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Lampiran 2

FORMULIR PENJELASAN SEBELUM PERSETUJUAN

Saya, dr Sri Lestari KS, Sp.KK(K), FAADV, FINSDV, Staf Medik Fungsional Bagian Ilmu Kesehatan Kulit dan Kelamin RSUP DR. M. Djamil Padang, dengan ini meminta kesediaan anda untuk berpartisipasi dengan sukarela dalam penelitian yang berjudul: **“Hubungan Alel HLA-Cw6 dan Alel HLA-Cw7 dengan Psoriasis Vulgaris Melalui Kadar IL-23”**.

1. Tujuan dari penelitian ini adalah membuktikan adanya pengaruh genetik dan imunologis seseorang terhadap penyakit psoriasis vulgaris.
2. Manfaat penelitian ini adalah agar dapat diketahui faktor-faktor yang berperan dalam terjadinya psoriasis vulgaris
3. Lembaran ini berisi informasi tentang penelitian tersebut di atas yang akan dilakukan terhadap Bapak/ Ibu. Sebelum Bapak/ Ibu menyetujui untuk ikut serta pada penelitian ini, terdapat beberapa hal yang akan dijelaskan dan diharapkan Bapak/ Ibu memahami semua informasi yang terkait dengan penelitian ini. Bila ada sesuatu yang tidak dipahami atau bila Bapak/ Ibu memerlukan informasi tambahan baik sebelum dan sesudah penelitian berlangsung, dapat segera meminta penjelasan lebih lanjut kepada dokter peneliti.

Latar Belakang Penelitian

Psoriasis vulgaris adalah suatu penyakit kulit autoimun dengan peradangan kronik, yang dimediasi oleh sel T. Etiologinya tidak diketahui serta penyakit yang menghasilkan bercak merah menebal ditutupi sisik tebal berwarna

keperakan yang secara kosmetik mengganggu pasien sehingga terjadi penurunan kualitas hidup seseorang dan secara umum mempengaruhi sistem kesehatan dan sosial. Psoriasis vulgaris merupakan penyakit kulit yang menimbulkan masalah yang besar dalam bidang kesehatan karena penyakit ini bersifat kronik dan residif, dapat mengganggu aktivitas kehidupan sehari-hari yang mengakibatkan angka kesakitan yang tinggi.

Adanya faktor genetik terutama HLA-Cw6 atau HLA-Cw7 sebagai predisposisi dan faktor pencetus yang berperan pada psoriasis vulgaris. Selain itu juga terdapat peningkatan kadar IL-23 pada pasien psoriasis vulgaris.

Sampai sekarang pengobatan penyakit ini masih menjadi masalah karena belum ada obat yang betul-betul efektif menyembuhkan penyakit ini. Hal ini disebabkan karena belum terungkap secara tuntas semua faktor yang terlibat dan berperan pada etiopatogenesis penyakit ini.

Berdasarkan latar belakang dimana faktor genetik yang berperan pada psoriasis vulgaris terutama alel HLA-Cw6, juga alel HLA-Cw7, melalui sitokin IL-23 serta adanya perbedaan faktor etnik dan geografikal, dan makin meningkatnya jumlah kasus psoriasis vulgaris, maka peneliti tertarik untuk melakukan penelitian ini.

Tujuan penelitian:

1. Menganalisis perbedaan alel HLA-Cw6 yang terdapat pada psoriasis vulgaris dengan non-psoriasis vulgaris.
2. Menganalisis perbedaan alel HLA-Cw7 yang terdapat pada psoriasis vulgaris dengan non-psoriasis vulgaris.

3. Menganalisis perbedaan kadar IL-23 antara psoriasis vulgaris dengan non-psoriasis vulgaris.
4. Menganalisis hubungan antara alel HLA-Cw6 dengan kadar IL-23 pada psoriasis vulgaris.
5. Menganalisis hubungan antara alel HLA-Cw7 dengan kadar IL-23 pada psoriasis vulgaris.
6. Menganalisis alel yang paling berhubungan dalam menimbulkan lesi psoriasis vulgaris melalui kadar IL-23.

Apa risiko dan efek samping yang tidak diharapkan selama penelitian?

Keikutsertaan Bapak/ Ibu dalam penelitian ini **tidak mempunyai risiko atau efek samping yang merugikan**. Komplikasi yang mungkin muncul pada Bapak/ Ibu (subyek penelitian) adalah berhubungan dengan pengambilan darah vena sebanyak 5cc (satu sendok teh) pada lengan oleh peneliti yaitu adanya rasa nyeri pada tempat suntikan namun bersifat ringan dan akan hilang dalam beberapa menit. Adapun untuk kemungkinan terjadinya infeksi sangat kecil karena dikerjakan dengan prosedur aseptik. Apabila terjadi infeksi pada tempat suntikan, maka peneliti akan memberikan pengobatan.

Kondisi keikutsertaan

Partisipasi Bapak/ Ibu dalam memberikan untuk ikut serta dalam penelitian ini sepenuhnya bersifat sukarela dan bebas memutuskan untuk ikut atau tidak, serta dapat mengundurkan diri kapan saja. Jika Bapak/ Ibu menolak berpartisipasi, hal ini tidak akan mengganggu hubungan Bapak/ Ibu dengan dokter yang meneliti dan tetap dilayani dan mendapat pengobatan sebagaimana mestinya.

Kerahasiaan medis dan catatan penelitian

Semua data pribadi dan hasil pemeriksaan Bapak/ Ibu akan dijaga kerahasiannya. Informasi penelitian ini akan disimpan oleh peneliti dan diperlakukan sebagai data rekam medis yang dijaga kerahasiannya. Bapak/ Ibu setuju bahwa data-data tersebut dapat diperiksa oleh mereka yang terkait dalam penelitian ini dengan sepengetahuan peneliti.

Siapa yang harus dihubungi selama penelitian?

Apabila Bapak/ Ibu/ Saudara/i mengalami keraguan setelah dilakukan pemeriksaan di atas, Bapak/ Ibu/ Saudara/i dapat menghubungi:

- Nama : dr. Sri Lestari K.S. Sp.KK(K), FAADV, FINSDV
- Alamat kantor : Bagian Ilmu Kesehatan Kulit dan Kelamin RSUP
DR. M. Djamil Padang
- No. HP : 08126603159
- Telp. kantor : (0751) 810256



Lampiran 3: Lembaran Informasi Pasien

Terimakasih kepada Bapak/Ibu yang telah bersedia turut serta mengikuti peneli ini secara sukarela, ini berarti Bapak/ Ibu berhak untuk menolak menjadi subjek penelitian. Lembaran informasi ini berisi tentang penjelasan prosedur pelaksanaan selama penelitian berlangsung, yaitu mengenai wawancara kepada Bapak/ Ibu, pemeriksaan fisik dan pemeriksaan laboratorium yang akan dilakukan. Bila ada hal yang belum jelas, dokter yang bertanggung jawab terhadap penelitian ini akan memberikan penjelasan lengkap, jelas dan benar sesuai yang Bapak/ Ibu minta. Setelah itu anda diharapkan dapat menandatangani formulir persetujuan yang menyatakan anda mengikuti studi ini secara sukarela.



Terimakasih
Peneliti

dr. Sri Lestari, Sp.KK(K), FAADV, FINSDV

Lampiran 4. Formulir Pernyataan Persetujuan Berpartisipasi Dalam Penelitian

Judul penelitian :

HUBUNGAN ALEL HLA-Cw6 DAN ALEL HLA-Cw7 DENGAN PSORIASIS VULGARIS MELALUI KADAR IL-23.

Tujuan penelitian ini untuk membuktikan bahwa terdapat hubungan antara alel HLA-Cw6 dan alel HLA-Cw7 dengan psoriasis vulgaris berdasarkan kadar IL-23.

Peneliti adalah seorang dokter spesialis kulit dan kelamin yang juga peserta program paska sarjana S3 Biomedik Fakultas Kedokteran Universitas Andalas.

Nama : Dr Sri Lestari kuncorowati Setyaningsih SpKK(K).

NIM : 06301052

Pelaksanaan penelitian ini di bawah bimbingan dan pengawasan:

1. Prof. DR. dr. Eryati Darwin, PA(K)
2. DR. dr. Tjut Nurul Alam Jacoeb, SpKK(K), FAADV, FINSDV
3. DR. Djong Hon Tjong, Msi

Penjelasan singkat tentang penelitian, kami ingin mengetahui apakah pemeriksaan alel HLA-Cw6, alel HLA-Cw7 dan kadar IL-23 memang benar-benar berhubungan dengan pasien psoriasis vulgaris.

Kesediaan ibu/ bapak/ saudara dalam penelitian ini sangat membantu upaya kami dalam meningkatkan ilmu pengetahuan tentang psoriasis vulgaris. Jika ibu/ bapak/ saudara tidak bersedia ikut dalam penelitian ini, tidak akan mengurangi mutu pelayanan yang akan diberikan.

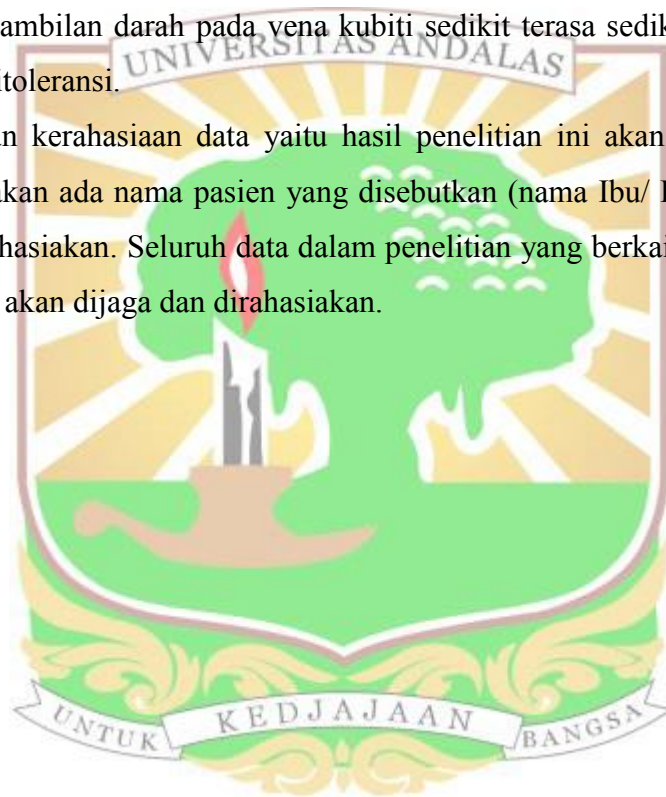
Tempat penelitian yaitu:

1. Di Poliklinik Ilmu Kesehatan Kulit dan Kelamin RSUP DR. M. Djamil Padang untuk pemeriksaan klinis dan *informed consent*.

2. Pengambilan darah pasien dari vena kubiti sebanyak 5 ml untuk pemeriksaan alel HLA-Cw6 dan alel HLA-Cw7 menggunakan *kit isolasi DNA GF-1 Blood DNA merek Vivantis (No. Katalog GF-BD-050 dan GF-BD-100)*, menggunakan metoda *polymerase chain reaction* dan pemeriksaan kadar IL-23 dengan ELISA.

Keuntungan penelitian ini bagi ibu/ bapak/ saudara yaitu hasil penelitian ini dapat digunakan untuk mengetahui apakah terdapat hubungan alel HLA-Cw6 dan alel HLA-Cw7 dengan psoriasis vulgaris melalui kadar IL-23. Risiko jika mengikuti penelitian ini, akan menyita waktu sedikit untuk wawancara dan saat tindakan pengambilan darah pada vena kubiti sedikit terasa sedikit nyeri, namun masih dapat ditoleransi.

Jaminan kerahasiaan data yaitu hasil penelitian ini akan dipublikasikan, namun tidak akan ada nama pasien yang disebutkan (nama Ibu/ Bapak/ Saudara) atau akan dirahasiakan. Seluruh data dalam penelitian yang berkaitan dengan data pribadi pasien akan dijaga dan dirahasiakan.



Lampiran 5: Informed Consent**FORMULIR PERSETUJUAN***(Informed Consent)*

PROGRAM STUDI S3 BIOMEDIK FAKULTAS KEDOKTERAN UNIVERSITAS ANDALAS	
SURAT PERSETUJUAN UJI KLINIK	
Saya yang bertanda tangan di bawah ini	
Nama	dr. Sri Lestari Kuncorowati Setyaningsih, SpKK(K)
Umur	58 tahun
Jenis Kelamin	1. Pria 2. Wanita (v)
Alamat Lengkap	Jl. Air Sirih no. 14 Padang 25128
Setelah mendapat keterangan secukupnya dan mengerti manfaat penelitian tersebut di bawah ini, yang berjudul	
HUBUNGAN ALEL HLA-Cw6 DAN ALEL HLA-Cw7 DENGAN PSORIASIS VULGARIS MELALUI KADAR IL-23.	

Dengan sukarela menyetujui diikutsertakan dalam penelitian di atas, dengan catatan bila sewaktu-waktu merasa dirugikan dalam bentuk apapun, saya berhak mengundurkan diri dari persetujuan ini.

Mengetahui
Penanggung jawab penelitian,

Padang, Juli 2016
Subjek penelitian,

dr. Sri Lestari K.S, Sp.KK(K), FAADV, FINS DV

(.....)





