

Lampiran 1. Certificate of Analysis (CoA)

Rat OLR1 / LOX1 Protein (Fc Tag)

Catalog Number: 80268-R01H



Sino Biological Inc.
Biological Solution Specialist

General Information

Gene Name Synonym:

OLR1, Lox1, Oldlr1

Protein Construction:

A DNA sequence encoding the rat OLR1 (O70156) (Leu60-Gln364) was expressed with Fc region of human IgG1 at the N-terminus.

Source: Rat

Expression Host: Human Cells

QC Testing

Purity: (90.4±8.5) % as determined by SDS-PAGE

Endotoxin:

< 1.0 EU per µg of the protein as determined by the LAL method

Stability:

Samples are stable for up to twelve months from date of receipt at -70 °C

Predicted N terminal: Glu

Molecular Mass:

The recombinant rat OLR1 comprises 565 amino acids and predicts a molecular mass of 63.9 kDa. The apparent molecular mass of the recombinant protein is approximately 66 and 35 kDa in SDS-PAGE under reducing conditions due to glycosylation.

Formulation:

Lyophilized from sterile PBS, pH 7.4

Usage Guide

Storage:

Store it under sterile conditions at -20°C to -80°C upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

Protein Description

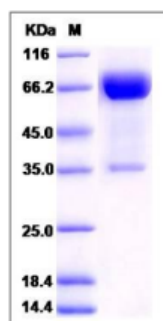
Oxidized low-density lipoprotein receptor 1 (Ox-LDL receptor 1) also known as lectin-type oxidized LDL receptor 1 (LOX-1) is a receptor protein which belongs to the C-type lectin superfamily. Lectin-like oxidized LDL receptor-1 (LOX-1) was isolated from an aortic endothelial cell, and recently it has been discovered in macrophages and vascular smooth muscle cells in artery vessels. The expression of LOX-1 is induced by inflammatory stimuli, so LOX-1 is thought to be involved in the development of atherosclerotic lesions. It is an important cell surface receptor for the progression of atherosclerosis. LOX-1 is a multi-ligand receptor originally identified as the endothelial oxidized LDL receptor. LOX-1 expression is also induced in smooth muscle cells in response to proinflammatory and oxidative stimuli. LOX-1 may play an important role in the progression of vulnerable carotid plaque and might regulate vulnerable plaque formation in cooperation with MMPs and TIMP-2.

References

1. Hinagata J. et al., 2006, Cardiovasc Res. 69 (1): 263-71.
2. Melan MA. et al., 1994, Plant Physiol. 105 (1): 385-93.
3. Saito A. et al., 2010, Acta Neurochir (Wien). 152 (4): 589-95.

Normally 5 % - 8 % trehalose and mannitol are added as protectants before lyophilization. Specific concentrations are included in the hardcopy of COA. Please contact us for any concerns or special requirements.

SDS-PAGE:



Manufactured By Sino Biological Inc., FOR RESEARCH USE ONLY. NOT FOR USE IN HUMANS.

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Lampiran 2. Perhitungan untuk Preparasi Vaksin

- Konsentrasi larutan stok protein = $\frac{100 \mu\text{g}}{400 \mu\text{l}} = 0,25 \mu\text{g}/\mu\text{l}$
- Pengenceran larutan stok protein dengan konsentrasi $25 \times 10^{-2} \mu\text{g}/\mu\text{l}$ menjadi $1 \times 10^{-2} - 10^{-5} \mu\text{g}/\mu\text{l}$

- Kelompok perlakuan 4 (P_4) : Larutan baku protein $1 \times 10^{-2} \mu\text{g}/\mu\text{l}$ dari larutan stok protein $25 \times 10^{-2} \mu\text{g}/\mu\text{l}$

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 25 \times 10^{-2} \mu\text{g}/\mu\text{l} = 500 \mu\text{l} \times 1 \times 10^{-2} \mu\text{g}/\mu\text{l}$$

$$V_1 = 20 \mu\text{l}$$

- Kelompok perlakuan 3 (P_3) : Larutan baku protein $1 \times 10^{-3} \mu\text{g}/\mu\text{l}$ dari larutan baku protein $1 \times 10^{-2} \mu\text{g}/\mu\text{l}$

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 1 \times 10^{-2} \mu\text{g}/\mu\text{l} = 500 \mu\text{l} \times 1 \times 10^{-3} \mu\text{g}/\mu\text{l}$$

$$V_1 = 50 \mu\text{l}$$

- Kelompok perlakuan 2 (P_2) : Larutan baku protein $1 \times 10^{-4} \mu\text{g}/\mu\text{l}$ dari larutan baku protein $1 \times 10^{-2} \mu\text{g}/\mu\text{l}$

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 1 \times 10^{-2} \mu\text{g}/\mu\text{l} = 500 \mu\text{l} \times 1 \times 10^{-4} \mu\text{g}/\mu\text{l}$$

$$V_1 = 5 \mu\text{l}$$

- Kelompok perlakuan 4 (P_4) : Larutan baku protein $1 \times 10^{-5} \mu\text{g}/\mu\text{l}$ dari larutan baku protein $1 \times 10^{-2} \mu\text{g}/\mu\text{l}$

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 1 \times 10^{-2} \mu\text{g}/\mu\text{l} = 500 \mu\text{l} \times 1 \times 10^{-5} \mu\text{g}/\mu\text{l}$$

$$V_1 = 0,5 \mu\text{l}$$

Perhitungan diatas dirangkum dalam tabel berikut:

Perlakuan	Konsentrasi protein ($\mu\text{g}/\mu\text{l}$)	Volume larutan protein (μl)	Volume PBS (μl)	Volume alum (μl)	Volume akhir (μl)
5		-	-	500	1000
4	1×10^{-2}	20 μl larutan stok	480	500	1000
3	1×10^{-3}	50 μl larutan protein P ₄	450	500	1000
2	1×10^{-4}	5 μl larutan protein P ₄	495	500	1000
1	1×10^{-5}	0,5 μl larutan protein P ₄	499,5	500	1000



Lampiran 3. Perhitungan untuk Pembuatan Larutan Standar 320, 160, 80, 40, 20, 10, dan 5 pg/ml

- Larutan standar 320 pg/ml dari larutan induk 640 pg/ml

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 640 \text{ pg/ml} = 240 \mu\text{l} \times 320 \text{ pg/ml}$$

$$V_1 = 120 \mu\text{l}$$

- Larutan standar 160 pg/ml dari larutan standar 320 pg/ml

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 320 \text{ pg/ml} = 240 \mu\text{l} \times 160 \text{ pg/ml}$$

$$V_1 = 120 \mu\text{l}$$

- Larutan standar 80 pg/ml dari larutan standar 160 pg/ml

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 160 \text{ pg/ml} = 240 \mu\text{l} \times 80 \text{ pg/ml}$$

$$V_1 = 120 \mu\text{l}$$

- Larutan standar 40 pg/ml dari larutan standar 80 pg/ml

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 80 \text{ pg/ml} = 240 \mu\text{l} \times 40 \text{ pg/ml}$$

$$V_1 = 120 \mu\text{l}$$

- Larutan standar 20 pg/ml dari larutan standar 40 pg/ml

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 40 \text{ pg/ml} = 240 \mu\text{l} \times 20 \text{ pg/ml}$$

$$V_1 = 120 \mu\text{l}$$

- Larutan standar 10 pg/ml dari larutan standar 20 pg/ml

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 20 \text{ pg/ml} = 240 \text{ } \mu\text{l} \times 10 \text{ pg/ml}$$

$$V_1 = 120 \text{ } \mu\text{l}$$

- Larutan standar 5 pg/ml dari larutan standar 10 pg/ml

$$V_1 \times M_1 = V_2 \times M_2$$

$$V_1 \times 10 \text{ pg/ml} = 240 \text{ } \mu\text{l} \times 5 \text{ pg/ml}$$

$$V_1 = 120 \text{ } \mu\text{l}$$

Perhitungan diatas dirangkum dalam tabel berikut:

No.	Konsentrasi (pg/ml)	Volume larutan standar yang diambil (μl)	Volume pelarut yang ditambahkan (μl)	Volume akhir (μl)
7	320	120 μl larutan induk	120	240
6	160	120 μl standar no.6	120	240
5	80	120 μl standar no.5	120	240
4	40	120 μl standar no.4	120	240
3	20	120 μl standar no.3	120	240
2	10	120 μl standar no.2	120	240
1	5	120 μl standar no.1	120	240
0	0	-	120	120



Lampiran 4. Hasil Pencarian Database Protein LOX-1

Names and origin

Protein names	Recommended name: Oxidized low-density lipoprotein receptor 1 Short name=Ox-LDL receptor 1 Alternative name(s): C-type lectin domain family 8 member A Lectin-like oxidized LDL receptor 1 Short name=LOX-1 Short name=Lectin-like oxLDL receptor 1 Short name=hLOX-1 Lectin-type oxidized LDL receptor 1 <u>Cleaved into the following chain:</u> 1. Oxidized low-density lipoprotein receptor 1, soluble form
Gene names	Name: OLR1 Synonyms: CLEC8A, LOX1
Organism	Homo sapiens (Human) [Reference proteome]
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota › Metazoa › Chordata › Craniata › Vertebrata › Euteleostomi › Mammalia › Eutheria › Euarchontoglires › Primates › Haplorhini › Catarrhini › Hominidae › Homo

Protein attributes

Sequence length	273 AA.
Sequence status	Complete.
Sequence processing	The displayed sequence is further processed into a mature form.
Protein existence	Evidence at protein level

General annotation (Comments)

Function	Receptor that mediates the recognition, internalization and degradation of oxidatively modified low density lipoprotein (oxLDL) by vascular endothelial cells. OxLDL is a marker of atherosclerosis that induces vascular endothelial cell activation and dysfunction, resulting in pro-inflammatory responses, pro-oxidative conditions and apoptosis. Its association with oxLDL induces the activation of NF-kappa-B through an increased production of intracellular reactive oxygen and a variety of pro-atherogenic cellular responses including a reduction of nitric oxide (NO) release, monocyte adhesion and apoptosis. In addition to binding oxLDL, it acts as a receptor for the HSP70 protein involved in antigen cross-presentation to naive T-cells in dendritic cells, thereby participating in cell-mediated antigen cross-presentation. Also involved in inflammatory process, by acting as a leukocyte-adhesion molecule at the vascular interface in endotoxin-induced inflammation. Also acts as a receptor for advanced glycation end (AGE) products, activated platelets, monocytes, apoptotic cells and both Gram-negative and Gram-positive bacteria. Ref.13 Ref.14
Subunit structure	Homodimer; disulfide-linked. May form a hexamer composed of 3 homodimers. Interacts with HSP70. Ref.3 Ref.19 Ref.27
Subcellular location	Cell membrane; Lipid-anchor. Cell membrane; Single-pass type II membrane protein. Membrane raft. Secreted. Note: A secreted form also exists. Localization to membrane rafts requires palmitoylation. Ref.24 Ref.26
Tissue specificity	Expressed at high level in endothelial cells and vascular-rich organs such as placenta, lung, liver and brain, aortic intima, bone marrow, spinal cord and substantia nigra. Also expressed at the surface of dendritic cells. Widely expressed at intermediate and low level. Ref.1 Ref.4 Ref.14
Induction	By inflammatory cytokines such as TNF, IFNG/IFN-gamma, IL6/interleukin-6 and by pathological conditions such as hyperlipidemia, hypertension and diabetes mellitus. Up-regulated in atherosclerotic lesions, by oxLDL, reactive oxygen species and fluid shear stress, suggesting that it may participate in amplification of oxLDL-induced vascular dysfunction. Ref.4 Ref.16
Domain	The cytoplasmic region is required for subcellular sorting on the cell surface. Ref.3 Ref.24 The C-type lectin domain mediates the recognition and binding of oxLDL. Ref.3 Ref.24
Post-translational modification	The intrachain disulfide-bonds prevent N-glycosylation at some sites. N-glycosylated. Ref.3 Ref.25
Involvement in disease	Independent association genetic studies have implicated OLR1 gene variants in myocardial infarction susceptibility. Ref.15 Ref.18 Ref.20 Ref.21 Ref.23 OLR1 may be involved in Alzheimer disease (AD). Involvement in AD is however unclear: according to some authors Ref.14, Ref.17 and Ref.22, variations in OLR1 modify the risk of AD, while according to other Ref.19 and Ref.20 they do not. Ref.15 Ref.18 Ref.20 Ref.21 Ref.23
Sequence similarities	Contains 1 C-type lectin domain.

Ontologies

Keywords

Biological process	Cell adhesion Immunity Inflammatory response
Cellular component	Cell membrane Membrane Secreted
Coding sequence diversity	Alternative splicing Polymorphism
Domain	Coiled coil Signal-anchor Transmembrane Transmembrane helix
Ligand	Lectin
Molecular function	Receptor
PTM	Disulfide bond Glycoprotein Lipoprotein Palmitate
Technical term	3D-structure Complete proteome Reference proteome

Gene Ontology (GO)

Biological_process	blood circulation Traceable author statement (Ref.1). Source: ProtInc blood coagulation Traceable author statement. Source: Reactome cell death Inferred from electronic annotation. Source: Ensembl inflammatory response Inferred from electronic annotation. Source: UniProtKB-KW leukocyte cell-cell adhesion Inferred from electronic annotation. Source: Ensembl leukocyte migration Traceable author statement. Source: Reactome lipoprotein metabolic process Inferred from electronic annotation. Source: Ensembl proteolysis Traceable author statement (Ref.1). Source: ProtInc response to hydrogen peroxide Inferred from electronic annotation. Source: Ensembl
Cellular_component	extracellular region Inferred from electronic annotation. Source: UniProtKB-SubCell integral component of plasma membrane Traceable author statement (Ref.1). Source: ProtInc intracellular membrane-bounded organelle Inferred from direct assay. Source: HPA membrane Traceable author statement (Ref.1). Source: ProtInc membrane raft Inferred from electronic annotation. Source: UniProtKB-SubCell nucleus Inferred from direct assay. Source: HPA plasma membrane Inferred from direct assay. Source: HPA receptor complex Inferred from direct assay (PubMed 23382219). Source: MGI
Molecular_function	carbohydrate binding Inferred from electronic annotation. Source: InterPro low-density lipoprotein receptor activity Inferred from electronic annotation. Source: Ensembl

Alternative products

This entry describes **3** isoforms produced by **alternative splicing**. [\[Align\]](#) [\[Select\]](#)

Isoform 1 (identifier: P78380-1)

This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

Isoform 2 (identifier: P78380-2)

The sequence of this isoform differs from the canonical sequence as follows:

142-273: APCQDWIWH...CQKKANLRAQ → GLHPASNFLF...GRFSFDAPLI

Note: No experimental confirmation available.

Isoform 3 (identifier: P78380-3)

The sequence of this isoform differs from the canonical sequence as follows:

189-273: DFIQQAISYS...CQKKANLRAQ → I

Note: No experimental confirmation available.

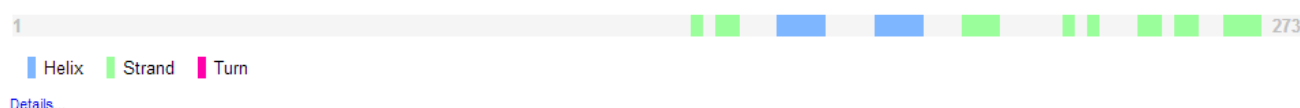
Sequence annotation (Features)

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
Molecule processing					
☐ Chain	1 – 273	273	Oxidized low-density lipoprotein receptor 1		PRO_0000017443
☐ Chain	? – 273		Oxidized low-density lipoprotein receptor 1, soluble form		PRO_0000017444
Regions					
☐ Topological domain	1 – 36	36	Cytoplasmic (Potential)		
☐ Transmembrane	37 – 57	21	Helical; Signal-anchor for type II membrane protein; (Potential)		
☐ Topological domain	58 – 273	216	Extracellular (Potential)		
☐ Domain	151 – 265	115	C-type lectin		
☐ Region	58 – 150	93	Neck		
☐ Coiled coil	64 – 123	60	(Potential)		
Sites					
☐ Site	183	1	Not glycosylated (Probable)		
Amino acid modifications					
☐ Lipidation	36	1	S-palmitoyl cysteine (Ref.26)		
☐ Lipidation	46	1	S-palmitoyl cysteine (Ref.26)		
☐ Glycosylation	73	1	N-linked (GlcNAc...) (Potential)		
☐ Glycosylation	139	1	N-linked (GlcNAc...) (complex) (Ref.25)		
☐ Disulfide bond	140		Interchain (Ref.3) (Ref.19) (Ref.27) (Ref.28)		
☐ Disulfide bond	144 ↔ 155		(Ref.3) (Ref.19) (Ref.27) (Ref.28)		
☐ Disulfide bond	172 ↔ 264		(Ref.3) (Ref.19) (Ref.27) (Ref.28)		
☐ Disulfide bond	243 ↔ 256		(Ref.3) (Ref.19) (Ref.27) (Ref.28)		
Natural variations					
☐ Alternative sequence	142 – 273	132	APCPQ...NLRAQ → GLHPASNFLFQFSILDGAVS EEPQLPMALGGGRFSFDAPLI in isoform 2 .		VSP_042555
☐ Alternative sequence	189 – 273	85	DFIQQ...NLRAQ → I in isoform 3 .		VSP_045277
☐ Natural variant	167	1	K → N Common polymorphism; myocardial infarction susceptibility. (Ref.5) (Ref.8) Corresponds to variant rs11053646 [dbSNP Ensembl] .		VAR_023200

Experimental info

☐	Mutagenesis	22 – 25	4	KKAK → EEAE: Impairs sorting into the cell surface but retains ability to bind oxLDL. Abolishes sorting into the cell surface; when associated with K-69. (Ref.24)	
☐	Mutagenesis	70	1	E → K: Abolishes sorting into the cell surface; when associated with 22-E-E-25. (Ref.24)	
☐	Mutagenesis	140	1	C → S: Abolishes homodimerization. (Ref.19)	
☐	Mutagenesis	144	1	C → S: Abolishes sorting into the cell surface and binding to acetylated LDL (AcLDL) while increasing N-glycosylation; when associated with S-155; S-172; S-243; S-256 and S-264. (Ref.3)	
☐	Mutagenesis	150	1	W → A: Abolishes binding to acetylated LDL (AcLDL), probably due to inappropriate homodimerization. (Ref.28)	
☐	Mutagenesis	155	1	C → S: Abolishes sorting into the cell surface and binding to acetylated LDL (AcLDL) while increasing N-glycosylation; when associated with S-144; S-172; S-243; S-256 and S-264. (Ref.3)	
☐	Mutagenesis	172	1	C → S: Abolishes sorting into the cell surface and binding to acetylated LDL (AcLDL) while increasing N-glycosylation; when associated with S-144; S-155; S-243; S-256 and S-264. (Ref.3)	
☐	Mutagenesis	183	1	N → Q: Does not affect glycosylation state. (Ref.3)	
☐	Mutagenesis	193	1	Q → L: Impairs binding to acetylated LDL (AcLDL); when associated with 198-AA-199.	
☐	Mutagenesis	198 – 199	2	SS → AA: Impairs binding to acetylated LDL (AcLDL); when associated with L-193.	
☐	Mutagenesis	208	1	R → N: Does not affect subcellular location but displays a strongly reduced affinity for acetylated LDL (AcLDL). (Ref.28)	
☐	Mutagenesis	209 – 210	2	RN → LL: Abolishes binding to acetylated LDL (AcLDL). (Ref.28)	
☐	Mutagenesis	209	1	R → N: Does not affect binding to acetylated LDL (AcLDL). (Ref.28)	
☐	Mutagenesis	226	1	H → A: No effect. (Ref.3) (Ref.28)	
☐	Mutagenesis	226	1	H → Q: Abolishes binding to acetylated LDL (AcLDL); when associated with N-229 and N-231. (Ref.3) (Ref.28)	
☐	Mutagenesis	229	1	R → N: Does not affect subcellular location but displays a reduced affinity for acetylated LDL (AcLDL). Abolishes binding to acetylated LDL (AcLDL); when associated with Q-226 and N-231. (Ref.3) (Ref.28)	
☐	Mutagenesis	231	1	R → N: Abolishes binding to acetylated LDL (AcLDL). Abolishes binding to AcLDL; when associated with Q-226 and N-229. (Ref.3) (Ref.28)	
☐	Mutagenesis	235 – 236	2	SQ → AL: Impairs binding to acetylated LDL (AcLDL); when associated with A-240.	
☐	Mutagenesis	240	1	S → A: Impairs binding to acetylated LDL (AcLDL); when associated with 235-AL-236. (Ref.3)	
☐	Mutagenesis	243	1	C → S: Abolishes sorting into the cell surface and binding to acetylated LDL (AcLDL) while increasing N-glycosylation; when associated with S-144; S-155; S-172; S-256 and S-264. (Ref.3)	
☐	Mutagenesis	248	1	R → N: Does not affect subcellular location but displays a reduced affinity for acetylated LDL (AcLDL). (Ref.28)	
☐	Mutagenesis	256	1	C → S: Abolishes sorting into the cell surface and binding to acetylated LDL (AcLDL) while increasing N-glycosylation; when associated with S-144; S-155; S-172; S-243 and S-264. (Ref.3)	
☐	Mutagenesis	264	1	C → S: Abolishes sorting into the cell surface and binding to acetylated LDL (AcLDL) while increasing N-glycosylation; when associated with S-144; S-155; S-172; S-243 and S-256. (Ref.3)	
☐	Mutagenesis	267 – 273	7	Missing: Impairs protein folding and transport. (Ref.3)	

