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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

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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 menandatanganni formulir persetujuan yang menyatakan anda mengikuti studi ini secara sukarela.

Terimakasih

Peneliti

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

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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.*

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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.

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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 Sirah 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, FINSDV (.....)

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Lampiran 7. Rekam Medik

REKAM MEDIK

JATI DIRI PASIEN

NAMA :
UMUR :
JENIS KELAMIN :
ALAMAT :
TELEPON :
PEKERJAAN :
NO REKAMAN MEDIK :
DOKTER YANG MERAWAT : 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

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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 derajad 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

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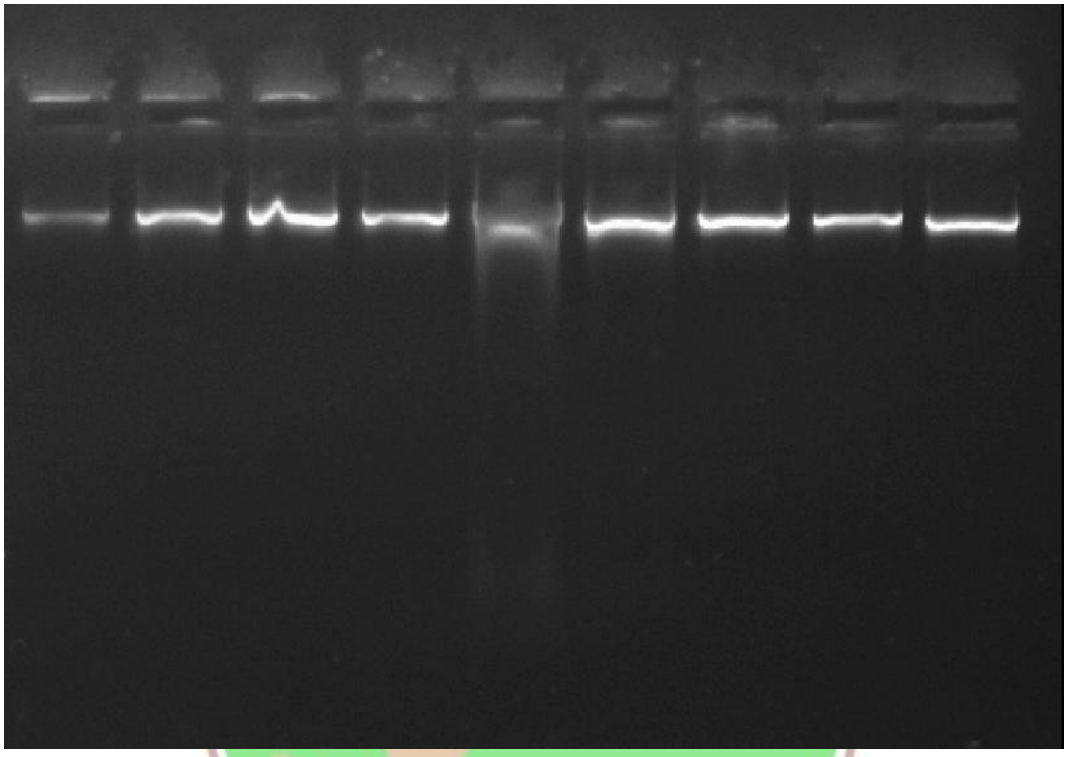
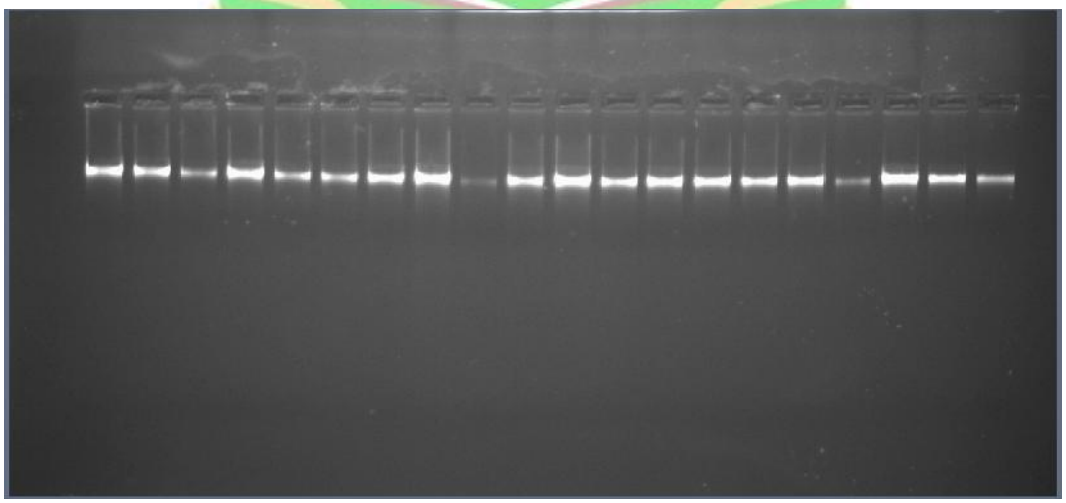
Lampiran 8

Metode Kerja Dan Hasil Genotyping HLA-C

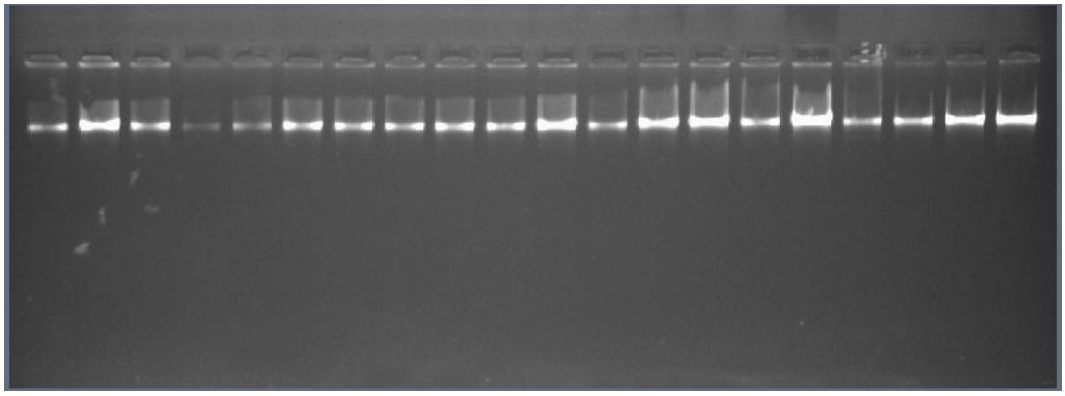
Elektroforegram Hasil Isolasi DNA



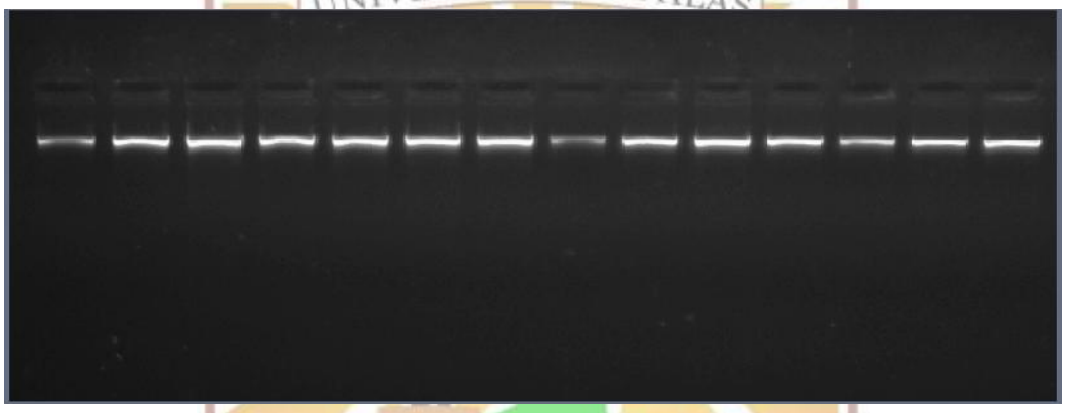
Gambar 1. Hasil isolasi DNA sampel SL1-SL9 (dari kiri ke kanan).



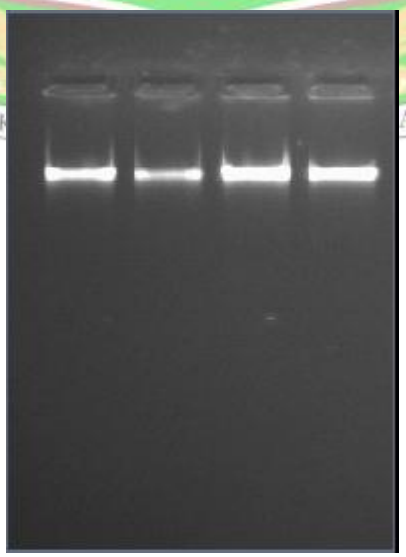
Gambar 2. Hasil isolasi DNA sampel SL18-SL27 dan SLK8-SLK18 (dari kiri ke kanan). SLK14 (-).



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

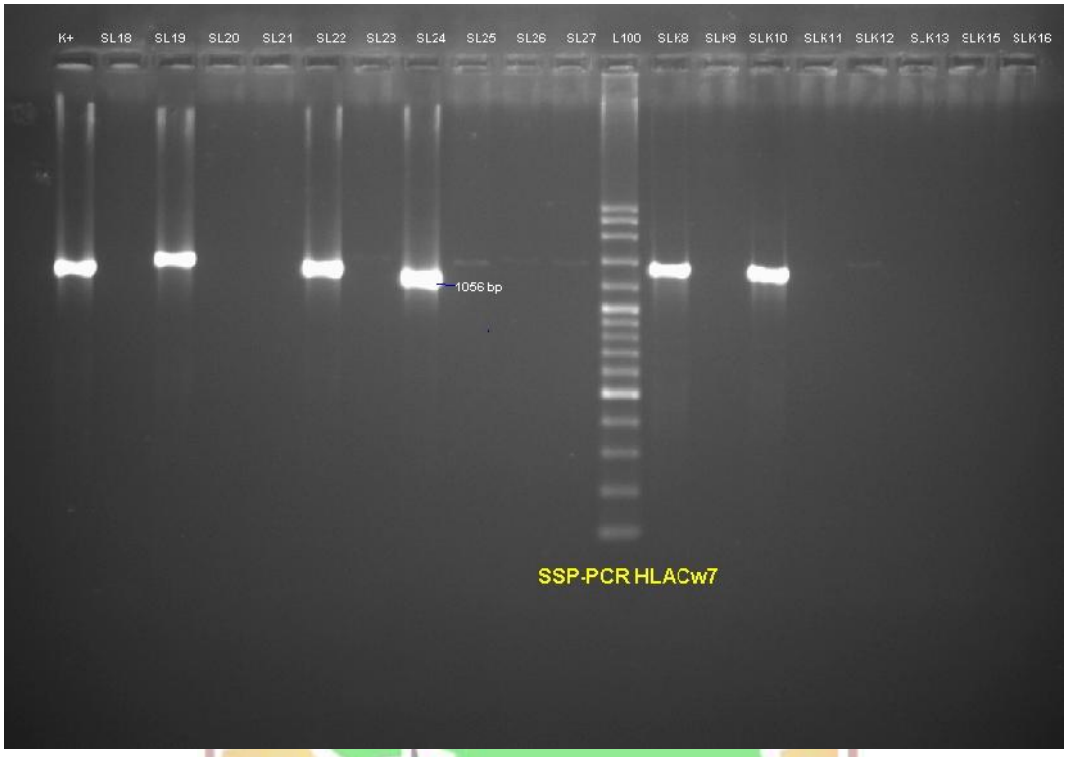


Gambar 4. Hasil isolasi DNA sampel SLK1-SLK7 dan SL11-SL17 (dari kiri ke kanan).

