2007184526

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 99 from patent US 8512711		1875	1875	100%	0.0	98%	AGV94249.1
☐ Sequence 8 from patent US 8394384		1871	1871	100%	0.0	98%	AGM89008.1
☐ Sequence 116 from patent US 8512711		1865	1865	100%	0.0	97%	AGV94286.1
☐ Sequence 4 from patent US 8086887		1865	1865	100%	0.0	97%	AKK41327.1
☐ Sequence 48 from patent US 8658354		1864	1864	100%	0.0	97%	AHL65192.1
☐ Sequence 118 from patent US 8512711		1860	1860	100%	0.0	97%	AGV94288.1
☐ Sequence 6 from patent US 8794819		1850	1850	100%	0.0	96%	AJM35741.1
☐ Sequence 53 from patent US 8080255		1847	1847	100%	0.0	97%	AEX16638.1
☐ Sequence 17 from patent US 8871220		1846	1846	100%	0.0	97%	AJM42919.1
☐ Sequence 40 from patent US 8815622		1842	1842	99%	0.0	97%	AJM85718.1

Query: SEQ ID NO: 9 de la solicitud
Sbjct: SEQ ID NO: 53 de US2007184526

US20070184526A1 53

Sequence ID: lc|Query_164903 Length: 564 Number of Matches: 1

Range 1: 1 to 564 Graphic					Next Match	Previous Match
Score	Expect	Method	Identities	Positives	Gaps	
1139 bits(2945)	0.0	Compositional matrix adjust.	549/568(97%)	555/568(97%)	5/568(0%)	
Query 1	MEKIMLLLAIVSLVKSQD	ICIGYHANNSTEQVD	TIMEKNVTVTHAQD	ILEKTHNGKLCNL	60	
Sbjct 1	MEKI+LLLAIVSLVKSQD	ICIGYHANNSTEQVD	TIMEKNVTVTHAQD	ILEKTHNGKLC+L	60	
Query 61	DGVKPLILRDCSVAGWLLGNPMCDEF	LNVPWSYIVEKINPANDLCYPG	KFN	DYEEKHL	120	
Sbjct 61	DGVKPLILRDCSVAGWLLGNPMCDEF	LNVPWSYIVEKINPANDLCYPG	FNDYEEKHL		120	
Query 121	LSRINHFKEKIIIPRNSWSDHE	-TSGVSSACQYQGRSSFFRN	VVWLTKKD	NAYSTIKRSY	179	
Sbjct 121	LSRINHFKEKIIIP++SWSDHE	+SGVSSAC YQGRSSFFRN	VVWL KK+NAY	TIKRSY	180	
Query 180	NNTNQEDLLVLWGIHHPNDAAEQ	TRLYQNPTTYISVGTSTLNQRL	VPKIATRSKVN	QSG	239	
Sbjct 181	NNTNQEDLLVLWGIHHPNDAAEQ	TRLYQNPTTYISVGTSTLNQRL	VPKIATRSKVN	QSG	240	
Query 240	RMEFFWTILKSNDAINFESNGNFI	APENAYKIVKKGDS	IMKSELYGNCN	TKCQTPIGA	299	
Sbjct 241	RMEFFWTILKPNDAINFESNGNFI	APENAYKIVKKGDS	IMKSELYGNCN	TKCQTPIGA	300	
Query 300	INSSMPFHNHPLTIGECPKYVKS	NRLVLATGLRNSPQE	ERRRKRGLFGA	IGFEGGW	359	
Sbjct 301	INSSMPFHNHPLTIGECPKYVKS	NRLVLATGLRNSPQIE----	TRGLFGA	IGFEGGW	356	
Query 360	QGMVDGWGYHHSNEQSGYAADKE	STQKAIDGVTNKVNSIIDKMNTQ	FEAVGREFN	NLE	419	
Sbjct 357	QGMVDGWGYHHSNEQSGYAADKE	STQKAIDGVTNKVNSIIDKMNTQ	FEAVGREFN	NLE	416	
Query 420	RRRIENLNKMKEDGFLDVWTYNAE	LLVLMENERTLDFHDSNVKNLYD	KVRLQLRDN	AKELG	479	
Sbjct 417	RRRIENLNKMKEDGFLDVWTYNAE	LLVLMENERTLDFHDSNVKNLYD	KVRLQLRDN	AKELG	476	
Query 480	NGCFEFYHRCDCNECMESVRNGTY	DYPOYSEEARLKREEISGVKLES	IGTYQILSIYSTVA		539	
Sbjct 477	NGCFEFYHRCDCNECMESVRNGTY	DYPOYSEEARLKREEISGVKLES	IGTYQILSIYSTVA		536	
Query 540	SSLALAIMVAGLFLWMC	SNGSLQCRICI	567			
Sbjct 537	SSLALAIMVAGLSLWMC	SNGSLQCRICI	564			