Secondary structure



Sequences

Sequence	Length	Mass (Da)	Tools
☐ Isoform 1 [UniParc]. FASTA	273	30,959	Blast go

Last modified May 1, 1997. Version 1.
Checksum: 852DE6595DC3D361

```

10      20      30      40      50      60
MTFDDLKIQT VKDQPDEKSN GKKAKGLQFL YSPWCLAA TLGVLCLGLV VTIMVLGMQL

70      80      90     100     110     120
SQVSDLLTQE QANLTHQKKK LEGQISARQQ AEEASQESN ELKEMIETLA RKLNEKSKEQ

130     140     150     160     170     180
MELHHQNLNL QETLKRIVANC SAPCPQDWIW HGENCYLFSS GSFNWEKSQE KCLSLDAKLL

190     200     210     220     230     240
KINSTADLDF IQQAISYSSF PFWMGLSRRN PSYPWLWEDG SPLMPHLFRV RGAVSQTYPS

250     260     270
GTCAYIQRGA VYAENCILAA FSICQKKANL RAQ

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☐ Isoform 2 [UniParc]. FASTA	181	20,227	Blast go
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Checksum: D9DFBBEB1948099

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10      20      30      40      50      60
MTFDDLKIQT VKDQPDEKSN GKKAKGLQFL YSPWCLAA TLGVLCLGLV VTIMVLGMQL

70      80      90     100     110     120
SQVSDLLTQE QANLTHQKKK LEGQISARQQ AEEASQESN ELKEMIETLA RKLNEKSKEQ

130     140     150     160     170     180
MELHHQNLNL QETLKRIVANC SGLHPASNFL FQFSILDGAV SEEPQLPMAL GGRFSFDAPL

I

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« Hide

☐ Isoform 3 [UniParc]. FASTA	189	21,425	Blast go
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Checksum: CA0E07E9A69E204F

```

10      20      30      40      50      60
MTFDDLKIQT VKDQPDEKSN GKKAKGLQFL YSPWCLAA TLGVLCLGLV VTIMVLGMQL

70      80      90     100     110     120
SQVSDLLTQE QANLTHQKKK LEGQISARQQ AEEASQESN ELKEMIETLA RKLNEKSKEQ

130     140     150     160     170     180
MELHHQNLNL QETLKRIVANC SAPCPQDWIW HGENCYLFSS GSFNWEKSQE KCLSLDAKLL

KINSTADLI

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« Hide

Sumber : UniProt

Link : <http://www.uniprot.org/uniprot/P78380>

Lampiran 5. Hasil Pemodelan Struktur 3D (SWISS MODEL)


BIOZENTRUM
 Universität Basel
 The Center for Molecular Life Sciences

SWISS-MODEL

Modelling Tools Repository Documentation Log in Create Account

All Projects

LOX-1 Created: today at 15:10

Summary

Templates 82

Models 3



Model Results



Model 03

Oligo-State MONOMER (matching prediction)

Ligands None

GMQE 0.49

QMEAN4 -0.85

QMEAN4: -0.85
 C β : 0.60
 All Atom: -0.37
 Solvation: 0.03
 Torsion: -1.30

Local Quality Estimate

Comparison with Non-redundant Set of PDB Structures

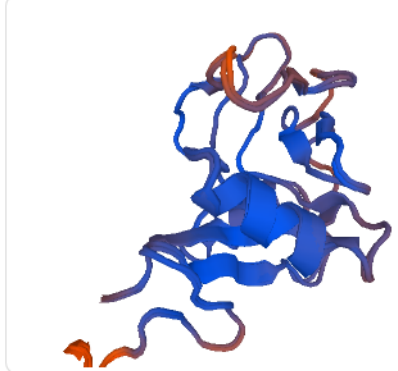
Template	Seq Identity	Description
1yxk.1.A	100.00%	oxidised low density lipoprotein (lectin-like) receptor 1

Oligo-state	Method	Seq Similarity	Range	Coverage
homo-dimer	X-ray, 2.40 Å	0.63	141 - 270	0.49

Model-Template Alignment

```

Model_03 MTFDDLKIQTVRKDPDEKSNKGKAKGLQFLYSPWWCLAAATLGVLCLGLV 50
1yxk.1.A -----
Model_03 VTIMVLGMQLSQVSDLLTQEQLNLTHQKKKLEGQISARQQAESEASQSEEN 100
1yxk.1.A -----
Model_03 ELKEMIELTLARKLNKESKEQMEHHQNLNQETLKRVCANCSAPCPQDWIW 150
1yxk.1.A -----RVANCSAPCPQDWIW 15
Model_03 HGENCYLFSSGSPFNWEKSQEKCLSLDAKLLKINSTADLDFIQQAISYSSF 200
1yxk.1.A HGENCYLFSSGSPFNWEKSQEKCLSLDAKLLKINSTADLDFIQQAISYSSF 65
Model_03 PFWMGLSRNPSYPWLWEDGSPMLPHLFRVRGAVSQTYPSTGTCAYIQRGA 250
1yxk.1.A PFWMGLSRNPSYPWLWEDGSPMLPHLFRVRGAVSQTYPSTGTCAYIQRGA 115
Model_03 VYAENCILAAFSICQKKANLRAQ 273
1yxk.1.A VYAENCILAAFSICQKKANL--- 135
    
```



View

Model 02

Model 01

Detach Reset



Model 02

Oligo-State MONOMER (matching prediction)

Ligands None

GMQE 0.51

QMEAN4 -1.02

QMEAN4: -1.02
 C β : 0.98
 All Atom: -0.82
 Solvation: -0.24
 Torsion: -1.50

Local Quality Estimate

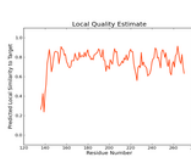
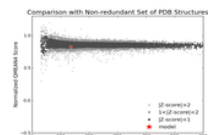


Model 01

Oligo-State **Ligands** **GMQE** ² **QMEAN** ⁴

MONOMER (matching prediction) None 0.52 -0.54

QMEAN4: -0.54
C β : 1.14
All Atom: -0.76
Solvation: -0.25
Torsion: -0.98

Template	Seq Identity	Description
1yxk.1.B	100.00%	oxidised low density lipoprotein (lectin-like) receptor 1

Oligo-state	Method	Seq Similarity	Range	Coverage
homo-dimer	X-ray, 2.40 Å	0.63		0.49

Model-Template Alignment

```

Model_02 MTFDDLKIQTVDKQPEKSNKGKAKGLQFLYSPWWCLAAATLGVLCLGLV 50
1yxk.1.B -----
Model_02 VTIMVLGMQLSQVSDLLTQEQLNTHQKKLEGQISARQQAEESQESN 100
1yxk.1.B -----
Model_02 ELKEMIETLARKLNESKEQMELEHQNINLQETLKRVANCSAPCPQDWIW 150
1yxk.1.B -----RVANCSAPCPQDWIW 15
Model_02 HGENCYLFSSGSFNWEKSQEKCLSLDAKLLKINSTADLDFIQQAISYSSF 200
1yxk.1.B HGENCYLFSSGSFNWEKSQEKCLSLDAKLLKINSTADLDFIQQAISYSSF 65
Model_02 PFWMGLSRNPSPYPLWEDGSLMPHLFRVRGAVSQTPSGTCAYIQRGA 250
1yxk.1.B PFWMGLSRNPSPYPLWEDGSLMPHLFRVRGAVSQTPSGTCAYIQRGA 115
Model_02 VYAENCILAAFSICQKKANLRAQ 273
1yxk.1.B VYAENCILAAFSICQKKANL--- 135
    
```

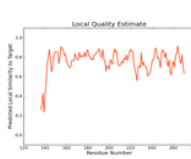
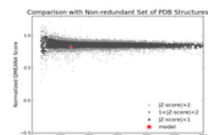


Model 01

Oligo-State **Ligands** **GMQE** ² **QMEAN** ⁴

MONOMER (matching prediction) None 0.52 -0.54

QMEAN4: -0.54
C β : 1.14
All Atom: -0.76
Solvation: -0.25
Torsion: -0.98

Sumber : SWISS MODEL
 Link : <http://swissmodel.expasy.org/interactive/WBjXZ/models/>

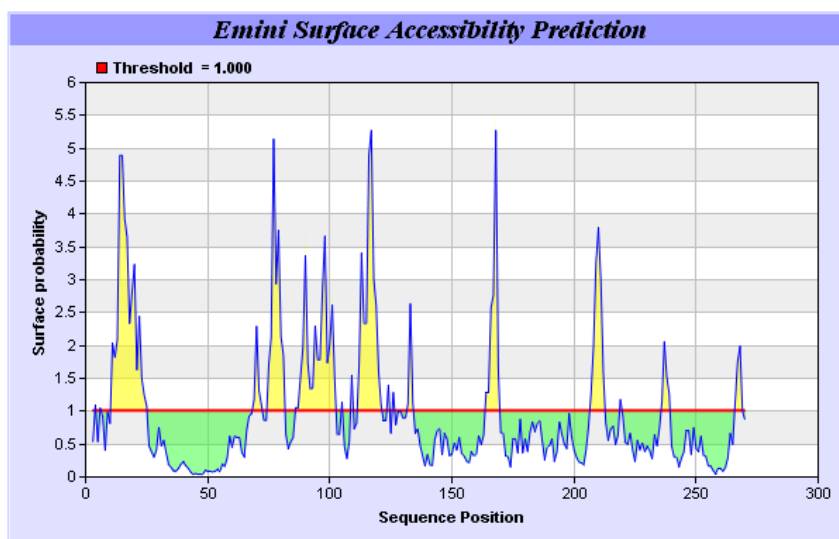
Lampiran 6. Hasil Prediksi Aksesibilitas Permukaan (*Emini Surface Accessibility Prediction*)

Emini Surface Accessibility Prediction

Sequence:

```
1  MTFDDLKIQT VKDQPDEKSN GKKAKGLQFL YSPWCLAAA TLGVLCLGLV VTIMVLGMQL
61  SQVSDLLTQE QANLTHQKKK LEGQISARQQ AEEASQESN ELKEMIETLA RKLNEKSKEQ
121 MELHHQNLNL QETLKRVCNC SAPCPQDWIW HGENCYLFSS GSFNWEKSQE KCLSLDAKLL
181 KINSTADLDF IQQAISYSSF PFWMGLSRN PSYPWLWEDG SPLMPHLFRV RGAVSQYTYS
241 GTCAYIQRGA VYAENCILAA FSICQKKANL RAQ
```

Center position: 3 Window size: 6



Average: 1.000 Minimum: 0.038 Maximum: 5.266 Threshold: 1.000

[Click here to view plotted values in table format](#)

Predicted peptides:

No.	Start Position	End Position	Peptide	Peptide Length
1	11	25	VKDQPDEKSNQKKAK	15
2	75	81	THQKKKL	7
3	86	102	SARQQAEESQESNEL	17
4	112	121	KLNEKSKEQM	10
5	164	169	NWEKSQ	6
6	207	212	SRRNPS	6

Reference: [Emini EA, Hughes JV, Perlow DS, Boger J. Induction of hepatitis A virus-neutralizing antibody by a virus-specific synthetic peptide. J Virol. 1985 Sep;55\(3\):836-9.](#)

Scale values: A:0.49, C:0.26, D:0.81, E:0.84, F:0.42, G:0.48, H:0.66, I:0.34, K:0.97, L:0.4, M:0.48, N:0.78, P:0.75, Q:0.84, R:0.95, S:0.65, T:0.7, V:0.36, W:0.51, Y:0.76

Sumber : IEDB

Link : <http://tools.immuneepitope.org/tools/bcell/SummaryDisplay>

Lampiran 7. Hasil Analisis Antigenisitas (*Kolaskar & Tongaonkar Antigenicity*)

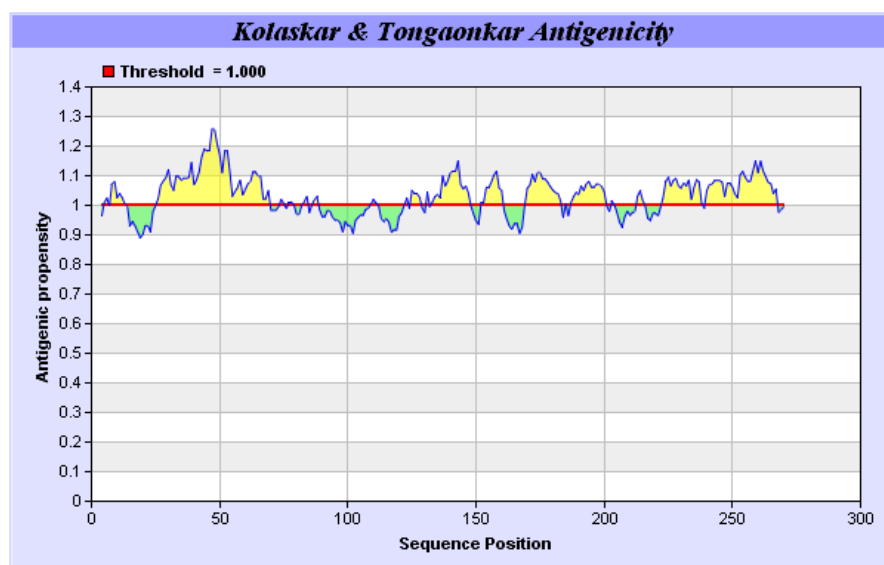
Kolaskar & Tongaonkar Antigenicity

Sequence:

```

1  MTFDDLKIQT VKDQPEKSN GKKAKGLQFL YSPWWCLAAA TLGVLCGLV VIMVLGMQL
61  SQVSDLLTQE QANLTHQKKK LEGQISARQQ AEEASQESN ELKEMIETLA RKLNEKSKEQ
121 MELHHQNLNL QETLKRVCNC SAPCPQDWI HGENCYLFSS GSFNWEKSQE KCLSLDAKLL
181 KINSTADLDF IQQAISYSSF PFWMGLSRN PSYPWLWEDG SPLMPHLFRV RGAVSQTYPS
241 GTCAYIQRGA VYAENCILAA FSICQKKANL RAQ
    
```

Center position: 4 Window size: 7



Average: 1.032 Minimum: 0.891 Maximum: 1.257 Threshold: 1.000

[Click here to view plotted values in table format](#)

Predicted peptides:

No.	Start Position	End Position	Peptide	Peptide Length
1	8	13	IQTVKD	6
2	26	69	GLQFLYSPWWCLAAATLGVLCGLVVTIMVLGMQLSQVSDLLTQ	44
3	133	147	TLKRVCNCSAPCPQD	15
4	152	160	GENCYLFSS	9
5	169	183	QEKCLSLDAKLLKIN	15
6	187	200	DLDIFIQQAISYSSF	14
7	223	238	LMPHLFRVRGAVSQTY	16
8	240	267	SGTCAYIQRGAVYAENCILAAFSICQKK	28

Reference: Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. *FEBS Lett.* 1990 Dec 10;276(1-2):172-4.

Scale values: A:1.064, C:1.412, D:0.866, E:0.851, F:1.091, G:0.874, H:1.105, I:1.152, K:0.93, L:1.25, M:0.826, N:0.776, P:1.064, Q:1.015, R:0.873, S:1.012, T:0.909, V:1.383, W:0.893, Y:1.161

Sumber : IEDB

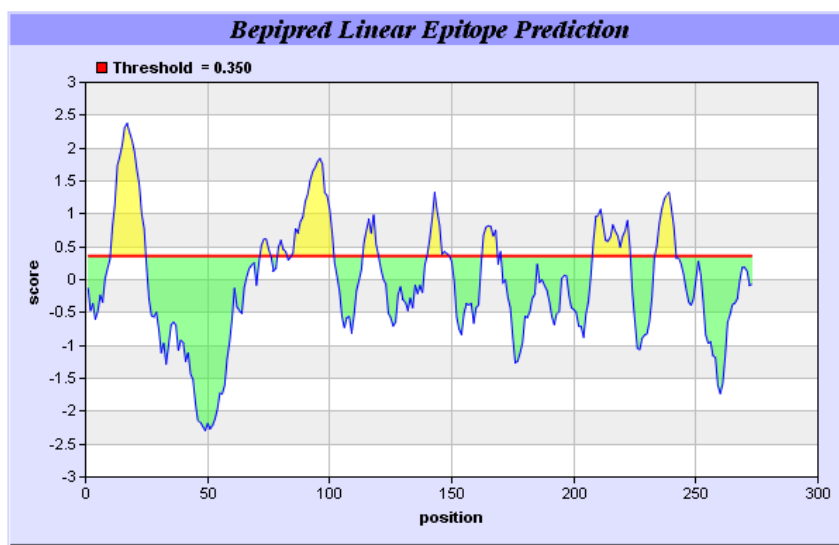
Link : <http://tools.immuneepitope.org/tools/bcell/SummaryDisplay>

Lampiran 8. Hasil Prediksi Epitop Sel B (*Bepipred Antibody Epitope Prediction*)

Sequence:

```

1  MTFDDLKIQT VKDQPDEKSN GKKAKGLQFL YSPWCLAAA TLGVLCLGLV VTIMVLGMQL
61  SQVSDLLTQE QANLTHQKKK LEGQISARQQ AEEASQESN ELKEMIETLA RKLNEKSKEQ
121 MELHHQNLNL QETLKRVCNC SAPCPQDWI HGENCYLFSS GSFNWEKSQE KCLSLDAKLL
181 KINSTADLDF IQQAISYSSS PFWMLSRRN PSYFPLWEDG SPLMPHLFRV RGAVSQTYPS
241 GTCAYIQRGA VYAENCILAA FSCQKKANL RAQ
    
```



Average:-0.04 Minimum:-2.295 Maximum:2.371 Threshold: 0.350

[Click here to view plotted values in table format](#)

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	11	24	VKDQPDEKSNKGKA	14
2	72	76	ANLTH	5
3	79	82	KKLE	4
4	85	101	ISARQQAEEASQESNE	17
5	114	120	NEKSKEQ	7
6	140	149	CSAPCPQDWI	10
7	163	168	FNWEKS	6
8	170	170	E	1
9	208	223	RRNPSYPWLWEDGSPL	16
10	234	241	VSQTYPSG	8

Reference: [Jens Erik Pontoppidan Larsen, Ole Lund and Morten Nielsen. Improved method for predicting linear B-cell epitopes. Immunome Res. 2006; 2: 2.](#)

Sumber : IEDB

Link : <http://tools.immuneepitope.org/tools/bcell/BepipredDisplayServlet>

Lampiran 9. Hasil Prediksi Epitop Sel T (Metode NetMHCIIpan)

allele	Seq num	start	end	peptida	Percentile rank	Netmhciipan core	Netmhciipan ic50	Netmhciipan rank	Afinitas
HLA-DRB1*1431	1	222	236	PLMPHLFRVRGAVSQ	0.69	LFRVRGAVS	4.79	0.69	Tinggi
HLA-DRB1*1431	1	223	237	LMPHLFRVRGAVSQT	0.8	LFRVRGAVS	5.04	0.8	Tinggi
HLA-DRB1*1431	1	221	235	SPLMPHLFRVRGAVS	0.9	LFRVRGAVS	5.23	0.9	Tinggi
HLA-DRB1*1431	1	224	238	MPHLFRVRGAVSQT	1.12	LFRVRGAVS	5.72	1.12	Tinggi
HLA-DRB1*1431	1	225	239	PHLFRVRGAVSQTYP	1.78	LFRVRGAVS	6.9	1.78	Tinggi
HLA-DRB3*0303	1	177	191	AKLLKINSTADLDFI	1.99	LKINSTADL	163.3	1.99	Intermediet
HLA-DRB3*0303	1	178	192	KLLKINSTADLDFIQ	2.58	LKINSTADL	188.22	2.58	Intermediet
HLA-DRB3*0303	1	176	190	DAKLLKINSTADLDF	3.97	LKINSTADL	268.45	3.97	Intermediet
HLA-DRB1*1431	1	226	240	HLFRVRGAVSQTYP	4.21	LFRVRGAVS	10.29	4.21	Tinggi
HLA-DRB3*0303	1	179	193	LLKINSTADLDFIQ	4.89	LKINSTADL	322.63	4.89	Intermediet
HLA-DRB3*0303	1	248	262	RGAVYAENCILAASF	5.44	VYAENCILA	348.93	5.44	Intermediet
HLA-DRB1*1431	1	258	272	LAAFSICQKKANLRA	6.28	FSICQKKAN	14.14	6.28	Tinggi
HLA-DRB3*0303	1	249	263	GAVYAENCILAAFSI	6.69	YAENCILAA	407.65	6.69	Intermediet
HLA-DRB3*0303	1	213	227	YPWLWEDGSPLMPHL	6.7	LWEDGSPLM	408	6.7	Intermediet
HLA-DRB1*1431	1	257	271	ILAAFSICQKKANLR	6.78	FSICQKKAN	14.95	6.78	Tinggi
HLA-DRB3*0303	1	186	200	ADLDFIQQAISYSS	7.09	FIQQAISYS	426.29	7.09	Intermediet
HLA-DRB3*0303	1	188	202	LDFIQQAISYSSP	7.23	FIQQAISYS	433.81	7.23	Intermediet
HLA-DRB3*0303	1	247	261	QRGAVYAENCILAAF	7.39	VYAENCILA	440.6	7.39	Intermediet
HLA-DRB1*1431	1	259	273	AAFSICQKKANLRAQ	7.68	FSICQKKAN	16.52	7.68	Tinggi
HLA-DRB3*0303	1	189	203	DFIQQAISYSSPFW	7.89	FIQQAISYS	479.86	7.89	Intermediet
HLA-DRB3*0303	1	187	201	DLDFIQQAISYSSP	8.3	FIQQAISYS	497.27	8.3	Intermediet
HLA-DRB1*1431	1	256	270	CILAAFSICQKKANL	8.48	AFSICQKKA	17.67	8.48	Tinggi
HLA-DRB3*0303	1	26	40	GLQFLYSPWWCLAAA	8.95	FLYSPWWCL	527.18	8.95	Rendah
HLA-DRB3*0303	1	175	189	LDKLLKINSTADLD	9.3	LKINSTADL	544.88	9.3	Rendah
HLA-DRB1*1431	1	220	234	GSPLMPHLFRVRGAV	9.36	HLFRVRGAV	19.56	9.36	Tinggi
HLA-DRB3*0303	1	25	39	KGLQFLYSPWWCLAA	9.65	FLYSPWWCL	563.9	9.65	Rendah
HLA-DRB3*0303	1	190	204	FIQQAISYSSPFW	9.66	FIQQAISYS	565.12	9.66	Rendah
HLA-DRB1*1431	1	255	269	NCILAAFSICQKKAN	9.85	AFSICQKKA	20.98	9.85	Tinggi
HLA-DRB3*0303	1	212	226	SYPWLWEDGSPLMPH	10.07	WLWEDGSPL	587.47	10.07	Rendah
HLA-DRB1*1431	1	103	117	KEMIETLARKLNEKS	10.17	MIETLARKL	21.68	10.17	Tinggi
HLA-DRB1*1431	1	102	116	LKEMIETLARKLNEK	10.78	MIETLARKL	23.03	10.78	Tinggi
HLA-DRB3*0303	1	250	264	AVYAENCILAAFSIC	10.94	YAENCILAA	635.63	10.94	Rendah
HLA-DRB1*1431	1	188	202	LDFIQQAISYSSP	11.16	FIQQAISYS	23.76	11.16	Tinggi
HLA-DRB3*0303	1	180	194	LKINSTADLDFIQQA	11.53	LKINSTADL	668.16	11.53	Rendah
HLA-DRB3*0303	1	174	188	SLDAKLLKINSTADL	11.76	LKINSTADL	681.3	11.76	Rendah
HLA-DRB3*0303	1	214	228	PWLWEDGSPLMPHLF	11.89	LWEDGSPLM	690.33	11.89	Rendah
HLA-DRB3*0303	1	170	184	EKCLSLDAKLLKINS	11.92	LSLDAKLLK	692.15	11.92	Rendah
HLA-DRB1*1431	1	254	268	ENCILAAFSICQKKA	12.08	ILAAFSICQ	25.4	12.08	Tinggi
HLA-DRB3*0303	1	27	41	LQFLYSPWWCLAAAT	12.17	FLYSPWWCL	708	12.17	Rendah
HLA-DRB1*1431	1	199	213	SFPFWMGLSRRNPSY	12.24	MGLSRRNPS	25.79	12.24	Tinggi