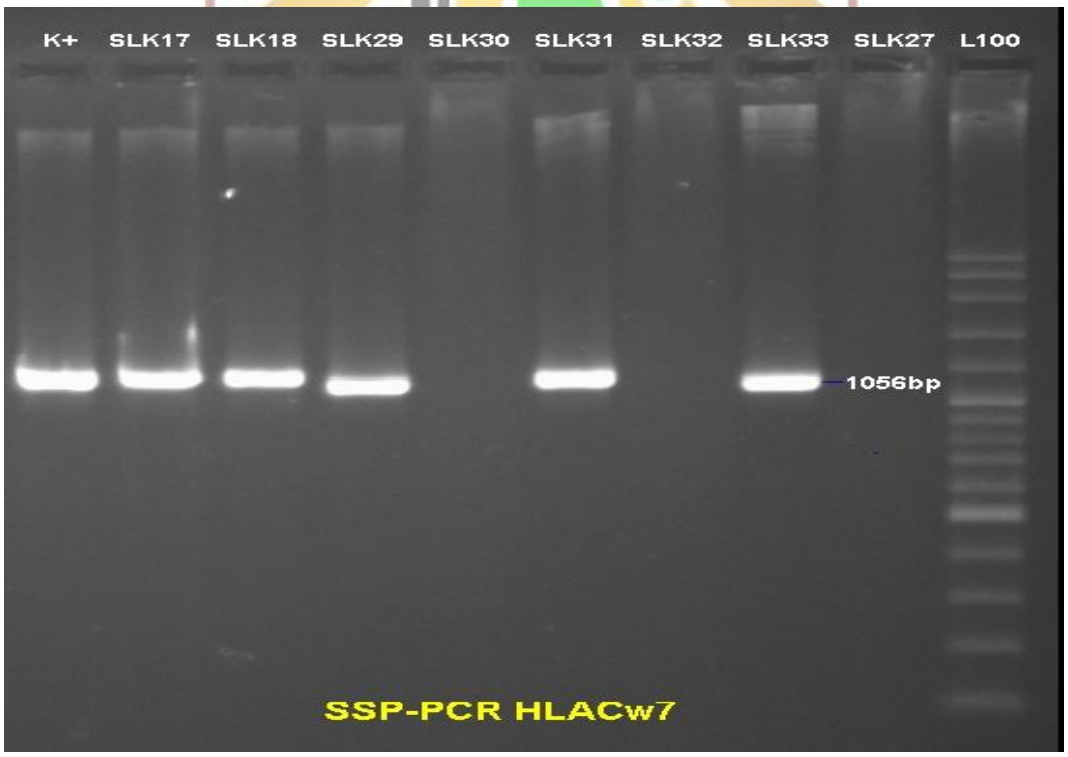


Gambar 5. Hasil isolasi DNA sampel SLK31-32-33-27 (dari kiri ke kanan).

Elektroforegram Hasil PCR HLA-Cw7



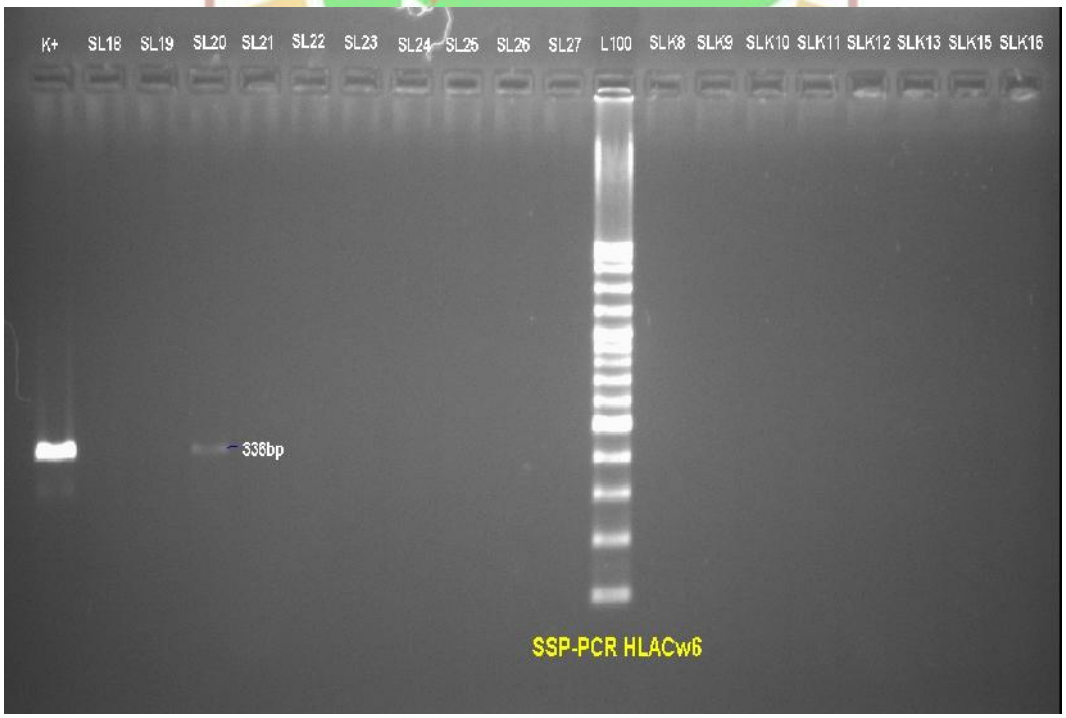
Gambar 6. PCR HLA-Cw7.



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   CTTCCCCATCTCCTATAGATCTCCCGGGATGGCCTCCCACGAGGAGGGGAGGAAAATGGG  239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1301  CTTCCCCATCTCCTATAGATCTCCCGGGATGGCCTCCCACGAGGAGGGGAGGAAAATGGG  1360

Query  240   ATCAGCACTGGAATATCGCCCTCCCTTGAATGGAGAATGGCATGAGTTTTCCTGAGTTTC  299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1361  ATCAGCACTGGAATATCGCCCTCCCTTGAATGGAGAATGGCATGAGTTTTCCTGAGTTTC  1420

Query  300   CTCTGAGGGCCCCCTCTGCTCTCTAGGACAATTAAGGGATGAAGTCTCTGAGGAAATGGA  359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1421  CTCTGAGGGCCCCCTCTGCTCTCTAGGACAATTAAGGGATGAAGTCTCTGAGGAAATGGA  1480

Query  360   GGGGAAGACAGTCCCTGGAATACTGATCAGGGGTCTCCTTTGACCACTTTGACCACTGCA  419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1481  GGGGAAGACAGTCCCTGGAATACTGATCAGGGGTCTCCTTTGACCACTTTGACCACTGCA  1540

Query  420   GCAGCTGTGGTCAGGCTGCTGACCTTTCTCTCAGGCCTTGTTCTCTGCCTCACACTCAAT  479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1541  GCAGCTGTGGTCAGGCTGCTGACCTTTCTCTCAGGCCTTGTTCTCTGCCTCACACTCAAT  1600

Query  480   GTGTCTGAAGGTTTGATTCCAGCTTTTCTGAGTCCTGCAGCCTCCACTCAGGTCAGGACC  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1601  GTGTCTGAAGGTTTGATTCCAGCTTTTCTGAGTCCTGCAGCCTCCACTCAGGTCAGGACC  1660

Query  540   AGAAGTCGCTGTTCCTCCCTCAGAGACTAGAACTTTCCAATGAATAGGAGATTATCCCAG  599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1661  AGAAGTCGCTGTTCCTCCCTCAGAGACTAGAACTTTCCAATGAATAGGAGATTATCCCAG  1720

Query  600   GTGCCTGTGTCCAGGCTGGCGTCTGGGTTCTGTGCCGCCTTCCCCACCCCAGGTGTCCTG  659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1721  GTGCCTGTGTCCAGGCTGGCGTCTGGGTTCTGTGCCGCCTTCCCCACCCCAGGTGTCCTG  1780

Query  660   TCCATTCTCAGGATGGTCACATGGGCGCTGCTGGAGTGTCCCAAGAGAGATGCAAAGTGT  719
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1781  TCCATTCTCAGGATGGTCACATGGGCGCTGCTGGAGTGTCCCAAGAGAGATGCAAAGTGT  1840

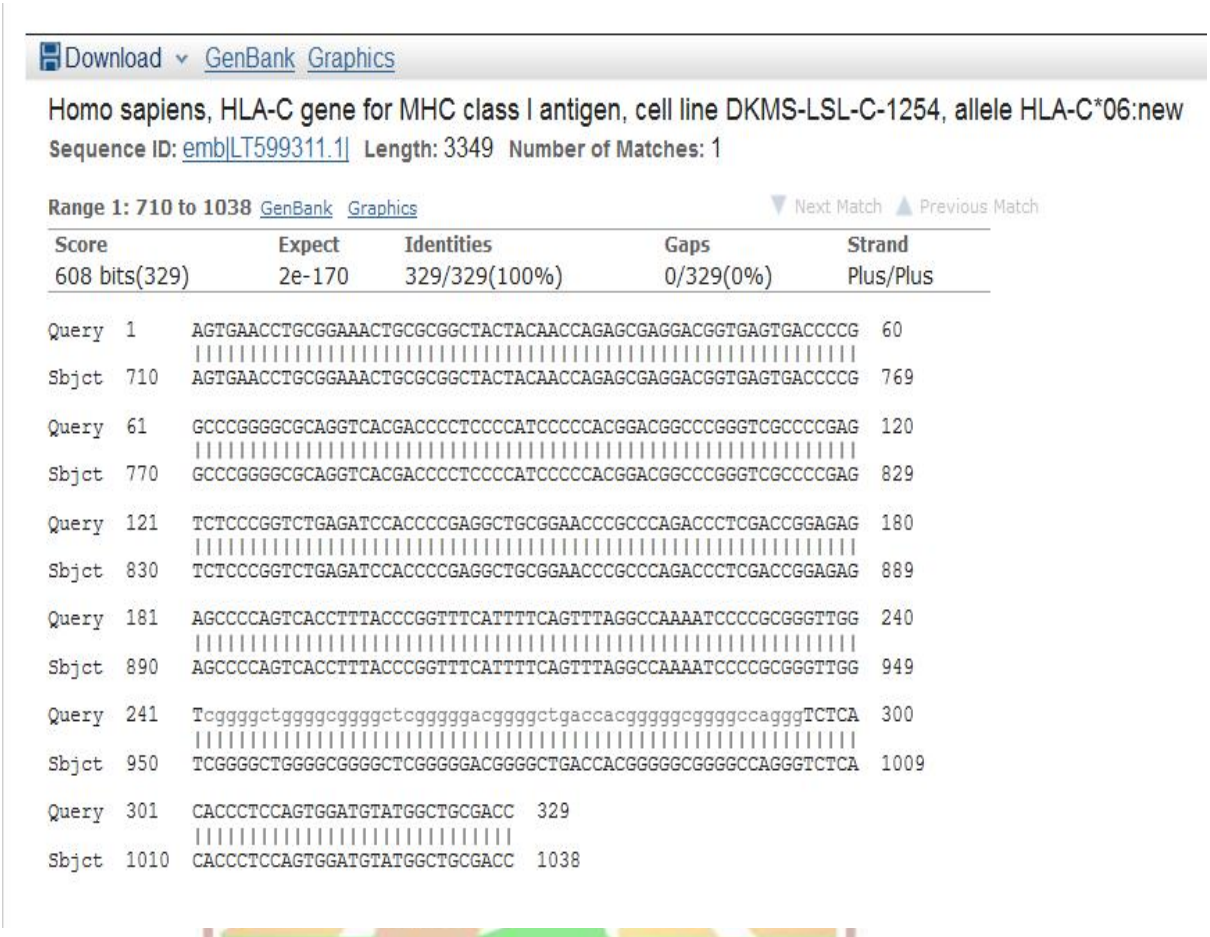
Query  720   CTGAATTTTCTGACTCTTCCCGTCAGAACCCCCAAAGACACACGTGACCCACCACCCCCT  779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1841  CTGAATTTTCTGACTCTTCCCGTCAGAACCCCCAAAGACACACGTGACCCACCACCCCCT  1900

Query  780   CTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCAC  839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1901  CTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCAC  1960

Query  840   ACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACCGAGCTTGTGGAGACCAG  899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1961  ACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACCGAGCTTGTGGAGACCAG  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     AGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACCCCG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  710   AGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACCCCG  769

Query  61    GCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCCGAG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  770   GCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCCGAG  829

Query  121   TCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGAGAG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  830   TCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGAGAG  889

Query  181   AGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGTTGG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  890   AGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGTTGG  949