Lampiran 7. Rekam Medik

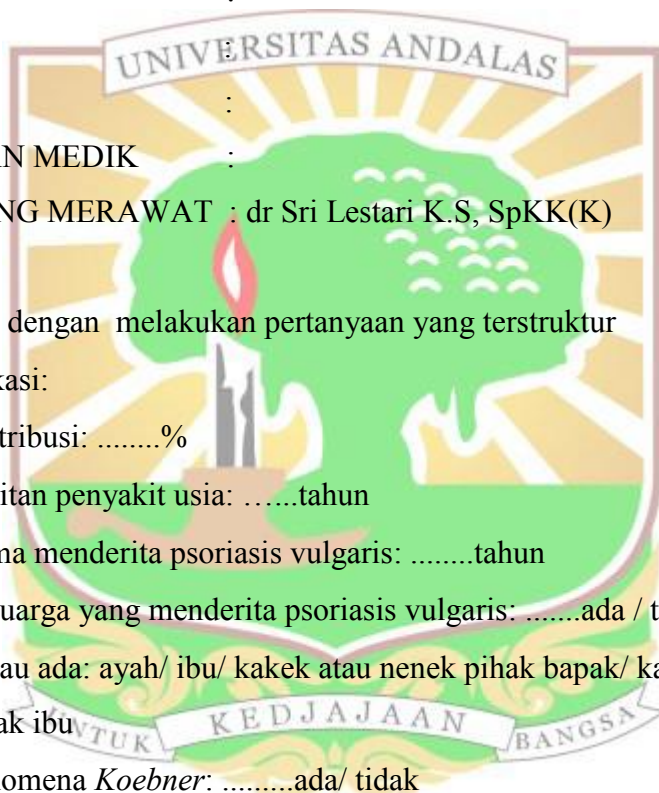
REKAM MEDIK

JATI DIRI PASIEN

NAMA :
 UMUR :
 JENIS KELAMIN :
 ALAMAT :
 TELEPON :
 PEKERJAAN :
 NO REKAMAN MEDIK :
 DOKTER YANG MERAawat : dr Sri Lestari K.S, SpKK(K)

Anamnesis dengan melakukan pertanyaan yang terstruktur

- Lokasi:
- Distribusi:%
- Awitan penyakit usia:tahun
- Lama menderita psoriasis vulgaris:tahun
- Keluarga yang menderita psoriasis vulgaris:ada / tidak
- Kalau ada: ayah/ ibu/ kakek atau nenek pihak bapak/ kakek atau nenek pihak ibu
- Fenomena *Koebner*:ada/ tidak
- Kelainan kuku:ada/ tidak
- Psoriasis artritis:ada/ tidak
- Perubahan klinis yang terjadi selama: infeksi/ stres/ pemakaian obat-obatan sistemik atau topikal/ trauma/ hormonal/ paparan ultra violet/ minum alkohol/ merokok



Pemeriksaan fisik : Lokasi:

Distribusi:%

Efloresensi: plak eritema, papul-papul eritema, pustul, skuama
tebal

skor PASI :

Skoring beratnya penyakit: Ringan / sedang / berat / sangat berat

Kelainan kuku tangan: *pitting* / onikolisis / hiperkeratosis subungual / distrofi
kuku

Diagnosis: Psoriasis vulgaris derajat ringan / sedang/ berat

Pemeriksaan laboratorium :

Pemeriksaan alel HLA-Cw6 dengan PCR-RT: terdeteksi/tidak terdeteksi

Pemeriksaan alel HLA-Cw7 dengan PCR-RT: terdeteksi/tidak terdeteksi

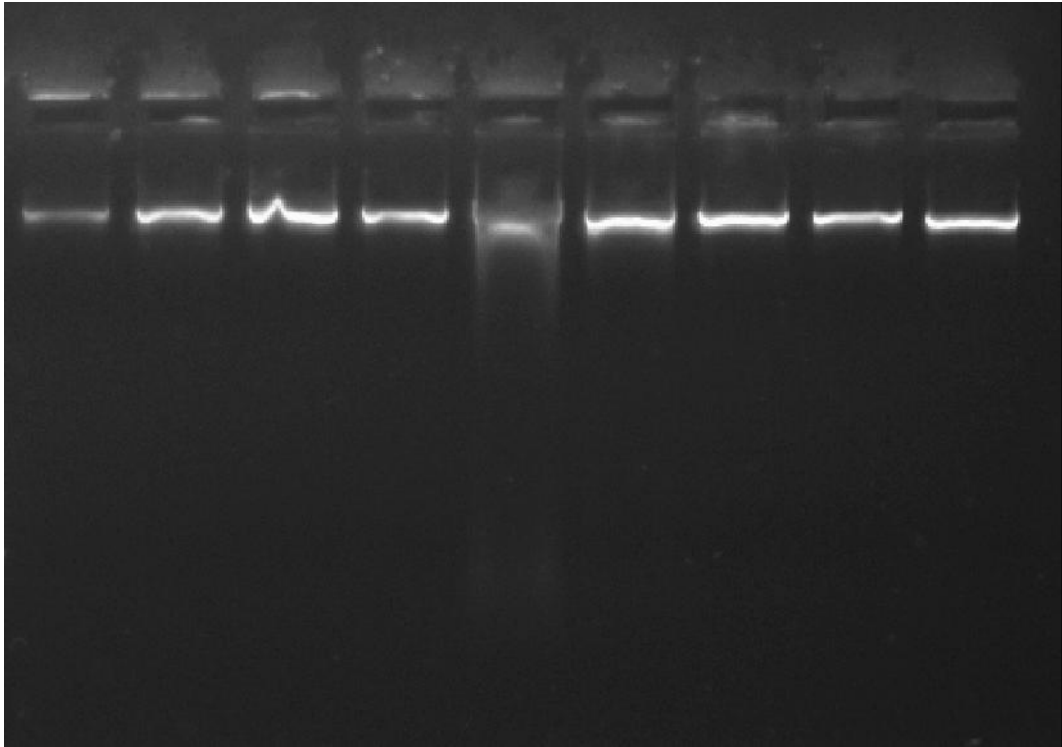
Pemeriksaan kadar IL-23 dengan ELISA:.....pg/ml



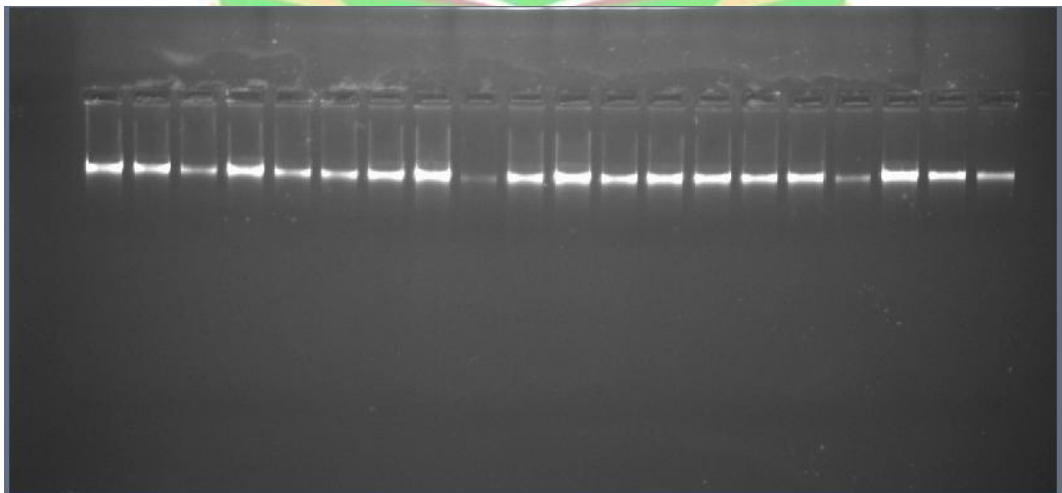
Lampiran 8

Metode Kerja Dan Hasil Genotyping HLA-C

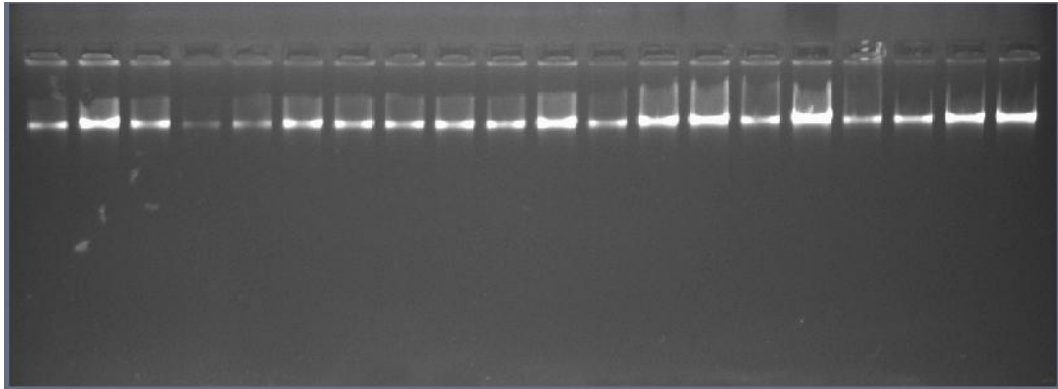
Elektroforegram Hasil Isolasi DNA



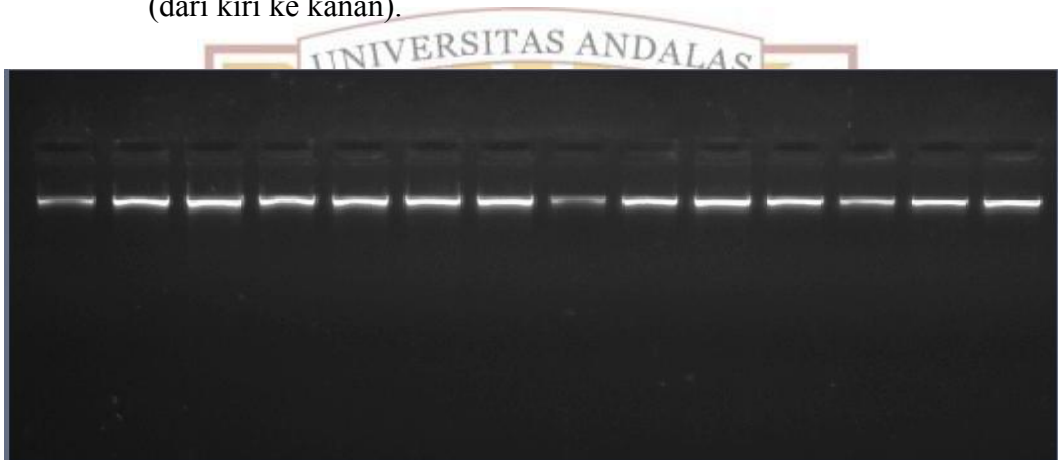
Gambar 1. Hasil isolasi DNA sampel SL1-SL9 (dari kiri ke kanan).



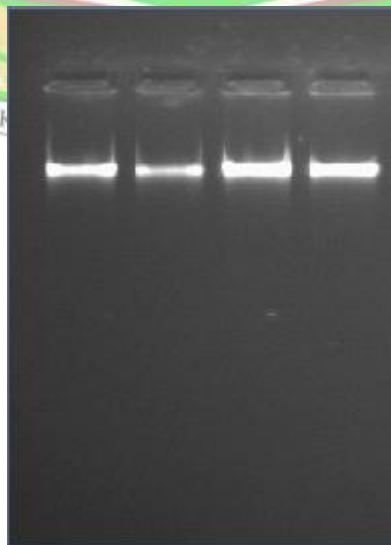
Gambar 2. Hasil isolasi DNA sampel SL18-SL27 dan SLK8-SLK18 (dari kiri ke kanan). SLK14 (-).



Gambar 3. Hasil isolasi DNA sampel SL28-SL34-SLMia dan SLK19-SLK30 (dari kiri ke kanan).

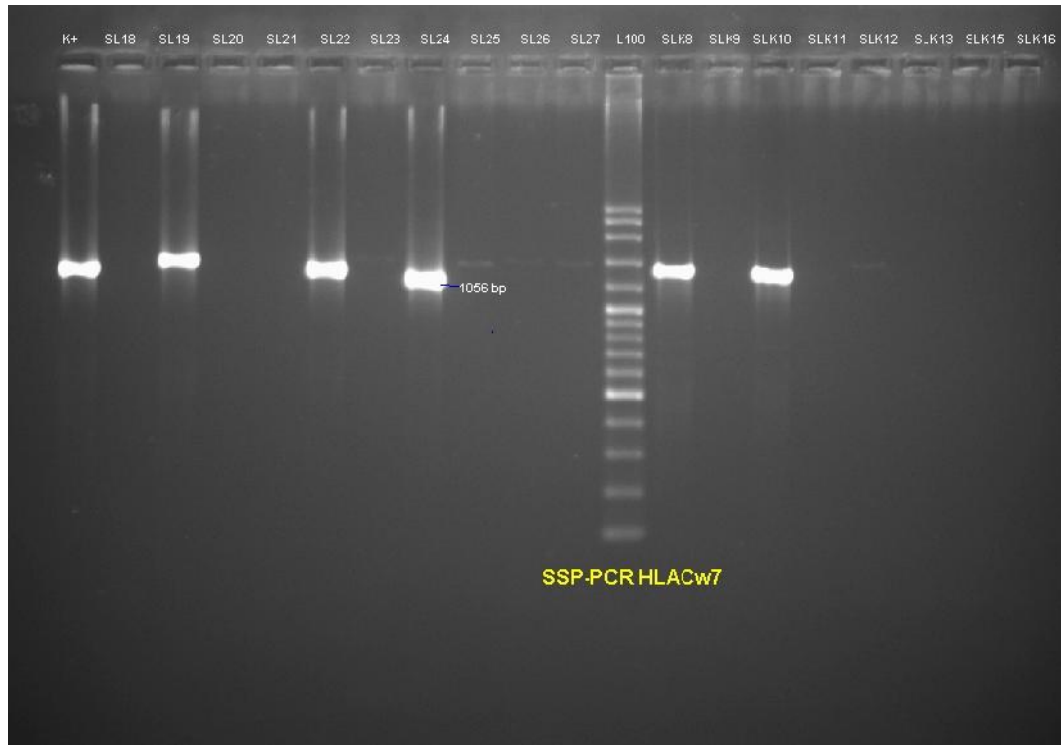


Gambar 4. Hasil isolasi DNA sampel SLK1-SLK7 dan SL11-SL17 (dari kiri ke kanan).