HLA-DRB3*0303	1	169	183	QEKLSDAKLLKIN	12.31	LSLDAKLLK	716.9	12.31	Rendah
HLA-DRB1*1431	1	24	38	AKGLQFLYSPWWCLA	12.9	LQFLYSPWW	27.01	12.9	Tinggi
HLA-DRB1*1431	1	25	39	KGLQFLYSPWWCLAA	12.94	LQFLYSPWW	27.17	12.94	Tinggi
HLA-DRB1*1431	1	23	37	KAKGLQFLYSPWWCL	13.13	GLQFLYSPW	27.64	13.13	Tinggi
HLA-DRB1*1431	1	104	118	EMIETLARKLNEKSK	13.49	MIETLARKL	28.25	13.49	Tinggi
HLA-DRB3*0303	1	185	199	TADLDFIQQAISYSS	13.54	FIQQAISYS	785.05	13.54	Rendah
HLA-DRB1*1431	1	190	204	FIQQAISYSSFPFWM	13.57	AISYSSFPF	28.5	13.57	Tinggi
HLA-DRB1*1431	1	227	241	LFRVRGAVSQTYPSG	14.18	LFRVRGAVS	29.74	14.18	Tinggi
HLA-DRB3*0303	1	24	38	AKGLQFLYSPWWCLA	14.28	FLYSPWWCL	822.3	14.28	Rendah
HLA-DRB1*1431	1	189	203	DFIQQAISYSSFPFW	14.29	FIQQAISYS	29.96	14.29	Tinggi
HLA-DRB1*1431	1	100	114	NELKEMIETLARKLN	14.33	MIETLARKL	30.06	14.33	Tinggi
HLA-DRB1*1431	1	186	200	ADLDFIQQAISYSSF	14.33	FIQQAISYS	30.05	14.33	Tinggi
HLA-DRB3*0303	1	171	185	KCLSLDAKLLKINST	14.49	LSLDAKLLK	834.08	14.49	Rendah
HLA-DRB1*1431	1	200	214	FPFWMGLSRRNPSYP	14.71	MGLSRRNPS	30.97	14.71	Tinggi
HLA-DRB1*1431	1	174	188	SLDAKLLKINSTADL	14.8	KLLKINSTA	31.3	14.8	Tinggi
HLA-DRB1*1431	1	239	253	PSGTCAIYQRGAVYA	14.91	CAYIQRGAV	31.51	14.91	Tinggi
HLA-DRB3*0303	1	146	160	QDWIWHGENCYLFSS	14.99	IWHGENCYL	862.52	14.99	Rendah
HLA-DRB3*0303	1	168	182	SQEKCLSLDAKLLKI	15.02	LSLDAKLLK	864.13	15.02	Rendah
HLA-DRB1*1431	1	47	61	LGLVVTIMVLGMQLS	15.5	IMVLGMQLS	33.24	15.5	Tinggi
HLA-DRB1*1431	1	101	115	ELKEMIETLARKLNE	15.5	MIETLARKL	33.24	15.5	Tinggi
HLA-DRB1*1431	1	201	215	PFWMGLSRRNPSYPW	15.51	MGLSRRNPS	33.26	15.51	Tinggi
HLA-DRB1*1431	1	187	201	DLDFIQQAISYSSFP	15.52	FIQQAISYS	33.3	15.52	Tinggi
HLA-DRB3*0303	1	246	260	IQRGAVYAENCILAA	15.58	VYAENCILA	893.02	15.58	Rendah
HLA-DRB1*1431	1	48	62	GLVVTIMVLGMQLSQ	15.72	IMVLGMQLS	33.73	15.72	Tinggi
HLA-DRB1*1431	1	240	254	SGTCAYIQRGAVYAE	15.76	YIQRGAVYA	33.87	15.76	Tinggi
HLA-DRB1*1431	1	172	186	CLSLDAKLLKINSTA	15.77	DAKLLKINS	33.92	15.77	Tinggi
HLA-DRB3*0303	1	28	42	QFLYSPWWCLAAATL	16.01	FLYSPWWCL	921.02	16.01	Rendah
HLA-DRB1*1431	1	49	63	LVVTIMVLGMQLSQV	16.01	IMVLGMQLS	34.65	16.01	Tinggi
HLA-DRB1*1431	1	241	255	GTCAYIQRGAVYAEN	16.23	YIQRGAVYA	35.17	16.23	Tinggi
HLA-DRB1*1431	1	50	64	VVTIMVLGMQLSQVS	16.32	IMVLGMQLS	35.55	16.32	Tinggi
HLA-DRB1*1431	1	198	212	SSFPFWMGLSRRNPS	16.32	FWMGLSRRN	35.59	16.32	Tinggi
HLA-DRB1*1431	1	191	205	IQQAISYSSFPFWMG	16.52	AISYSSFPF	35.98	16.52	Tinggi
HLA-DRB1*1431	1	105	119	MIETLARKLNEKSKE	16.8	MIETLARKL	36.72	16.8	Tinggi
HLA-DRB3*0303	1	211	225	PSYPWLWEDGSPLMP	16.82	WLWEDGSPL	969.48	16.82	Rendah
HLA-DRB3*0303	1	147	161	DWIIWHGENCYLFSSG	16.96	IWHGENCYL	978.42	16.96	Rendah
HLA-DRB1*1431	1	185	199	TADLDFIQQAISYSS	17.4	FIQQAISYS	38.43	17.4	Tinggi
HLA-DRB3*0303	1	148	162	WIIWHGENCYLFSSGS	17.63	IWHGENCYL	1018.78	17.63	Rendah
HLA-DRB1*1431	1	26	40	GLQFLYSPWWCLAAA	17.71	FLYSPWWCL	39.45	17.71	Tinggi
HLA-DRB1*1431	1	175	189	LDKLLKINSTADLD	17.75	KLLKINSTA	39.67	17.75	Tinggi
HLA-DRB1*1431	1	173	187	LSLDAKLLKINSTAD	17.86	DAKLLKINS	40.04	17.86	Tinggi
HLA-DRB1*1431	1	171	185	KCLSLDAKLLKINST	17.87	DAKLLKINS	40.15	17.87	Tinggi
HLA-DRB3*0303	1	125	139	HQNLNLQETLKR VAN	18.18	LNLQETLKR	1050.72	18.18	Rendah
HLA-DRB3*0303	1	153	167	ENCYLFSSGSFNWEK	18.36	YLFSSGSFN	1060.6	18.36	Rendah
HLA-DRB1*1431	1	177	191	AKLLKINSTADLDFI	18.56	LLKINSTAD	42.33	18.56	Tinggi
HLA-DRB1*1431	1	176	190	DAKLLKINSTADLDF	18.66	LLKINSTAD	42.56	18.66	Tinggi
HLA-DRB1*1431	1	22	36	KKAKGLQFLYSPWWC	18.79	GLQFLYSPW	43.01	18.79	Tinggi

HLA-DRB1*1431	1	21	35	GKKAKGLQLFLYSPWW	18.92	GLQFLYSPW	43.39	18.92	Tinggi
HLA-DRB3*0303	1	124	138	HHQNLNLQETLKRVA	18.97	LNLQETLKR	1094.49	18.97	Rendah
HLA-DRB1*1431	1	202	216	FWMGLSRRNPSYPWL	19.15	MGLSRRNPS	44	19.15	Tinggi
HLA-DRB3*0303	1	215	229	WLWEDGSPLMPHLFR	19.34	LWEDGSPLM	1116.77	19.34	Rendah
HLA-DRB3*0303	1	191	205	IQQAISYSSFPFWMG	19.49	AISYSSFPF	1130.06	19.49	Rendah
HLA-DRB3*0303	1	210	224	NPSYPWLWEDGSPLM	19.61	WLWEDGSPL	1136.54	19.61	Rendah
HLA-DRB3*0303	1	251	265	VYAENCILAAFSICQ	19.85	YAENCILAA	1151.02	19.85	Rendah
HLA-DRB3*0303	1	145	159	PQDWIWHGENCYLFS	20.23	IWHGENCYL	1176.52	20.23	Rendah
HLA-DRB1*1431	1	253	267	AENCILAAFSICQKK	20.38	ILAAFSICQ	47.97	20.38	Tinggi
HLA-DRB1*1431	1	170	184	EKCLSLDAKLLKINS	20.74	LSLDAKLLK	48.88	20.74	Tinggi
HLA-DRB3*0303	1	154	168	NCYLFSSGSFNWEKS	20.78	YLFSSGSFN	1209.67	20.78	Rendah
HLA-DRB1*1431	1	203	217	WMGLSRRNPSYPWLW	20.83	MGLSRRNPS	49.14	20.83	Tinggi
HLA-DRB1*1431	1	242	256	TCAYIQRGAVYAENC	20.97	YIQRGAVYA	49.6	20.97	Tinggi
HLA-DRB1*1431	1	128	142	LNLQETLKRVANCSA	21.31	LKRVANCSA	50.76	21.31	Intermediet
HLA-DRB1*1431	1	51	65	VTIMVLGMQLSQVSD	21.34	IMVLGMQLS	50.79	21.34	Intermediet
HLA-DRB3*0303	1	152	166	GENCYLFSSGSFNWE	21.63	YLFSSGSFN	1260.95	21.63	Rendah
HLA-DRB3*0303	1	149	163	IWHGENCYLFSSGSF	21.65	IWHGENCYL	1264.29	21.65	Rendah
HLA-DRB1*1431	1	196	210	SYSSFPFWMGLSRRN	21.78	FWMGLSRRN	52.01	21.78	Intermediet
HLA-DRB3*0303	1	184	198	STADLDFIQQAISYS	22.14	FIQQAISYS	1288.71	22.14	Rendah
HLA-DRB3*0303	1	23	37	KAKGLQLFLYSPWWCL	22.65	FLYSPWWCL	1316.92	22.65	Rendah
HLA-DRB1*1431	1	192	206	QQAISYSSFPFWMGL	22.7	AISYSSFPF	55.25	22.7	Intermediet
HLA-DRB3*0303	1	102	116	LKEMIETLARKLNEK	23.34	MIETLARKL	1361.46	23.34	Rendah
HLA-DRB1*1431	1	99	113	ENELKEMIETLARKL	23.41	MIETLARKL	57.87	23.41	Intermediet
HLA-DRB3*0303	1	126	140	QNLNLQETLKRVA	23.53	LNLQETLKR	1375.24	23.53	Rendah
HLA-DRB1*1431	1	238	252	YPSGTCAIYIQRGAVY	23.58	CAYIQRGAV	58.56	23.58	Intermediet
HLA-DRB3*0303	1	151	165	HGENCYLFSSGSFNW	24.35	CYLFSSGSF	1431.31	24.35	Rendah
HLA-DRB3*0303	1	172	186	CLSLDAKLLKINSTA	24.43	LSLDAKLLK	1436.18	24.43	Rendah
HLA-DRB1*1431	1	197	211	YSSFPFWMGLSRRNP	24.46	FWMGLSRRN	61.84	24.46	Intermediet
HLA-DRB3*0303	1	123	137	LHHQNLNLQETLKR	24.54	LNLQETLKR	1443.43	24.54	Rendah
HLA-DRB1*1431	1	46	60	CLGLVVTIMVLGMQL	24.54	VTIMVLGMQ	62.41	24.54	Intermediet
HLA-DRB1*1431	1	52	66	TIMVLGMQLSQVSDL	24.58	IMVLGMQLS	62.55	24.58	Intermediet
HLA-DRB3*0303	1	100	114	NELKEMIETLARKLN	24.71	MIETLARKL	1453.28	24.71	Rendah
HLA-DRB3*0303	1	101	115	ELKEMIETLARKLNE	24.77	MIETLARKL	1460.2	24.77	Rendah
HLA-DRB1*1431	1	219	233	DGSPLMPHLFRVRGA	24.78	PHLFRVRGA	63.37	24.78	Intermediet
HLA-DRB1*1431	1	124	138	HHQNLNLQETLKRVA	24.97	LNLQETLKR	64.23	24.97	Intermediet
HLA-DRB3*0303	1	55	69	VLGMQLSQVSDLLTQ	25.23	MQLSQVSDL	1491.94	25.23	Rendah
HLA-DRB1*1431	1	178	192	KLLKINSTADLDFIQ	25.48	LLKINSTAD	65.8	25.48	Intermediet
HLA-DRB3*0303	1	192	206	QQAISYSSFPFWMGL	25.74	AISYSSFPF	1517.79	25.74	Rendah
HLA-DRB1*1431	1	193	207	QAISYSSFPFWMGLS	25.79	AISYSSFPF	66.98	25.79	Intermediet
HLA-DRB1*1431	1	125	139	HQNLNLQETLKRVA	26.08	LNLQETLKR	68.68	26.08	Intermediet
HLA-DRB1*1431	1	151	165	HGENCYLFSSGSFNW	26.2	CYLFSSGSF	69.05	26.2	Intermediet
HLA-DRB3*0303	1	167	181	KSQEKCLSLDAKLLK	26.38	LSLDAKLLK	1557.21	26.38	Rendah
HLA-DRB1*1431	1	184	198	STADLDFIQQAISYS	26.58	FIQQAISYS	70.09	26.58	Intermediet
HLA-DRB1*1431	1	129	143	NLQETLKRVANCSAP	26.69	LKRVANCSA	70.45	26.69	Intermediet
HLA-DRB1*1431	1	27	41	LQFLYSPWWCLAAAT	26.99	FLYSPWWCL	71.85	26.99	Intermediet
HLA-DRB3*0303	1	245	259	YIQRGAVYAENCILA	27.41	VYAENCILA	1623.96	27.41	Rendah

HLA-DRB3*0303	1	54	68	MVLGMQLSQVSDLLT	27.63	MQLSQVSDL	1643.01	27.63	Rendah
HLA-DRB1*1431	1	169	183	QEKLCLSLDAKLLKIN	27.66	LSLDAKLLK	75.84	27.66	Intermediet
HLA-DRB3*0303	1	150	164	WHGENCYLFSSGSFN	27.95	WHGENCYLF	1672.44	27.95	Rendah
HLA-DRB1*1431	1	127	141	NLNLQETLKRVANCS	28.18	LQETLKRVA	77.93	28.18	Intermediet
HLA-DRB1*1431	1	106	120	IETLARKLNEKSKEQ	28.59	LARKLNEKS	79.49	28.59	Intermediet
HLA-DRB1*1431	1	168	182	SQEKCLSLDAKLLKI	28.77	KCLSLDAKL	80.43	28.77	Intermediet
HLA-DRB1*1431	1	130	144	LQETLKRVANCSAPC	28.84	LKRVANCSA	80.66	28.84	Intermediet
HLA-DRB1*1431	1	123	137	LHHQNLNLQETLKR	28.91	LNQETLKR	81.23	28.91	Intermediet
HLA-DRB1*1431	1	252	266	YAENCILAAFSICQK	29.12	ILAAFSICQ	82.63	29.12	Intermediet
HLA-DRB1*1431	1	194	208	AISYSSFPFWMGLSR	29.18	YSSFPFWMG	83.04	29.18	Intermediet
HLA-DRB3*0303	1	99	113	ENELKEMIETLARKL	29.49	MIETLARKL	1789.74	29.49	Rendah
HLA-DRB3*0303	1	103	117	KEMIETLARKLNEKS	29.55	MIETLARKL	1795.76	29.55	Rendah
HLA-DRB3*0303	1	144	158	CPQDWIWHGENCYLF	29.69	IWHGENCYL	1803.3	29.69	Rendah
HLA-DRB1*1431	1	195	209	ISYSSFPFWMGLSRR	29.72	YSSFPFWMG	86.31	29.72	Intermediet
HLA-DRB3*0303	1	29	43	FLYSPWWCLAAATLG	29.94	FLYSPWWCL	1822.39	29.94	Rendah
HLA-DRB1*1431	1	152	166	GENCYLFSSGSFNWE	29.96	YLFSSGSFN	88.11	29.96	Intermediet
HLA-DRB1*1431	1	153	167	ENCYLFSSGSFNWEK	30.04	YLFSSGSFN	88.57	30.04	Intermediet
HLA-DRB3*0303	1	56	70	LGMQLSQVSDLLTQE	30.06	MQLSQVSDL	1833.55	30.06	Rendah
HLA-DRB3*0303	1	155	169	CYLFSSGSFNWEKSQ	30.06	YLFSSGSFN	1833.96	30.06	Rendah
HLA-DRB1*1431	1	204	218	MGLSRRNPSYPWLWE	30.1	MGLSRRNPS	88.86	30.1	Intermediet
HLA-DRB1*1431	1	126	140	QNLNLQETLKRVANC	30.35	LNQETLKR	90.41	30.35	Intermediet
HLA-DRB1*1431	1	53	67	IMVLGMQLSQVSDLL	30.52	IMVLGMQLS	91.63	30.52	Intermediet
HLA-DRB1*1431	1	20	34	NGKKAKGLQFLYSPW	30.57	GLQFLYSPW	91.96	30.57	Intermediet
HLA-DRB3*0303	1	31	45	YSPWWCLAAATLGVL	30.91	WWCLAAATL	1888.65	30.91	Rendah
HLA-DRB3*0303	1	53	67	IMVLGMQLSQVSDLL	31.25	MQLSQVSDL	1910.94	31.25	Rendah
HLA-DRB1*1431	1	243	257	CAYIQRGAVYAENCI	31.97	YIQRGAVYA	98.26	31.97	Intermediet
HLA-DRB3*0303	1	127	141	NLNLQETLKRVANCS	32.43	LNQETLKR	1980.49	32.43	Rendah
HLA-DRB1*1431	1	154	168	NCYLFSSGSFNWEKS	32.63	YLFSSGSFN	101.99	32.63	Intermediet
HLA-DRB3*0303	1	193	207	QAISYSSFPFWMGLS	32.64	AISYSSFPF	1992.37	32.64	Rendah
HLA-DRB3*0303	1	181	195	KINSTADLDFIQAI	32.76	INSTADLDF	2000.34	32.76	Rendah
HLA-DRB3*0303	1	120	134	QMEHHQNLNLQETL	33.37	LHHQNLNLQ	2049.19	33.37	Rendah
HLA-DRB3*0303	1	122	136	ELHHQNLNLQETLKR	33.89	LHHQNLNLQ	2079.74	33.89	Rendah
HLA-DRB1*1431	1	167	181	KSQEKCLSLDAKLLK	34.02	KCLSLDAKL	109.14	34.02	Intermediet
HLA-DRB3*0303	1	33	47	PWWCLAAATLGVLC	34.13	CLAAATLGV	2089.88	34.13	Rendah
HLA-DRB3*0303	1	32	46	SPWWCLAAATLGVLC	34.29	CLAAATLGV	2098.82	34.29	Rendah
HLA-DRB3*0303	1	183	197	NSTADLDFIQQAISY	34.49	ADLDFIQQA	2118.07	34.49	Rendah
HLA-DRB1*1431	1	28	42	QFLYSPWWCLAAATL	34.56	FLYSPWWCL	112.69	34.56	Intermediet
HLA-DRB3*0303	1	64	78	SDLLTQEANLTHQK	34.81	LTQEANLT	2133.91	34.81	Rendah
HLA-DRB1*1431	1	122	136	ELHHQNLNLQETLKR	34.82	LHHQNLNLQ	114.12	34.82	Intermediet
HLA-DRB1*1431	1	150	164	WHGENCYLFSSGSFN	34.88	CYLFSSGSF	114.51	34.88	Intermediet
HLA-DRB3*0303	1	259	273	AAFSICQKKANLRAQ	35.32	ICQKKANLR	2180.06	35.32	Rendah
HLA-DRB1*1431	1	45	59	LCLGLVVTIMVLGMQ	35.56	VTIMVLGMQ	119.22	35.56	Intermediet
HLA-DRB3*0303	1	252	266	YAENCILAAFSICQK	35.77	YAENCILAA	2219.82	35.77	Rendah
HLA-DRB1*1431	1	131	145	QETLKRVANCSAPCP	35.84	LKRVANCSA	121.17	35.84	Intermediet
HLA-DRB3*0303	1	224	238	MPHLFRVRGAVSQTY	36.84	LFRVRGAVS	2303.7	36.84	Rendah
HLA-DRB3*0303	1	258	272	LAAFSICQKKANLRA	36.87	ICQKKANLR	2305.21	36.87	Rendah