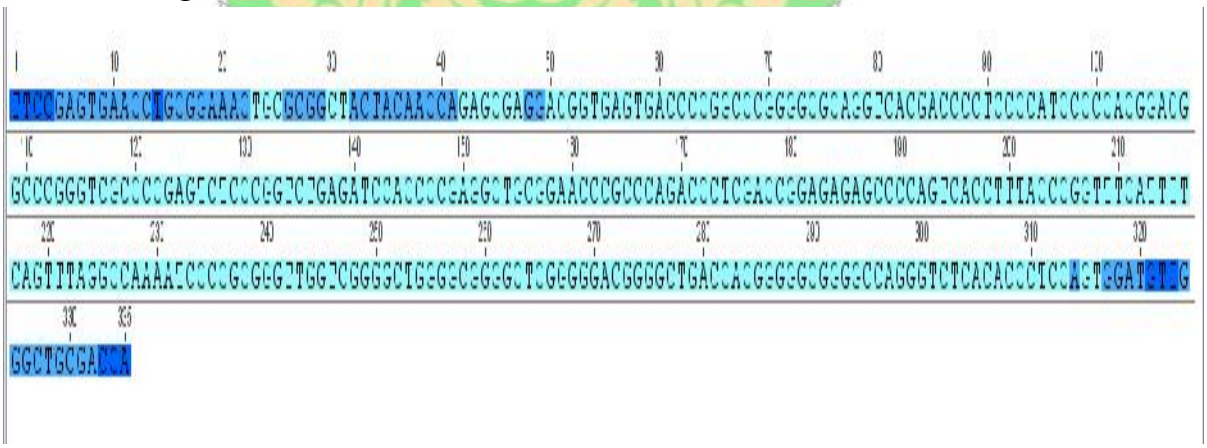
Query  241   TcggggctggggcggggctcgggggacggggctgaccacgggggcggggccagggTCTCA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  950   TCGGGGCTGGGGCGGGGCTCGGGGGACGGGGCTGACCACGGGGGCGGGGCCAGGGTCTCA  1009

Query  301   CACCCTCCAGTGGATGTATGGCTGCGACC  329
             |||||||||||||||||||||||||||||
Sbjct  1010  CACCCTCCAGTGGATGTATGGCTGCGACC  1038
```

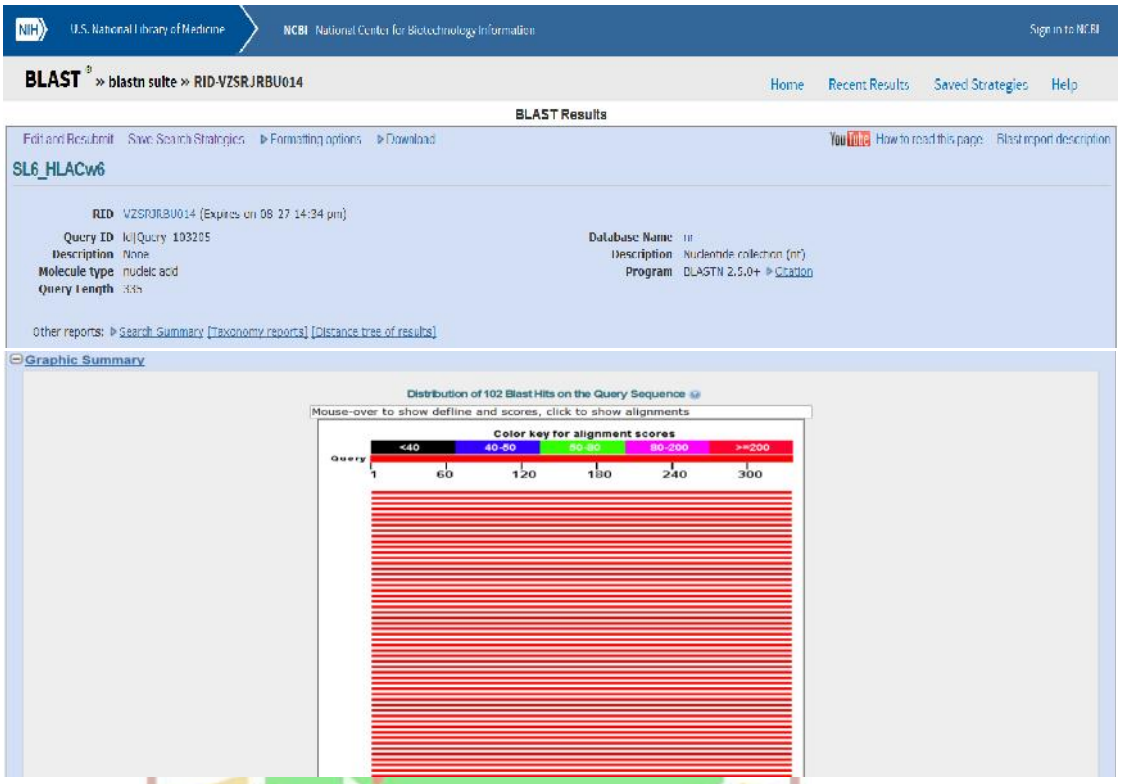
Gambar 12. *Homo sapiens.*

Sampel SL6_HLA-Cw6

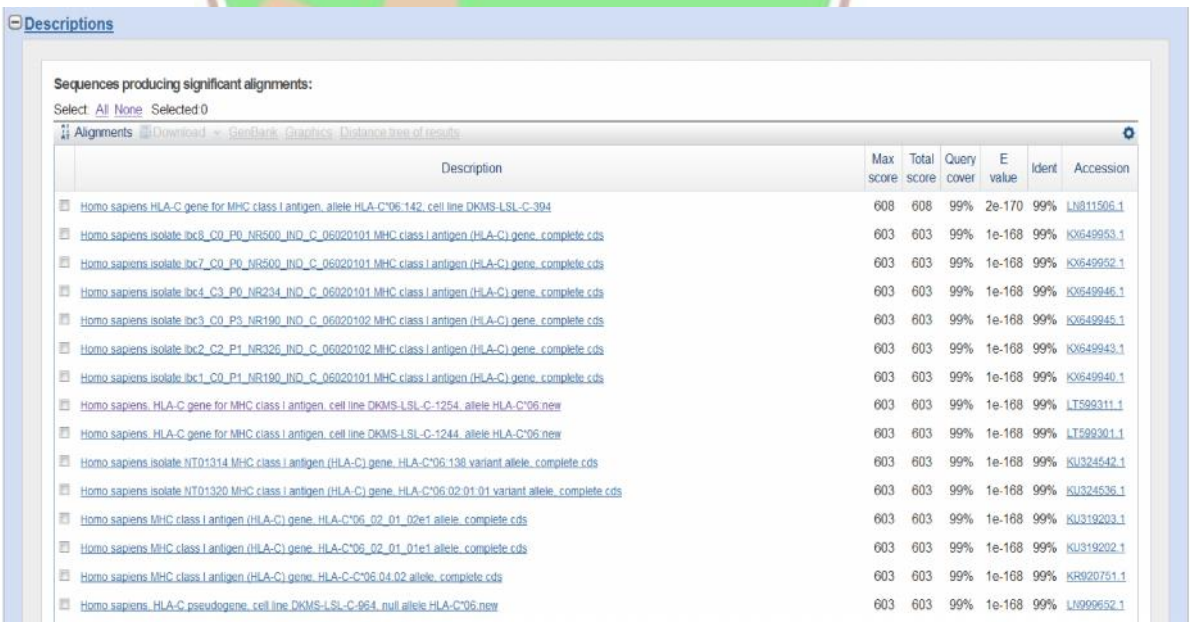
Contig



Gambar 13. Sampel SL6_HLA-Cw6.



Gambar 14. BLAST *result.*



Gambar 15. *Squences producing significant aligment.*

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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     CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  707   CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC  766

Query  63    CCGGCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCC  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  767   CCGGCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCC  826

Query  123   GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGA  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  827   GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGA  886

Query  183   GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  887   GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT  946

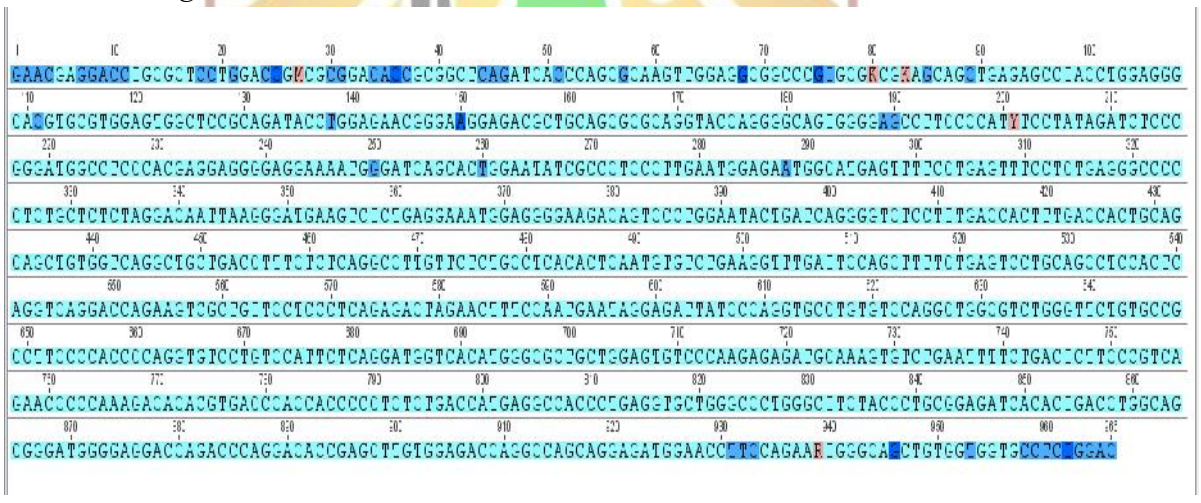
Query  243   TGGTcggggctggggcggggctcgggggacggggctgaccacgggggcgggggccagggTC  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  947   TGGTCGGGGCTGGGGCGGGGCTCGGGGGACGGGGCTGACCACGGGGGCGGGGCCAGGGTC  1006

Query  303   TCACACCCTCCAGTGGATGTTGGGCTGCGACC  334
             ||||||||||||||||||| ||||||||||
Sbjct  1007  TCACACCCTCCAGTGGATGTATGGCTGCGACC  1038
```