Query: SEQ ID NO: 15 de la solicitud
Sbjct: SEQ ID NO: 34 de US2007184526

US_2007_0184526_A1_34

Sequence ID: lc|Query_111719 Length: 572 Number of Matches: 1

Range 1: 15 to 553		Graphics				Next Match	Previous Match
Score	Expect	Method	Identities	Positives	Gaps		
1080 bits(2793)	0.0	Compositional matrix adjust.	517/539(96%)	526/539(97%)	1/539(0%)		
Query 3	VSIVKSQD	ICIGYHANNSTEQVD	TIMEKNVTVTHAQD	ILEKTHNGKLCNL	DGVKPLILRD	62	
Sbjct 15	VS DQICIGYHANNSTEQVD	TIMEKNVTVTHAQD	ILEKTHNGKLC+LDGVKPLILRD	74			
Query 63	CSVAGWLLGNPMCDEF	LNVPWSYIVEKINPNDLCYPG	FNDYEEKHL	SRINHFKEI	122		
Sbjct 75	CSVAGWLLGNPMCDEF	LNVPWSYIVEKANPANDLCYPG	FNDYEEKHL	SRINHFKEI	134		
Query 123	QIIPKNSWSDHEAS	-GVSSACPYQGRSSFFRN	VVWLTKKNNAYPTIKSYNNT	NQEDLLV	181		
Sbjct 135	QIIPKNSWS HEAS	GVSSACPYQG+SSFFRN	VVWL KNNAYPTIK+SYNNT	NQEDLLV	194		
Query 182	LWGIHHPNDAAEQ	TRLYQNPTTYISVGTSTLNQRL	VPKIATRSKVN	QSGRMEFFWTILK	241		
Sbjct 195	LWGIHHPNDAAEQ	TRLYQNPTTYISVGTSTLNQRL	VPKIATRSKVN	QSGRMEFFWTILK	254		
Query 242	SNDAINFESNGNFI	APENAYKIVKKGDS	IMKSELYGNCN	TKCQTPIGAIN	SSMPFHN	301	
Sbjct 255	PNDAINFESNGNFI	APAYAYKIVKKGDS	AIMKSELYGNCN	TKCQTPMGA	INSSMPFHN	314	
Query 302	HPLTIGECPKYVKS	NRLVLATGLRNSPQGERRR	KRGLFGA	IGFEGGW	QGMVDGWYGY	361	
Sbjct 315	HPLTIGECPKYVKS	NRLVLATGLRNSPQERRRR	KRGLFGA	IGFEGGW	QGMVDGWYGY	374	
Query 362	HHSNEQSGYAADKE	STQKAIDGVTNKVNSIIDKMNTQ	FEAVGREFN	LNERRIENLN	NKMK	421	
Sbjct 375	HHSNEQSGYAADKE	STQKAIDGVTNKVNSIIDKMNTQ	FEAVGREFN	LNERRIENLN	NKMK	434	
Query 422	EDGFLDVWTYNAE	LLVLMENERTLDFHDSNVKNLYD	KVRLQLRDN	AKELGNGCFE	FYHRC	481	
Sbjct 435	EDGFLDVWTYNAE	LLVLMENERTLDFHDSNVKNLYD	KVRLQLRDN	AKELGNGCFE	FYHRC	494	
Query 482	DNECMESVRNGTY	DYPOYSEEARLKREEISGVKLES	IGTYQILSI	YSTVASS	LALAIMV	540	
Sbjct 495	DNECMESVRNGTY	DYPOYSEEARLKREEISGVKLES	IGTYQILSI	YSTVASS	LALAIMV	553	

Sequences producing significant alignments:

Select: All None Selected:0

Alignments  GenPept  Distance tree of results 								
		Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 99 from patent US 8512711		1107	1107	99%	0.0	98%	AGV94249.1
☐	Sequence 8 from patent US 8394384		1106	1106	99%	0.0	98%	AGM89008.1
☐	Sequence 48 from patent US 8658354		1106	1106	99%	0.0	98%	AHL65192.1
☐	Sequence 4 from patent US 8986987		1105	1105	99%	0.0	98%	AKX41327.1
☐	Sequence 116 from patent US 8512711		1104	1104	99%	0.0	98%	AGV94266.1
☐	Sequence 24 from patent US 8784819		1102	1102	99%	0.0	98%	AJM35759.1
☐	Sequence 118 from patent US 8512711		1102	1102	99%	0.0	98%	AGV94268.1
☐	Sequence 6 from patent US 8784819		1095	1095	99%	0.0	97%	AJM35741.1
☐	Sequence 40 from patent US 8815522		1093	1093	99%	0.0	98%	AJM65718.1
☐	Sequence 17 from patent US 7981428		1091	1091	97%	0.0	98%	AEL90884.1
☐	Sequence 3 from patent US 8202967		1091	1091	99%	0.0	96%	AFN93794.1
☐	Sequence 112 from patent US 8192927		1091	1091	99%	0.0	96%	AFL38733.1
☐	Sequence 7 from patent US 7981428		1091	1091	99%	0.0	96%	AEL90875.1