HLA-DRB3*0303	1	63	77	VSDLLTQEQLNLTHQ	37.14	LTQEQLNL	2322.36	37.14	Rendah
HLA-DRB3*0303	1	182	196	INSTADLDIFIQQAIS	37.16	ADLDIFIQQA	2323.28	37.16	Rendah
HLA-DRB3*0303	1	121	135	MELHHQNLNLQETLK	37.5	LHHQNLNLQ	2342.97	37.5	Rendah
HLA-DRB3*0303	1	257	271	ILAAFSICQKKANLR	38.59	ILAAFSICQ	2420.79	38.59	Rendah
HLA-DRB3*0303	1	254	268	ENCILAAFSICQKKA	38.8	ILAAFSICQ	2430.38	38.8	Rendah
HLA-DRB3*0303	1	226	240	HLFRVRGAVSQTYPS	38.89	VRGAVSQTY	2438.57	38.89	Rendah
HLA-DRB1*1431	1	120	134	QMEHLHHQNLNLQETL	39.35	LHHQNLNLQ	147.86	39.35	Intermediet
HLA-DRB3*0303	1	255	269	NCILAAFSICQKKAN	39.47	ILAAFSICQ	2478.83	39.47	Rendah
HLA-DRB3*0303	1	242	256	TCAYIQRGAVYAENC	39.8	YIQRGAVYA	2504.33	39.8	Rendah
HLA-DRB1*1431	1	77	91	QKKKLEGQISARQQA	39.95	LEGQISARQ	152.79	39.95	Intermediet
HLA-DRB1*1431	1	237	251	TYPSTGTCAYIQRGAV	40	CAYIQRGAV	152.9	40	Intermediet
HLA-DRB3*0303	1	199	213	SFPFWMGLSRRNPSY	40.29	FWMGLSRRN	2544.7	40.29	Rendah
HLA-DRB3*0303	1	227	241	LFRVRGAVSQTYPSG	40.29	VRGAVSQTY	2544.99	40.29	Rendah
HLA-DRB3*0303	1	161	175	GSFNWEKSQEKCLSL	40.31	FNWEKSQEK	2547.22	40.31	Rendah
HLA-DRB3*0303	1	225	239	PHLFRVRGAVSQTY	40.35	VRGAVSQTY	2554.09	40.35	Rendah
HLA-DRB1*1431	1	132	146	ETLKRVCANCSAPCPQ	40.95	LKRVCANCSA	160.35	40.95	Intermediet
HLA-DRB3*0303	1	52	66	TIMVLGMQLSQVSD	41.06	MQLSQVSD	2604.23	41.06	Rendah
HLA-DRB3*0303	1	173	187	LSDAKLLKINSTAD	41.13	LSDAKLLK	2608.94	41.13	Rendah
HLA-DRB1*1431	1	54	68	MVLGMQLSQVSDLLT	41.16	MQLSQVSD	162.65	41.16	Intermediet
HLA-DRB3*0303	1	57	71	GMQLSQVSDLLTQEQ	41.23	MQLSQVSD	2616.3	41.23	Rendah
HLA-DRB1*1431	1	107	121	ETLARKLNEKSKEQM	41.3	LARKLNEKS	164.5	41.3	Intermediet
HLA-DRB3*0303	1	216	230	LWEDGSPLMPHLFRV	41.66	LWEDGSPLM	2648.53	41.66	Rendah
HLA-DRB3*0303	1	256	270	CILAAFSICQKKANL	41.67	ILAAFSICQ	2648.58	41.67	Rendah
HLA-DRB1*1431	1	121	135	MELHHQNLNLQETLK	41.93	LHHQNLNLQ	170.86	41.93	Intermediet
HLA-DRB1*1431	1	18	32	KSNKKKAGLQFLYS	42.23	KKAGLQFL	173.42	42.23	Intermediet
HLA-DRB3*0303	1	194	208	AISYSSFPFWMGLSR	42.77	AISYSSFPF	2727.72	42.77	Rendah
HLA-DRB1*1431	1	149	163	IWHGENCYLFSSGSF	42.79	CYLFSSGSF	178.24	42.79	Intermediet
HLA-DRB3*0303	1	241	255	GTCAYIQRGAVYAEN	42.84	YIQRGAVYA	2730.53	42.84	Rendah
HLA-DRB3*0303	1	243	257	CAYIQRGAVYAENCI	42.86	YIQRGAVYA	2732.47	42.86	Rendah
HLA-DRB1*1431	1	244	258	AYIQRGAVYAENCIL	42.95	YIQRGAVYA	179.86	42.95	Intermediet
HLA-DRB1*1431	1	251	265	VYAENCILAAFSICQ	43.06	ILAAFSICQ	180.72	43.06	Intermediet
HLA-DRB1*1431	1	108	122	TLARKLNEKSKEQME	43.13	LARKLNEKS	182.04	43.13	Intermediet
HLA-DRB3*0303	1	119	133	EQMELHHQNLNLQET	43.19	LHHQNLNLQ	2749.95	43.19	Rendah
HLA-DRB3*0303	1	65	79	DLTTQEQLNLTHQKK	43.37	LTQEQLNL	2766.71	43.37	Rendah
HLA-DRB1*1431	1	179	193	LLKINSTADLDIFIQ	43.37	LLKINSTAD	184.68	43.37	Intermediet
HLA-DRB3*0303	1	34	48	WWCLAAATLGVLC	43.38	CLAAATLGV	2768.71	43.38	Rendah
HLA-DRB1*1431	1	155	169	CYLFSSGSFNWEKSQ	43.44	YLFSSGSFN	185.82	43.44	Intermediet
HLA-DRB3*0303	1	196	210	SYSSFPFWMGLSRRN	43.6	FWMGLSRRN	2794.14	43.6	Rendah
HLA-DRB1*1431	1	218	232	EDGSPLMPHLFRVRG	43.77	LMPHLFRVR	188.25	43.77	Intermediet
HLA-DRB3*0303	1	104	118	EMIETLARKLNEKSK	43.99	MIETLARKL	2828.34	43.99	Rendah
HLA-DRB3*0303	1	128	142	LNLQETLKRVCANCSA	44.07	LNLQETLKR	2841.12	44.07	Rendah
HLA-DRB1*1431	1	249	263	GAVYAENCILAAFSI	44.08	VYAENCILA	191.11	44.08	Intermediet
HLA-DRB3*0303	1	198	212	SSFPFWMGLSRRNPS	44.14	FWMGLSRRN	2845.17	44.14	Rendah
HLA-DRB1*1431	1	119	133	EQMELHHQNLNLQET	44.46	LHHQNLNLQ	195.83	44.46	Intermediet
HLA-DRB1*1431	1	166	180	EKSQEKCLSLDAKLL	44.71	KCLSLDAKL	198.4	44.71	Intermediet
HLA-DRB3*0303	1	162	176	SFNWEKSQEKCLSLD	44.82	FNWEKSQEK	2905.97	44.82	Rendah

HLA-DRB1*1431	1	133	147	TLKRVANCSAPCPQD	44.82	LKRVANCSA	199.75	44.82	Intermediet
HLA-DRB1*1431	1	19	33	SNGKKAKGLQFLYSP	44.88	AKGLQFLYS	200.1	44.88	Intermediet
HLA-DRB1*1431	1	228	242	FRVRGAVSQTYPSGT	44.96	FRVRGAVSQ	201.3	44.96	Intermediet
HLA-DRB1*1431	1	76	90	HQKKKLEGQISARQQ	45.15	LEGQISARQ	203.1	45.15	Intermediet
HLA-DRB3*0303	1	160	174	SGSFNWEKSQEKCCLS	45.27	FNWEKSQEK	2930.21	45.27	Intermediet
HLA-DRB3*0303	1	244	258	AYIQRGAVYAENCIL	45.27	YIQRGAVYA	2929.9	45.27	Intermediet
HLA-DRB1*1431	1	29	43	FLYSPWWCLAAATLG	45.47	FLYSPWWCL	205.89	45.47	Intermediet
HLA-DRB1*1431	1	78	92	KKKLEGQISARQQAE	45.49	LEGQISARQ	206.27	45.49	Intermediet
HLA-DRB1*1431	1	55	69	VLGMQLSQVSDLLTQ	45.54	MQLSQVSDL	207.03	45.54	Intermediet
HLA-DRB1*1431	1	248	262	RGAVYAENCILAAFS	45.72	VYAENCILA	208.79	45.72	Intermediet
HLA-DRB1*1431	1	117	131	SKEQMELHHQNLNLQ	45.98	LHHQNLNLQ	212.23	45.98	Intermediet
HLA-DRB1*1431	1	72	86	ANLTHQKKKLEGQIS	46.08	LTHQKKKLE	213.51	46.08	Intermediet
HLA-DRB1*1431	1	245	259	YIQRGAVYAENCILA	46.13	YIQRGAVYA	214.51	46.13	Intermediet
HLA-DRB3*0303	1	253	267	AENCILAAFSICQKK	46.45	ILAAFSICQ	3029.43	46.45	Rendah
HLA-DRB1*1431	1	118	132	KEQMELHHQNLNLQE	46.73	LHHQNLNLQ	222.09	46.73	Intermediet
HLA-DRB1*1431	1	31	45	YSPWWCLAAATLGV	47.02	CLAAATLGV	226.45	47.02	Intermediet
HLA-DRB3*0303	1	228	242	FRVRGAVSQTYPSGT	47.03	VRGAVSQTY	3086.06	47.03	Rendah
HLA-DRB1*1431	1	73	87	NLTHQKKKLEGQISA	47.14	LTHQKKKLE	228.12	47.14	Intermediet
HLA-DRB3*0303	1	62	76	QVSDLLTQEQANLTH	47.44	LTQEQANLT	3124.7	47.44	Intermediet
HLA-DRB1*1431	1	75	89	THQKKKLEGQISARQ	47.79	LEGQISARQ	236.74	47.79	Intermediet
HLA-DRB3*0303	1	197	211	YSSFPFWMGLSRRNP	48.37	FWMGLSRRN	3187.15	48.37	Rendah
HLA-DRB3*0303	1	200	214	FPFWMGLSRRNPSYP	48.37	FWMGLSRRN	3187.12	48.37	Rendah
HLA-DRB3*0303	1	66	80	LLTQEQANLTHQKKK	48.38	LTQEQANLT	3188.13	48.38	Rendah
HLA-DRB1*1431	1	247	261	QRGAVYAENCILAAF	48.54	VYAENCILA	245.78	48.54	Intermediet
HLA-DRB1*1431	1	30	44	LYSPWWCLAAATLGV	48.65	WWCLAAATL	247.27	48.65	Intermediet
HLA-DRB1*1431	1	71	85	QANLTHQKKKLEGQI	48.96	LTHQKKKLE	250.99	48.96	Intermediet
HLA-DRB1*1431	1	74	88	LTHQKKKLEGQISAR	49.64	LTHQKKKLE	259.58	49.64	Intermediet
HLA-DRB3*0303	1	30	44	LYSPWWCLAAATLGV	50.11	WWCLAAATL	3354.43	50.11	Rendah
HLA-DRB3*0303	1	118	132	KEQMELHHQNLNLQE	50.27	LHHQNLNLQ	3368.59	50.27	Rendah
HLA-DRB1*1431	1	205	219	GLSRRNPSYPWLWED	50.32	LSRRNPSYP	269.27	50.32	Intermediet
HLA-DRB3*0303	1	240	254	SGTCAYIQRGAVYAE	50.35	YIQRGAVYA	3378.29	50.35	Rendah
HLA-DRB3*0303	1	166	180	EKSQEKCLSLDAKLL	50.95	CLSLDAKLL	3428.46	50.95	Rendah
HLA-DRB1*1431	1	246	260	IQRGAVYAENCILAA	51.36	VYAENCILA	285.55	51.36	Intermediet
HLA-DRB3*0303	1	156	170	YLFSSGSFNWEKSQE	51.39	YLFSSGSFN	3463.18	51.39	Rendah
HLA-DRB3*0303	1	223	237	LMPHLFRVRGAVSQT	51.59	LFRVRGAVS	3482.08	51.59	Rendah
HLA-DRB1*1431	1	217	231	WEDGSPLMPHLFRVR	51.67	LMPHLFRVR	292.36	51.67	Intermediet
HLA-DRB3*0303	1	203	217	WMGLSRRNPSYPWLW	51.81	SRRNPSYPW	3497.05	51.81	Rendah
HLA-DRB3*0303	1	159	173	SSGSFNWEKSQEKCL	51.86	FNWEKSQEK	3503.44	51.86	Rendah
HLA-DRB3*0303	1	204	218	MGLSRRNPSYPWLWE	51.86	SRRNPSYPW	3503.48	51.86	Rendah
HLA-DRB1*1431	1	44	58	VLCLGLVVTIMVLGM	51.93	LGLVVTIMV	296.66	51.93	Intermediet
HLA-DRB1*1431	1	32	46	SPWWCLAAATLGVL	51.99	CLAAATLGV	297.79	51.99	Intermediet
HLA-DRB1*1431	1	250	264	AVYAENCILAAFSIC	52.02	VYAENCILA	298.44	52.02	Intermediet
HLA-DRB3*0303	1	195	209	ISYSSFPFWMGLSRR	52.03	YSSFPFWMG	3520.33	52.03	Rendah
HLA-DRB3*0303	1	18	32	KSNGKKAKGLQFLYS	52.04	GKKAKGLQF	3521.14	52.04	Rendah
HLA-DRB3*0303	1	163	177	FNWEKSQEKCLSLDA	52.33	WEKSQEKCL	3549.46	52.33	Rendah
HLA-DRB3*0303	1	201	215	PFWMGLSRRNPSYPW	52.45	FWMGLSRRN	3557.04	52.45	Rendah

HLA-DRB1*1431	1	17	31	EKSNGKKAKGLQFLY	52.87	KKAKGLQFL	312.59	52.87	Intermediet
HLA-DRB1*1431	1	183	197	NSTADLDIFIQQAISY	52.91	LDIFIQQAIS	313.15	52.91	Intermediet
HLA-DRB3*0303	1	1	15	MTFDDLKIQTVKDQP	53.09	MTFDDLKIQ	3618.97	53.09	Rendah
HLA-DRB1*1431	1	33	47	PWWCLAAATLGVLC	53.46	CLAAATLGV	320.93	53.46	Intermediet
HLA-DRB3*0303	1	222	236	PLMPHLFRVRGAVSQ	53.52	LFRVRGAVS	3658.69	53.52	Rendah
HLA-DRB3*0303	1	209	223	RNPSYPWLWEDGSPL	53.95	WLWEDGSPL	3692.44	53.95	Rendah
HLA-DRB3*0303	1	117	131	SKEQMELHHQNLNLQ	54.02	LHHQNLNLQ	3698.76	54.02	Rendah
HLA-DRB3*0303	1	77	91	QKKKLEGQISARQQA	54.09	LEGQISARQ	3705.17	54.09	Rendah
HLA-DRB1*1431	1	56	70	LGMQLSQVSDLLTQE	54.55	MQLSQVSDL	340.59	54.55	Intermediet
HLA-DRB3*0303	1	58	72	MQLSQVSDLLTQEQA	55.47	QLSQVSDLL	3859.32	55.47	Rendah
HLA-DRB1*1431	1	41	55	TLGVLCGLVVTIMV	55.59	LGLVVTIMV	358.4	55.59	Intermediet
HLA-DRB1*1431	1	70	84	EQANLTHQKKKLEGQ	55.74	LTHQKKKLE	361.73	55.74	Intermediet
HLA-DRB1*1431	1	79	93	KKLEGQISARQQAEE	56.17	LEGQISARQ	368.96	56.17	Intermediet
HLA-DRB3*0303	1	78	92	KKKLEGQISARQQAEE	56.81	LEGQISARQ	3986.01	56.81	Rendah
HLA-DRB3*0303	1	21	35	GKKAKGLQFLYSPWW	57.25	KKAKGLQFL	4034.48	57.25	Rendah
HLA-DRB1*1431	1	69	83	QEQLNTHQKKKLEG	57.49	NLTHQKKKL	399.59	57.49	Intermediet
HLA-DRB3*0303	1	35	49	WCLAAATLGVLCGL	57.67	CLAAATLGV	4072.56	57.67	Rendah
HLA-DRB3*0303	1	221	235	SPLMPHLFRVRGAVS	57.87	LFRVRGAVS	4093.88	57.87	Rendah
HLA-DRB1*1431	1	68	82	TQEQLNTHQKKKLE	58.01	NLTHQKKKL	414.21	58.01	Intermediet
HLA-DRB1*1431	1	1	15	MTFDDLKIQTVKDQP	58.04	LKIQTVKDQ	414.77	58.04	Intermediet
HLA-DRB1*1431	1	42	56	LGVLCGLVVTIMVL	58.04	LGLVVTIMV	415.57	58.04	Intermediet
HLA-DRB1*1431	1	148	162	WIWHGENCYLFSSGS	58.31	IWHGENCYL	422.67	58.31	Intermediet
HLA-DRB1*1431	1	67	81	LTQEQLNTHQKKKL	58.34	NLTHQKKKL	423.23	58.34	Intermediet
HLA-DRB1*1431	1	206	220	LSRRNPSYPWLWEDG	58.34	LSRRNPSYP	423.24	58.34	Intermediet
HLA-DRB3*0303	1	202	216	FWMGLSRRNPSYPWL	58.4	SRRNPSYPW	4149.21	58.4	Rendah
HLA-DRB3*0303	1	205	219	GLSRRNPSYPWLWED	58.47	SRRNPSYPW	4157.79	58.47	Rendah
HLA-DRB1*1431	1	43	57	GVLCGLVVTIMVLG	58.54	LGLVVTIMV	426.86	58.54	Intermediet
HLA-DRB3*0303	1	61	75	SQVSDLLTQEQLNLT	58.59	LTQEQLNLT	4172.33	58.59	Rendah
HLA-DRB3*0303	1	239	253	PSGTCAYIQRGAVYA	58.67	CAYIQRGAV	4178.92	58.67	Rendah
HLA-DRB3*0303	1	19	33	SNGKKAKGLQFLYSP	59	GKKAKGLQF	4215.6	59	Rendah
HLA-DRB1*1431	1	165	179	WEKSQEKCLSLDAKL	59.07	KCLSLDAKL	441.87	59.07	Intermediet
HLA-DRB3*0303	1	50	64	VVTIMVLGMQLSQVS	59.48	IMVLGMQLS	4256.29	59.48	Rendah
HLA-DRB1*1431	1	156	170	YLFSSGSFNWEKSQE	59.48	LFSSGSFNW	453.41	59.48	Intermediet
HLA-DRB1*1431	1	236	250	QTYPSGTCAYIQRGA	59.76	TCAYIQRGA	460.74	59.76	Intermediet
HLA-DRB1*1431	1	109	123	LARKLNEKSKEQMEL	59.9	LARKLNEKS	463.67	59.9	Intermediet
HLA-DRB3*0303	1	17	31	EKSNGKKAKGLQFLY	59.98	GKKAKGLQF	4307.97	59.98	Rendah
HLA-DRB3*0303	1	47	61	LGLVVTIMVLGMQLS	60.02	LGLVVTIMV	4312.49	60.02	Rendah
HLA-DRB3*0303	1	129	143	NLQETLKRVANCSAP	60.33	LKRVANCSA	4343.87	60.33	Rendah
HLA-DRB1*1431	1	116	130	KSKEQMELHHQNLNL	60.78	ELHHQNLNL	485.27	60.78	Intermediet
HLA-DRB3*0303	1	22	36	KKAKGLQFLYSPWWC	60.94	KKAKGLQFL	4408.76	60.94	Rendah
HLA-DRB3*0303	1	20	34	NGKKAKGLQFLYSPW	61.02	GKKAKGLQF	4421.58	61.02	Rendah
HLA-DRB3*0303	1	51	65	VTIMVLGMQLSQVSD	61.03	IMVLGMQLS	4422.51	61.03	Rendah
HLA-DRB1*1431	1	229	243	RVRGAVSQTYPSGTC	61.05	GAVSQTYPS	492.49	61.05	Intermediet
HLA-DRB3*0303	1	234	248	VSQTYPSGTCAYIQR	61.24	YPSGTCAYI	4443.4	61.24	Rendah
HLA-DRB3*0303	1	157	171	LFSSGSFNWEKSQEK	61.29	LFSSGSFNW	4448.83	61.29	Rendah
HLA-DRB3*0303	1	220	234	GSPLMPHLFRVRGAV	61.85	LMPHLFRVR	4516.33	61.85	Rendah