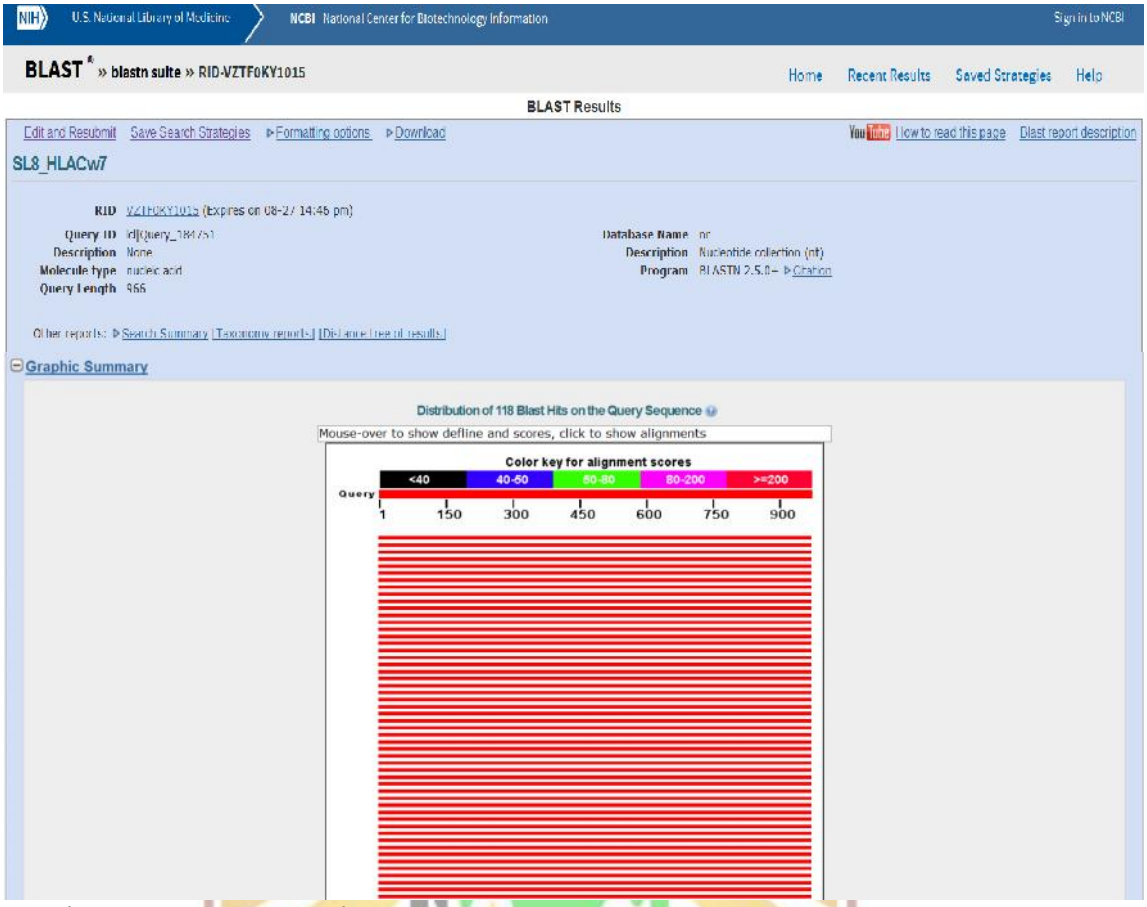
Gambar 16. *Homo sapiens.*

Sampel SL8_HLACw7

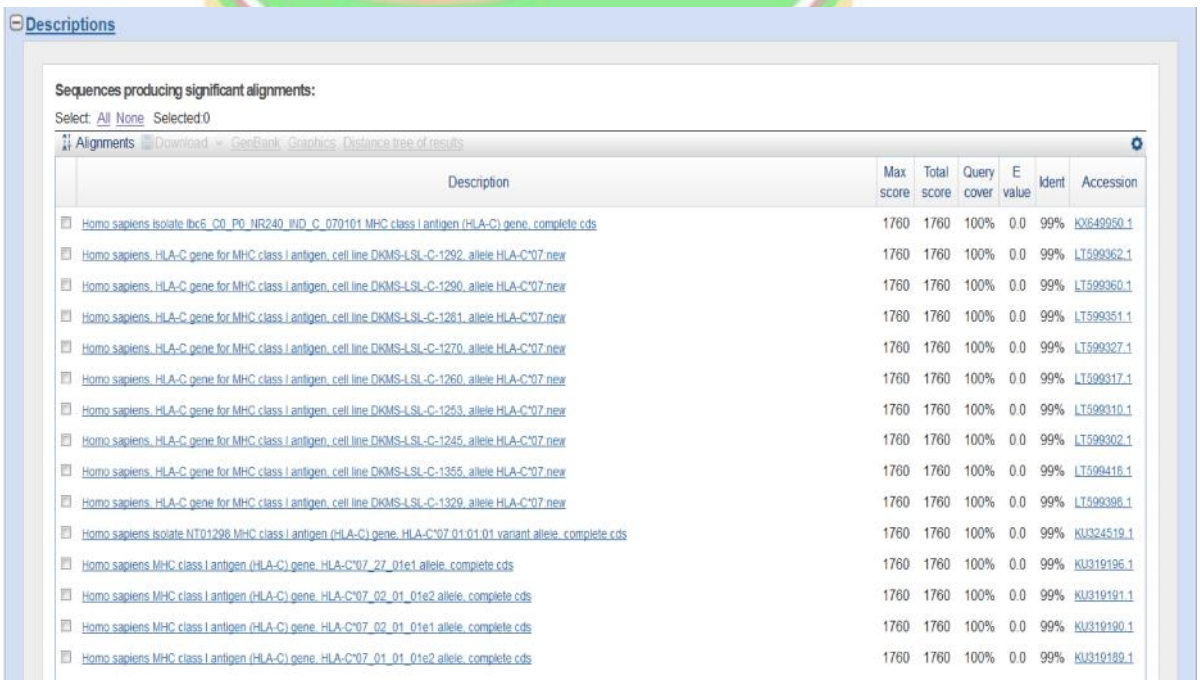
Contig



Gambar 17. Sampel SL8_HLACw7.



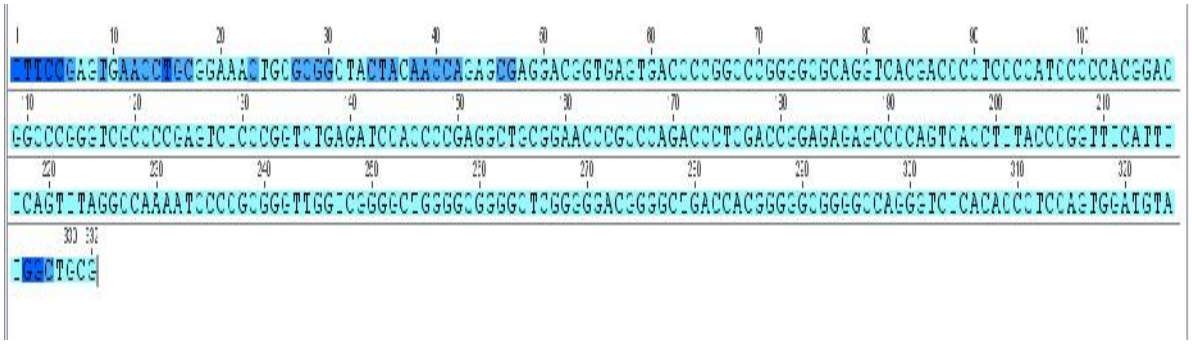
Gambar 18. BLAST *result.*



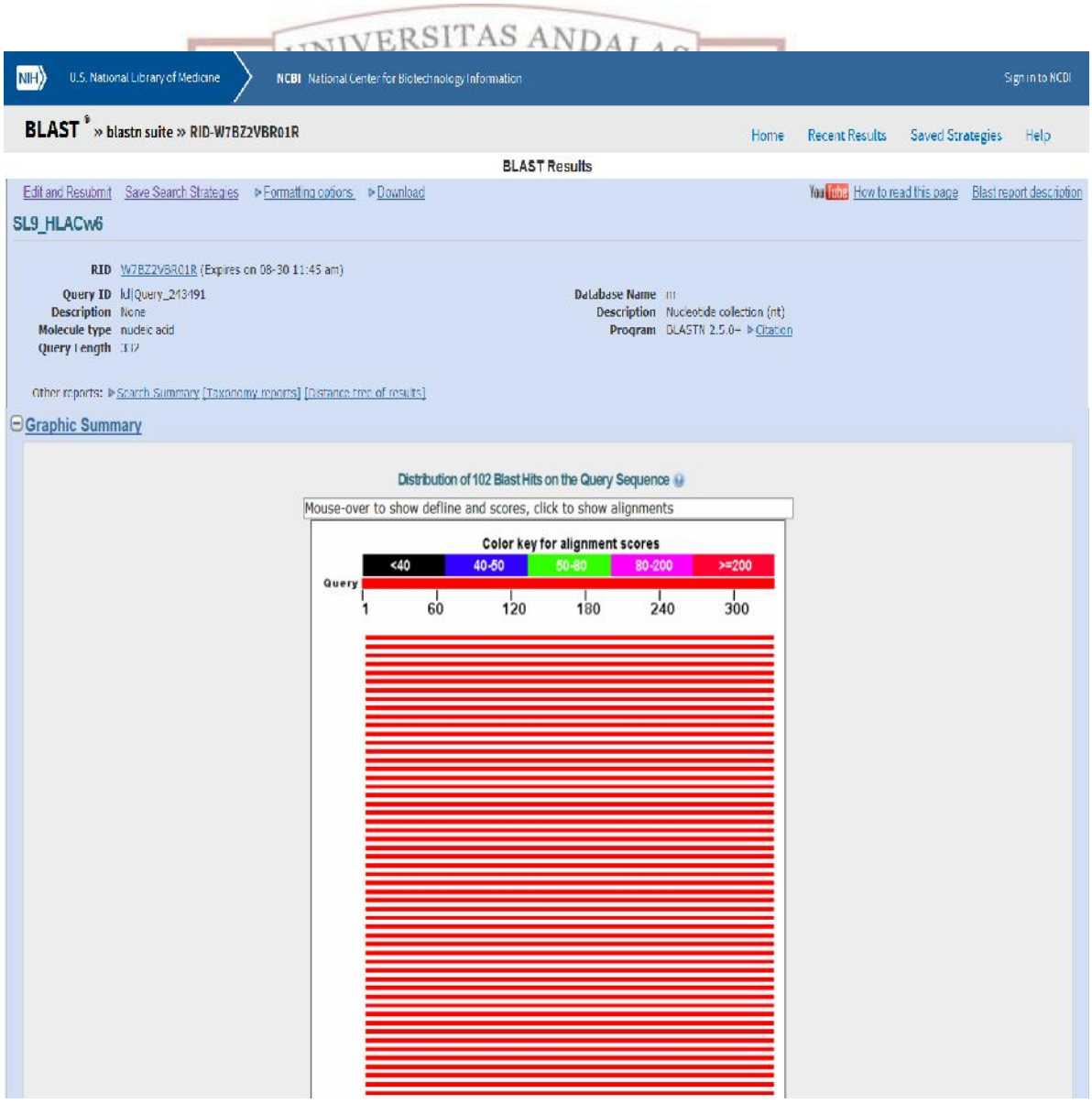
Gambar 19. *Squences producing significant aligment.*

Gambar 20. *Homo sapiens*.

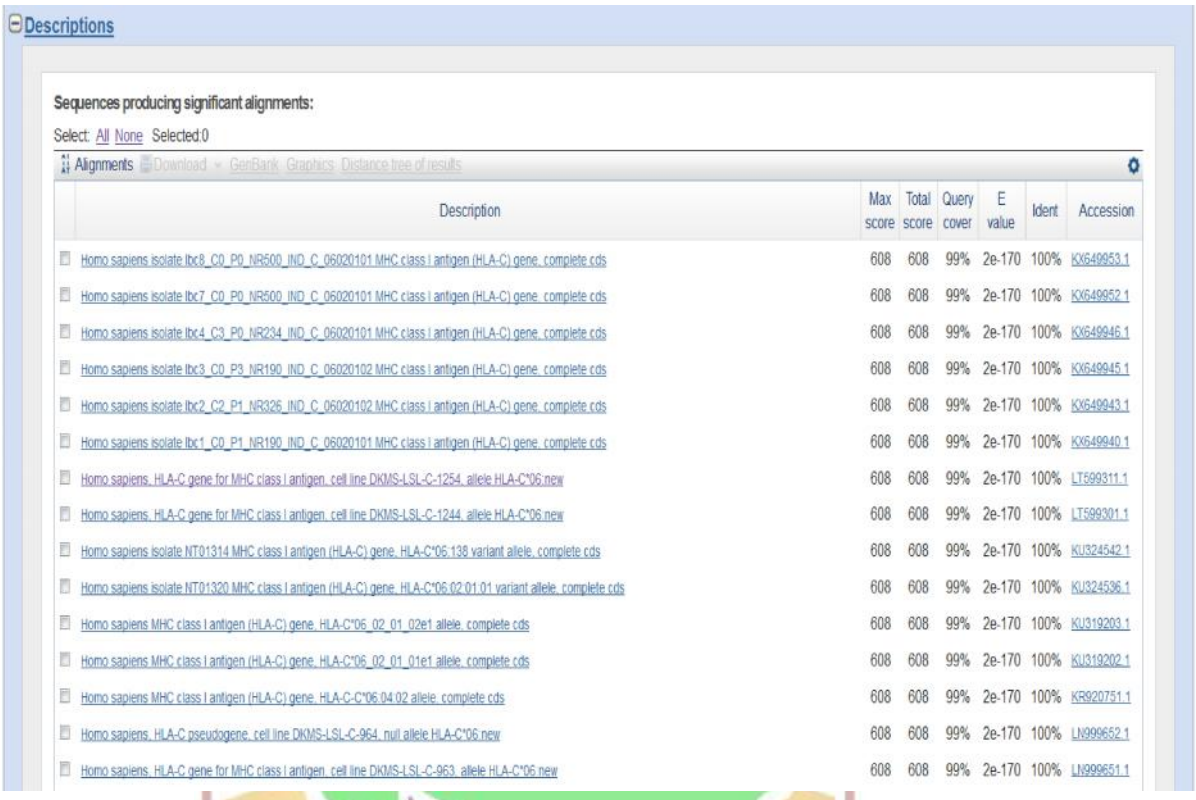
Contig



Gambar 21. Sampel SL9_HLACw6.