Gambar 5. Hasil isolasi DNA sampel SLK31-32-33-27 (dari kiri ke kanan).

Elektroforegram Hasil PCR HLA-Cw7



Gambar 6. PCR HLA-Cw7.



Gambar 7. PCR HLA-Cw7.

Elektroforegram Hasil SSP-PCR HLA-Cw6



Gambar 8. PCR HLA-Cw6 .



Gambar 9. PCR HLA-Cw6.



Gambar 10. PCR HLA-Cw6.



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Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1292, allele HLA-C*07:new
 Sequence ID: [emb|LT599362.1](#) Length: 3354 Number of Matches: 1

Range 1: 1121 to 2054 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1718 bits(930)	0.0	933/934(99%)	1/934(0%)	Plus/Plus
Query 1	TGCGCTCCTGGACCGCCGCGGACACCGCGGCTCA-ATCACCCAGCGCAAGTTGGAGGCGG			59
Sbjct 1121	TGCGCTCCTGGACCGCCGCGGACACCGCGGCTCAGATCACCCAGCGCAAGTTGGAGGCGG			1180
Query 60	CCCGTGCGGCGGAGCAGCTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCA			119
Sbjct 1181	CCCGTGCGGCGGAGCAGCTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCA			1240
Query 120	GATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCAGGTACCAGGGGCAGTGGGGAGC			179
Sbjct 1241	GATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCAGGTACCAGGGGCAGTGGGGAGC			1300
Query 180	CTTCCCATCTCCTATAGATCTCCCGGGATGGCCTCCACGAGGAGGGGAGGAAAATGGG			239
Sbjct 1301	CTTCCCATCTCCTATAGATCTCCCGGGATGGCCTCCACGAGGAGGGGAGGAAAATGGG			1360
Query 240	ATCAGCACTGGAATATCGCCCTCCCTTGAATGGAGAATGGCATGAGTTTCTGAGTTTC			299
Sbjct 1361	ATCAGCACTGGAATATCGCCCTCCCTTGAATGGAGAATGGCATGAGTTTCTGAGTTTC			1420
Query 300	CTCTGAGGGCCCCCTCTGCTCTCTAGGACAATTAAGGGATGAAGTCTCTGAGGAAATGGA			359
Sbjct 1421	CTCTGAGGGCCCCCTCTGCTCTCTAGGACAATTAAGGGATGAAGTCTCTGAGGAAATGGA			1480
Query 360	GGGGAAGACAGTCCCTGGAATACTGATCAGGGGTCTCCTTTGACCACTTTGACCACTGCA			419
Sbjct 1481	GGGGAAGACAGTCCCTGGAATACTGATCAGGGGTCTCCTTTGACCACTTTGACCACTGCA			1540
Query 420	GCAGCTGTGTCAGGCTGCTGACCTTTCTCTCAGGCCTTGTTCTCTGCCTCACACTCAAT			479
Sbjct 1541	GCAGCTGTGTCAGGCTGCTGACCTTTCTCTCAGGCCTTGTTCTCTGCCTCACACTCAAT			1600
Query 480	GTGTCTGAAGTTTGATCCAGCTTTTCTGAGTCTGACGCTCCACTCAGGTGAGGACC			539
Sbjct 1601	GTGTCTGAAGTTTGATCCAGCTTTTCTGAGTCTGACGCTCCACTCAGGTGAGGACC			1660
Query 540	AGAAGTCGCTGTTCCTCCCTCAGAGACTAGAACTTTCCAATGAATAGGAGATTATCCCAG			599
Sbjct 1661	AGAAGTCGCTGTTCCTCCCTCAGAGACTAGAACTTTCCAATGAATAGGAGATTATCCCAG			1720
Query 600	GTGCCTGTGTCAGGCTGGGCTCTGGGTTCTGTGCCGCTTCCCCACCCAGGTGTCCTG			659
Sbjct 1721	GTGCCTGTGTCAGGCTGGGCTCTGGGTTCTGTGCCGCTTCCCCACCCAGGTGTCCTG			1780
Query 660	TCCATTCTCAGGATGGTCACATGGGCGCTGCTGGAGTGTCCTCAAGAGAGATGCAAGTGT			719
Sbjct 1781	TCCATTCTCAGGATGGTCACATGGGCGCTGCTGGAGTGTCCTCAAGAGAGATGCAAGTGT			1840
Query 720	CTGAATTTTCTGACTCTTCCCGTCAGAACCCCAAGACACACGTGACCCACCACCCCT			779
Sbjct 1841	CTGAATTTTCTGACTCTTCCCGTCAGAACCCCAAGACACACGTGACCCACCACCCCT			1900
Query 780	CTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCTGCGGAGATCAC			839
Sbjct 1901	CTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCTGCGGAGATCAC			1960
Query 840	ACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACCCGAGCTTGTGGAGACCAG			899
Sbjct 1961	ACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACCCGAGCTTGTGGAGACCAG			2020
Query 900	GCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCA 933			
Sbjct 2021	GCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCA 2054			

Gambar 11. *Homo sapiens*.

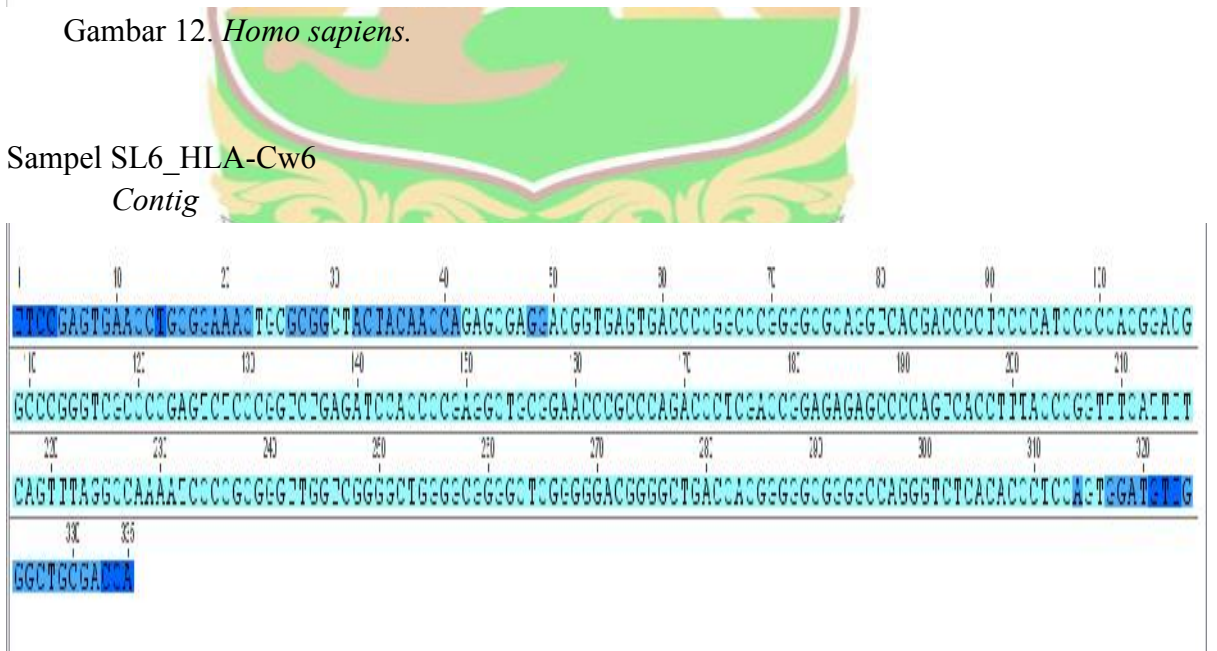
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Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1254, allele HLA-C*06:new
 Sequence ID: [emb|LT599311.1](#) Length: 3349 Number of Matches: 1

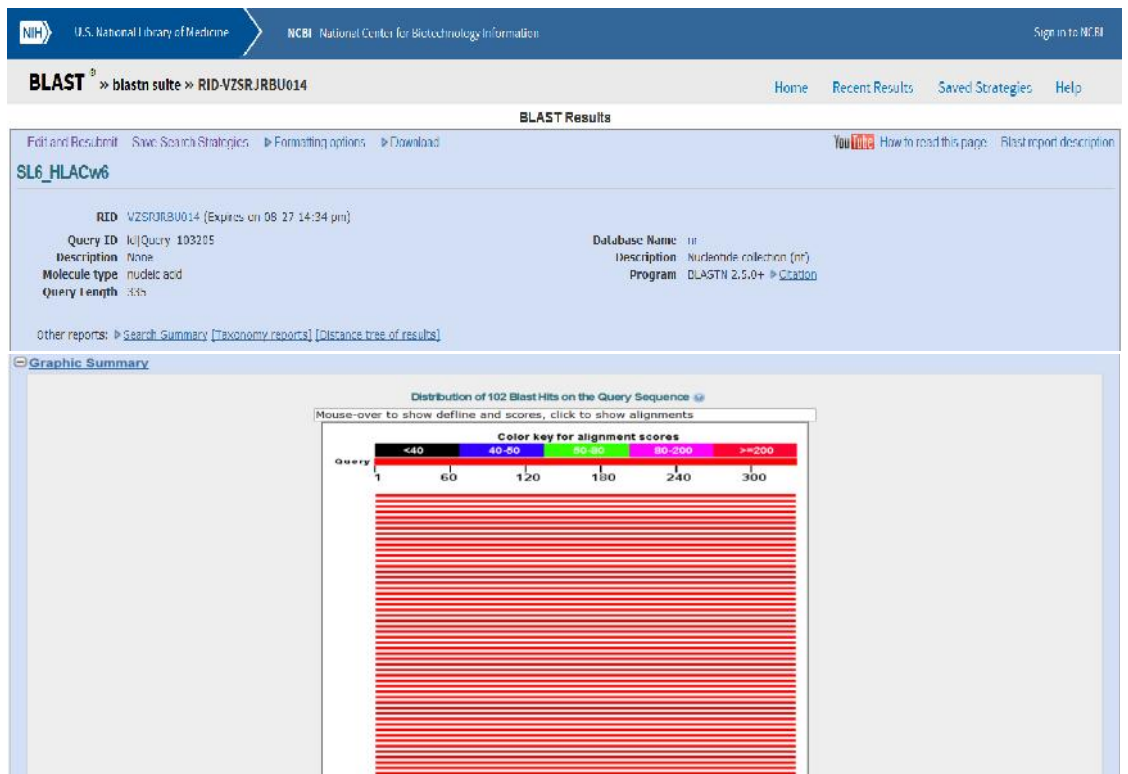
Range 1: 710 to 1038 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
608 bits(329)	2e-170	329/329(100%)	0/329(0%)	Plus/Plus
Query 1	AGTGAACCTGCGGAAACTGCGGGCTACTACAACCAGAGCGAGGACGGTGAGTGACCCCG	60		
Sbjct 710	AGTGAACCTGCGGAAACTGCGGGCTACTACAACCAGAGCGAGGACGGTGAGTGACCCCG	769		
Query 61	GCCCCGGGCGCAGGTCACGACCCCTCCCCATCCCCACGGACGGCCGGGTGCCCCGAG	120		
Sbjct 770	GCCCCGGGCGCAGGTCACGACCCCTCCCCATCCCCACGGACGGCCGGGTGCCCCGAG	829		
Query 121	TCTCCGGTCTGAGATCCACCCGAGGCTGCGGAACCCGCCAGACCCCTCGACCGGAGAG	180		
Sbjct 830	TCTCCGGTCTGAGATCCACCCGAGGCTGCGGAACCCGCCAGACCCCTCGACCGGAGAG	889		
Query 181	AGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGTTGG	240		
Sbjct 890	AGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGTTGG	949		
Query 241	TcggggctggggcggggctcgggggacggggctgaccacggggcggggccagggTCTCA	300		
Sbjct 950	TCGGGGCTGGGCGGGGCTCGGGGACGGGGTGACCACGGGGCGGGGCCAGGGTCTCA	1009		
Query 301	CACCCTCCAGTGGATGTATGGCTGCGACC	329		
Sbjct 1010	CACCCTCCAGTGGATGTATGGCTGCGACC	1038		

Gambar 12. *Homo sapiens*.