HLA-DRB1*1431	1	57	71	GMQLSQVSDLLTQE	61.88	LSQVSDLLT	518.67	61.88	Rendah
HLA-DRB1*1431	1	34	48	WWCLAATLGVLC	62.1	CLAAATLGV	527.28	62.1	Rendah
HLA-DRB1*1431	1	134	148	LKRVANCSAPCPQDW	62.56	LKRVANCSA	542.52	62.56	Rendah
HLA-DRB3*0303	1	49	63	LVVTIMVLGMQLSQV	62.6	IMVLGMQLS	4608.5	62.6	Rendah
HLA-DRB3*0303	1	44	58	VLCLGLVVTIMVLGM	62.68	LGLVVTIMV	4621.02	62.68	Rendah
HLA-DRB3*0303	1	76	90	HQKKKLEGQISARQQ	62.86	LEGQISARQ	4645.29	62.86	Rendah
HLA-DRB3*0303	1	105	119	MIETLARKLNEKSKE	62.96	MIETLARKL	4655.49	62.96	Rendah
HLA-DRB1*1431	1	182	196	INSTADLDFIQQAIS	63.17	LDFIQQAIS	561.54	63.17	Rendah
HLA-DRB3*0303	1	131	145	QETLKRVANCSAPCP	63.31	LKRVANCSA	4698.08	63.31	Rendah
HLA-DRB1*1431	1	80	94	KLEGQISARQQAEAA	63.37	LEGQISARQ	566.44	63.37	Rendah
HLA-DRB3*0303	1	235	249	SQTYPSTGTCAYIQRG	63.41	YPSGTTCAYI	4706.76	63.41	Rendah
HLA-DRB3*0303	1	46	60	CLGLVVTIMVLGMQL	63.71	LGLVVTIMV	4740.64	63.71	Rendah
HLA-DRB3*0303	1	133	147	TLKRVANCSAPCPQD	63.71	LKRVANCSA	4741.69	63.71	Rendah
HLA-DRB3*0303	1	206	220	LSRRNPSYPWLWEDG	63.75	SRRNPSYPW	4750.59	63.75	Rendah
HLA-DRB3*0303	1	130	144	LQETLKRVANCSAPC	63.86	LKRVANCSA	4765.28	63.86	Rendah
HLA-DRB3*0303	1	229	243	RVRGAVSQTYPSTGTC	63.9	VRGAVSQTY	4775.46	63.9	Rendah
HLA-DRB1*1431	1	2	16	TFDDLKIQTVDKQPD	63.9	LKIQTVDKQ	589.04	63.9	Rendah
HLA-DRB3*0303	1	132	146	ETLKRVANCSAPCPQ	63.92	LKRVANCSA	4776.75	63.92	Rendah
HLA-DRB3*0303	1	43	57	GVLCGLVVTIMVLG	64.17	LGLVVTIMV	4807.39	64.17	Rendah
HLA-DRB3*0303	1	42	56	LGVLCLGLVVTIMVL	64.43	LGLVVTIMV	4838.74	64.43	Rendah
HLA-DRB1*1431	1	230	244	VRGAVSQTYPSTGTC	64.52	AVSQTYPSTG	609.07	64.52	Rendah
HLA-DRB1*1431	1	146	160	QDWIWHGENCYLFSS	64.64	IWHGENCYL	613.4	64.64	Rendah
HLA-DRB3*0303	1	164	178	NWEKSQEKCLSLDAK	64.67	WEKSQEKCL	4873.48	64.67	Rendah
HLA-DRB3*0303	1	45	59	LCLGLVVTIMVLGMQ	64.79	LGLVVTIMV	4891.32	64.79	Rendah
HLA-DRB1*1431	1	63	77	VSDLLTQEANLTHQ	64.85	LLTQEANL	622.04	64.85	Rendah
HLA-DRB1*1431	1	180	194	LKINSTADLDFIQQA	64.87	LKINSTADL	622.54	64.87	Rendah
HLA-DRB3*0303	1	143	157	PCPDWVWHGENCYL	65.05	IWHGENCYL	4919.91	65.05	Rendah
HLA-DRB1*1431	1	147	161	DWVWHGENCYLFSSG	65.82	IWHGENCYL	658.5	65.82	Rendah
HLA-DRB3*0303	1	98	112	SENEKEMIETLARK	65.95	ELKEMIETL	5016.26	65.95	Rendah
HLA-DRB1*1431	1	66	80	LLTQEANLTHQKKK	66.08	LLTQEANL	664.93	66.08	Rendah
HLA-DRB1*1431	1	58	72	MQLSQVSDLLTQEQA	66.17	LSQVSDLLT	670.24	66.17	Rendah
HLA-DRB1*1431	1	64	78	SDLLTQEANLTHQK	66.24	LLTQEANL	674.16	66.24	Rendah
HLA-DRB1*1431	1	16	30	DEKSNGKAKGLQFL	66.29	KKAKGLQFL	675.48	66.29	Rendah
HLA-DRB1*1431	1	65	79	DLTQEANLTHQKK	66.57	LLTQEANL	686.43	66.57	Rendah
HLA-DRB1*1431	1	62	76	QVSDLLTQEANLTH	66.97	LLTQEANL	703.61	66.97	Rendah
HLA-DRB3*0303	1	48	62	GLVVTIMVLGMQLSQ	67.01	IMVLGMQLS	5142.26	67.01	Rendah
HLA-DRB1*1431	1	145	159	PQDWVWHGENCYLFS	67.43	IWHGENCYL	722.99	67.43	Rendah
HLA-DRB3*0303	1	219	233	DGSPLMPHLFRVRGA	67.62	PLMPHLFRV	5210.06	67.62	Rendah
HLA-DRB3*0303	1	75	89	THQKKKLEGQISARQ	68.38	LEGQISARQ	5285.24	68.38	Rendah
HLA-DRB1*1431	1	231	245	RGAVSQTYPSTGTCAY	68.48	VSQTYPSTG	765.11	68.48	Rendah
HLA-DRB1*1431	1	3	17	FDDLKIQTVDKQPD	68.9	LKIQTVDKQ	783.71	68.9	Rendah
HLA-DRB1*1431	1	40	54	ATLGLVLCGLVVTIM	68.91	LGLVLCGLV	785.21	68.91	Rendah
HLA-DRB1*1431	1	98	112	SENEKEMIETLARK	69.4	EMIETLARK	809.6	69.4	Rendah
HLA-DRB3*0303	1	79	93	KKLEGQISARQAAEE	69.8	LEGQISARQ	5461.78	69.8	Rendah
HLA-DRB3*0303	1	233	247	AVSQTYPSTGTCAYIQ	69.88	YPSGTTCAYI	5481.62	69.88	Rendah
HLA-DRB1*1431	1	35	49	WCLAATLGVLCGL	69.99	CLAAATLGV	839.72	69.99	Rendah

HLA-DRB1*1431	1	36	50	CLAAATLGVLCGLV	70.06	LGVLCGLV	842.58	70.06	Rendah
HLA-DRB1*1431	1	61	75	SQVSDLLTQEANLT	70.11	LLTQEANL	843.59	70.11	Rendah
HLA-DRB3*0303	1	165	179	WEKSQEKCLSLDAKL	70.42	KCLSLDAKL	5537.94	70.42	Rendah
HLA-DRB3*0303	1	41	55	TLGVLCGLVVTIMV	70.62	LGLVVTIMV	5570.46	70.62	Rendah
HLA-DRB3*0303	1	158	172	FSSGSFNWEKSQEK	70.62	FNWEKSQEK	5571.37	70.62	Rendah
HLA-DRB3*0303	1	230	244	VRGAVSQTYPSGTCA	70.72	VRGAVSQTY	5583.01	70.72	Rendah
HLA-DRB1*1431	1	60	74	LSQVSDLLTQEANL	70.72	LLTQEANL	871.96	70.72	Rendah
HLA-DRB3*0303	1	36	50	CLAAATLGVLCGLV	71.28	CLAAATLGV	5647.1	71.28	Rendah
HLA-DRB3*0303	1	59	73	QLSQVSDLLTQEAN	71.28	QLSQVSDLL	5648.95	71.28	Rendah
HLA-DRB3*0303	1	238	252	YPSGTCAYIQRGAVY	71.54	AYIQRGAVY	5678.25	71.54	Rendah
HLA-DRB1*1431	1	59	73	QLSQVSDLLTQEAN	71.74	LSQVSDLLT	937.19	71.74	Rendah
HLA-DRB1*1431	1	115	129	EKSKEQMELHHQNLN	71.84	MELHHQNLN	947.06	71.84	Rendah
HLA-DRB1*1431	1	144	158	CPQDWIWHGENCYLF	71.9	IWHGENCYL	950.23	71.9	Rendah
HLA-DRB3*0303	1	217	231	WEDGSPLMPHLFRVR	72.25	PLMPHLFRV	5779.83	72.25	Rendah
HLA-DRB3*0303	1	134	148	LKRVANCAPCPQDW	72.34	LKRVANCSA	5789.01	72.34	Rendah
HLA-DRB3*0303	1	232	246	GAVSQTYPSGTCAIY	72.72	YPSGTCAIY	5829.56	72.72	Rendah
HLA-DRB1*1431	1	216	230	LWEDGSPLMPHLFRV	72.73	PLMPHLFRV	997.02	72.73	Rendah
HLA-DRB3*0303	1	236	250	QTYPSGTCAYIQRGA	72.78	YPSGTCAIY	5843.31	72.78	Rendah
HLA-DRB3*0303	1	60	74	LSQVSDLLTQEANL	72.83	LLTQEANL	5851.29	72.83	Rendah
HLA-DRB3*0303	1	218	232	EDGSPLMPHLFRVRG	72.95	PLMPHLFRV	5872.66	72.95	Rendah
HLA-DRB1*1431	1	232	246	GAVSQTYPSGTCAIY	73.07	VSQTYPSGT	1016.23	73.07	Rendah
HLA-DRB3*0303	1	67	81	LTQEANLTHQKKKL	73.12	LTQEANLT	5892.85	73.12	Rendah
HLA-DRB1*1431	1	39	53	AATLGVLCGLVVTI	73.28	LGVLCGLV	1027.03	73.28	Rendah
HLA-DRB1*1431	1	81	95	LEGQISARQQAEEAS	73.93	ISARQQAEE	1076.85	73.93	Rendah
HLA-DRB1*1431	1	38	52	AAATLGVLCGLVVT	74.51	LGVLCGLV	1126.85	74.51	Rendah
HLA-DRB1*1431	1	181	195	KINSTADLDFIQQAI	75.15	INSTADLDF	1174.22	75.15	Rendah
HLA-DRB1*1431	1	5	19	DLKIQTVKDQPDEKS	75.27	LKIQTVKDQ	1182.47	75.27	Rendah
HLA-DRB1*1431	1	4	18	DDLKIQTVKDQPDEK	75.3	LKIQTVKDQ	1186.7	75.3	Rendah
HLA-DRB1*1431	1	161	175	GSFNWEKSQEKCLSL	75.34	WEKSQEKCL	1189.22	75.34	Rendah
HLA-DRB3*0303	1	2	16	TFDDLKIQTVKDQPD	75.37	FDDLKIQTV	6201.44	75.37	Rendah
HLA-DRB1*1431	1	37	51	LAAATLGVLCGLVV	75.57	LGVLCGLV	1208.39	75.57	Rendah
HLA-DRB1*1431	1	164	178	NWEKSQEKCLSLDAK	75.61	EKCLSLDAK	1211.87	75.61	Rendah
HLA-DRB3*0303	1	116	130	KSKEQMELHHQNLNL	75.89	MELHHQNLN	6301.16	75.89	Rendah
HLA-DRB1*1431	1	234	248	VSQTYPSGTCAIYQR	75.89	YPSGTCAIY	1240.3	75.89	Rendah
HLA-DRB1*1431	1	157	171	LFSSGSFNWEKSQEK	76.01	LFSSGSFNW	1251.9	76.01	Rendah
HLA-DRB1*1431	1	233	247	AVSQTYPSGTCAIYQ	76.47	YPSGTCAIY	1282.96	76.47	Rendah
HLA-DRB3*0303	1	237	251	TYPSTGTCAYIQRGAV	76.77	YPSGTCAIY	6440.27	76.77	Rendah
HLA-DRB1*1431	1	6	20	LKIQTVKDQPDEKSN	77.1	LKIQTVKDQ	1339.65	77.1	Rendah
HLA-DRB1*1431	1	235	249	SQTYPSGTCAIYQRG	77.38	YPSGTCAIY	1365.57	77.38	Rendah
HLA-DRB3*0303	1	16	30	DEKSNGKKAKGLQFL	77.79	GKKAKGLQF	6616.73	77.79	Rendah
HLA-DRB3*0303	1	231	245	RGAVSQTYPSGTCAIY	78.21	VSQTYPSGT	6689.27	78.21	Rendah
HLA-DRB1*1431	1	114	128	NEKSKEQMELHHQNL	78.31	EQMELHHQN	1453.71	78.31	Rendah
HLA-DRB1*1431	1	160	174	SGSFNWEKSQEKCLS	79.16	FNWEKSQEK	1542.78	79.16	Rendah
HLA-DRB1*1431	1	143	157	PCPQDWIWHGENCYL	79.41	IWHGENCYL	1563.36	79.41	Rendah
HLA-DRB1*1431	1	215	229	WLWEDGSPLMPHLFR	79.66	SPLMPHLFR	1587.06	79.66	Rendah
HLA-DRB3*0303	1	3	17	FDDLKIQTVKDQPDE	79.69	LKIQTVKDQ	6953.45	79.69	Rendah

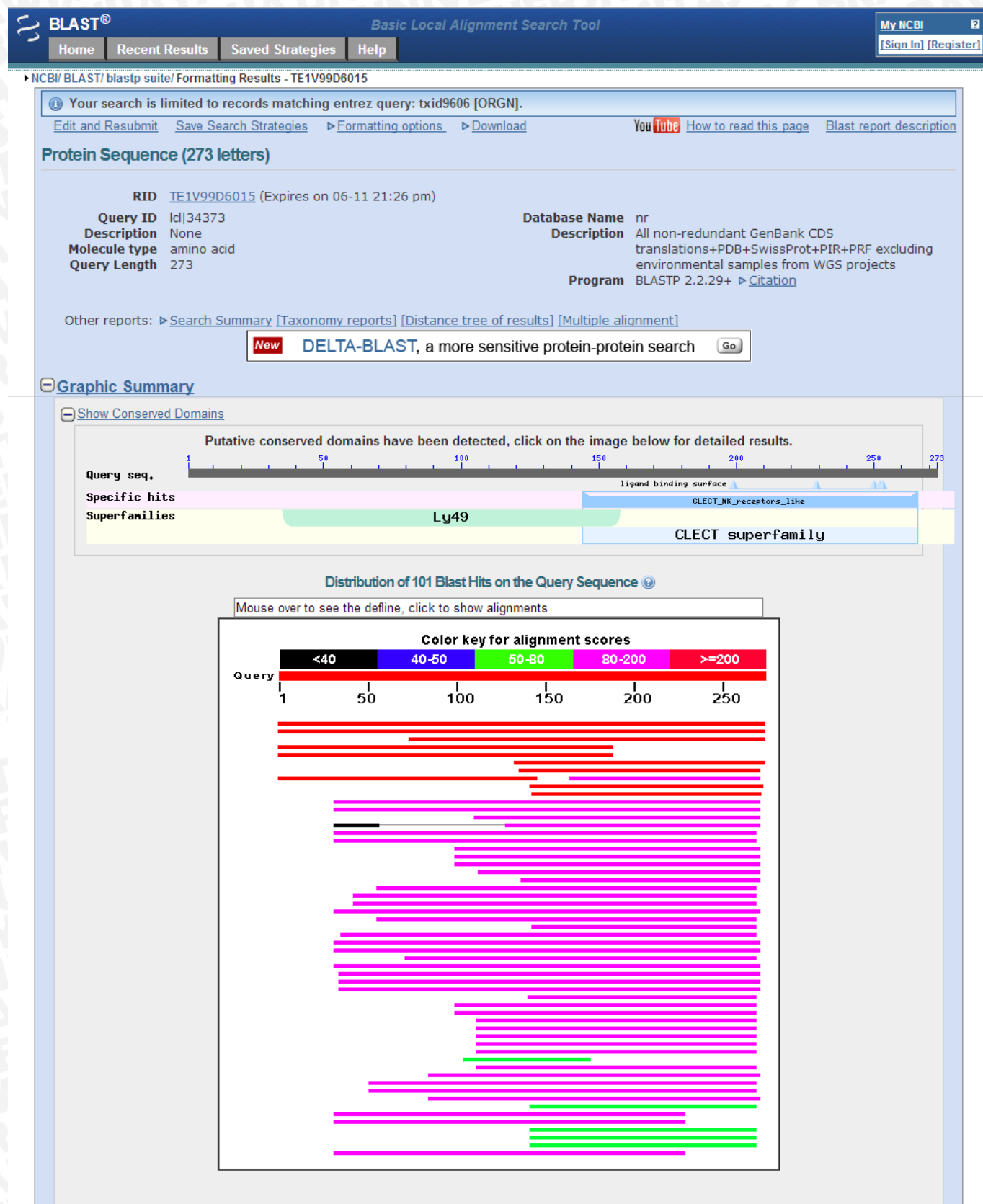
HLA-DRB1*1431	1	163	177	FNWEKSQEKLCLSLDA	79.77	NWEKSQEKC	1607.1	79.77	Rendah
HLA-DRB1*1431	1	162	176	SFNWEKSQEKLCLSLD	79.8	FNWEKSQEK	1611.58	79.8	Rendah
HLA-DRB3*0303	1	80	94	KLEGQISARQQAEEA	80.33	LEGQISARQ	7054.13	80.33	Rendah
HLA-DRB3*0303	1	97	111	ESENELKEMIETLAR	80.54	ELKEMIETL	7093.31	80.54	Rendah
HLA-DRB3*0303	1	74	88	LTHQKKKLEGQISAR	80.73	KKKLEGQIS	7141.35	80.73	Rendah
HLA-DRB1*1431	1	135	149	KRVANCSAPCPQDWI	80.79	RVANCSAPC	1717.61	80.79	Rendah
HLA-DRB1*1431	1	97	111	ESENELKEMIETLAR	81.06	ELKEMIETL	1758.19	81.06	Rendah
HLA-DRB1*1431	1	113	127	LNEKSQEQMELHHQN	81.19	EQMELHHQN	1773.78	81.19	Rendah
HLA-DRB1*1431	1	82	96	EGQISARQQAEEASQ	81.25	ISARQQAEE	1780.17	81.25	Rendah
HLA-DRB1*1431	1	213	227	YPWLWEDGSPLMPHL	81.51	LWEDGSPLM	1819.87	81.51	Rendah
HLA-DRB1*1431	1	110	124	ARKLNEKSQEQMELH	81.56	LNEKSQEQM	1827.27	81.56	Rendah
HLA-DRB1*1431	1	15	29	PDEKSNKGKAKGLQF	81.63	GKKAKGLQF	1840.36	81.63	Rendah
HLA-DRB1*1431	1	83	97	GQISARQQAEEASQE	82.36	ISARQQAEE	1931.28	82.36	Rendah
HLA-DRB1*1431	1	212	226	SYPLWEDGSPLMPH	82.67	WLWEDGSPL	1967.72	82.67	Rendah
HLA-DRB1*1431	1	159	173	SSGSFNWEKSQEKL	83.41	FNWEKSQEK	2062.83	83.41	Rendah
HLA-DRB1*1431	1	214	228	PWLWEDGSPLMPHLF	83.61	LWEDGSPLM	2082.76	83.61	Rendah
HLA-DRB3*0303	1	40	54	ATLGLVCLGLVVTIM	84.61	LCLGLVVTI	7873.65	84.61	Rendah
HLA-DRB3*0303	1	135	149	KRVANCSAPCPQDWI	84.8	RVANCSAPC	7929.57	84.8	Rendah
HLA-DRB1*1431	1	207	221	SRRNPSYPWLWEDGS	85.08	SRRNPSYPW	2298.06	85.08	Rendah
HLA-DRB1*1431	1	112	126	KLNEKSQEQMELHHQ	85.1	LNEKSQEQM	2301.2	85.1	Rendah
HLA-DRB3*0303	1	207	221	SRRNPSYPWLWEDGS	85.37	SRRNPSYPW	8058.95	85.37	Rendah
HLA-DRB3*0303	1	6	20	LKIQTVDQDPDEKSN	85.39	LKIQTVDQD	8063.6	85.39	Rendah
HLA-DRB1*1431	1	210	224	NPSYPWLWEDGSPLM	85.63	WLWEDGSPL	2381.91	85.63	Rendah
HLA-DRB1*1431	1	111	125	RKLNEKSQEQMELHH	85.72	LNEKSQEQM	2400	85.72	Rendah
HLA-DRB3*0303	1	5	19	DLKIQTVDQDPDEKS	85.76	LKIQTVDQD	8152.4	85.76	Rendah
HLA-DRB1*1431	1	211	225	PSYPWLWEDGSPLMP	85.81	WLWEDGSPL	2415.68	85.81	Rendah
HLA-DRB3*0303	1	39	53	AATLGLVCLGLVVTI	85.89	LGLVCLGLV	8184.05	85.89	Rendah
HLA-DRB3*0303	1	96	110	QESANELKEMIETLA	86.36	ELKEMIETL	8307.42	86.36	Rendah
HLA-DRB3*0303	1	37	51	LAAATLGLVCLGLVV	86.76	LGLVCLGLV	8417.34	86.76	Rendah
HLA-DRB1*1431	1	96	110	QESANELKEMIETLA	86.81	ELKEMIETL	2645.93	86.81	Rendah
HLA-DRB3*0303	1	68	82	TQEQANLTHQKKKLE	87.09	EQANLTHQK	8499.33	87.09	Rendah
HLA-DRB3*0303	1	115	129	EKSQEQMELHHQNLN	87.51	MELHHQNLN	8615.68	87.51	Rendah
HLA-DRB1*1431	1	158	172	FSSGSFNWEKSQEKC	87.6	FNWEKSQEK	2839.67	87.6	Rendah
HLA-DRB3*0303	1	4	18	DDLKIQTVDQDPDEK	87.72	LKIQTVDQD	8668.53	87.72	Rendah
HLA-DRB3*0303	1	73	87	NLTHQKKKLEGQISA	87.77	KKKLEGQIS	8682.63	87.77	Rendah
HLA-DRB1*1431	1	136	150	RVANCSAPCPQDWIW	88.29	RVANCSAPC	3032	88.29	Rendah
HLA-DRB3*0303	1	69	83	QEANLTHQKKKLEG	88.42	EQANLTHQK	8839.23	88.42	Rendah
HLA-DRB3*0303	1	38	52	AAATLGLVCLGLVVT	88.63	LGLVCLGLV	8900.9	88.63	Rendah
HLA-DRB1*1431	1	209	223	RNPSYPWLWEDGSPL	88.87	WLWEDGSPL	3160.38	88.87	Rendah
HLA-DRB3*0303	1	95	109	SQESANELKEMIETL	89.49	ELKEMIETL	9146.44	89.49	Rendah
HLA-DRB1*1431	1	84	98	QISARQQAEEASQES	89.56	ISARQQAEE	3362.83	89.56	Rendah
HLA-DRB3*0303	1	110	124	ARKLNEKSQEQMELH	89.69	LNEKSQEQM	9209.1	89.69	Rendah
HLA-DRB1*1431	1	7	21	KIQTVDQDPDEKSNG	89.76	IQTVDQDPD	3430.87	89.76	Rendah
HLA-DRB3*0303	1	15	29	PDEKSNKGKAKGLQF	90	GKKAKGLQF	9291.11	90	Rendah
HLA-DRB3*0303	1	106	120	IETLARKLNEKSQEQ	90.11	LARKLNEKS	9341.45	90.11	Rendah
HLA-DRB3*0303	1	136	150	RVANCSAPCPQDWIW	90.2	RVANCSAPC	9361.78	90.2	Rendah