Gambar 22. BLAST *result.*



Descriptions

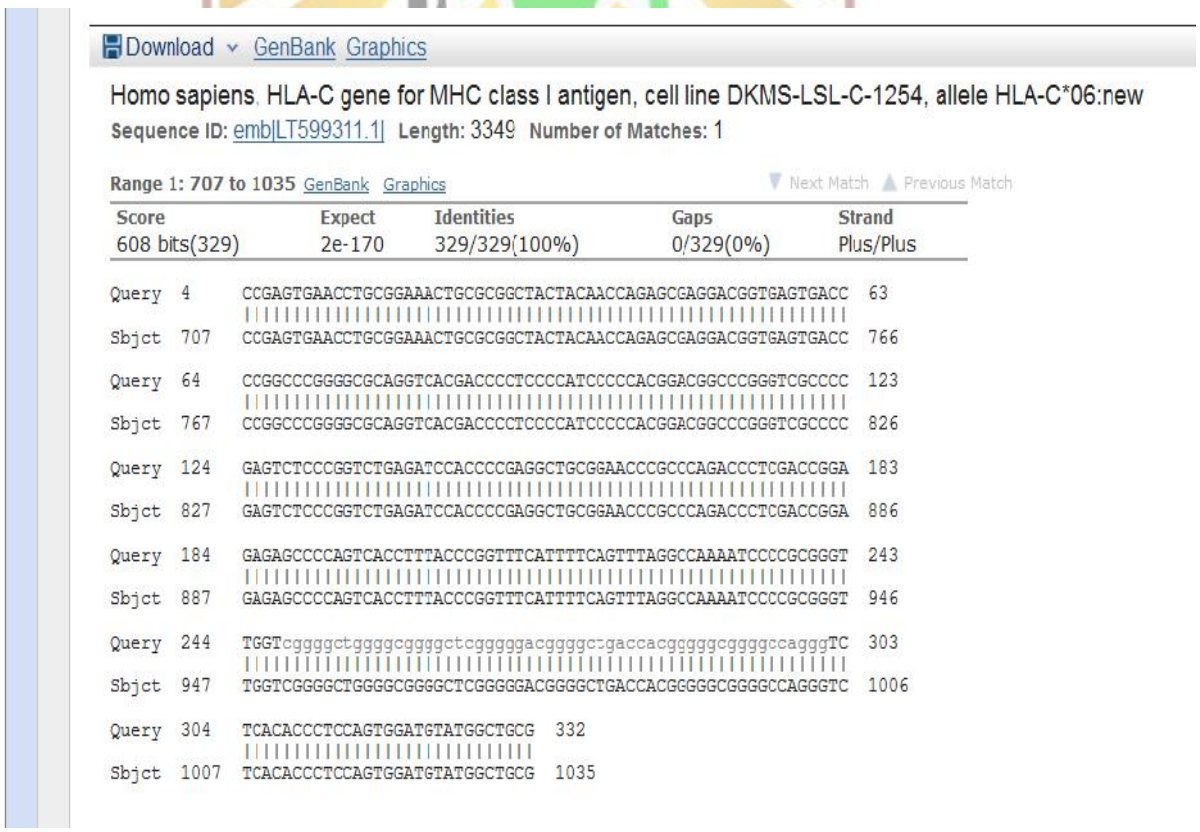
Sequences producing significant alignments:

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 Ibc8_C0_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 Ibc7_C0_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 Ibc4_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 Ibc3_C0_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 Ibc2_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 Ibc1_C0_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%	LN999652.1
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%	LN999651.1

Gambar 23. *Squences producing significant aligment.*



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 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

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Query  4     CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC  63
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Sbjct  707   CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC  766

Query  64    CCGGCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCC  123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  767   CCGGCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCC  826

Query  124   GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGA  183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  827   GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGA  886

Query  184   GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT  243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  887   GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT  946

Query  244   TGGTcggggctggggcggggctcgggggacggggctgaccacgggggcggggccagggTC  303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  947   TGGTCGGGGCTGGGGCGGGGCTCGGGGGACGGGGCTGACCACGGGGGCGGGGCCAGGGTC  1006

Query  304   TCACACCCTCCAGTGGATGTATGGCTGCG  332
             ||||||||||||||||||||||||||||
Sbjct  1007  TCACACCCTCCAGTGGATGTATGGCTGCG  1035
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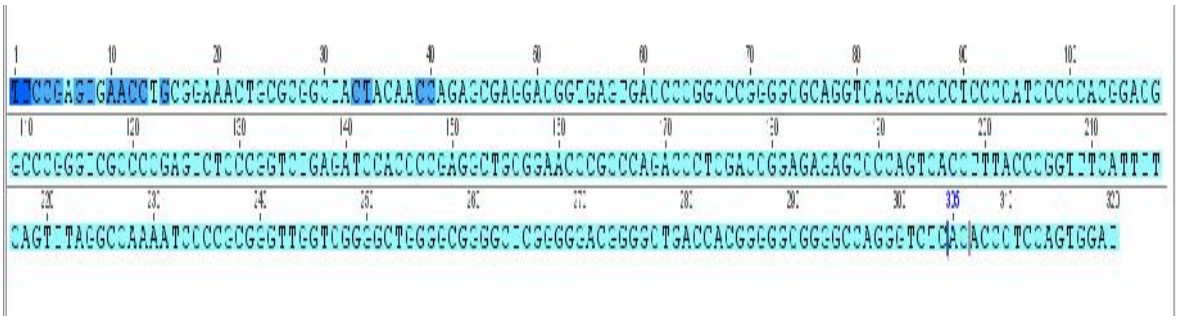
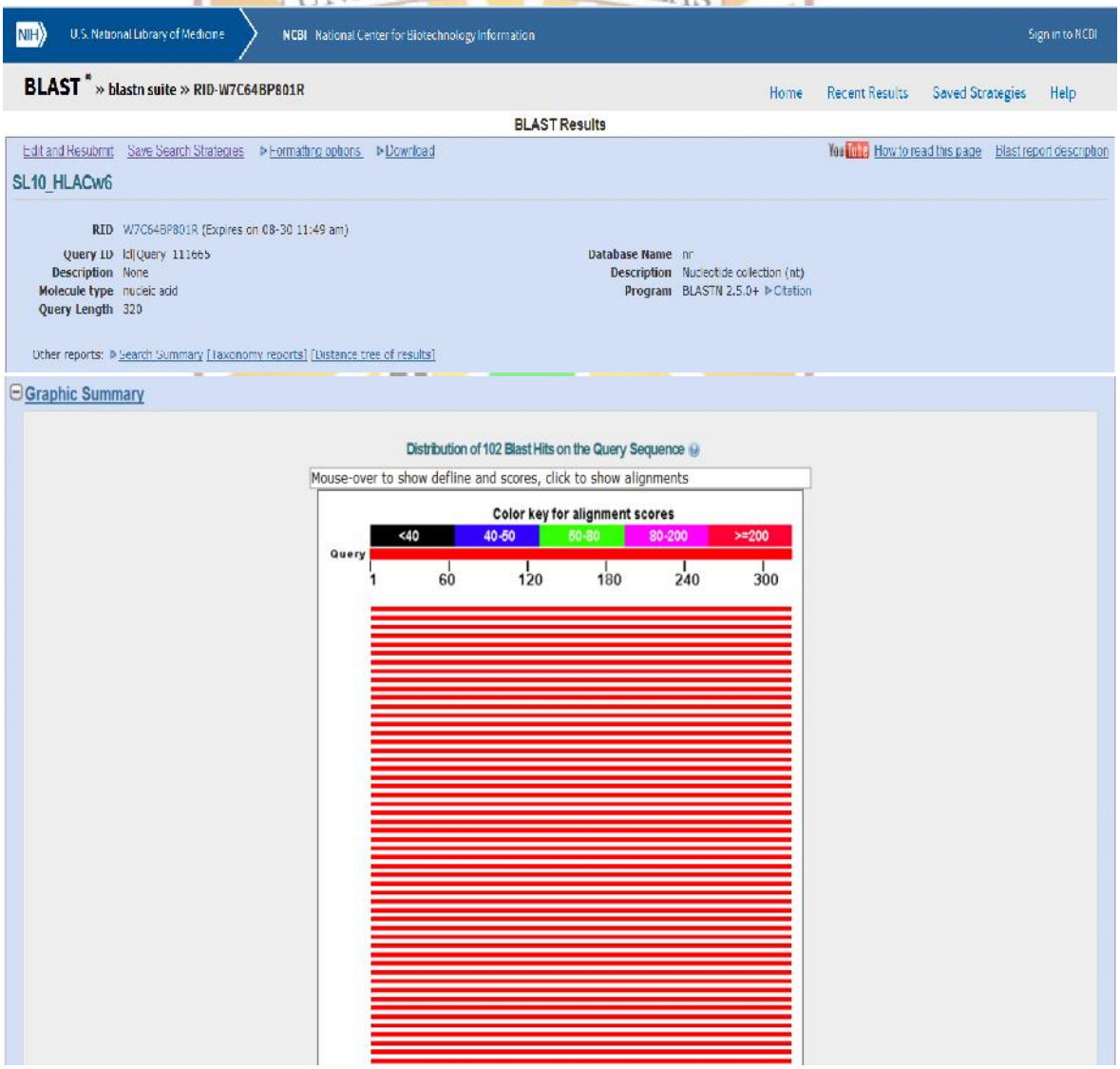
Gambar 24. *Homo sapiens.*

Contig

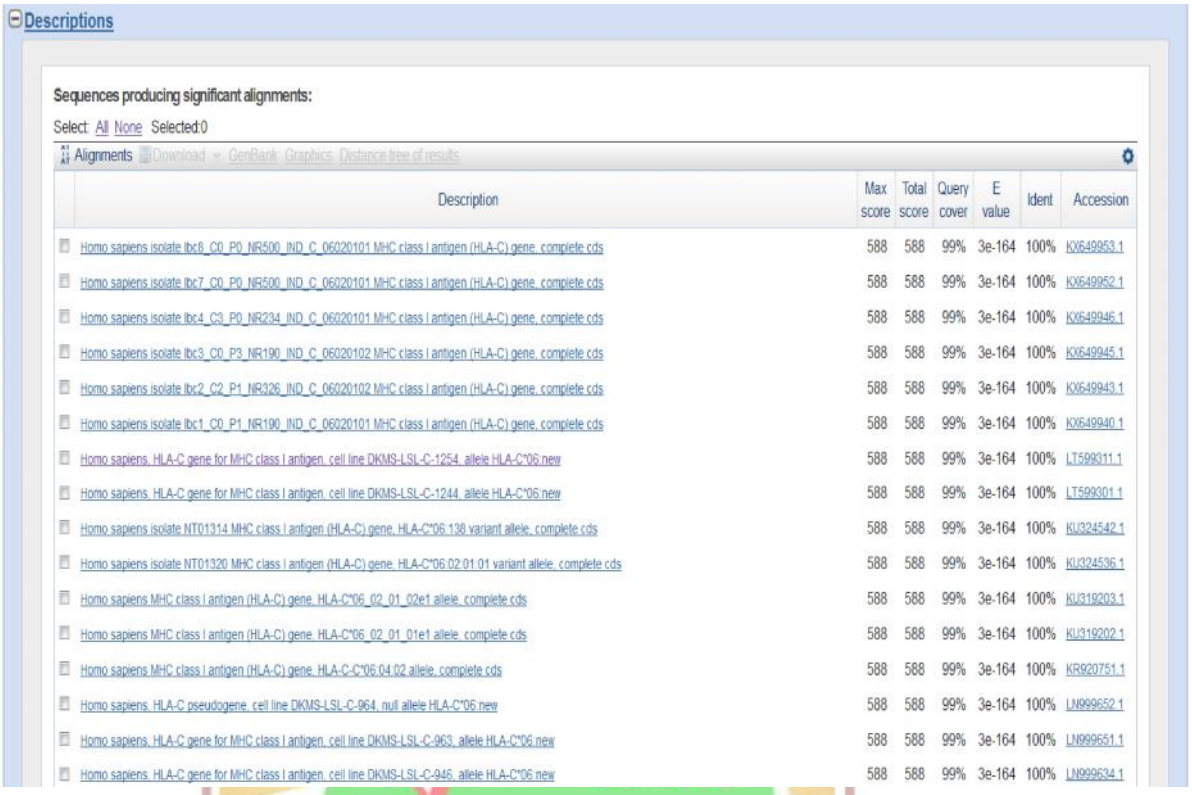


Gambar 25. Sampel SL10_HLACw6.