Gambar 13. Sampel SL6_HLA-Cw6.



Gambar 14. BLAST result.

Descriptions

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens HLA-C gene for MHC class I antigen, allele HLA-C*06:142, cell line DKMS-LSL-C-394	608	608	99%	2e-170	99%	LN811508.1
Homo sapiens isolate hbc8_C0_P0_NR500_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	603	603	99%	1e-168	99%	KX649953.1
Homo sapiens isolate hbc7_C0_P0_NR500_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	603	603	99%	1e-168	99%	KX649952.1
Homo sapiens isolate hbc4_C3_P0_NR234_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	603	603	99%	1e-168	99%	KX649946.1
Homo sapiens isolate hbc3_C0_P3_NR190_IND_C_06020102 MHC class I antigen (HLA-C) gene, complete cds	603	603	99%	1e-168	99%	KX649945.1
Homo sapiens isolate hbc2_C2_P1_NR326_IND_C_06020102 MHC class I antigen (HLA-C) gene, complete cds	603	603	99%	1e-168	99%	KX649943.1
Homo sapiens isolate hbc1_C0_P1_NR190_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	603	603	99%	1e-168	99%	KX649940.1
Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1254, allele HLA-C*06: new	603	603	99%	1e-168	99%	LT599311.1
Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1244, allele HLA-C*06: new	603	603	99%	1e-168	99%	LT599301.1
Homo sapiens isolate NT01314 MHC class I antigen (HLA-C) gene, HLA-C*06:138 variant allele, complete cds	603	603	99%	1e-168	99%	KU324542.1
Homo sapiens isolate NT01320 MHC class I antigen (HLA-C) gene, HLA-C*06:02:01:01 variant allele, complete cds	603	603	99%	1e-168	99%	KU324536.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:02:01:02e1 allele, complete cds	603	603	99%	1e-168	99%	KU319203.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:02:01:01e1 allele, complete cds	603	603	99%	1e-168	99%	KU319202.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:04:02 allele, complete cds	603	603	99%	1e-168	99%	KR920751.1
Homo sapiens HLA-C pseudogene, cell line DKMS-LSL-C-964, null allele HLA-C*06: new	603	603	99%	1e-168	99%	LN999652.1

Gambar 15. Sequences producing significant alignment.

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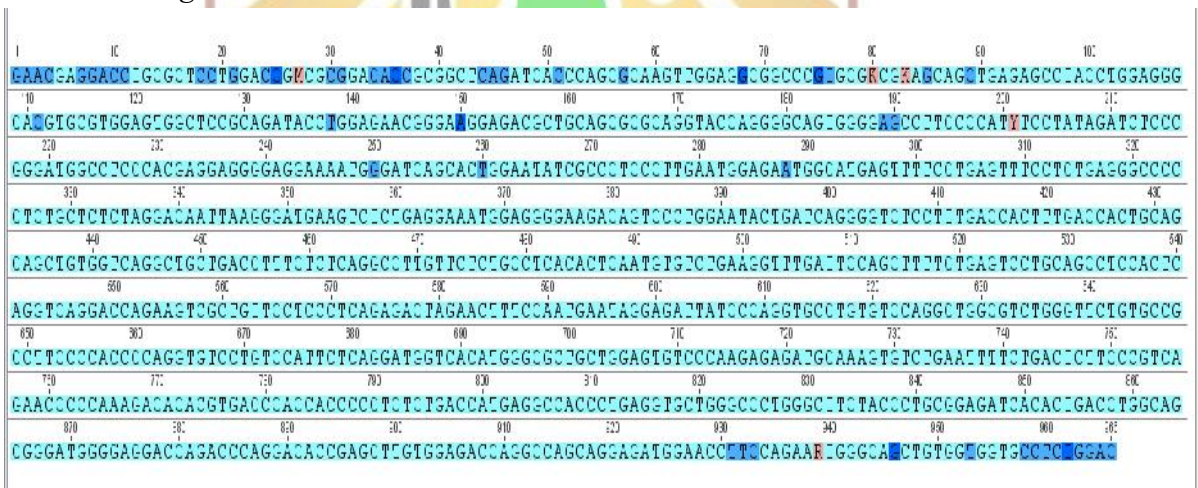
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1244, allele HLA-C*06:new
 Sequence ID: [emb|LT599301.1|](#) Length: 3349 Number of Matches: 1

Range 1: 707 to 1038 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

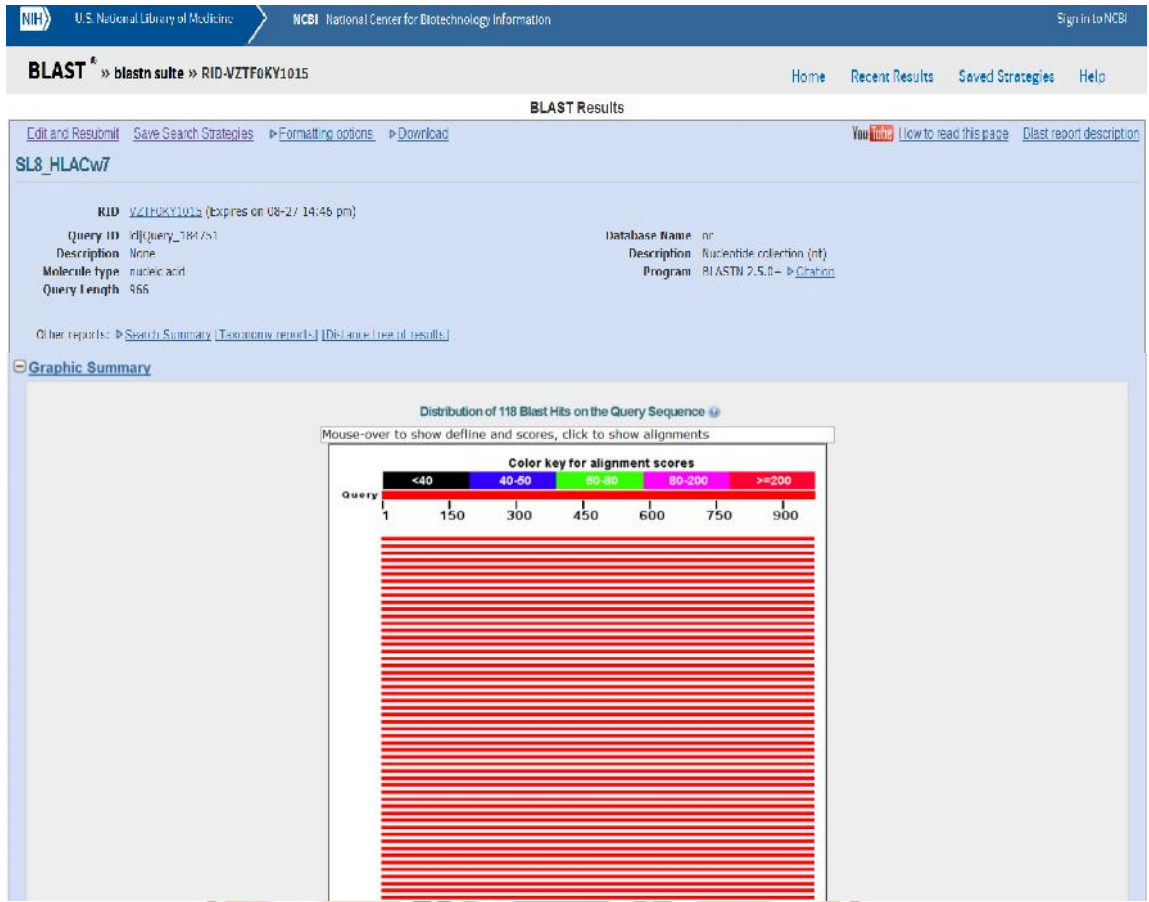
Score	Expect	Identities	Gaps	Strand
603 bits(326)	1e-168	330/332(99%)	0/332(0%)	Plus/Plus
Query 3	CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCGAGCGAGGACGGTGAGTGACC			62
Sbjct 707	CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCGAGCGAGGACGGTGAGTGACC			766
Query 63	CCGGCCCGGGGCGCAGGTCACGACCCCTCCCATCCCCACGGACGGCCCGGGTCGCCCC			122
Sbjct 767	CCGGCCCGGGGCGCAGGTCACGACCCCTCCCATCCCCACGGACGGCCCGGGTCGCCCC			826
Query 123	GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCAGACCCCTCGACCGGA			182
Sbjct 827	GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCAGACCCCTCGACCGGA			886
Query 183	GAGAGCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT			242
Sbjct 887	GAGAGCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT			946
Query 243	TGGTcggggctggggcggggctgggggacggggctgaccacggggcggggcccagggtc			302
Sbjct 947	TGGTCGGGCTGGGCGGGGCTCGGGGACGGGCTGACCACGGGGCGGGGCCAGGGTC			1006
Query 303	TCACACCTCCAGTGGATGTTGGGCTGCGACC		334	
Sbjct 1007	TCACACCTCCAGTGGATGTTGGGCTGCGACC		1038	

Gambar 16. *Homo sapiens*.

Sampel SL8_HLACw7
 Contig



Gambar 17. Sampel SL8_HLACw7.



Gambar 18. BLAST result.

Descriptions

Sequences producing significant alignments:

Select: All None Selected: 0

[Alignments](#) [Download](#) [GeoBank](#) [Graphics](#) [Distance tree of results](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Homo sapiens isolate tbc6_CO_P0_NR240 IND_C_070101 MHC class I antigen (HLA-C) gene, complete cds	1760	1760	100%	0.0	99%	K0649950.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1292, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599362.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1290, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599360.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1281, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599351.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1270, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599327.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1260, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599317.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1253, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599310.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1245, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599302.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1355, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599416.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1329, allele HLA-C*07:neq	1760	1760	100%	0.0	99%	LT599396.1
<input type="checkbox"/> Homo sapiens isolate NT01298 MHC class I antigen (HLA-C) gene, HLA-C*07:01:01:01 variant allele, complete cds	1760	1760	100%	0.0	99%	K0324519.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_27_01e1 allele, complete cds	1760	1760	100%	0.0	99%	K0319195.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_02_01_01e2 allele, complete cds	1760	1760	100%	0.0	99%	K0319191.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_02_01_01e1 allele, complete cds	1760	1760	100%	0.0	99%	K0319190.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_01_01_01e2 allele, complete cds	1760	1760	100%	0.0	99%	K0319189.1

Gambar 19. Sequences producing significant alignment.

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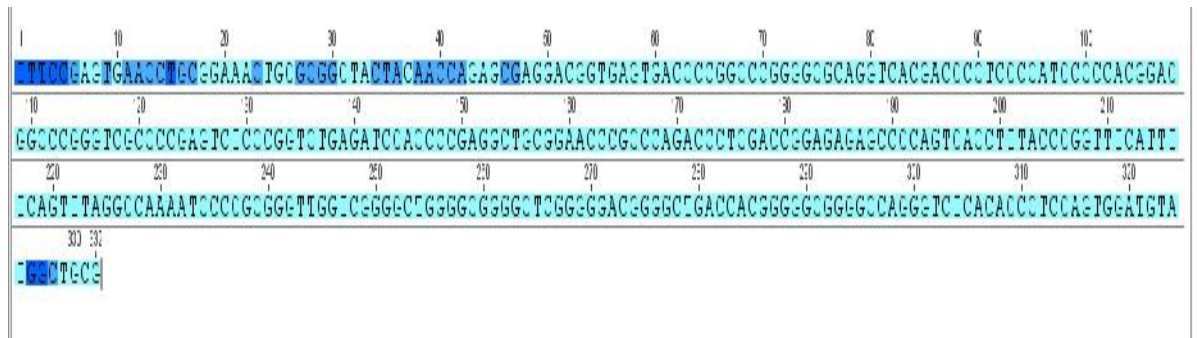
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1292, allele HLA-C*07:new
 Sequence ID: cmb|L1599362.1| Length: 3354 Number of Matches: 1