HLA-DRB1*1431	1	137	151	VANCSAPCPQDWIWH	90.32	PCPQDWIWH	3589.72	90.32	Rendah
HLA-DRB3*0303	1	109	123	LARKLNEKSKEQMEL	90.37	LNEKSKEQM	9399.58	90.37	Rendah
HLA-DRB3*0303	1	7	21	KIQTVDQPDDEKSNG	90.57	IQTVDQPD	9444.42	90.57	Rendah
HLA-DRB1*1431	1	208	222	RRNPSYPWLWEDGSP	91.13	RNPSYPWLW	3842.4	91.13	Rendah
HLA-DRB3*0303	1	114	128	NEKSKEQMELHHQNL	91.29	KSKEQMELH	9651.72	91.29	Rendah
HLA-DRB3*0303	1	81	95	LEGQISARQQAEEAS	91.37	LEGQISARQ	9679.61	91.37	Rendah
HLA-DRB1*1431	1	138	152	ANCSAPCPQDWIWHG	91.37	PCPQDWIWH	3945.97	91.37	Rendah
HLA-DRB3*0303	1	111	125	RKLNEKSKEQMELHH	91.48	LNEKSKEQM	9727.85	91.48	Rendah
HLA-DRB3*0303	1	107	121	ETLARKLNEKSKEQM	91.68	LARKLNEKS	9792.61	91.68	Rendah
HLA-DRB3*0303	1	108	122	TLARKLNEKSKEQME	91.73	LARKLNEKS	9812.4	91.73	Rendah
HLA-DRB3*0303	1	70	84	EQANLTHQKKKLEGQ	92.09	NLTHQKKKL	9891.31	92.09	Rendah
HLA-DRB1*1431	1	142	156	APCPQDWIWHGENCY	92.09	PCPQDWIWH	4246.85	92.09	Rendah
HLA-DRB3*0303	1	112	126	KLNEKSKEQMELHHQ	92.25	LNEKSKEQM	9929.62	92.25	Rendah
HLA-DRB1*1431	1	95	109	SQESENELKEMIETL	92.48	ELKEMIETL	4409.35	92.48	Rendah
HLA-DRB3*0303	1	72	86	ANLTHQKKKLEGQIS	92.71	NLTHQKKKL	10093.47	92.71	Rendah
HLA-DRB3*0303	1	71	85	QANLTHQKKKLEGQI	92.76	NLTHQKKKL	10116.3	92.76	Rendah
HLA-DRB1*1431	1	139	153	NCSAPCPQDWIWHGE	92.76	PCPQDWIWH	4542.46	92.76	Rendah
HLA-DRB1*1431	1	140	154	CSAPCPQDWIWHGEN	93.1	PCPQDWIWH	4693.79	93.1	Rendah
HLA-DRB3*0303	1	113	127	LNEKSKEQMELHHQN	93.27	KSKEQMELH	10317.8	93.27	Rendah
HLA-DRB3*0303	1	137	151	VANCSAPCPQDWIWH	93.27	ANCSAPCPQ	10321.47	93.27	Rendah
HLA-DRB1*1431	1	14	28	QPDEKSNGKKAKGLQ	93.29	EKSNGKKAK	4811.18	93.29	Rendah
HLA-DRB1*1431	1	85	99	ISARQQAEEASQESE	93.56	ISARQQAEE	4975.67	93.56	Rendah
HLA-DRB3*0303	1	8	22	IQTVDQPDDEKSNGK	94.11	IQTVDQPD	10654.25	94.11	Rendah
HLA-DRB3*0303	1	138	152	ANCSAPCPQDWIWHG	94.16	SAPCPQDWI	10663.37	94.16	Rendah
HLA-DRB3*0303	1	142	156	APCPQDWIWHGENCY	94.28	WIWHGENCY	10704.05	94.28	Rendah
HLA-DRB1*1431	1	141	155	SAPCPQDWIWHGENC	94.35	PCPQDWIWH	5407.38	94.35	Rendah
HLA-DRB1*1431	1	13	27	DQPDEKSNGKKAKGL	94.94	EKSNGKKAK	5835.73	94.94	Rendah
HLA-DRB1*1431	1	8	22	IQTVDQPDDEKSNGK	95.35	IQTVDQPD	6147.29	95.35	Rendah
HLA-DRB3*0303	1	139	153	NCSAPCPQDWIWHGE	95.44	SAPCPQDWI	11192.67	95.44	Rendah
HLA-DRB3*0303	1	208	222	RRNPSYPWLWEDGSP	95.61	RNPSYPWLW	11243.69	95.61	Rendah
HLA-DRB3*0303	1	94	108	ASQESENELKEMIET	96.04	SENELKEMI	11464.77	96.04	Rendah
HLA-DRB1*1431	1	11	25	VKDQPDDEKSNGKKAK	96.18	EKSNGKKAK	6834.2	96.18	Rendah
HLA-DRB3*0303	1	9	23	QTVKDQPDDEKSNGKK	96.25	VKDQPDDEKS	11573.32	96.25	Rendah
HLA-DRB3*0303	1	82	96	EGQISARQQAEEASQ	96.25	ISARQQAEE	11573.65	96.25	Rendah
HLA-DRB3*0303	1	140	154	CSAPCPQDWIWHGEN	96.33	PCPQDWIWH	11608.98	96.33	Rendah
HLA-DRB3*0303	1	83	97	GQISARQQAEEASQE	96.34	ISARQQAEE	11614.79	96.34	Rendah
HLA-DRB3*0303	1	93	107	EASQESENELKEMIE	96.69	SENELKEMI	11808.49	96.69	Rendah
HLA-DRB3*0303	1	141	155	SAPCPQDWIWHGENC	96.7	CPQDWIWHG	11813.49	96.7	Rendah
HLA-DRB1*1431	1	12	26	KDQPDDEKSNGKKAKG	96.76	EKSNGKKAK	7489.78	96.76	Rendah
HLA-DRB3*0303	1	92	106	EEASQESENELKEMI	97.08	SENELKEMI	12028.29	97.08	Rendah
HLA-DRB3*0303	1	14	28	QPDEKSNGKKAKGLQ	97.33	DEKSNGKKA	12175.03	97.33	Rendah
HLA-DRB3*0303	1	84	98	QISARQQAEEASQES	97.41	ISARQQAEE	12219.6	97.41	Rendah
HLA-DRB1*1431	1	10	24	TVKDQPDDEKSNGKKA	97.57	VKDQPDDEKS	8348.82	97.57	Rendah
HLA-DRB3*0303	1	10	24	TVKDQPDDEKSNGKKA	97.59	TVKDQPDDEK	12327.71	97.59	Rendah
HLA-DRB3*0303	1	13	27	DQPDEKSNGKKAKGL	97.79	DEKSNGKKA	12417.17	97.79	Rendah
HLA-DRB1*1431	1	9	23	QTVKDQPDDEKSNGKK	98.08	VKDQPDDEKS	9143.98	98.08	Rendah

HLA-DRB3*0303	1	11	25	VKDQPDEKSNGKKAK	98.2	DEKSNGKKA	12686.68	98.2	Rendah
HLA-DRB1*1431	1	94	108	ASQSENELKEMIET	98.3	SENELKEMI	9404.82	98.3	Rendah
HLA-DRB3*0303	1	85	99	ISARQQAEEASQESE	98.32	ISARQQAEE	12784.15	98.32	Rendah
HLA-DRB3*0303	1	91	105	AEEASQSENELKEM	98.35	ASQSENEL	12824.92	98.35	Rendah
HLA-DRB3*0303	1	12	26	KDQPDEKSNGKKAKG	98.65	DEKSNGKKA	13048.07	98.65	Rendah
HLA-DRB1*1431	1	93	107	EASQSENELKEMIE	98.9	SENELKEMI	10703.53	98.9	Rendah
HLA-DRB1*1431	1	86	100	SARQQAEEASQESEN	98.98	ARQQAEEAS	10904.66	98.98	Rendah
HLA-DRB1*1431	1	92	106	EEASQSENELKEMI	99.01	SENELKEMI	10980.1	99.01	Rendah
HLA-DRB3*0303	1	86	100	SARQQAEEASQESEN	99.05	SARQQAEEA	13379.56	99.05	Rendah
HLA-DRB3*0303	1	90	104	QAEEASQSENELKE	99.23	ASQSENEL	13532.75	99.23	Rendah
HLA-DRB3*0303	1	88	102	RQQAEEASQSENEL	99.3	ASQSENEL	13612.76	99.3	Rendah
HLA-DRB3*0303	1	89	103	QQAEEASQSENELK	99.31	ASQSENEL	13622.84	99.31	Rendah
HLA-DRB1*1431	1	87	101	ARQQAEEASQSENE	99.33	ARQQAEEAS	12022.63	99.33	Rendah
HLA-DRB3*0303	1	87	101	ARQQAEEASQSENE	99.38	ARQQAEEAS	13699.56	99.38	Rendah
HLA-DRB1*1431	1	91	105	AEEASQSENELKEM	99.39	ASQSENEL	12159.47	99.39	Rendah
HLA-DRB1*1431	1	89	103	QQAEEASQSENELK	99.54	ASQSENEL	12598.18	99.54	Rendah
HLA-DRB1*1431	1	90	104	QAEEASQSENELKE	99.54	ASQSENEL	12635.06	99.54	Rendah
HLA-DRB1*1431	1	88	102	RQQAEEASQSENEL	99.61	ASQSENEL	12773.22	99.61	Rendah



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Descriptions

Sequences producing significant alignments:

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

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	oxidized low-density lipoprotein receptor 1 isoform 1 [Homo sapiens]	568	568	100%	0.0	100%	NP_002534.1
☐	oxidised low density lipoprotein (lectin-like) receptor 1 [Homo sapiens]	566	566	100%	0.0	99%	BAC81565.1
☐	unnamed protein product [Homo sapiens]	419	419	73%	8e-148	99%	BAG60339.1
☐	oxidized low-density lipoprotein receptor 1 isoform 3 [Homo sapiens]	383	383	68%	4e-134	100%	NP_001166104.1
☐	PREDICTED: oxidized low-density lipoprotein receptor 1 isoform X1 [Homo sapiens]	383	383	68%	1e-133	100%	XP_006719144.1
☐	Chain A, Crystal Structure Of The W150a Mutant Lox-1 CtlD Showing Impaired Oxidl Bindir	299	299	51%	1e-101	99%	3VLG_A
☐	Chain A, Human Oxidized Low Density Lipoprotein Receptor Lox-1 Dioxane Complex [Hor	291	291	49%	7e-99	100%	1YPQ_A
☐	oxidized low-density lipoprotein receptor 1 isoform 2 [Homo sapiens]	285	285	53%	8e-96	98%	NP_001166103.1
☐	Chain A, Human Oxidized Low Density Lipoprotein Receptor Lox-1 P3.1 21 Space Group [	283	283	47%	1e-95	100%	1YPQ_A
☐	Chain A, Crystal Structure Of Human Lectin-like Oxidized Low-density Lipoprotein Recept	274	274	47%	4e-92	98%	1YXJ_A
☐	C-type lectin domain family 7 member A isoform a [Homo sapiens]	127	127	87%	1e-33	32%	NP_922938.1
☐	C-type lectin domain family 7, member A, isoform CRA_k [Homo sapiens]	126	126	87%	3e-33	34%	EAW96155.1
☐	C-type lectin domain family 7 member A isoform e [Homo sapiens]	116	116	58%	2e-30	36%	NP_922941.1
☐	C-type lectin domain family 7 member A isoform b [Homo sapiens]	114	145	61%	2e-29	39%	NP_072092.2
☐	C-type lectin domain family 12 member B, isoform CRA_a [Homo sapiens]	107	107	86%	5e-26	33%	EAW96135.1
☐	C-type lectin domain family 12 member B isoform 1 [Homo sapiens]	106	106	86%	1e-25	32%	NP_001123470.1
☐	C-type lectin domain family 1, member A, isoform CRA_c [Homo sapiens]	103	103	62%	6e-25	33%	EAW96142.1
☐	PREDICTED: C-type lectin domain family 1 member A isoform X1 [Homo sapiens]	103	103	62%	6e-25	33%	XP_005253440.1
☐	C-type lectin-like receptor-1 [Homo sapiens]	103	103	62%	2e-24	32%	AAF36830.1
☐	unnamed protein product [Homo sapiens]	99.4	99.4	57%	7e-24	33%	BAG62601.1
☐	C-type lectin domain family 7, member A, isoform CRA_d [Homo sapiens]	91.3	91.3	39%	9e-22	40%	EAW96147.1
☐	C-type lectin domain family 1, member A, isoform CRA_a [Homo sapiens]	92.8	92.8	49%	1e-21	36%	EAW96140.1
☐	sDC-SIGN1A type III isoform [Homo sapiens]	94.4	94.4	78%	1e-21	31%	AAK91852.1
☐	mDC-SIGN1A type III isoform [Homo sapiens]	94.4	94.4	82%	2e-21	31%	AAK91848.1
☐	CD209 antigen isoform 7 [Homo sapiens]	93.2	93.2	82%	5e-21	31%	NP_001138367.1
☐	C-type lectin domain family 1, member B [Homo sapiens]	91.3	91.3	87%	1e-20	25%	EAW96134.1
☐	CD209 antigen isoform 5 [Homo sapiens]	91.3	91.3	78%	1e-20	31%	NP_001138365.1
☐	PREDICTED: C-type lectin domain family 12 member B isoform X5 [Homo sapiens]	89.7	89.7	46%	1e-20	38%	XP_006719136.1
☐	C-type lectin domain family 9 member A [Homo sapiens]	90.9	90.9	85%	2e-20	29%	NP_997228.1
☐	QDED721 [Homo sapiens]	90.5	90.5	87%	2e-20	25%	AAQ88962.1
☐	C-type lectin domain family 1 member B isoform a [Homo sapiens]	90.5	90.5	87%	2e-20	25%	NP_057593.3
☐	PREDICTED: CD209 antigen isoform X4 [Homo sapiens]	89.4	89.4	72%	7e-20	33%	XP_005272529.1
☐	C-type lectin-like receptor-2 [Homo sapiens]	87.0	87.0	87%	3e-19	25%	AAF36777.1
☐	unnamed protein product [Homo sapiens]	87.0	87.0	86%	5e-19	29%	BAF84273.1
☐	C-type lectin domain family 1 member A [Homo sapiens]	86.7	86.7	86%	6e-19	29%	NP_057595.2
☐	unnamed protein product [Homo sapiens]	86.7	86.7	86%	7e-19	29%	BAC11410.1
☐	Chain A, Crystal Structure Of The Human Clec9a C-type Lectin-like Domain [Homo sapier	83.2	83.2	46%	1e-18	35%	3VPP_A
☐	sDC-SIGN1B type II isoform [Homo sapiens]	85.9	85.9	61%	2e-18	33%	AAK91856.1
☐	CD209 antigen, isoform CRA_i [Homo sapiens]	85.9	85.9	61%	2e-18	33%	EAW69000.1
☐	CD209 antigen isoform 6 [Homo sapiens]	85.1	85.1	57%	5e-18	35%	NP_001138366.1
☐	CD209 antigen isoform 3 [Homo sapiens]	85.1	85.1	57%	6e-18	35%	NP_001138368.1
☐	sDC-SIGN1B type I isoform [Homo sapiens]	84.7	84.7	57%	7e-18	35%	AAK91855.1
☐	unnamed protein product [Homo sapiens]	85.1	85.1	57%	8e-18	35%	BAG36354.1
☐	CD209 antigen isoform 1 [Homo sapiens]	85.1	85.1	57%	8e-18	35%	NP_066978.1
☐	unnamed protein product [Homo sapiens]	79.3	79.3	26%	9e-18	61%	BAH14724.1
☐	mDC-SIGN1B type I isoform [Homo sapiens]	84.7	84.7	57%	9e-18	35%	AAK91854.1
☐	C-type lectin domain family 1 member B isoform b [Homo sapiens]	81.6	81.6	68%	1e-17	27%	NP_001092901.1

☐ C-type lectin domain family 4 member M isoform 7 [Homo sapiens]	82.4	82.4	79%	1e-17	31%	NP_001138378.1
☐ sDC-SIGN2 type III isoform [Homo sapiens]	82.4	82.4	79%	1e-17	31%	AAK91865.1
☐ CLEC1B protein [Homo sapiens]	81.6	81.6	68%	1e-17	27%	AAH29554.1
☐ Chain A, Crystal Structure Of The Free Human Nkg2d Immunoreceptor [Homo sapiens]	79.3	79.3	46%	3e-17	38%	1MPU_A
☐ macrophage antigen h [Homo sapiens]	81.3	81.3	72%	3e-17	32%	AAQ89170.1
☐ unnamed protein product [Homo sapiens]	81.3	81.3	72%	3e-17	32%	BAC87350.1
☐ Chain B, Crystal Structure Of Human Mica In Complex With Natural Killer Cell Receptor N	79.3	79.3	46%	3e-17	38%	1HYR_B
☐ Chain A, Crystal Structure Of Cowpox Virus Cpx018 (omcp) Bound To Human Nkg2d [Ho	78.6	78.6	46%	4e-17	38%	4PDC_A
☐ Chain A, Nkg2d In Complex With Ulbp3 [Homo sapiens]	78.6	78.6	46%	5e-17	38%	1KCG_A
☐ C-type lectin domain family 12 member B isoform 2 [Homo sapiens]	80.1	80.1	72%	6e-17	32%	NP_995324.2
☐ Chain B, Crystal Structure Of Nkp65 Bound To Its Liqand Kac1 [Homo sapiens]	78.6	78.6	46%	9e-17	36%	4IOP_B
☐ Chain A, Crvstal Structure Of Human Clec-2 (Clec1b) [Homo sapiens]	77.0	77.0	46%	1e-16	29%	2C6U_A
☐ killer cell lectin-like receptor subfamily F member 2 [Homo sapiens]	78.6	78.6	46%	2e-16	36%	NP_001177694.1
☐ CD209 antigen isoform 8 [Homo sapiens]	79.0	79.0	52%	2e-16	35%	NP_001138371.1
☐ NKG2-D type II integral membrane protein [Homo sapiens]	78.2	78.2	46%	2e-16	38%	NP_031386.2
☐ RecName: Full=NKG2-D type II integral membrane protein; AltName: Full=Killer cell lectin	78.2	78.2	46%	3e-16	38%	P26718.1
☐ unnamed protein product [Homo sapiens]	78.2	78.2	46%	3e-16	38%	BAF84709.1
☐ Chain A, Crystal Structure Of The Complex Of The Carbohydrate Recognition Domain Of I-	77.0	77.0	46%	4e-16	36%	2XR6_A
☐ PREDICTED: C-type lectin domain family 12 member B isoform X2 [Homo sapiens]	78.2	78.2	72%	4e-16	31%	XP_006719133.1
☐ Chain A, Crystal Structure Of Dc-Sign Carbohydrate Recognition Domain Complexed With	75.5	75.5	46%	7e-16	36%	1SL5_A
☐ Chain A, Complex Of Dc-Sign And Glnac2man3 [Homo sapiens]	75.9	75.9	46%	7e-16	36%	1K9I_A
☐ Chain A, Crystal Structure Of Dc-Sign Carbohydrate Recognition Domain Complexed With	75.9	75.9	46%	7e-16	36%	1SL4_A
☐ C-type lectin domain family 12 member A isoform 2 [Homo sapiens]	76.6	76.6	62%	9e-16	30%	NP_963917.2
☐ Chain D, Cryo Em Structure Of Denque Complexed With Crd Of Dc-Sign [Homo sapiens]	75.9	75.9	46%	1e-15	36%	2B6B_D
☐ Chain A, Crystal Structure Of The Complex Of The Carbohydrate Recognition Domain Of I-	75.5	75.5	46%	1e-15	36%	2XR5_A
☐ myeloid inhibitory C-type lectin-like receptor isoform beta [Homo sapiens]	76.6	76.6	62%	1e-15	30%	AAS00606.1
☐ C-type lectin domain family 12 member A isoform 1 [Homo sapiens]	76.3	76.3	62%	2e-15	30%	NP_612210.4
☐ C-type lectin protein CLL-1 [Homo sapiens]	75.9	75.9	62%	3e-15	30%	AAL95693.1
☐ C-type lectin domain family 4 member M isoform 11 [Homo sapiens]	76.6	76.6	63%	3e-15	32%	NP_001138379.1
☐ C-type lectin domain family 12 member A isoform 3 [Homo sapiens]	75.9	75.9	62%	3e-15	30%	NP_001193939.1
☐ C-type lectin domain family 12, member A, isoform CRA_a [Homo sapiens]	75.9	75.9	62%	4e-15	30%	EAW96132.1
☐ PREDICTED: C-type lectin domain family 12 member A isoform X2 [Homo sapiens]	75.9	75.9	62%	4e-15	30%	XP_006719096.1
☐ Chain A, Crystal Structure Of A Fragment Of Dc-signr (containing The Carbohydrate Recon	74.3	74.3	63%	4e-15	30%	1SL6_A
☐ hCG16425, isoform CRA_a [Homo sapiens]	73.6	73.6	50%	8e-15	28%	EAW83922.1
☐ C-type lectin domain family 2 member L [Homo sapiens]	73.2	73.2	49%	1e-14	28%	NP_001073980.2
☐ CD209 antigen isoform 4 [Homo sapiens]	75.1	75.1	57%	2e-14	33%	NP_001138369.1
☐ L-SIGN variant [Homo sapiens]	74.7	74.7	63%	2e-14	30%	AAR04559.1
☐ C-type lectin domain family 4 member M isoform 9 [Homo sapiens]	74.7	74.7	63%	2e-14	30%	NP_001138381.1
☐ C-type lectin domain family 4 member M isoform 2 [Homo sapiens]	74.7	74.7	57%	2e-14	31%	NP_001138376.1
☐ unnamed protein product [Homo sapiens]	74.7	74.7	57%	2e-14	31%	BAG65307.1
☐ PREDICTED: C-type lectin domain family 4 member M isoform X4 [Homo sapiens]	74.3	74.3	57%	2e-14	30%	XP_006722677.1
☐ PREDICTED: C-type lectin domain family 4 member M isoform X3 [Homo sapiens]	74.3	74.3	57%	3e-14	31%	XP_006722676.1
☐ C-type lectin domain family 4 member M isoform 8 [Homo sapiens]	74.3	74.3	63%	3e-14	30%	NP_001138382.1
☐ C-type lectin domain family 4 member M isoform 12 [Homo sapiens]	74.3	74.3	63%	3e-14	30%	NP_001138377.1
☐ CLEC4M protein [Homo sapiens]	74.3	74.3	57%	3e-14	31%	AAI10615.1
☐ PREDICTED: C-type lectin domain family 4 member M isoform X2 [Homo sapiens]	73.9	73.9	57%	4e-14	30%	XP_006722675.1
☐ C-type lectin domain family 4 member M isoform 1 [Homo sapiens]	73.9	73.9	57%	4e-14	30%	NP_055072.3