UNIVERSITAS ANDALAS



Gambar 26. BLAST *result.*



Descriptions

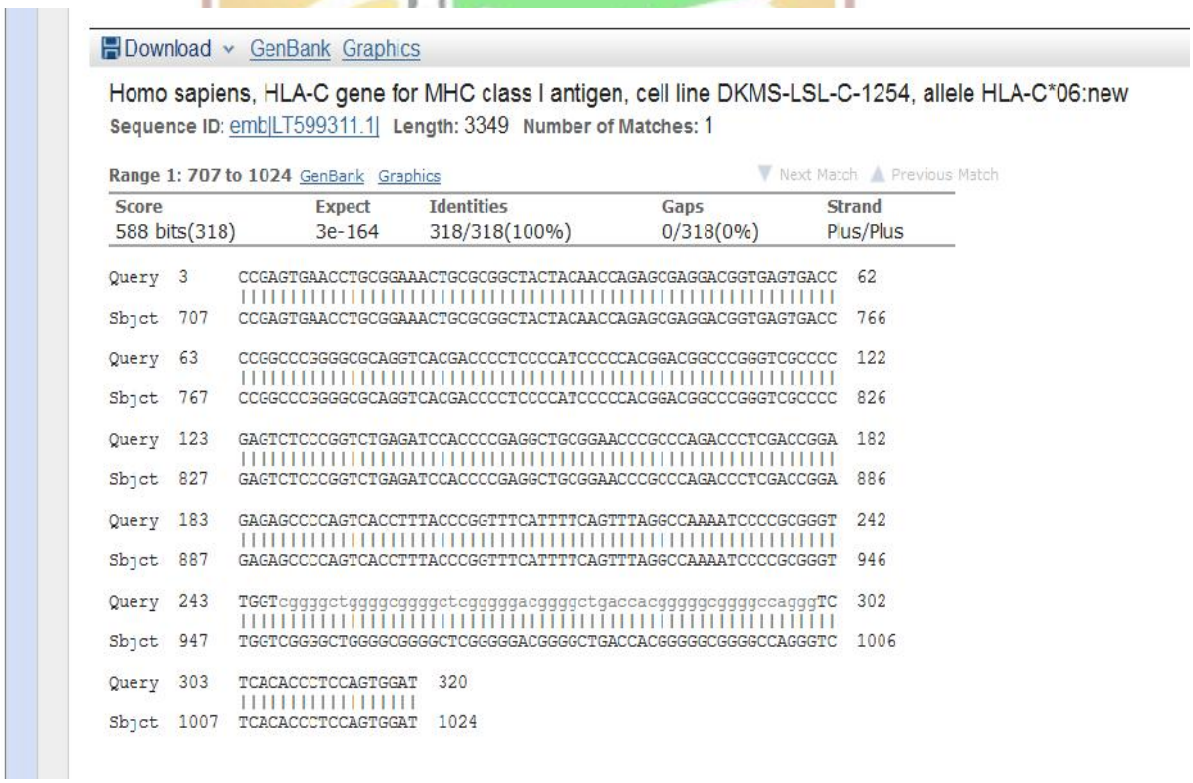
Sequences producing significant alignments:

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 tbc8_C0_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 tbc7_C0_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 tbc4_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 tbc3_C0_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 tbc2_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 tbc1_C0_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%	KU324542.1
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%	KU324536.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06_02_01_02e1 allele, complete cds	588	588	99%	3e-164	100%	KU319203.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*06_02_01_01e1 allele, complete cds	588	588	99%	3e-164	100%	KU319202.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C-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. *Squences producing significant aligment.*



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

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Query  3     CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC  62
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Sbjct  707   CCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACGGTGAGTGACC  766

Query  63    CCGGCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCC  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  767   CCGGCCCGGGGCGCAGGTCACGACCCCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCC  826

Query  123   GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGA  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  827   GAGTCTCCCGGTCTGAGATCCACCCCGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGA  886

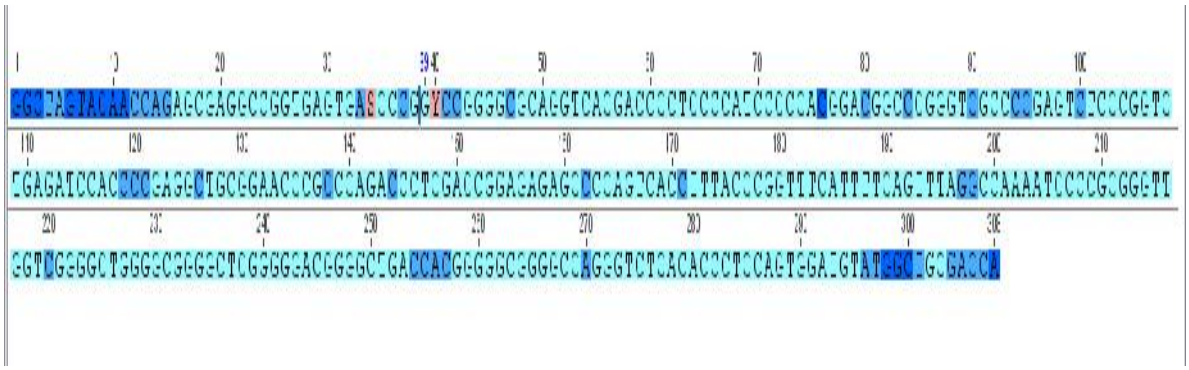
Query  183   GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  887   GAGAGCCCCAGTCACCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGT  946

Query  243   TGGTcggggctggggcggggctcgggggacggggctgaccacgggggcggggccagggTC  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  947   TGGTCGGGGCTGGGGCGGGGCTCGGGGGACGGGGCTGACCACGGGGGCGGGGCCAGGGTC  1006