Range 1: 1110 to 2076 [GenBank Graphics](#) ▼ Next Match ▲ Previous Match

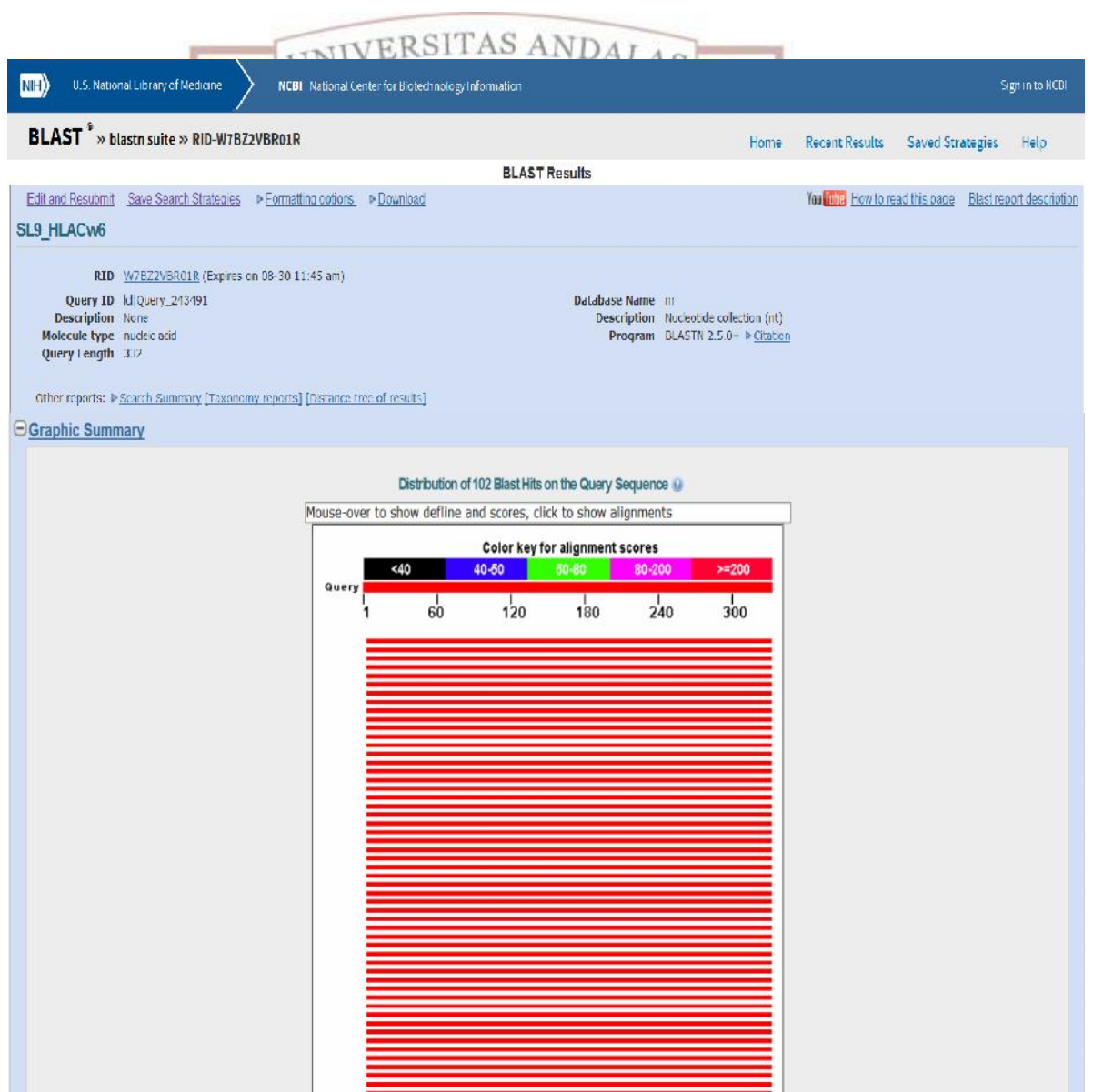
Score	Expect	Identities	Gaps	Strand
1760 bits(953)	0.0	961/967(99%)	1/967(0%)	Plus/Plus
Query 1	CAACCACGACCTCCGCTCCTCGACCCMCCCGCACACCCCGGCTCAGATCACCCACCCGAA	60		
Sbjct 1110	GRACGAGGACCTGCGCTCCTGGACCGCCGGGACACCCGGGCTCAGATCACCCACCCGAA	1169		
Query 61	GTTCGAGGACCTCCGCTCCTCGACCCMCCCGCACACCCCGGCTCAGATCACCCACCCGAA	120		
Sbjct 1170	GTTGGAGGCGCCCGTGGCGGGGAGCAGCTGAGAGCTTACCTGGAGGGCACCTGCGTGGAA	1229		
Query 121	CTCCCTCCCCACATACCTGCCAACCCCAACCCACACCCCTCCACCCCGGACCTACCCAGCC	180		
Sbjct 1230	GTGGCTCCGCAGATACCTGGAGAACGGGAAGGAGACGGCTGCAGCGCGCAGGTACCAGGGG	1289		
Query 181	CAGTGGGAGACCTTCCCATCTCCTATAGATCTCCCGGGATGGCCCTCCACAGGAGGGGG	240		
Sbjct 1290	CAGTGGGAGACCTTCCCATCTCCTATAGATCTCCCGGGATGGCCCTCCACAGGAGGGGG	1349		
Query 241	AGCAAAATCCGATCAGCACTGCAATATCCCCCTCCCTTCAATCCAGAAATCCCATCACTTT	300		
Sbjct 1350	AGGAAATGGGATCAGCACTGGAATATCGCCCTCCCTTGAATGGAGAAATGGCATGAGTTT	1409		
Query 301	TCCTGAGTTTCCCTCTGAGGGCCCGCTCTGCTCTCTAGGACAATTAAGGGATGAAGTCTCT	360		
Sbjct 1410	TCCTGAGTTTCCCTCTGAGGGCCCGCTCTGCTCTCTAGGACAATTAAGGGATGAAGTCTCT	1469		
Query 361	CACCAATCCAGCCCAAGACACTCCCTCCAACTATCAGCCCTCTCCTTTGACCACTT	420		
Sbjct 1470	GAGGAAATGGAGGGGAAAGACAGTCCCTGGAACTACTATCAGGGGTCTCCTTTGACCACTT	1529		
Query 421	TGACCCTCAGCAGCTGTGGTCAGGCTGCTGACCTTTCTCTCAGGCCTTGTCTCTGCCC	480		
Sbjct 1530	TGACCCTCAGCAGCTGTGGTCAGGCTGCTGACCTTTCTCTCAGGCCTTGTCTCTGCCC	1589		
Query 481	TCACACTCAATCTGCTCAAGCTTTCATTCACGCTTTCTCAGCTCCTCCACCTCCAGTCTC	540		
Sbjct 1590	TCACACTCAATGTGTCTGAAGGTTTGTATCCAGCTTTCTGAGTCTCAGCCTCCAGTCTC	1649		
Query 541	AGGTCAAGGACAGAAAGTCTGCTGCTCCCTCAGGACTAGAACTTTCCAAATGAATAGGA	600		
Sbjct 1650	AGGTCAAGGACAGAAAGTCTGCTGCTCCCTCAGGACTAGAACTTTCCAAATGAATAGGA	1709		
Query 601	GATTATCCCAAGTGCCTGTGTCCAGGCTGGCGTCTGGGTTCTGTGCCGCTTCCCCACCC	660		
Sbjct 1710	GATTATCCCAAGTGCCTGTGTCCAGGCTGGCGTCTGGGTTCTGTGCCGCTTCCCCACCC	1769		
Query 661	CAGGTGTCTGTCCATTCTCAGGATGGTCACATGGGCGCTGCTGGAGTGTCCCAAGAGAG	720		
Sbjct 1770	CAGGTGTCTGTCCATTCTCAGGATGGTCACATGGGCGCTGCTGGAGTGTCCCAAGAGAG	1829		
Query 721	ATGCAAAAGTGTCTGAATTTTCTGACTCTTCCCGTCAGAACCCCAAGACACACGTGACC	780		
Sbjct 1830	ATGCAAAAGTGTCTGAATTTTCTGACTCTTCCCGTCAGAACCCCAAGACACACGTGACC	1889		
Query 781	CACCACCCCTCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGGCTTCTACCTT	840		
Sbjct 1890	CACCACCCCTCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGGCTTCTACCTT	1949		
Query 841	GCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGACACCGAGCTT	900		
Sbjct 1950	GCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGACACCGAGCTT	2009		
Query 901	GTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAARTGGGCAGCTGTGGTGTGCCT	960		
Sbjct 2010	GTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAARTGGGCAGCTGTGGTGTGCCT	2069		
Query 961	-CTGGAC 966			
Sbjct 2070	TCTGGAC 2076			

Gambar 20. *Homo sapiens*.

Contig



Gambar 21. Sampel SL9_HLACw6.



Gambar 22. BLAST result.

Descriptions

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens isolate tbc8_CO_P0_NR500_IND_C_06020101.MHC class I antigen (HLA-C) gene, complete cds	608	608	99%	2e-170	100%	KX649953.1
Homo sapiens isolate tbc7_CO_P0_NR500_IND_C_06020101.MHC class I antigen (HLA-C) gene, complete cds	608	608	99%	2e-170	100%	KX649952.1
Homo sapiens isolate tbc4_C3_P0_NR234_IND_C_06020101.MHC class I antigen (HLA-C) gene, complete cds	608	608	99%	2e-170	100%	KX649946.1
Homo sapiens isolate tbc3_CO_P3_NR190_IND_C_06020102.MHC class I antigen (HLA-C) gene, complete cds	608	608	99%	2e-170	100%	KX649945.1
Homo sapiens isolate tbc2_C2_P1_NR326_IND_C_06020102.MHC class I antigen (HLA-C) gene, complete cds	608	608	99%	2e-170	100%	KX649943.1
Homo sapiens isolate tbc1_CO_P1_NR190_IND_C_06020101.MHC class I antigen (HLA-C) gene, complete cds	608	608	99%	2e-170	100%	KX649940.1
Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1254, allele: HLA-C*06:new	608	608	99%	2e-170	100%	LT599311.1
Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1244, allele: HLA-C*06:new	608	608	99%	2e-170	100%	LT599301.1
Homo sapiens isolate NT01314.MHC class I antigen (HLA-C) gene, HLA-C*06:138 variant allele, complete cds	608	608	99%	2e-170	100%	KU324542.1
Homo sapiens isolate NT01320.MHC class I antigen (HLA-C) gene, HLA-C*06:02:01:01 variant allele, complete cds	608	608	99%	2e-170	100%	KU324536.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06_02_01_02e1 allele, complete cds	608	608	99%	2e-170	100%	KU319203.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06_02_01_01e1 allele, complete cds	608	608	99%	2e-170	100%	KU319202.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:04:02 allele, complete cds	608	608	99%	2e-170	100%	KR920751.1
Homo sapiens_HLA-C pseudogene, cell line DKMS-LSL-C-964, null allele: HLA-C*06:new	608	608	99%	2e-170	100%	LI999652.1
Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-963, allele: HLA-C*06:new	608	608	99%	2e-170	100%	LI999651.1

Gambar 23. Sequences producing significant alignment.

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Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1254, allele HLA-C*06:new
 Sequence ID: [emb|LT599311.1](#) Length: 3349 Number of Matches: 1

Range 1: 707 to 1035 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
608 bits(329)	2e-170	329/329(100%)	0/329(0%)	Plus/Plus
Query 4	CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC	63		
Sbjct 707	CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC	766		
Query 64	CCGGCCCGGGGCGCAGGTACGACCCCTCCCCATCCCCACGGACGGCCCGGGTCGCCCC	123		
Sbjct 767	CCGGCCCGGGGCGCAGGTACGACCCCTCCCCATCCCCACGGACGGCCCGGGTCGCCCC	826		
Query 124	GAGTCTCCCGTCTGAGATCCACCCGAGGCTGCGGAACCCGCCAGACCTCGACCGGA	183		
Sbjct 827	GAGTCTCCCGTCTGAGATCCACCCGAGGCTGCGGAACCCGCCAGACCTCGACCGGA	886		
Query 184	GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCCGGGT	243		
Sbjct 887	GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCCGGGT	946		
Query 244	TGGTcggggctggggcggggctcgggggacggggctgaccacggggcggggcagggtc	303		
Sbjct 947	TGGTCGGGCTGGGGCGGGCTCGGGGACGGGCTGACCACGGGGCGGGCCAGGGTC	1006		
Query 304	TCACACCCTCCAGTGGATGTATGGCTGCG	332		
Sbjct 1007	TCACACCCTCCAGTGGATGTATGGCTGCG	1035		

Gambar 24. Homo sapiens.