☐	PREDICTED: C-type lectin domain family 4 member M isoform X1 [Homo sapiens]	73.9	73.9	57%	4e-14	31%	XP_006722674.1
☐	Chain A, Structure Of Dc-Signr And A Portion Of Repeat Domain 8 [Homo sapiens]	69.7	69.7	45%	9e-14	34%	1XPH_A
☐	Chain A, Complex Of Dc-signr And Glnac2man3 [Homo sapiens]	69.3	69.3	45%	1e-13	34%	1K9J_A
☐	probable mannose binding C-type lectin DC-SIGNR [Homo sapiens]	72.8	72.8	43%	1e-13	34%	AAG13848.2
☐	PREDICTED: C-type lectin domain family 12 member A isoform X6 [Homo sapiens]	68.6	68.6	39%	7e-13	32%	XP_006719100.1
☐	PREDICTED: C-type lectin domain family 12 member A isoform X5 [Homo sapiens]	68.2	68.2	39%	1e-12	32%	XP_006719099.1

Alignments

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oxidized low-density lipoprotein receptor 1 isoform 1 [Homo sapiens]

Sequence ID: [ref|NP_002534.1|](#) Length: 273 Number of Matches: 1

[See 9 more title\(s\)](#)

Range 1: 1 to 273 [GenPept](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
568 bits(1464)	0.0	Compositional matrix adjust.	273/273(100%)	273/273(100%)	0/273(0%)
Query 1	MTFDDLKIQTVKDPDEKSNKKKAGLQFLYSPWWCLAAATLGVLCGLVVTIMVLGMQL				60
Sbjct 1	MTFDDLKIQTVKDPDEKSNKKKAGLQFLYSPWWCLAAATLGVLCGLVVTIMVLGMQL				60
Query 61	SQVSDLLTQEQANLTHQKKKLEGQISARQQAEASQESSELKEMETLARKLNEKSKEQ				120
Sbjct 61	SQVSDLLTQEQANLTHQKKKLEGQISARQQAEASQESSELKEMETLARKLNEKSKEQ				120
Query 121	MELHHQNLNLQETLKRNVANCSAPCPQDWIWHGENCYLFSSGSGFNWKSQEKCLSLDAKLL				180
Sbjct 121	MELHHQNLNLQETLKRNVANCSAPCPQDWIWHGENCYLFSSGSGFNWKSQEKCLSLDAKLL				180
Query 181	KINSTADLDFIQQAISYSSFFFWMGLSRRNPSYPWLWEDGSPLMPHLFRVRGAVSQTYPS				240
Sbjct 181	KINSTADLDFIQQAISYSSFFFWMGLSRRNPSYPWLWEDGSPLMPHLFRVRGAVSQTYPS				240
Query 241	GTCAYIQRGAVYAENCILAAFSICQKKANLRAQ		273		
Sbjct 241	GTCAYIQRGAVYAENCILAAFSICQKKANLRAQ		273		

Related Information

[Gene](#) - associated gene details
[UniGene](#) - clustered expressed sequence tags
[Map Viewer](#) - aligned genomic context
[Identical Proteins](#) - Proteins identical to the subject

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oxidised low density lipoprotein (lectin-like) receptor 1 [Homo sapiens]

Sequence ID: [dbj|BAC81565.1|](#) Length: 273 Number of Matches: 1

[See 1 more title\(s\)](#)

unnamed protein product [Homo sapiens]

Sequence ID: [dbj|BAF84813.1|](#)

Range 1: 1 to 273 [GenPept](#) [Graphics](#)

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Score	Expect	Method	Identities	Positives	Gaps
566 bits(1458)	0.0	Compositional matrix adjust.	272/273(99%)	272/273(99%)	0/273(0%)
Query 1	MTFDDLKIQTVKDPDEKSNKKKAGLQFLYSPWWCLAAATLGVLCGLVVTIMVLGMQL				60
Sbjct 1	MTFDDLKIQTVKDPDEKSNKKKAGLQFLYSPWWCLAAATLGVLCGLVVTIMVLGMQL				60
Query 61	SQVSDLLTQEQANLTHQKKKLEGQISARQQAEASQESSELKEMETLARKLNEKSKEQ				120
Sbjct 61	SQVSDLLTQEQANLTHQKKKLEGQISARQQAEASQESSELKEMETLARKLNEKSKEQ				120
Query 121	MELHHQNLNLQETLKRNVANCSAPCPQDWIWHGENCYLFSSGSGFNWKSQEKCLSLDAKLL				180
Sbjct 121	MELHHQNLNLQETLKRNVANCSAPCPQDWIWHGENCYLFSSGSGFNWKSQEKCLSLDAKLL				180
Query 181	KINSTADLDFIQQAISYSSFFFWMGLSRRNPSYPWLWEDGSPLMPHLFRVRGAVSQTYPS				240
Sbjct 181	KINSTADLDFIQQAISYSSFFFWMGLSRRNPSYPWLWEDGSPLMPHLFRVRGAVSQTYPS				240
Query 241	GTCAYIQRGAVYAENCILAAFSICQKKANLRAQ		273		
Sbjct 241	GTCAYIQRGAVYAENCILAAFSICQKKANLRAQ		273		

Related Information

[Gene](#) - associated gene details
[Identical Proteins](#) - Proteins identical to the subject

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unnamed protein product [Homo sapiens]

Sequence ID: [dbj|BAG60339.1](#) Length: 214 Number of Matches: 1**Related Information**[Gene](#) - associated gene detailsRange 1: 15 to 214 [GenPept](#) [Graphics](#)

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Score	Expect	Method	Identities	Positives	Gaps
419 bits(1076)	8e-148	Compositional matrix adjust.	199/200(99%)	199/200(99%)	0/200(0%)
Query 74	LTHQKKKLEGQISARQAAEEASQES	ENELKEM	ETLARKLNEKSKEQ	MELHHQNLNLQET	133
Sbjct 15	FTHQKKKLEGQISARQAAEEASQES	ENELKEM	ETLARKLNEKSKEQ	MELHHQNLNLQET	74
Query 134	LKRVANCSAPCPQDWIWHG	ENCYLFSSGSFNWEKSQEK	CLSLDAKLLKIN	STADLDFIQQ	193
Sbjct 75	LKRVANCSAPCPQDWIWHG	ENCYLFSSGSFNWEKSQEK	CLSLDAKLLKIN	STADLDFIQQ	134
Query 194	AISYSSFPFWMGLSRNPSPY	PWLWEDGSP	LMPLFRVRGAVSQT	YPSGTCAYIQRGAVYA	253
Sbjct 135	AISYSSFPFWMGLSRNPSPY	PWLWEDGSP	LMPLFRVRGAVSQT	YPSGTCAYIQRGAVYA	194
Query 254	ENCILAAFSICQKKANLRAQ	273			
Sbjct 195	ENCILAAFSICQKKANLRAQ	214			

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oxidized low-density lipoprotein receptor 1 isoform 3 [Homo sapiens]

Sequence ID: [ref|NP_001166104.1](#) Length: 189 Number of Matches: 1[▶ See 1 more title\(s\)](#)**Related Information**[Gene](#) - associated gene details[Map Viewer](#) - aligned genomic context[Identical Proteins](#) - Proteins identical to the subjectRange 1: 1 to 188 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
383 bits(984)	4e-134	Compositional matrix adjust.	188/188(100%)	188/188(100%)	0/188(0%)
Query 1	MTFDDLKIQTIVKDQPEK	SNKKAKGLQFLYSP	WWCLAAATLGVL	CLGLVVTIMVLGMQL	60
Sbjct 1	MTFDDLKIQTIVKDQPEK	SNKKAKGLQFLYSP	WWCLAAATLGVL	CLGLVVTIMVLGMQL	60
Query 61	SQVSDLLTQEQANLTHQ	KKKLEGQISARQAAEEASQES	ENELKEM	ETLARKLNEKSKEQ	120
Sbjct 61	SQVSDLLTQEQANLTHQ	KKKLEGQISARQAAEEASQES	ENELKEM	ETLARKLNEKSKEQ	120
Query 121	MELHHQNLNLQETLKR	VANCSAPCPQDWIWHG	ENCYLFSSGSFNWEKSQEK	CLSLDAKLL	180
Sbjct 121	MELHHQNLNLQETLKR	VANCSAPCPQDWIWHG	ENCYLFSSGSFNWEKSQEK	CLSLDAKLL	180
Query 181	KINSTADL	188			
Sbjct 181	KINSTADL	188			

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PREDICTED: oxidized low-density lipoprotein receptor 1 isoform X1 [Homo sapiens]

Sequence ID: [ref|XP_006719144.1](#) Length: 217 Number of Matches: 1**Related Information**[Gene](#) - associated gene detailsRange 1: 1 to 188 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
383 bits(983)	1e-133	Compositional matrix adjust.	188/188(100%)	188/188(100%)	0/188(0%)
Query 1	MTFDDLKIQTIVKDQPEK	SNKKAKGLQFLYSP	WWCLAAATLGVL	CLGLVVTIMVLGMQL	60
Sbjct 1	MTFDDLKIQTIVKDQPEK	SNKKAKGLQFLYSP	WWCLAAATLGVL	CLGLVVTIMVLGMQL	60
Query 61	SQVSDLLTQEQANLTHQ	KKKLEGQISARQAAEEASQES	ENELKEM	ETLARKLNEKSKEQ	120
Sbjct 61	SQVSDLLTQEQANLTHQ	KKKLEGQISARQAAEEASQES	ENELKEM	ETLARKLNEKSKEQ	120
Query 121	MELHHQNLNLQETLKR	VANCSAPCPQDWIWHG	ENCYLFSSGSFNWEKSQEK	CLSLDAKLL	180
Sbjct 121	MELHHQNLNLQETLKR	VANCSAPCPQDWIWHG	ENCYLFSSGSFNWEKSQEK	CLSLDAKLL	180
Query 181	KINSTADL	188			
Sbjct 181	KINSTADL	188			

Sumber : NCBI

Link : <http://blast.ncbi.nlm.nih.gov/Blast.cgi>

Lampiran 11 . FASTA Sekuens Asam Amino Penyusun Protein LOX-1 Manusia dan Tikus

FASTA Sekuens Asam Amino Penyusun Protein LOX-1 Manusia (*Homo sapiens*)

>sp|P78380|OLR1_HUMAN Oxidized low-density lipoprotein receptor 1 OS=Homo sapiens
GN=OLR1 PE=1 SV=1
MTFDDLKIQTVDQDEKSNKGKAKGLQFLYSPWWCLAAATLGVLCGLVVTIMVLGMQL
SQVSDLLTQEQANLTHQKKKLEGQISARQQAEEASQESNELKEMIETLARKLNEKSKEQ
MELHHQNLNLQETLKRVANCSAPCPQDWIWHGENCYLFSSGSFNWEKSQEKCLSLDAKL
LKINSTADLDFIQQAISYSSFPFWMGLSRRNPSPWLWEDGSPLMPHLFRVRGAVSQTYP
SGTCAYIQRGAVYAENCILAAFSICQKKANLRAQ

Sumber : UniProt

Link : <http://www.uniprot.org/uniprot/P78380.fasta>

FASTA Sekuens Asam Amino Penyusun Protein LOX-1 Tikus (*Rattus norvegicus*)

>sp|O70156|OLR1_RAT Oxidized low-density lipoprotein receptor 1 OS=Rattus norvegicus
GN=Olrl PE=2 SV=1
MAFDDKMKPVNGQPDQKSCGKKPKGLHLLSSTWWCPAAVTLAILCLVLSVTLIVQQTQLL
QVSDLLKQYQANLTQQDHILEGQMSAQKKAENASQESKRELKEQIDTLTWKLNEKSKEQE
KLLQQNQNLQEALQRAVNASEESKWELKEQIDILNWKLNGISKEQKELLQQNQNLQEALQ
KAEKYSEESQRELKEQIDTLWKLNEKSKEQEELLQQNQNLQEALQRAANSSGPCPDW
IWHKENCYLFHGPFNWEKSRENCLSLDAQLLQISTDDLNFLVLAQATSHSTSPFWMGLHRK
NPNHPWLWENGSPFSFQFFRTRGVSLQMYSSGTCAYIQGGVFAENCILTAFSICQKKAN
LLLTQ

Sumber : UNIPROT

Link : <http://www.uniprot.org/uniprot/O70156.fasta>

Lampiran 12. Hasil Analisis Homologi Protein LOX-1 Manusia dan Tikus

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NCBI/BLAST/blastp suite-2sequences/Formatting Results - V6VJ0P55114

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Blast 2 sequences

sp|P78380|OLR1_HUMAN Oxidized low-density...

RID	V6VJ0P55114 (Expires on 07-03 10:28 am)	Subject ID	Id 17757
Query ID	Id 17755	Description	sp O70156 OLR1_RAT Oxidized low-density lipoprotein receptor 1 OS=Rattus norvegicus GN=Olr1 PE=2 SV=1
Description	sp P78380 OLR1_HUMAN Oxidized low-density lipoprotein receptor 1 OS=Homo sapiens GN=OLR1 PE=1 SV=1	Molecule type	amino acid
Molecule type	amino acid	Subject Length	364
Query Length	273	Program	BLASTP 2.2.29+ Citation

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#)

Graphic Summary

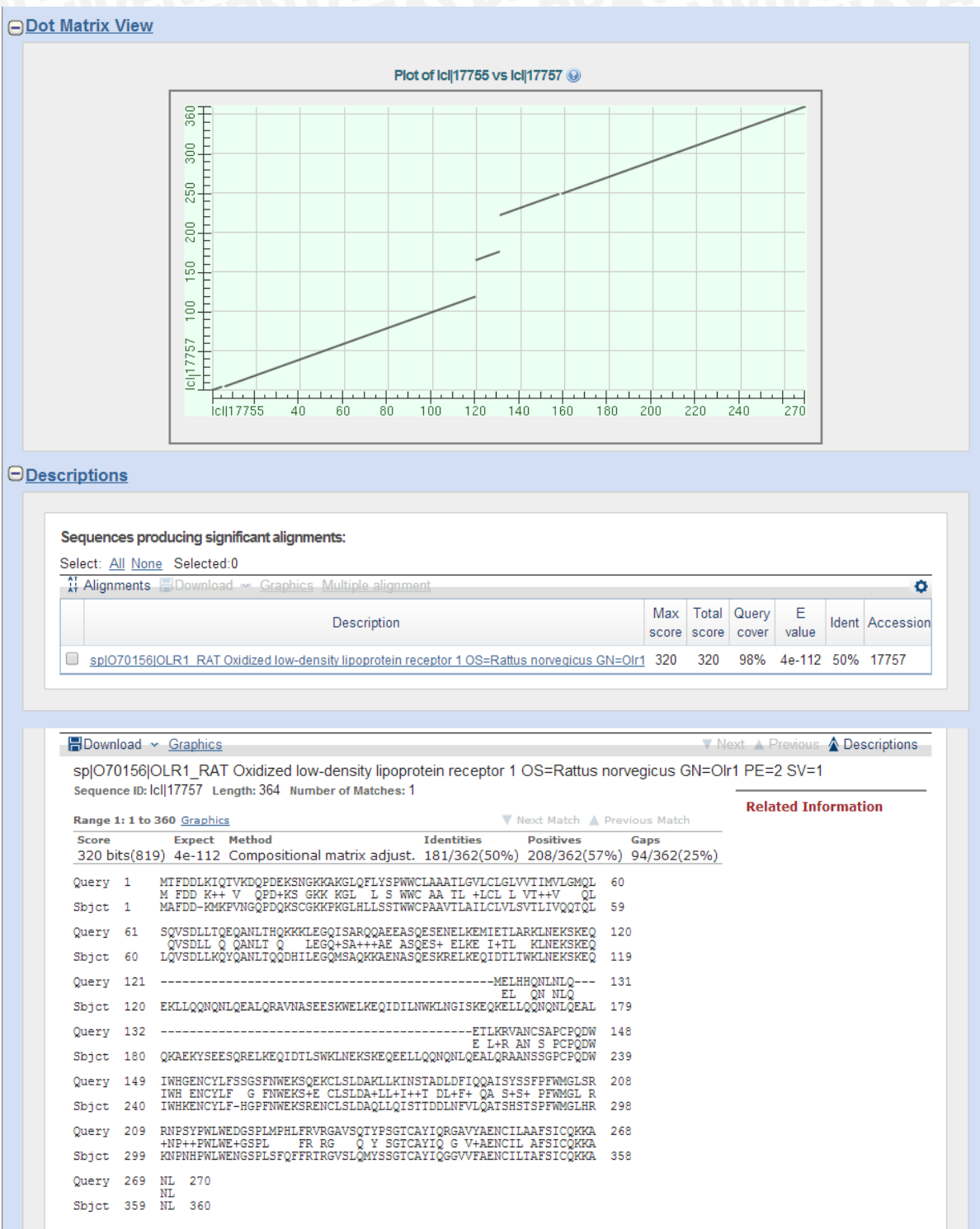
Distribution of 1 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments

Color key for alignment scores	
Score Range	Color
<40	Black
40-50	Blue
50-80	Green
80-200	Yellow
>=200	Red

Query 1 50 100 150 200 250





Sumber : NCBI

Link : <http://blast.ncbi.nlm.nih.gov/Blast.cgi>

Lampiran 13. Rancangan Acak Kelompok

Adapun prosedur pengambilan sampel menggunakan Rancangan Acak Kelompok (RAK) sebagai berikut: dari jumlah 28 tekor tikus ini dilakukan sistem *lotree*, sebanyak 2 kali. *Lotree* pertama menentukan kelompok yang akan diambil terlebih dahulu, sedangkan *lotree* ke dua untuk mengelompokkan tikus.