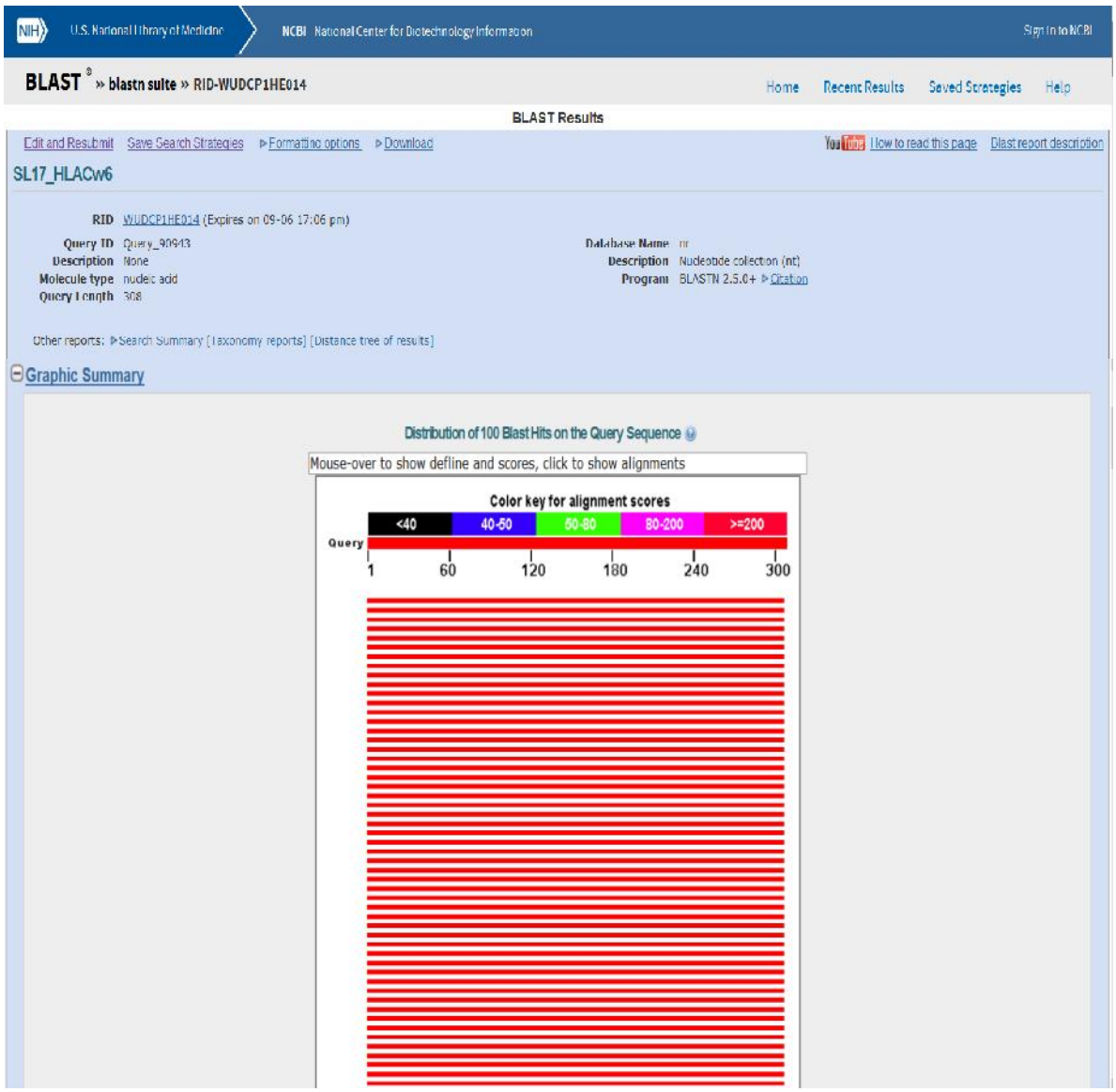
Query  303   TCACACCCTCCAGTGGAT  320
             |||||||||||||||||
Sbjct  1007  TCACACCCTCCAGTGGAT  1024
```

Gambar 28. *Homo sapiens.*

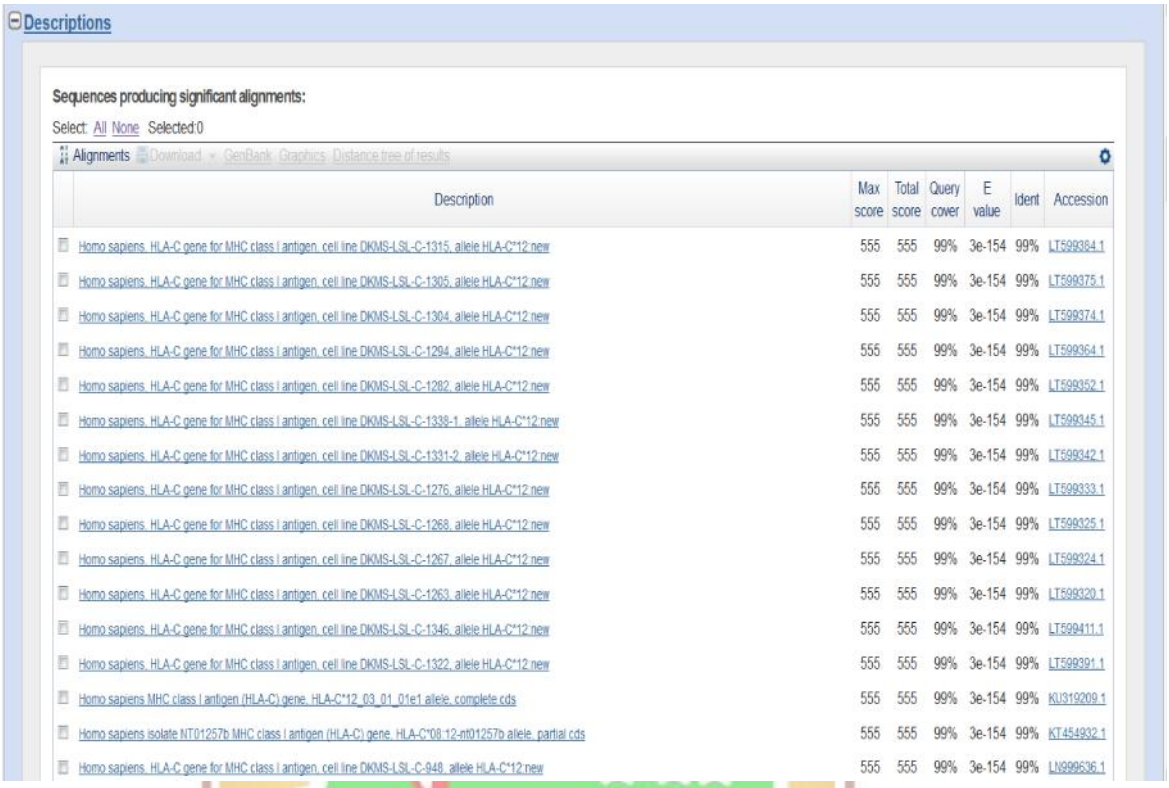
Contig



Gambar 29. Sampel SL17_HLACw6.



Gambar 30. *BLAST result.*



Descriptions

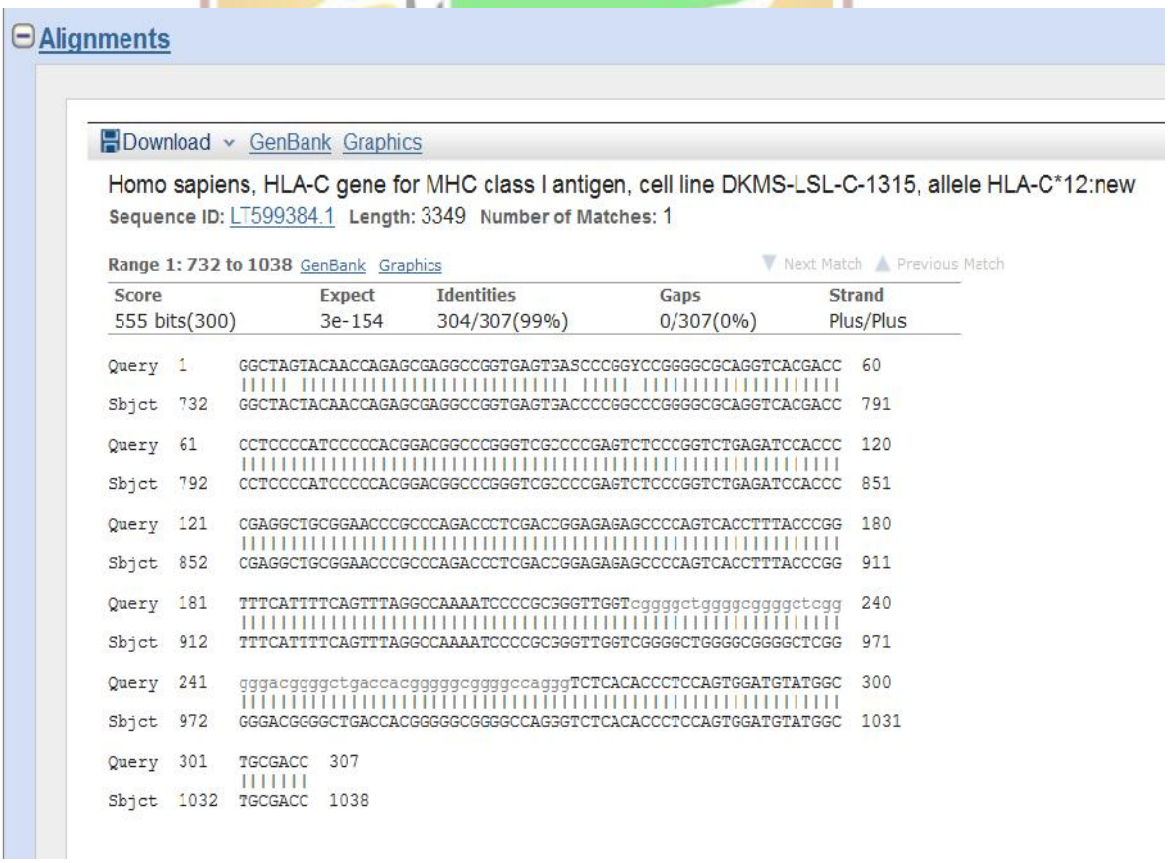
Sequences producing significant alignments:

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%	LN999536.1

Gambar 31. *Squences producing significant aligment.*



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

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Query  1     GGCTAGTACAACCAGAGCGAGGCCGGTGAGTGASCCCGGYCCGGGGCGCAGGTCACGACC  60
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Sbjct  732   GGCTACTACAACCAGAGCGAGGCCGGTGAGTGACCCCGGCCCGGGGCGCAGGTCACGACC  791

Query  61    CCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCCGAGTCTCCCGGTCTGAGATCCACCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  792   CCTCCCCATCCCCCACGGACGGCCCGGGTCGCCCCGAGTCTCCCGGTCTGAGATCCACCC  851

Query  121   CGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGAGAGAGCCCCAGTCACCTTTACCCGG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  852   CGAGGCTGCGGAACCCGCCCAGACCCTCGACCGGAGAGAGCCCCAGTCACCTTTACCCGG  911

Query  181   TTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGTTGGTcggggctggggcggggctcgg  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  912   TTTCATTTTCAGTTTAGGCCAAAATCCCCGCGGGTTGGTCGGGGCTGGGGCGGGGCTCGG  971

Query  241   gggacggggctgaccacgggggcggggccagggTCTCACACCCTCCAGTGGATGTATGGC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  972   GGGACGGGGCTGACCACGGGGGCGGGGCCAGGGTCTCACACCCTCCAGTGGATGTATGGC  1031

Query  301   TGCGACC  307
             |||||||
Sbjct  1032  TGCGACC  1038
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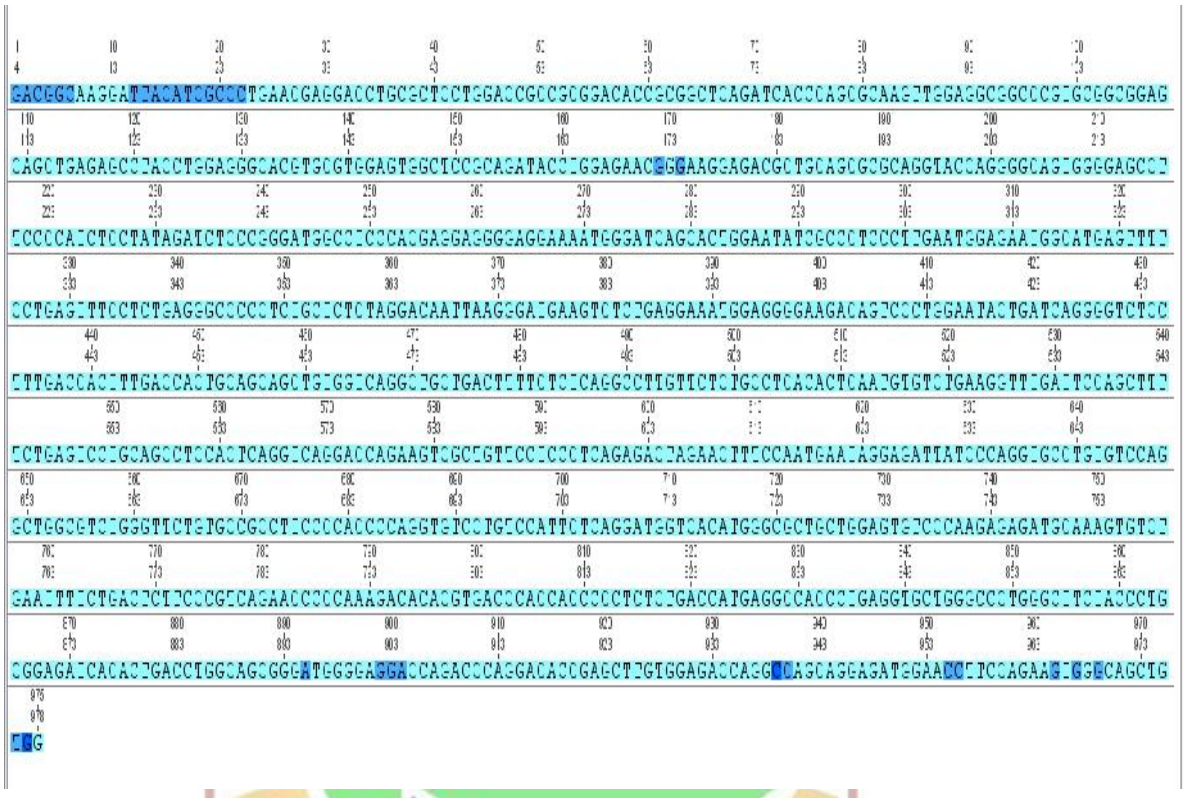
Gambar 32. *Homo sapiens*.

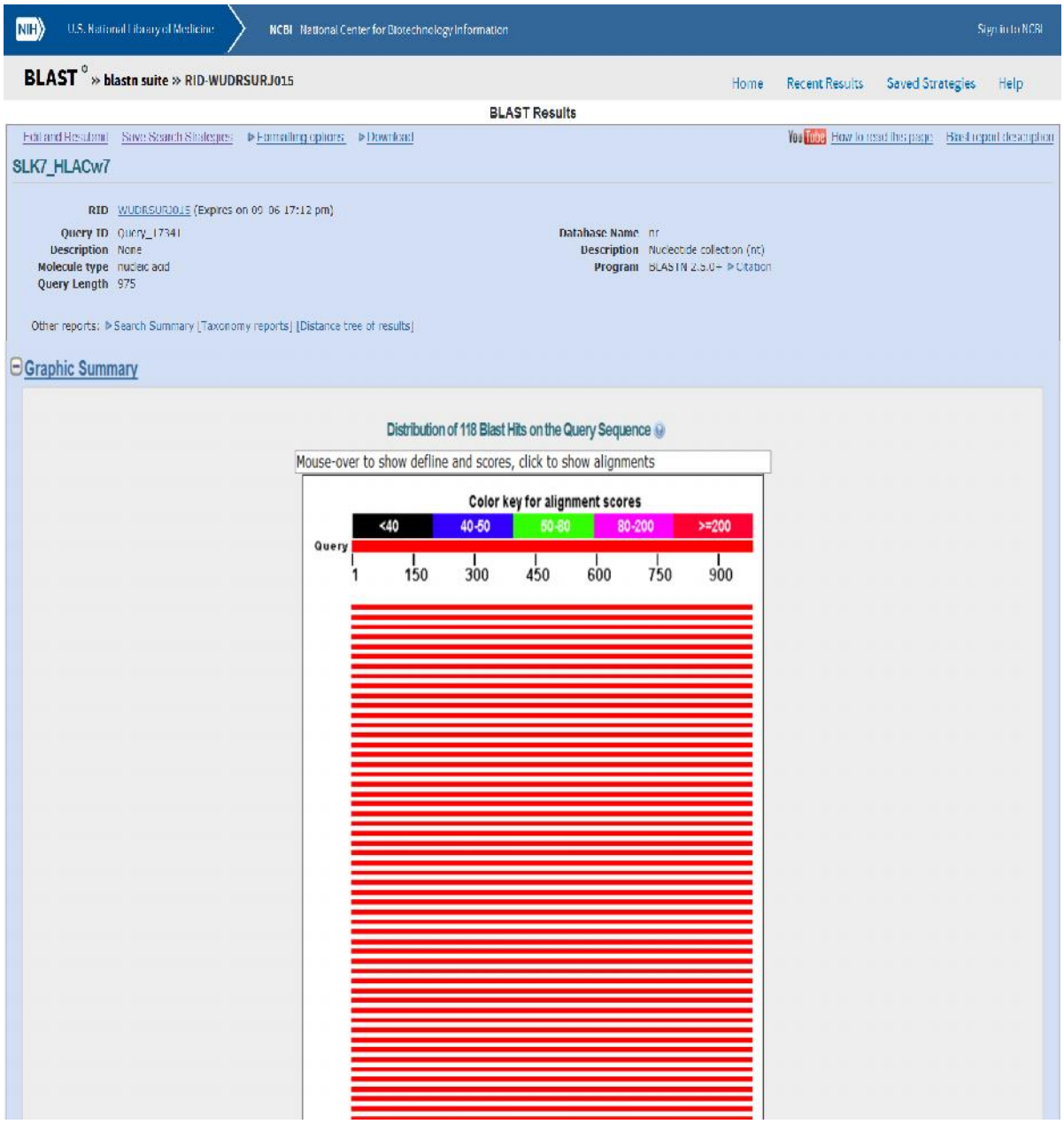
Contig



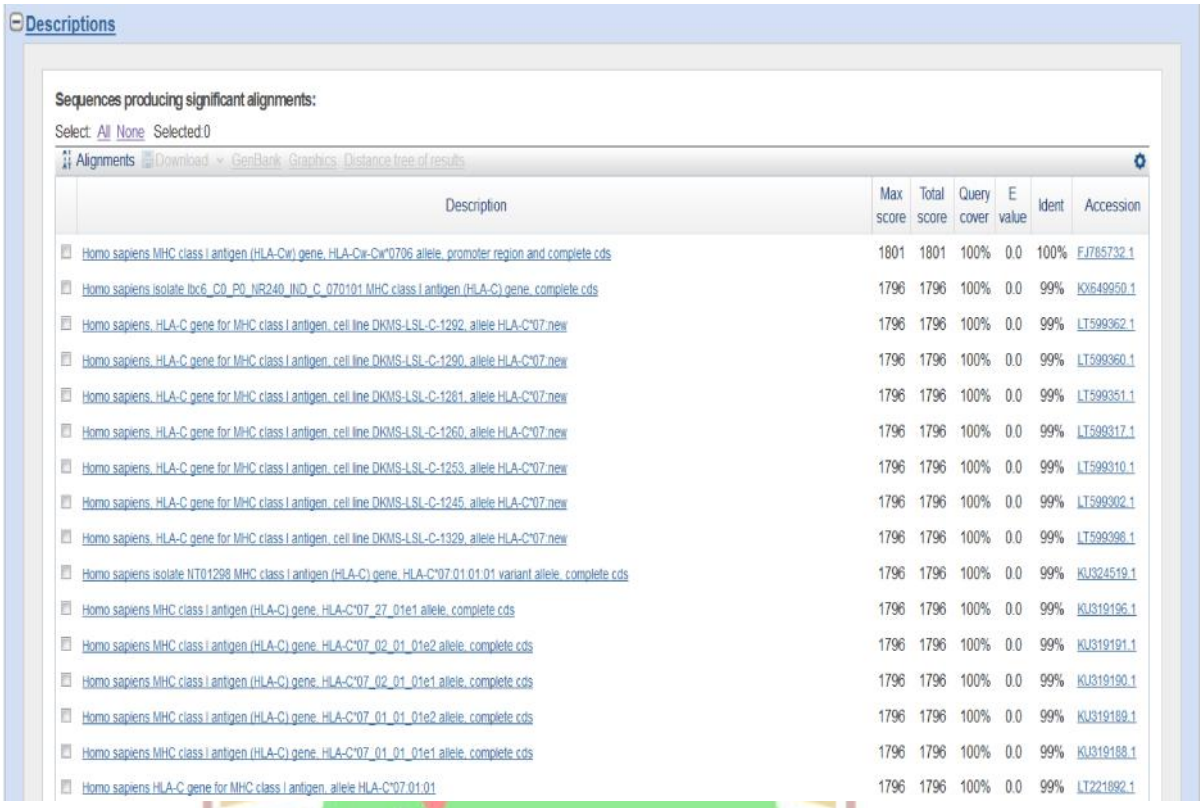
Gambar 33. Sampel SLK7_HLACw7.

UNTUK KEDJAJAAN BANGSA

BLAST *result*



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
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
Homo sapiens isolate tbc6_C0_P0_NR240_IND_C_070101 MHC class I antigen (HLA-C) gene, complete cds	1796	1796	100%	0.0	99%	KX649950.1