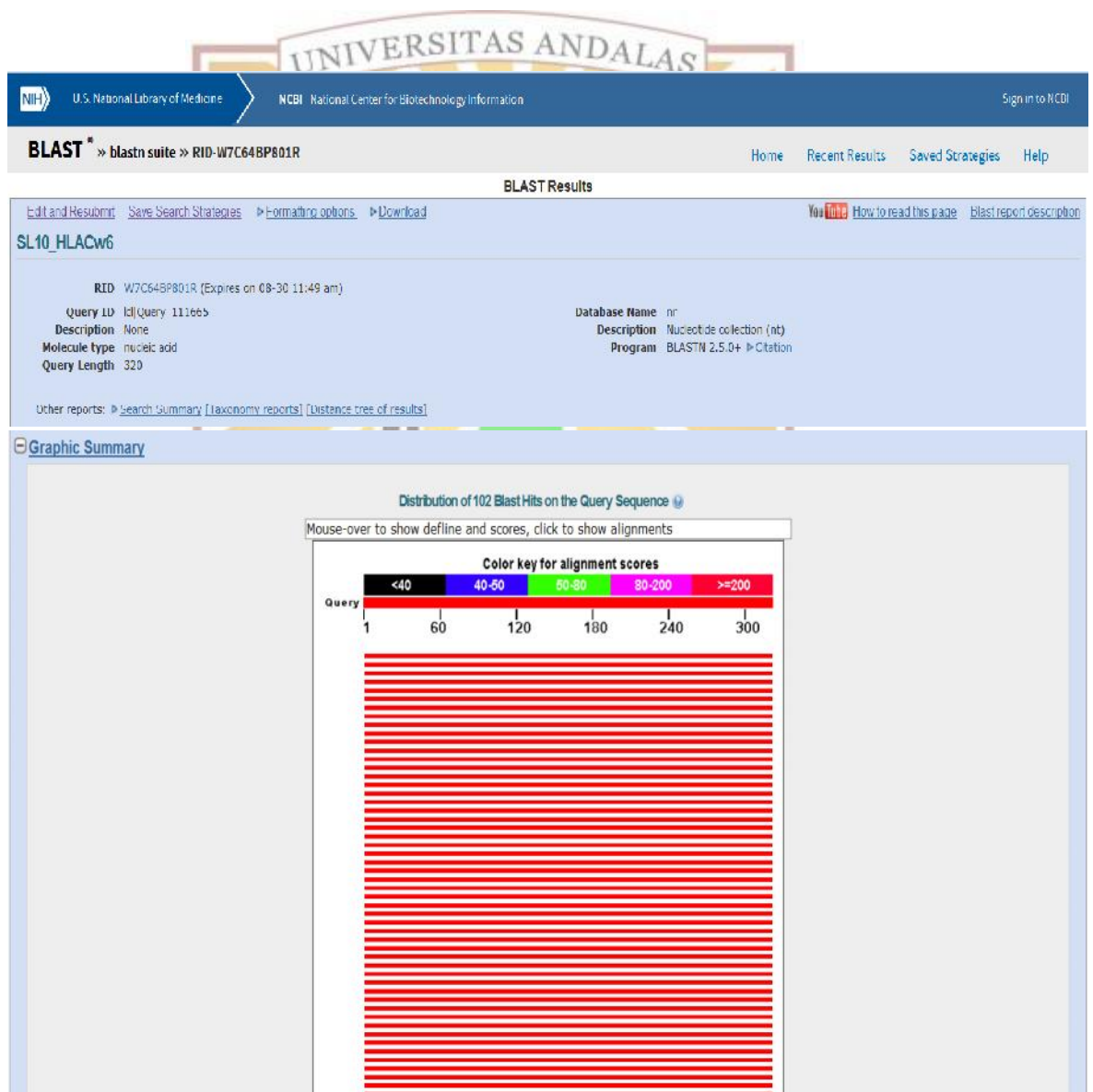
Contig

```

1      10      20      30      40      50      60      70      80      90      100
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
TCCGAGTGAACCTTCGCAAACTGCGGCGACTACAACAGAGCGAAGACGGTGAGTACCCGGCCCGGGCCGAGGTCAAGACCCCTCCCAATCCCCACGAGG
110      120      130      140      150      160      170      180      190      200      210
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GCCCCGGTGGCCCGAGTCTCCCGTCTGAGATCCACCCGAGGCTGCGGAACCCGCGCCAGACCTCGACCGSAGAGAGCCCGAGTCCCTTACCCGGTTCATTIT
220      230      240      250      260      270      280      290      300      310      320
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
CAGTITAGGCCAAAATCCCCGCGGTTGGTGGGCGCTGGCGGGGTCGCGGACCGGGTGAACACGGGCGCGGGCCAGGATCTCACACCCCTCCAGTGGAA

```

Gambar 25. Sampel SL10_HLACw6.



Gambar 26. BLAST result.

Descriptions

Sequences producing significant alignments:

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

Alignments [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens isolate lbc6_CO_P0_NR500_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	588	588	99%	3e-164	100%	KX649953.1
Homo sapiens isolate lbc7_CO_P0_NR500_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	588	588	99%	3e-164	100%	KX649952.1
Homo sapiens isolate lbc4_C3_P0_NR234_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	588	588	99%	3e-164	100%	KX649946.1
Homo sapiens isolate lbc3_CO_P3_NR190_IND_C_06020102 MHC class I antigen (HLA-C) gene, complete cds	588	588	99%	3e-164	100%	KX649945.1
Homo sapiens isolate lbc2_C2_P1_NR326_IND_C_06020102 MHC class I antigen (HLA-C) gene, complete cds	588	588	99%	3e-164	100%	KX649943.1
Homo sapiens isolate lbc1_CO_P1_NR190_IND_C_06020101 MHC class I antigen (HLA-C) gene, complete cds	588	588	99%	3e-164	100%	KX649940.1
Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1254, allele HLA-C*06:new	588	588	99%	3e-164	100%	LT599311.1
Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1244, allele HLA-C*06:new	588	588	99%	3e-164	100%	LT599301.1
Homo sapiens isolate NT01314 MHC class I antigen (HLA-C) gene, HLA-C*06:138 variant allele, complete cds	588	588	99%	3e-164	100%	KJ324542.1
Homo sapiens isolate NT01320 MHC class I antigen (HLA-C) gene, HLA-C*06:02.01.01 variant allele, complete cds	588	588	99%	3e-164	100%	KJ324536.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:02_01_02e1 allele, complete cds	588	588	99%	3e-164	100%	KJ319203.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:02_01_01e1 allele, complete cds	588	588	99%	3e-164	100%	KJ319202.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:04.02 allele, complete cds	588	588	99%	3e-164	100%	KR920751.1
Homo sapiens HLA-C pseudogene, cell line DKMS-LSL-C-964, null allele HLA-C*06:new	588	588	99%	3e-164	100%	LN999652.1
Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-963, allele HLA-C*06:new	588	588	99%	3e-164	100%	LN999651.1
Homo sapiens HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-946, allele HLA-C*06:new	588	588	99%	3e-164	100%	LN999634.1

Gambar 27. Sequences producing significant alignment.

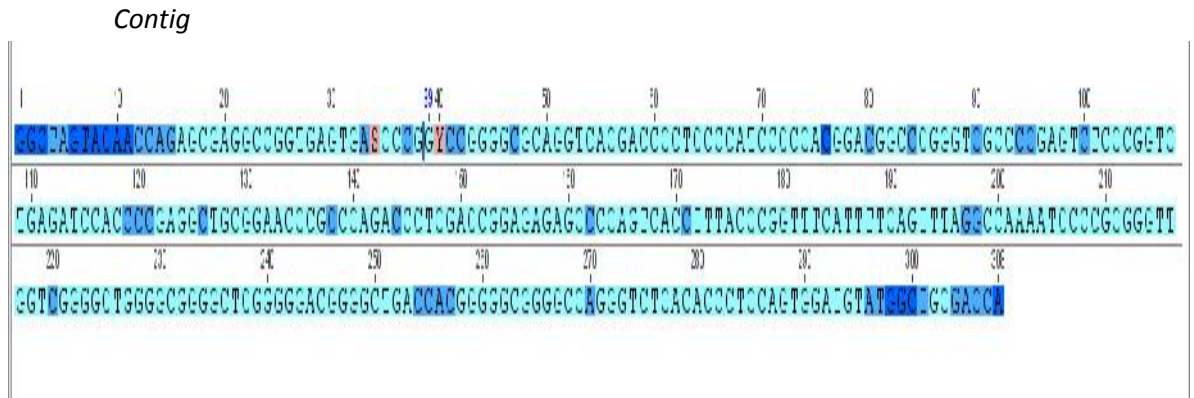
[Download](#) [GenBank](#) [Graphics](#)

Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1254, allele HLA-C*06:new
 Sequence ID: [emb|LT599311.1](#) Length: 3349 Number of Matches: 1

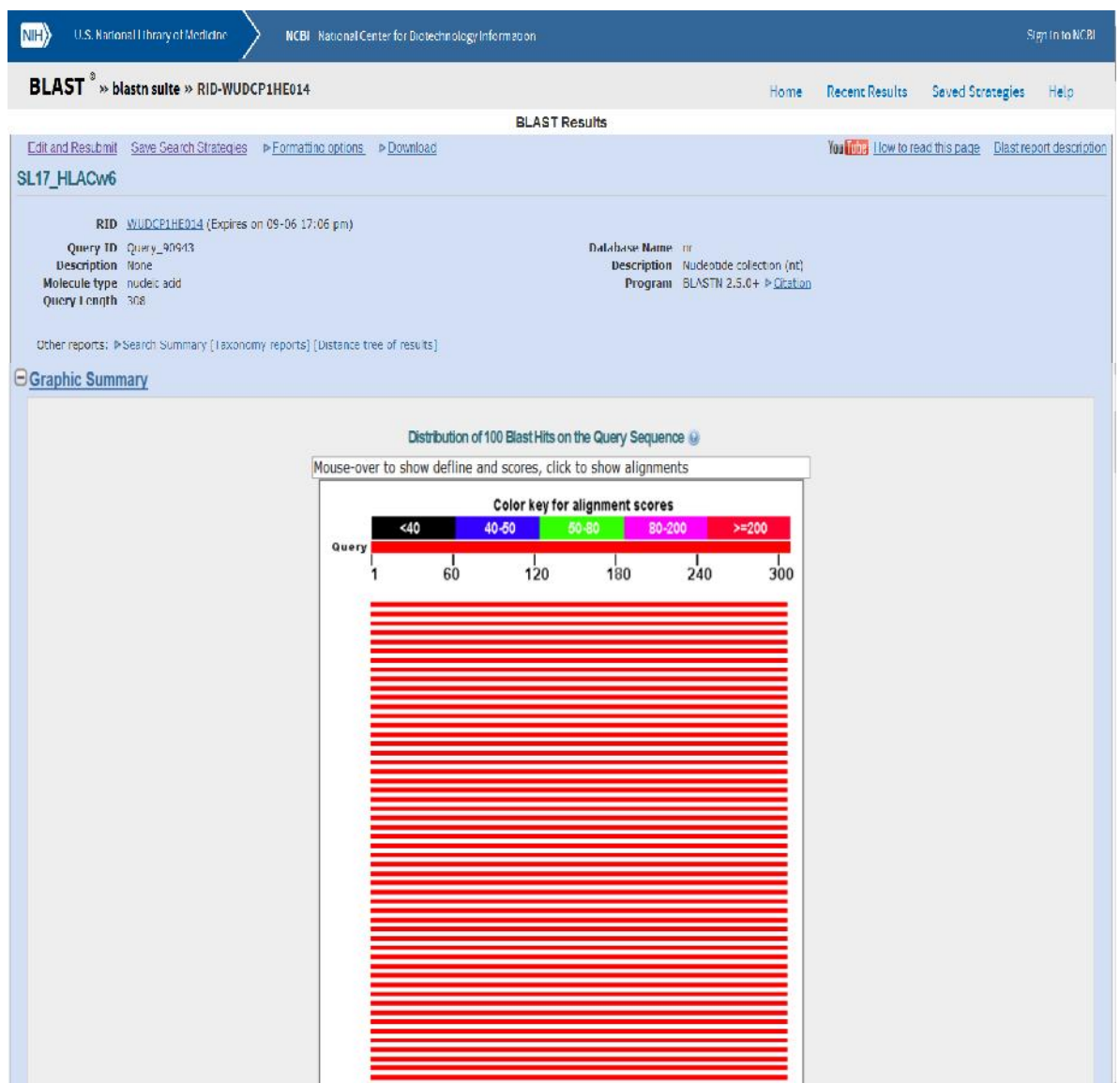
Range 1: 707 to 1024 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
588 bits(318)	3e-164	318/318(100%)	0/318(0%)	Plus/Plus
Query 3	CCGAGTGAACCTGCGGAACTGCGGGCTACTACAACCGAGCGAGGACGGTGAGTGACC	62		
Sbjct 707	CCGAGTGAACCTGCGGAACTGCGGGCTACTACAACCGAGCGAGGACGGTGAGTGACC	766		
Query 63	CCGGCCC3GGGGCGCAGGTCACGACCCCTCCCCATCCCCACGGACGGCCGGGTCGCCCC	122		
Sbjct 767	CCGGCCC3GGGGCGCAGGTCACGACCCCTCCCCATCCCCACGGACGGCCGGGTCGCCCC	826		
Query 123	GAGTCTCCGGTCTGAGATCCACCCGAGGCTGCGGAACCCGCCAGACCTCGACCGGA	182		
Sbjct 827	GAGTCTCCGGTCTGAGATCCACCCGAGGCTGCGGAACCCGCCAGACCTCGACCGGA	886		
Query 183	GAGAGCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGGGGT	242		
Sbjct 887	GAGAGCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGGGGT	946		
Query 243	TGGTcggggctggggcggggctcggggacggggctgaccagggggcgggccagggTC	302		
Sbjct 947	TGcTCGG3GCTGGGGCGGGGCTCGGGGACGGGGCTGACCAGGGGGCGGGGCCAGGGTC	1006		
Query 303	TCACACCTCCAGTGGAT	320		
Sbjct 1007	TCACACCTCCAGTGGAT	1024		

Gambar 28. Homo sapiens.



Gambar 29. Sampel SL17_HLACw6.

Gambar 30. *BLAST* result.

Descriptions

Sequences producing significant alignments:

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

Alignments [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1315, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599384.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1305, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599375.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1304, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599374.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1294, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599364.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1282, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599352.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1338-1, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599345.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1331-2, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599342.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1276, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599333.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1268, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599325.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1267, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599324.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1263, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599320.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1346, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599411.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1322, allele HLA-C*12:new	555	555	99%	3e-154	99%	LT599391.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*12_03_01_01e1 allele, complete cds	555	555	99%	3e-154	99%	KU319209.1
Homo sapiens isolate NT01257b MHC class I antigen (HLA-C) gene, HLA-C*08:12-nt01257b allele, partial cds	555	555	99%	3e-154	99%	KT454932.1
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-948, allele HLA-C*12:new	555	555	99%	3e-154	99%	LN999636.1

Gambar 31. Sequences producing significant alignment.

Alignments

[Download](#) [GenBank](#) [Graphics](#)

Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1315, allele HLA-C*12:new
 Sequence ID: [LT599384.1](#) Length: 3349 Number of Matches: 1

Range 1: 732 to 1038 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
555 bits(300)	3e-154	304/307(99%)	0/307(0%)	Plus/Plus
Query 1	GGCTAGTACAACAGAGCGAGGCCGGTGAGTGASCCCGGYCCGGGCGCAGGTACAGACC	60		
Sbjct 732	GGCTACTACAACAGAGCGAGGCCGGTGAGTGACCCCGGCCGGGCGCAGGTACAGACC	791		
Query 61	CCTCCCCATCCCCACGGACGGCCCGGGTCGCCCGAGTCTCCCGTCTGAGATCCACCC	120		
Sbjct 792	CCTCCCCATCCCCACGGACGGCCCGGGTCGCCCGAGTCTCCCGTCTGAGATCCACCC	851		
Query 121	CGAGGCTGCGGAACCCGCCAGACCCTCGACCGGAGAGAGCCCCAGTCACCTTTACCCGG	180		
Sbjct 852	CGAGGCTGCGGAACCCGCCAGACCCTCGACCGGAGAGAGCCCCAGTCACCTTTACCCGG	911		
Query 181	TTTCATITTCAGTTTAGGCCAAAATCCCGCGGGTGGToggggctggggoggggctcgg	240		
Sbjct 912	TTTCATITTCAGTTTAGGCCAAAATCCCGCGGGTGGTGGGGCTGGGGCGGGGCTCGG	971		
Query 241	gggacgggctgaccacggggcggggcoagggtCTCACACCCCTCCAGTGGATGTATGGC	300		
Sbjct 972	GGGACGGGCTGACCACGGGGCGGGGCCAG3GTCTCACACCCCTCCAGTGGATGTATGGC	1031		
Query 301	TGCGACC 307			
Sbjct 1032	TGCGACC 1038			

Gambar 32. Homo sapiens.

Contig

1	10	20	30	40	50	60	70	80	90	100
4	13	23	31	43	51	61	71	81	91	101
GACGGCAAGGATACATCGCCCTGAACGAGGACCTGCCTCCTGGACCGCCGCGSACACCCGGCTCAGATCACCCAGCGCAAGCTGGAGGCGGCCGCGGGGGAG										
110	120	130	140	150	160	170	180	190	200	210
113	123	133	143	153	163	173	183	193	203	213
CAGCTGAGACCCACCTGGAGGGCACCTGCTGGAGTGGCTCCCGACATACCTGGAGAACCAGGAGGAGCGCTSCAGCGCGCAGGTACCAGCGGCAGTGGGAGGCC										
220	230	240	250	260	270	280	290	300	310	320
223	233	243	253	263	273	283	293	303	313	323
TCCCCAICTCCTATAGACTCCCGGGATGCCCCACGAGGAGGGGAGGAAAAATGGSATCAGCACGGAAATATCCCTCCCTGGAATGGAGAAATGGCATGAGTTT										
330	340	350	360	370	380	390	400	410	420	430
333	343	353	363	373	383	393	403	413	423	433
CCTGASITTCCTCTGAGGGCCCCCTCIGGCTCTTAGGACAATAAGCGAIGAAGTCTCIGAGGAAAATGGAGGGAAGACAGTCCCTGGAATACTGATCAGGEGTCTCC										
440	450	460	470	480	490	500	510	520	530	540
443	453	463	473	483	493	503	513	523	533	543
TTTGACCAGTTTGAACCATGACAGAGCTGIGGICAGGCGGTGACTTTCTCAGGCTGTGTCTCTGCTCACACTCAAGTGTCTGAAGGTTTGAATCCAGCTT										
550	560	570	580	590	600	610	620	630	640	650
553	563	573	583	593	603	613	623	633	643	653
TCTGASICCTGACGCTCCACTCAGGICAGGACCCAGAGTCCGCTGCTCCCTCAGAGACAGAACTTCCCAATGAATAGGAGATATCCAGGIGCTGTGTCCAG										
660	670	680	690	700	710	720	730	740	750	760
663	673	683	693	703	713	723	733	743	753	763
GCTGGGCTGIGGGTCTGIGCGGCTTCCCAACCCAGGTTCTGTCATTCTCAGSATGGTCACAIGSGCCCTECTEGAGTSCCCAGAGAGATGCAAAGTGT										
770	780	790	800	810	820	830	840	850	860	870
773	783	793	803	813	823	833	843	853	863	873
GAAITTTCTGACCTCTCCCGCCAGAAACCCCAAAGACACAGTGAACCCACCACCCTCTCTGACCATGAGGCGCACCCGAGGTTGCTGGGCCCTGEGGCTCTACCCCTG										
880	890	900	910	920	930	940	950	960	970	980
883	893	903	913	923	933	943	953	963	973	983
CGGAGATCACAGTGACCTGGCAGCGGGATGGGGAAGTCCAGACCCAGGACACCGAGCTTGIGGAGAACAGCTDASCAGGAGATGGAACTTCCAGAAAGGTCAGCTG										
990										
993										
G										

Gambar 33. Sampel SLK7_HLACw7.



BLAST result

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SLK7_HLACw7

RID [WUDRSURJ015](#) (Expires on 09/06/17 12 pm)

Query ID Query_17341 **Database Name** nr

Description None **Description** Nucleotide collection (nr)

Molecule type nucleic acid **Program** BLASTN 2.6.0+ P-Clustalw

Query Length 975

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

Graphic Summary

Distribution of 118 Blast Hits on the Query Sequence

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

Color key for alignment scores

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

Query

1 150 300 450 600 750 900

Gambar 34. BLAST result.

Descriptions

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-Cw) gene, HLA-Cw*0706 allele, promoter region and complete cds	1801	1801	100%	0.0	100%	FJ785732.1
<input type="checkbox"/> Homo sapiens isolate bx6_C0_P0_NR240_IND_C_070191 MHC class I antigen (HLA-C) gene, complete cds	1796	1796	100%	0.0	99%	KX649950.1
<input type="checkbox"/> Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1292, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599362.1
<input type="checkbox"/> Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1290, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599360.1
<input type="checkbox"/> Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1281, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599351.1
<input type="checkbox"/> Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1260, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599317.1
<input type="checkbox"/> Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1259, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599310.1
<input type="checkbox"/> Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1245, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599302.1
<input type="checkbox"/> Homo sapiens_HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1329, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599398.1
<input type="checkbox"/> Homo sapiens isolate NT01298 MHC class I antigen (HLA-C) gene, HLA-C*07:01:01:01 variant allele, complete cds	1796	1796	100%	0.0	99%	KJ324519.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_27_01e1 allele, complete cds	1796	1796	100%	0.0	99%	KJ319196.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_02_01_01e2 allele, complete cds	1796	1796	100%	0.0	99%	KJ319191.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_02_01_01e1 allele, complete cds	1796	1796	100%	0.0	99%	KJ319190.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_01_01_01e2 allele, complete cds	1796	1796	100%	0.0	99%	KJ319188.1
<input type="checkbox"/> Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_01_01_01e1 allele, complete cds	1796	1796	100%	0.0	99%	KJ319188.1
<input type="checkbox"/> Homo sapiens HLA-C gene for MHC class I antigen, allele HLA-C*07:01:01	1796	1796	100%	0.0	99%	LT221892.1

Gambar 35. Sequences producing significant alignment.



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Homo sapiens MHC class I antigen (HLA-Cw) gene, HLA-Cw-Cw*0706 allele, promoter region and complete cds
 Sequence ID: [FJ785732.1](#) Length: 4551 Number of Matches: 1

Range 1: 1773 to 2747 GenBank Graphics ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1801 bits(975)	0.0	975/975(100%)	0/975(0%)	Plus/Plus
Query 1	GTCGGCAAGGATTACATCGCCCTGAAAGAGGACCTGCGCTCCTGGACCGCCGGGACACC			60
Subject 1773	GTGGGCAAGGATTACATCGCCCTGAAAGAGGACCTGCGCTCCTGGACCGCCGGGACACC			1832
Query 61	GCGGCTCAGATCAACCAGCGCAAGTTGAGGGCGGCGCGTGGCGGCGAGCAGCTGAGAGCC			120
Subject 1833	GCGGCTCAGATCAACCAGCGCAAGTTGAGGGCGGCGCGTGGCGGCGAGCAGCTGAGAGCC			1892
Query 121	TACCTGSRGGGCACGTCGTTGGAGTGGCTCCGACAGATCCTGGAGAACGGAAAGGAGCG			180
Subject 1893	TACCTGACCCACCCACTCCCTCCACTCCCTCCGACATACCTCCGACAAACCCGAAACACACC			1952
Query 181	CTGCAGTGTGGCAGGTACAGGGGCAGTGGGAGGCTTCCGCACTCTTATAGATCTCTGG			240
Subject 1953	CTGCAGGCGGCAGGTACAGGGGCAGTGGGAGGCTTCCGCACTCTTATAGATCTCTGG			2012
Query 241	GGATGGCCCTCCACGAGGGGGAGGAAATGGGATCGCACTGGAAATTCGCCCTCCCT			300
Subject 2013	GGATGGCCCTCCACGAGGGGGAGGAAATGGGATCGCACTGGAAATTCGCCCTCCCT			2072
Query 301	TGAATGAGAAATGGCATGAGTTTCTCTGAGTTTCTCTGAGGGCCCGCTGCTCTCTAG			360
Subject 2073	TGAATGAGAAATGGCATGAGTTTCTCTGAGTTTCTCTGAGGGCCCGCTGCTCTCTAG			2132
Query 361	GCAAAATAGGGATGAAGTCTCTGAGGAATGGAGGGAGACAGTCCCTGGAAATCTGA			420
Subject 2133	GCAAAATAGGGATGAAGTCTCTGAGGAATGGAGGGAGACAGTCCCTGGAAATCTGA			2192
Query 421	TCAGGGTCTCTCTTGACCACTTGTGACTGCACTGACTGAGTGGTGGTGGTGGTGGTGGT			480
Subject 2193	TCAGGGTCTCTCTTGACCACTTGTGACTGCACTGACTGAGTGGTGGTGGTGGTGGTGGT			2252
Query 481	TCTCTGAGGCTTGTGTTCTGCTCAGCACTCAATGTTGGAAGTTTATATCCACTTT			540
Subject 2253	TCTCTGAGGCTTGTGTTCTGCTCAGCACTCAATGTTGGAAGTTTATATCCACTTT			2312
Query 541	TCTCAGTCCCTCCAGCCCTCCACTGACCTCACCACCAACTCCCTCTCCCTCCCTCAGACA			600
Subject 2313	TCTGAGTCTGAGGCTTCCACTCAGGTCAGGATCAGAAATCGTGTCTCTCTCTCTCAGACA			2372
Query 601	CTAGACTTTTCCAATGAATAGGAGATTATCCAGGTGCTGTGTCCAGGCTGGCGTCTGG			660
Subject 2373	CTAGACTTTTCCAATGAATAGGAGATTATCCAGGTGCTGTGTCCAGGCTGGCGTCTGG			2432
Query 661	GTTCTGTGCCCTTCCCAACCCAGTGTCTCTGCTCATTCTCAGGATGTCACATGGGC			720
Subject 2433	GTTCTGTGCCCTTCCCAACCCAGTGTCTCTGCTCATTCTCAGGATGTCACATGGGC			2492
Query 721	GCTGCTGGAGTGTCCCAAGAGAGATSCAAGTGTCTGAATTTTCTGACTCTTCCCGTCAG			780
Subject 2493	GCTGCTGGAGTGTCCCAAGAGAGATSCAAGTGTCTGAATTTTCTGACTCTTCCCGTCAG			2552
Query 781	AACCCCAAAAGACACACCTGACCCACCACCCCTCTCTGACCATGAGGCCACCCCTGAGGT			840
Subject 2553	AACCCCAAAAGACACACCTGACCCACCACCCCTCTCTGACCATGAGGCCACCCCTGAGGT			2612
Query 841	GCTGGGCCCTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGATGGGGAGG			900
Subject 2613	GCTGGGCCCTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGATGGGGAGG			2672
Query 901	ACCAGACCCAGGACACCGAGCTTGTGGAGACAGGCCAGCAGGAGATGGAACCTTCCAGA			960
Subject 2673	ACCAGACCCAGGACACCGAGCTTGTGGAGACAGGCCAGCAGGAGATGGAACCTTCCAGA			2732
Query 961	AGTGGCCAGCTGTGG 975			
Subject 2733	AGTGGCCAGCTGTGG 2747			

Gambar 36. *Homo sapiens*.