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
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
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1261, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599351.1
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
Homo sapiens, HLA-C gene for MHC class I antigen, cell line DKMS-LSL-C-1253, allele HLA-C*07:new	1796	1796	100%	0.0	99%	LT599310.1
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
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%	LT599396.1
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%	KU324519.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_27_01e1 allele, complete cds	1796	1796	100%	0.0	99%	KU319196.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_02_01_01e2 allele, complete cds	1796	1796	100%	0.0	99%	KU319191.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_02_01_01e1 allele, complete cds	1796	1796	100%	0.0	99%	KU319190.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_01_01_01e2 allele, complete cds	1796	1796	100%	0.0	99%	KU319189.1
Homo sapiens MHC class I antigen (HLA-C) gene, HLA-C*07_01_01_01e1 allele, complete cds	1796	1796	100%	0.0	99%	KU319188.1
Homo sapiens HLA-C gene for MHC class I antigen, allele HLA-C*07:01:01	1796	1796	100%	0.0	99%	LT221892.1

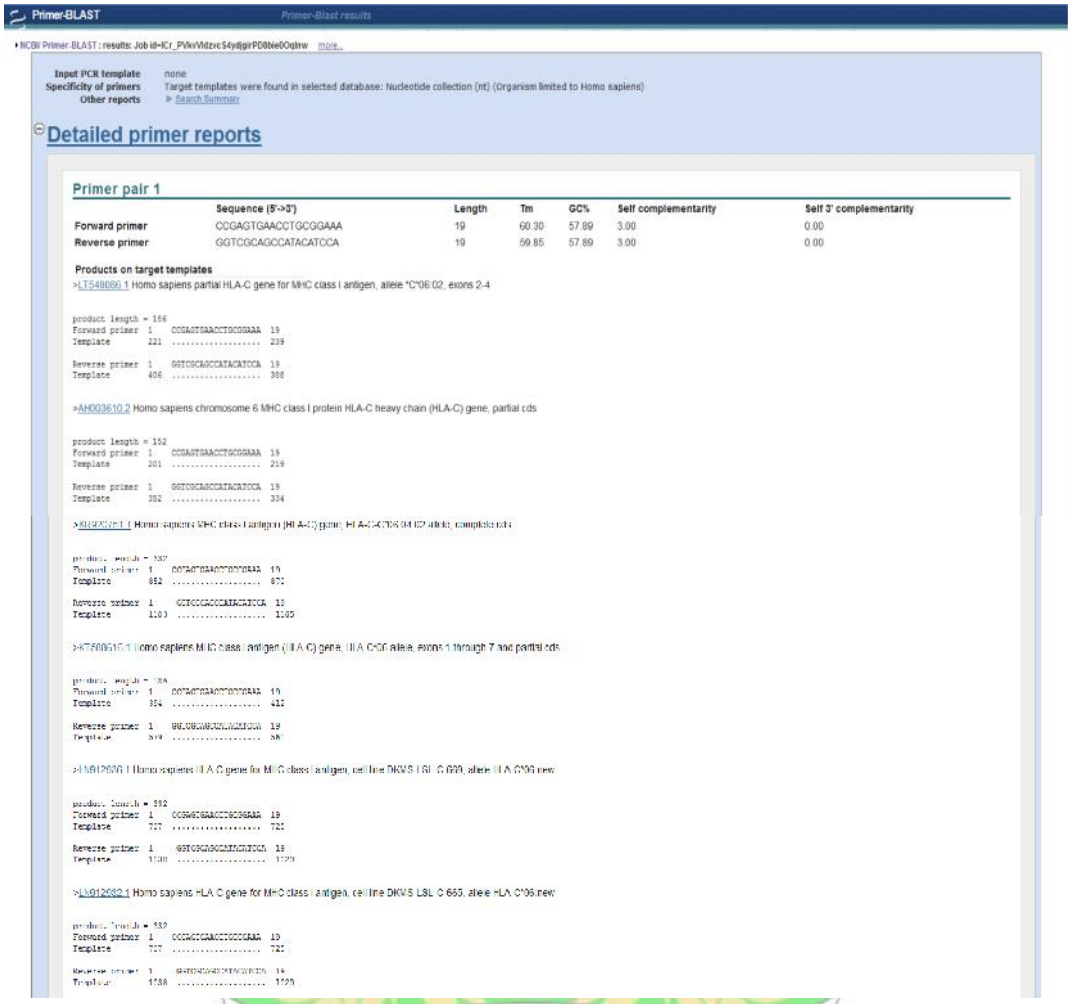
Gambar 35. *Squences producing significant aligment.*

UNTUK KEDJAJAAN BANGSA

Gambar 36. *Homo sapiens*.

Hasil *Primer* BLAST

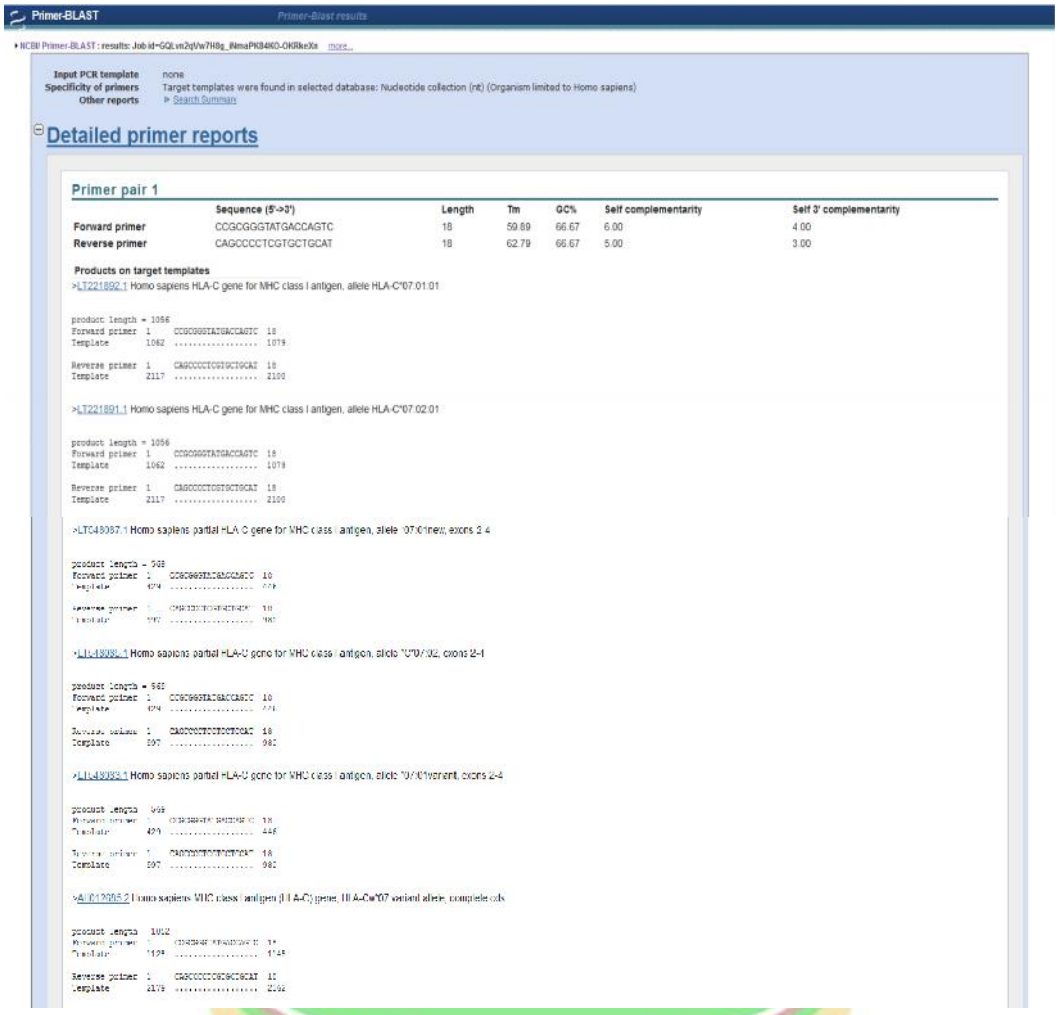
Pasangan *primer* HLA-Cw6



Gambar 37. Pasangan *primer* HLA-Cw6

UNTUK KEDJAJAAN BANGSA

Pasangan *primer* HLA-Cw7



Gambar 38. Pasangan *primer* HLA-Cw7

UNTUK KEDJAJAAN BANGSA

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 mem*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	2255800714,223
	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	2257850406,339
	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.

UNIVERSITAS ANDALAS

Risk Estimate

Risk Estimate

	Value	95% Confidence Interval	
	Lower	Upper	Lower
For cohort GROUP = Kasus	2,250	1,670	3,032
N of Valid Cases	60		

	Value	95% Confidence Interval	
	Lower	Upper	Lower
Odds Ratio for HLA-Cw7 (1,00 / 2,00)	,710	,225	2,246
For cohort GROUP = 1,00	,837	,449	1,561
For cohort GROUP = 2,00	1,179	,693	2,005
N of Valid Cases	60		