Hasil *Primer* BLAST

Pasangan *primer* HLA-Cw6

Primer-BLAST
Primer-BLAST results

NCBI Primer-BLAST: results: Job ID=ICr_PkVvMzrc5ydtgrPD0bte0Qnlw [more...](#)

Input PCR template: none
Specificity of primers: Target templates were found in selected database: Nucleotide collection (nt) (Organism limited to Homo sapiens)
Other reports: [Search Summary](#)

Detailed primer reports

Primer pair 1

	Sequence (5'→3')	Length	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CCGAGTGAACCTGCGGAAA	19	60.30	57.89	3.00	0.00
Reverse primer	GGTCGCGGCATACATCCA	19	59.85	57.89	3.00	0.00

Products on target templates

>U54909.1 Homo sapiens partial HLA-C gene for MHC class I antigen, allele *C*06:02, exons 2-4

product length = 158
 Forward primer: 1 CCGAGTGAACCTGCGGAAA 19
 Template: 221 239
 Reverse primer: 1 GGTCGCGGCATACATCCA 19
 Template: 406 388

>AH003610.2 Homo sapiens chromosome 6 MHC class I protein HLA-C heavy chain (HLA-C) gene, partial cds

product length = 152
 Forward primer: 1 CCGAGTGAACCTGCGGAAA 19
 Template: 201 219
 Reverse primer: 1 GGTCGCGGCATACATCCA 19
 Template: 392 374

>U54909.1 Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06:02:01:02 allele, complete cds

product length = 167
 Forward primer: 1 CCGAGTGAACCTGCGGAAA 19
 Template: 812 830
 Reverse primer: 1 GGTCGCGGCATACATCCA 19
 Template: 1103 1085

>AF005110.1 Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06 allele, exons 1 through 7 and partial cds

product length = 164
 Forward primer: 1 CCGAGTGAACCTGCGGAAA 19
 Template: 514 496
 Reverse primer: 1 GGTCGCGGCATACATCCA 19
 Template: 514 532

>U54909.1 Homo sapiens HLA-C gene for MHC class I antigen, cell line DKW5 LSL C 659, allele HLA-C*06:02

product length = 152
 Forward primer: 1 CCGAGTGAACCTGCGGAAA 19
 Template: 717 735
 Reverse primer: 1 GGTCGCGGCATACATCCA 19
 Template: 918 899

>U54909.1 Homo sapiens HLA-C gene for MHC class I antigen, cell line DKW5 LSL C 655, allele HLA-C*06:02

product length = 150
 Forward primer: 1 CCGAGTGAACCTGCGGAAA 19
 Template: 717 735
 Reverse primer: 1 GGTCGCGGCATACATCCA 19
 Template: 918 899

Gambar 37. Pasangan *primer* HLA-Cw6



Pasangan *primer* HLA-Cw7

Primer-BLAST

Primer-Blast results

NCBI Primer-BLAST : results: Job id=GLvzYvW7H8g_NmaPK34KD-ORRkexa_mss_...

Input PCR template: none
 Specificity of primers: Target templates were found in selected database: Nucleotide collection (nt) (Organism limited to Homo sapiens)
 Other reports: Search Summary

Detailed primer reports

Primer pair 1

	Sequence (5'→3')	Length	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	COGGGGTATGACCAATC	18	59.89	66.67	6.00	4.00
Reverse primer	CAGCCCTCGTGTGCAT	18	62.79	66.67	5.00	3.00

Products on target templates

>L1221892.1 Homo sapiens HLA-C gene for MHC class I antigen, allele HLA-C*07:01:01

product length = 1056
 Forward primer 1 COGGGGTATGACCAATC 18
 Template 1062 1079
 Reverse primer 1 CAGCCCTCGTGTGCAT 18
 Template 2117 2134

>L1221891.1 Homo sapiens HLA-C gene for MHC class I antigen, allele HLA-C*07:02:01

product length = 1056
 Forward primer 1 COGGGGTATGACCAATC 18
 Template 1062 1079
 Reverse primer 1 CAGCCCTCGTGTGCAT 18
 Template 2117 2134

>L1048007.1 Homo sapiens partial HLA-C gene for MHC class I antigen, allele *07:01new, exons 2-4

product length = 968
 Forward primer 1 COGGGGTATGACCAATC 18
 Template 474 491
 Reverse primer 1 CAGCCCTCGTGTGCAT 18
 Template 1062 1079

>L1148006.1 Homo sapiens partial HLA-C gene for MHC class I antigen, allele *07:01new, exons 2-4

product length = 968
 Forward primer 1 COGGGGTATGACCAATC 18
 Template 474 491
 Reverse primer 1 CAGCCCTCGTGTGCAT 18
 Template 1062 1079

>L1148005.1 Homo sapiens partial HLA-C gene for MHC class I antigen, allele *07:01new, exons 2-4

product length = 968
 Forward primer 1 COGGGGTATGACCAATC 18
 Template 474 491
 Reverse primer 1 CAGCCCTCGTGTGCAT 18
 Template 1062 1079

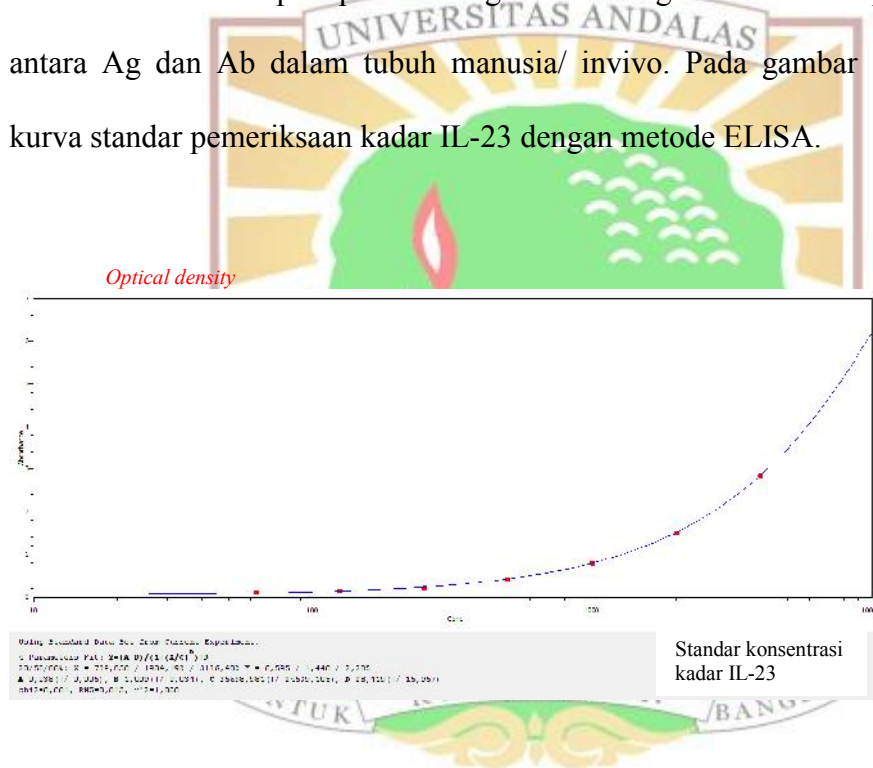
>L112095.21 Homo sapiens MHC class I antigen (HLA-C) gene, HLA-Cw*07 variant allele, complete cds

product length = 1052
 Forward primer 1 COGGGGTATGACCAATC 18
 Template 1062 1079
 Reverse primer 1 CAGCCCTCGTGTGCAT 18
 Template 2117 2134

Gambar 38. Pasangan *primer* HLA-Cw7

Metode Kerja ELISA Pada Pemeriksaan IL-23

Prinsip pemeriksaan ELISA pada umumnya berdasarkan pada interaksi antigen (Ag) dan antibodi (Ab). Interaksi antigen dan antibodi tba melalui tiga tingkatan yaitu tingkat primer, tingkat sekunder dan tingkat tersier. Tingkat primer merupakan awal reaksi ikatan molekuler antara Ag dan Ab dan diperlukan indikator (enzim), indikator tersebut dilengketkan ke Ag atau Ab. Tingkat sekunder terdiri dari presipitasi dan aglutinasi. Tingkat tersier merupakan interaksi antara Ag dan Ab dalam tubuh manusia/ *invivo*. Pada gambar 5.4 didapatkan kurva standar pemeriksaan kadar IL-23 dengan metode ELISA.



Gambar 39. Nilai Kurva Standar Kadar IL-23.

Merupakan kurva kadar IL-23 yang diperoleh dengan cara *plotting* nilai konsentrasi hasil pengenceran berseri kadar IL-23 dengan satuan pg/ml (sumbu X) terhadap nilai absorbansinya pada panjang gelombang 450 nm (sumbu Y).

Lampiran 9. Analisis Statistik

[DataSet0] I:\SRI KULIT\DATA SRI 8 NOV.sav

One-Sample Kolmogorov-Smirnov Test

		IL23
N		60
Normal Parameters(a,b)	Mean	28,3964
	Std. Deviation	8,79698
Most Extreme Differences	Absolute	,168
	Positive	,168
	Negative	-,101
Kolmogorov-Smirnov Z		1,300
Asymp. Sig. (2-tailed)		,068

a Test distribution is normal.

b Calculated from data.

Umur responden * GROUP

Crosstab

			GROUP		Total
			1,00	2,00	1,00
Umur responden	<= 40 tahun	Count	14	15	29
		% within GROUP	46,7%	50,0%	48,3%
	> 40 tahun	Count	16	15	31
		% within GROUP	53,3%	50,0%	51,7%
Total		Count	30	30	60
		% within GROUP	100,0%	100,0%	100,0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	,067(b)	1	,796		
Continuity Correction(a)	,000	1	1,000		
Likelihood Ratio	,067	1	,796		
Fisher's Exact Test				1,000	,500
Linear-by-Linear Association	,066	1	,798		
N of Valid Cases	60				

a Computed only for a 2x2 table

b 0 cells (.0%) have expected count less than 5. The minimum expected count is 14,50.

Frequency Table

DURASI

	Frequency	Percent	Valid Percent	Cumulative Percent
Valid 1,00	14	46,7	46,7	46,7
2,00	15	50,0	50,0	96,7
3,00	1	3,3	3,3	100,0
Total	30	100,0	100,0	

ONSET

	Frequency	Percent	Valid Percent	Cumulative Percent
Valid 1,00	23	76,7	76,7	76,7
2,00	7	23,3	23,3	100,0
Total	30	100,0	100,0	

DDK * GROUP Crosstabulation

			GROUP		Total
			1,00	2,00	1,00
DDK 1,00	Count		11	1	12
	% within GROUP		36,7%	3,3%	20,0%
2,00	Count		13	15	28
	% within GROUP		43,3%	50,0%	46,7%
3,00	Count		6	14	20
	% within GROUP		20,0%	46,7%	33,3%
Total	Count		30	30	60
	% within GROUP		100,0%	100,0%	100,0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	11,676(a)	2	,003
Likelihood Ratio	13,186	2	,001
Linear-by-Linear Association	10,300	1	,001
N of Valid Cases	60		

a 0 cells (,0%) have expected count less than 5. The minimum expected count is 6,00.

JENIS KELAMIN

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	1,00	16	53,3	53,3	53,3
	2,00	14	46,7	46,7	100,0
	Total	30	100,0	100,0	

SKOR PASI

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	1,00	23	76,7	73,3	73,3
	2,00	5	16,7	16,7	90,0
	3,00	2	6,6	10,0	100,0
Total		30	100,0	100,0	

HLA-Cw6 * GROUP*Crosstab*

			GROUP		Total
			1,00	2,00	1,00
HLA-Cw6	1,00	Count	6	0	6
		% within HLA-Cw6	100,0%	,0%	100,0%
	2,00	Count	24	30	54
		% within HLA-Cw6	44,4%	55,6%	100,0%
Total		Count	30	30	60
		% within HLA-Cw6	50,0%	50,0%	100,0%

Chi-Square Tests

	Value	Df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	6,667(b)	1	,010		
Continuity Correction(a)	4,630	1	,031		
Likelihood Ratio	8,986	1	,003		
Fisher's Exact Test				,024	,012
Linear-by-Linear Association	6,556	1	,010		
N of Valid Cases	60				

a Computed only for a 2x2 table

b 2 cells (50,0%) have expected count less than 5. The minimum expected count is 3,00.

HLA-Cw7 * GROUP

Crosstab

			GROUP		Total
			1,00	2,00	1,00
HLA-Cw7	1,00	Count	6	7	13
		% within HLA-Cw7	20%	23,3%	100,0%
	2,00	Count	24	23	47
		% within HLA-Cw7	80%	76,7%	100,0%
Total		Count	30	30	60
		% within HLA-Cw7	50,0%	50,0%	100,0%

Chi-Square Tests

	Value	Df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	,341(b)	1	,559		
Continuity Correction(a)	,085	1	,770		
Likelihood Ratio	,342	1	,559		
Fisher's Exact Test				,771	,386
Linear-by-Linear Association	,335	1	,563		
N of Valid Cases	60				

a Computed only for a 2x2 table

b 0 cells (,0%) have expected count less than 5. The minimum expected count is 8,00.

Group Statistics

GROUP	N	Mean	Std. Deviation	Std. Error Mean
IL-23 1,00	30	31,2088	10,58093	1,93180
2,00	30	25,5839	5,39638	,98524

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means						
		F	Sig.	T	df	Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference	
IL23	Equal variances assumed	9,243	,004	2,594	58	,012	5,62493	2,16854	1,28413	9,96574
	Equal variances not assumed			2,594	43,130	,013	5,62493	2,16854	1,25204	9,99783

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1(a)	HLA-Cw6	21,537	15364,131	,000	1	,999	22558007 14,223
	HLA-Cw7	-,003	,641	,000	1	,996	,997
	IL-23	-,100	,042	5,575	1	,018	,905
	Constant	-40,037	30728,263	,000	1	,999	,000
Step 2(a)	HLA-Cw6	21,538	15363,841	,000	1	,999	22578504 06,339
	IL-23	-,100	,042	5,582	1	,018	,905
	Constant	-40,044	30727,683	,000	1	,999	,000

a Variable(s) entered on step 1: HLA-Cw6, HLA-Cw7, IL-23.