Tabel 5.5 Randomisasi Acak Kelompok

Kelompok	Nomor Urut Tikus	Pengelompokan
Kn	18	Kn C
	6	Kn A
	10	Kn B
	22	Kn D
Kp	5	Kp A
	20	Kp C
	9	Kp B
	28	Kp D
P1	1	P1 A
	17	P1 D
	4	P1 C
	2	P1 B
P2	27	P2 D
	21	P2 C
	3	P2 A
	7	P2 B
P3	19	P3 D
	11	P3 B
	8	P3 A
	13	P3 C
P4	12	P4 A
	15	P4 B
	24	P4 D
	23	P4 C
P5	14	P5 A
	16	P5 B
	25	P5 D
	22	P5 C

Lampiran 14. Data Asupan Pakan Tikus

Tabel 5.7 Data Asupan Pakan Tikus Bulan Maret 2014 (Tanggal 15-31 Maret 2014)

Kelompok	Sampel (tikus)	Jumlah asupan pakan per hari (gram)																		
		14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	
Kn	A	13	14	14	3	12	9	12	15	14	13	14	15	14	14	14	14	16	9	
	B	16	17	15	18	14	11	16	18	11	15	17	20	18	15	17	18	16	15	
	C	10	10	8	12	9	8	13	20	18	12	17	17	17	15	27	17	17	19	
	D	13	9	14	15	9	10	12	13	12	13	15	17	13	13	17	13	16	15	
Kp	A	11	6	17	14	5	8	11	12	13	12	14	14	13	13	9	14	9	14	
	B	17	13	13	10	9	15	15	14	16	18	19	15	13	18	13	13	19	15	
	C	10	13	13	9	9	9	14	15	15	13	14	16	12	13	14	17	14	9	
	D	17	26	16	16	25	7	16	16	12	16	17	15	17	15	6	16	20	14	
P1	A	19	17	17	12	13	30	21	19	14	22	14	20	14	16	8	14	11	9	
	B	16	14	16	15	19	13	11	17	18	12	15	17	12	18	6	21	14	15	
	C	11	13	13	13	10	11	17	14	15	23	11	13	13	13	7	13	12	8	
	D	13	13	11	13	11	16	17	22	1										

Tabel 5.8 Data Asupan Pakan Tikus Bulan April 2014 (Tanggal 1 - 30 April 2014)

Kelompok	Sampel (tikus)	Jumlah asupan pakan per hari (gram)																													
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Kn	A	4	3	6	6	6	7	3	13	7	5	12	9	15	17	14	14	12	14	16	14	20	13	14	16	15	14	16	16	19	14
	B	10	12	9	11	12	12	13	14	15	4	3	14	15	21	19	20	13	24	15	19	12	21	17	19	22	14	15	19	20	11
	C	3	7	8	10	9	14	15	9	14	6	11	10	12	20	13	18	14	15	16	19	16	18	22	19	18	15	17	19	20	13
	D	7	7	6	7	7	7	8	13	13	7	6	17	16	18	14	13	13	14	14	15	14	13	16	16	17	11	14	15	17	14
Kp	A	17	3	15	12	12	12	16	7	8	12	2	9	6	6	7	7	6	8	9	7	4	7	8	5	6	7	7	5	4	4
	B	10	20	22	20	20	20	16	11	13	13	6	5	6	5	6	8	10	10	8	5	8	7	7	5	8	7	7	7	7	5
	C	8	10	12	8	10	10	9	10	13	8	4	12	3	7	6	5	7	11	9	8	8	9	3	9	7	5	2	6	6	6
	D	8	11	20	15	9	9	9	12	9	12	6	6	9	6	11	7	11	8	11	6	7	8	6	6	7	9	7	6	13	8
P1	A	6	2	6	16	11	11	5	11	11	10	4	7	3	6	7	6	5	5	8	6	6	6	7	8	6	7	4	4	4	9
	B	13	11	15	15	15	15	7	7	2	14	11	5	2	7	11	11	8	9	8	7	9	15	9	9	7	9	6	7	13	10
	C	6	5	5	10	10	10	6	8	6	14	7	6	8	7	11	9	7	6	6	5	5	6	7	7	8	6	5	4	7	7
	D	6	5	11	13	13	13	6	10	14	14	7	8	2	2	6	7	10	5	7	6	9	10	3	7	8	10	8	6	7	6
P2	A	9	11	8	15	11	11	9	13	10	14	8	7	7	9	10	7	9	2	7	4	8	9	5	7	5	6	6	6	13	4
	B	9	2	12	13	12	12	3	8	10	12	10	9	9	9	10	7	9	2	7	4	8	9	5	7	5	6	6	6	13	4
	C	9	3	9	15	9	9	4	10	11	13	4	5	5	7	8	6	9	4	10	2	8	8	5	9	5	6	5	6	7	7
	D	9	5	12	6	12	12	4	6	15	13	6	9	9	6	9	7	7	7	9	6	9	13	6	10	7	8	7	13	7	10
P3	A	6	10	5	11	7	11	6	13	15	12	7	8	5	5	9	6	9	5	10	8	6	7	6	9	5	11	8	5	4	8
	B	9	11	4	4	4	8	6	8	8	13	3	9	5	7	8	8	6	4	8	4	4	3	1	9	7	10	8	6	5	7
	C	6	5	8	12	12	12	2	11	7	14	7	12	5	7	3	5	5	6	12	9	6	8	7	5	7	9	7	6	5	10
	D	8	3	8	17	8	8	10	5	16	9	9	6	8	7	6	6	8	6	10	7	7	10	6	5	4	9	6	6	5	7
P4	A	7	8	10	17	8	8	5	8	5	10	5	8	6	8	10	6	5	5	7	7	7	8	6	5	8	5	7	5	5	6
	B	17	11	16	14	14	14	15	10	16	9	10	12	12	2	5	11	8	8	6	8	9	7	6	12	9	12	6	9	10	9
	C	5	10	8	18	10	8	8	11	8	15	10	22	6	9	8	6	7	5	8	9	9	12	3	6	6	9	10	6	4	8
	D	6	6	13	15	6	6	6	11	8	13	8	5	4	5	30	3	9	3	6	6	9	5	5	7	5	6	7	6	5	8
P5	A	1	13	10	19	10	8	4	7	12	5	7	5	9	2	3	8	9	7	8	7	8	8	4	4	7	6	4	8	3	5
	B	5	12	12	14	12	12	5	8	7	10	7	6	7	7	5	7	8	4	9	3	11	7	2	5	3	2	1	2	1	5
	C	9	10	25	9	9	9	2	8	15	8	8	7	7	4	5	8	8	7	10	2	9	9	5	8	3	4	8	5	8	8
	D	7	12	11	12	12	12	6	4	5	13	9	11	8	5	9	5	10	4	12	9	9	9								

Tabel 5.9 Data Asupan Pakan Tikus Bulan Mei 2014 (Tanggal 1 - 23 Mei 2014)

Kelompok	Sampel (tikus)	Jumlah asupan pakan per hari (gram)																						
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
Kn	A	13	16	18	16	16	17	14	14	17	12	16	14	16	18	20	19	18	17					

Tabel 5.10 Data Rerata Asupan Pakan Tikus Setiap Minggu

Kelompok	Sampel (tikus)	Rerata asupan pakan tikus per minggu (gram)										Total rerata/hari (gram)	
		Minggu aklimatisasi		Minggu Perlakuan								Minggu Aklimatisasi	Minggu Perlakuan
		1	2	1	2	3	4	5	6	7	8		
Kn	A	11.0	14.1	9.4	6.7	13.3	15.3	16.0	15.1	17.4	15.8	12.6	13.6
	B	15.3	16.3	13.9	11.6	15.0	18.1	18.6	17.3	19.3	16.6	15.8	16.3
	C	10.0	16.6	14.0	11.0	14.0	17.9	18.7	17.9	19.1	18.4	13.3	16.4
	D	11.7	13.7	11.6	8.9	13.9	14.6	14.9	14.3	15.7	15.6	12.7	13.7
Kp	A	10.3	13.0	11.6	11.3	6.1	6.9	5.7	5.9	5.3	6.6	11.6	7.4
	B	13.1	16.1	16.0	16.1	6.6	7.1	6.9	7.0	5.9	6.6	14.6	9.0
	C	11.0	14.0	12.0	9.7	6.3	8.1	5.6	6.6	5.7	7.6	12.5	7.7
	D	17.6	15.4	13.6	10.7	8.0	7.4	8.1	7.1	6.9	8.8	16.5	8.8
P1	A	18.4	17.0	8.0	10.7	5.4	6.6	6.6	6.3	6.1	6.8	17.7	7.1
	B	14.9	15.6	13.6	10.7	7.9	9.4	8.3	7.4	5.9	9.4	15.2	9.1
	C	12.6	14.6	8.0	9.1	7.9	6.0	5.1	5.0	5.4	7.0	13.6	6.7
	D	13.4	17.6	11.7	11.9	6.0	6.7	7.0	7.4	7.1	7.2	15.5	8.1
P2	A	14.0	16.1	10.3	11.9	8.1	6.0	8.0	8.3	7.0	7.8	15.1	8.4
	B	10.0	16.1	10.4	10.0	9.0	6.0	6.6	5.3	6.1	8.6	13.1	7.8
	C	13.3	15.3	10.3	10.1	6.3	6.6	6.3	7.7	7.1	8.2	14.3	7.8
	D	14.1	16.7	9.9	9.7	7.6	8.6	8.7	9.1	7.6	8.4	15.4	8.7
P3	A	15.1	18.0	9.1	10.7	7.0	7.3	6.6	5.7	7.0	10.4	16.6	8.0
	B	19.4	17.3	11.1	7.3	6.6	4.7	6.1	6.3	6.3	9.0	18.4	7.2
	C	15.0	16.0	9.1	10.0	6.3	7.6	6.6	6.1	5.1	7.6	15.5	7.3
	D	14.7	15.3	9.4	10.4	7.1	7.3	6.4	7.6	6.7	6.6	15.0	7.7
P4	A	14.0	11.9	10.4	8.7	6.9	6.4	5.3	5.3	6.1	4.8	12.9	6.7
	B	15.3	26.1	15.7	13.1	8.6	8.0	8.9	8.1	5.4	8.4	20.7	9.5
	C	15.1	22.6	11.0	11.1	9.7	7.4	6.1	7.3	7.1	8.6	18.9	8.6
	D	13.3	17.0	12.1	9.3	9.1	5.9	5.7	6.9	5.0	7.4	15.1	7.7
P5	A	12.6	10.6	12.3	9.3	6.1	6.6	5.7	4.7	4.7	5.0	11.6	6.8
	B	14.0	16.1	14.3	9.7	6.7	5.9	4.4	7.4	5.6	6.8	15.1	7.6
	C	12.1	13.6	12.7	8.6	6.7	7.1	6.0	6.4	5.0	7.2	12.9	7.5
	D	15.1	14.7	13.9	9.1	8.1	8.4	7.0	0.0	0.0	0.0	14.9	5.8



Lampiran 15. Hasil Analisis Data Asupan Pakan Tikus

Tabel 5.11 Uji Normalitas Data Asupan Pakan Tikus Semua Kelompok

Tests of Normality							
Kelompok		Kolmogorov-Smirnov ^a			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Asupan Pakan Tikus	Kn	.307	4	.	.729	4	.024
	Kp	.283	4	.	.863	4	.272
	P1	.283	4	.	.863	4	.272
	P2	.441	4	.	.630	4	.001
	P3	.307	4	.	.729	4	.024
	P4	.151	4	.	.993	4	.972
	P5	.250	4	.	.945	4	.683

a. Lilliefors Significance Correction

Tabel 5.12 Uji Kruskal Wallis Data Asupan Pakan Tikus Semua Kelompok

Test Statistics ^{a,b}	
	Asupan Pakan Tikus
Chi-Square	15.408
df	6
Asymp. Sig.	.017

a. Kruskal Wallis Test

b. Grouping Variable: Kelompok

Tabel 5.13 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_n dan K_p

Test Statistics ^b	
	Asupan Pakan Tikus
Mann-Whitney U	.000
Wilcoxon W	10.000
Z	-2.352
Asymp. Sig. (2-tailed)	.019
Exact Sig. [2*(1-tailed Sig.)]	.029 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.14 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_n dan P_1

Test Statistics ^b	
	Asupan Pakan Tikus
Mann-Whitney U	.000
Wilcoxon W	10.000
Z	-2.352
Asymp. Sig. (2-tailed)	.019
Exact Sig. [2*(1-tailed Sig.)]	.029 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.15 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_n dan P_2

Test Statistics ^b	
	Asupan Pakan Tikus
Mann-Whitney U	.000
Wilcoxon W	10.000
Z	-2.397
Asymp. Sig. (2-tailed)	.017
Exact Sig. [2*(1-tailed Sig.)]	.029 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.16 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_n dan P_3

Test Statistics ^b	
	Asupan Pakan Tikus
Mann-Whitney U	.000
Wilcoxon W	10.000
Z	-2.366
Asymp. Sig. (2-tailed)	.018
Exact Sig. [2*(1-tailed Sig.)]	.029 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.17 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_n dan P_4

Test Statistics^b

	Asupan Pakan Tikus
Mann-Whitney U	.000
Wilcoxon W	10.000
Z	-2.337
Asymp. Sig. (2-tailed)	.019
Exact Sig. [2*(1-tailed Sig.)]	.029 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.18 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_n dan P_5

Test Statistics^b

	Asupan Pakan Tikus
Mann-Whitney U	.000
Wilcoxon W	10.000
Z	-2.352
Asymp. Sig. (2-tailed)	.019
Exact Sig. [2*(1-tailed Sig.)]	.029 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.19 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_p dan P_1

Test Statistics^b

	Asupan Pakan Tikus
Mann-Whitney U	5.500
Wilcoxon W	15.500
Z	-.764
Asymp. Sig. (2-tailed)	.445
Exact Sig. [2*(1-tailed Sig.)]	.486 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.20 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_p dan P_2

Test Statistics^b

	Asupan Pakan Tikus
Mann-Whitney U	7.500
Wilcoxon W	17.500
Z	-.158

Asymp. Sig. (2-tailed)	.874
Exact Sig. [2*(1-tailed Sig.)]	.886 ^a

Tabel 5.21 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_p dan P₃
Test Statistics^b

	Asupan Pakan Tikus
Mann-Whitney U	4.000
Wilcoxon W	14.000
Z	-1.222
Asymp. Sig. (2-tailed)	.222
Exact Sig. [2*(1-tailed Sig.)]	.343 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.22 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_p dan P₄
Test Statistics^b

	Asupan Pakan Tikus
Mann-Whitney U	7.000
Wilcoxon W	17.000
Z	-.300
Asymp. Sig. (2-tailed)	.765
Exact Sig. [2*(1-tailed Sig.)]	.886 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Tabel 5.23 Uji Post Hoc Mann Whitney Data Asupan Pakan Tikus antara Kelompok K_p dan P₅
Test Statistics^b

	Asupan Pakan Tikus
Mann-Whitney U	2.500
Wilcoxon W	8.500
Z	-1.310
Asymp. Sig. (2-tailed)	.190
Exact Sig. [2*(1-tailed Sig.)]	.229 ^a

a. Not corrected for ties.

b. Grouping Variable: Kelompok

Lampiran 16. Data Berat Badan Tikus

Tabel 5.25 Data Berat Badan Tikus

Kelompok		Kode tikus	Rerata Berat Badan Tikus											Kenaikan Berat Badan
			Berat awal	Minggu Aklimatisasi		Minggu Perlakuan								
				1	2	1	2	3	4	5	6	7	8	
Kn		A	154	156	158	154	150	153	155	161	169	172	175	21
		B	146	148	148	148	145	152	166	179	193	195	198	52
		C	148	150	152	151	150	148	155	168	177	180	184	36
		D	142	142	143	137	133	136	138	145	141	144	146	4
Kp		A	158	159	160	162	166	166	168	165	171	176	179	21
		B	125	125	126	127	131	130	128	125	128	131	132	7
		C	134	135	135	131	132	128	131	134	136	139	145	11
		D	158	159	160	157	153	152	160	162	167	171	176	18
P1		A	145	146	147	140	136	133	140	141	148	151	155	10
		B	125	126	126	127	123	136	153	158	163	166	168	43
		C	159	160	160	160	162	159	163	161	159	162	167	8
		D	157	158	159	159	165	169	162	163	166	169	175	18
P2		A	124	125	125	130	135	149	155	166	166	168	170	46
		B	154	155	155	156	167	165	162	162	157	160	164	10
		C	151	152	152	147	150	151	152	156	151	154	158	7
		D	132	133	133	133	135	128	140	155	157	160	162	30
P3		A	160	161	161	160	159	160	167	168	170	172	174	14
		B	141	142	142	142	143	141	151	152	148	150	152	11
		C	134	135	136	136	136	145	138	145	142	146	147	13
		D	160	160	161	161	161	164	171	171	171	173	176	16
P4		A	126	127	128	128	125	136	139	143	143	145	148	22

Lampiran 17. Hasil Analisis Data Kenaikan Berat Badan Tikus

Tabel 5.26 Uji Normalitas Data Kenaikan Berat Badan Tikus Semua Kelompok Penelitian

Tests of Normality						
Kelompok	Kolmogorov-Smirnov ^a			Shapiro-Wilk		
	Statistic	df	Sig.	Statistic	df	Sig.
Kn	.147	4	.	.996	4	.984
Kp	.221	4	.	.948	4	.702
P1	.293	4	.	.830	4	.167
P2	.266	4	.	.905	4	.458
P3	.155	4	.	.998	4	.995
P4	.214	4	.	.963	4	.798
P5	.298	4	.	.849	4	.224

a. Lilliefors Significance Correction

Tabel 5.27 Uji Varians Data Kenaikan Berat Badan Tikus Semua Kelompok

Test of Homogeneity of Variances			
Kenaikan_BB			
Levene Statistic	df1	df2	Sig.
4.383	6	21	.005

Tabel 5.28 Uji Kruskal Wallis Data Kenaikan Berat Badan Tikus Semua Kelompok

Test Statistics ^{a,b}	
	Kenaikan_BB
Chi-Square	4.494
df	6
Asymp. Sig.	.610

a. Kruskal Wallis Test

b. Grouping Variable: Kelompok

Lampiran 18. Data Hasil *Optical Density* (OD) Larutan Standar

Pengukuran *optical density* atau absorbansi dari larutan standar dengan beberapa konsentrasi dilakukan sebanyak dua kali (duplo), dengan tujuan untuk mendapatkan persamaan regresi dengan nilai R^2 yang baik, yaitu mendekati satu ($R^2 \approx 1$). Berikut adalah hasil OD larutan standar:

Tabel 5.29 Hasil *Optical Density* Larutan Standar

Standar No.	Konsentrasi (pg/ml)	OD Uji 1	OD Uji 2	Rerata OD
1	0	0.08	0.102	0.091
2	5	0.134	0.129	0.1315
3	10	0.153	0.178	0.1655
4	20	0.253	0.258	0.2555
5	40	0.429	0.404	0.4165
6	80	0.761	0.711	0.736
7	160	1.286	1.202	1.244

Dari kedua hasil OD diatas maka dibuat kurva standar untuk mendapatkan persamaan regresi dan nilai R^2 ,

Lampiran 19. Data Hasil *Optical Density* (OD) dan Kadar IgG anti-LOX-1

Tabel 5.30. Hasil OD dan Kadar IgG anti-LOX-1

Kelompok	Sampel	OD	Kadar antibodi	Rerata / kelompok
Kn	A	0.573	66.71429	66.14±4.58
	B	0.584	68.28571	
	C	0.596	70	
	D	0.523	59.57143	
Kp	A	0.618	73.14286	67.64±5.51
	B	0.589	69	
	C	0.585	68.42857	
	D	0.526	60	
P1	A	0.541	62.14286	68.79±4.69
	B	0.591	69.28571	
	C	0.601	70.71429	
	D	0.617	73	
P2	A	0.559	64.71429	69.18±3.73
	B	0.579	67.57143	
	C	0.616	72.85714	
	D	0.607	71.57143	
P3	A	0.559	64.71429	71.25±5.29
	B	0.591	69.28571	
	C	0.629	74.71429	
	D	0.64	76.28571	
P4	A	0.686	82.85714	75.4±6.95
	B	0.62	73.42857	
	C	0.573	66.71429	
	D	0.656	78.57143	
P5	A	0.617	73	80.71±5.36
	B	0.676	81.42857	
	C	0.689	83.28571	
	D	0.702	85.14286	

Lampiran 20. Analisis Data Kadar IgG anti-LOX-1

Tabel 5.31 Uji Normalitas Data Kadar IgG Anti-LOX-1 Serum Tikus Semua Kelompok Penelitian

		Tests of Normality					
	Kelompok	Kolmogorov-Smirnov ^a			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Kadar antibodi	Kn	.300	4	.	.876	4	.323
	Kp	.307	4	.	.914	4	.506
	P1	.292	4	.	.900	4	.432
	P2	.239	4	.	.939	4	.646
	P3	.244	4	.	.934	4	.620
	P4	.176	4	.	.985	4	.930
	P5	.303	4	.	.868	4	.292

a. Lilliefors Significance Correction

Descriptives						
	Kelompok			Statistic	Std. Error	
Kadar antibodi	Kn	Mean		66.1429	2.29092	
		95% Confidence Interval for Mean	Lower Bound	58.8521		
			Upper Bound	73.4336		
		5% Trimmed Mean		66.2937		
		Median		67.5000		
		Variance		20.993		
		Std. Deviation		4.58183		
		Minimum		59.57		
		Maximum		70.00		
		Range		10.43		
	Kp	Interquartile Range		8.21		
		Skewness		-1.500	1.014	
		Kurtosis		2.439	2.619	
		Mean		67.6429	2.75564	
		95% Confidence Interval for Mean	Lower Bound	58.8732		
			Upper Bound	76.4125		
		5% Trimmed Mean		67.7619		
		Median		68.7143		
		Variance		30.374		
		Std. Deviation		5.51127		
		Minimum		60.00		
		Maximum		73.14		
		Range		13.14		
		Interquartile Range		10.00		

P1	Skewness	-1.103	1.014
	Kurtosis	2.148	2.619
	Mean	68.7857	2.34267
	95% Confidence Interval for Mean	Lower Bound	61.3303
		Upper Bound	76.2411
	5% Trimmed Mean	68.9206	
	Median	70.0000	
	Variance	21.952	
	Std. Deviation	4.68534	
	Minimum	62.14	
	Maximum	73.00	
	Range	10.86	
	Interquartile Range	8.50	
	Skewness	-1.368	1.014
	Kurtosis	2.247	2.619
P2	Mean	69.1786	1.86571
	95% Confidence Interval for Mean	Lower Bound	63.2411
		Upper Bound	75.1161
	5% Trimmed Mean	69.2222	
	Median	69.5714	
	Variance	13.923	
	Std. Deviation	3.73142	
	Minimum	64.71	
	Maximum	72.86	
	Range	8.14	
	Interquartile Range	7.11	
	Skewness	-.380	1.014
	Kurtosis	-2.844	2.619
	Mean	71.2500	2.64471
	95% Confidence Interval for Mean	Lower Bound	62.8334
P3		Upper Bound	79.6666
	5% Trimmed Mean	71.3333	
	Median	72.0000	
	Variance	27.978	
	Std. Deviation	5.28941	
	Minimum	64.71	
	Maximum	76.29	
	Range	11.57	
	Interquartile Range	10.04	
	Skewness	-.529	1.014
	Kurtosis	-2.315	2.619
	Mean	75.3929	3.47605
	95% Confidence Interval for Mean	Lower Bound	64.3305
P4			

	Mean	Upper Bound	86.4552	
	5% Trimmed Mean		75.4603	
	Median		76.0000	
	Variance		48.332	
	Std. Deviation		6.95210	
	Minimum		66.71	
	Maximum		82.86	
	Range		16.14	
	Interquartile Range		13.39	
	Skewness		-.423	1.014
	Kurtosis		-.809	2.619
	Mean		80.7143	2.68087
	95% Confidence Interval for Mean	Lower Bound	72.1826	
		Upper Bound	89.2460	
	5% Trimmed Mean		80.8968	
	Median		82.3571	
	Variance		28.748	
P5	Std. Deviation		5.36174	
	Minimum		73.00	
	Maximum		85.14	
	Range		12.14	
	Interquartile Range		9.57	
	Skewness		-1.535	1.014
	Kurtosis		2.512	2.619

Tabel 5.32 Uji Varians Data Kadar IgG anti-LOX-1 Serum Tikus Semua Kelompok Penelitian

Test of Homogeneity of Variance					
		Levene Statistic	df1	df2	Sig.
Kadar antibodi	Based on Mean	.336	6	21	.910
	Based on Median	.280	6	21	.940
	Based on Median and with adjusted df	.280	6	17.051	.938
	Based on trimmed mean	.332	6	21	.912

Tabel 5.33 Uji One Way ANOVA Data Kadar IgG anti-LOX-1 Serum Tikus Semua Kelompok Penelitian

ANOVA					
Kadar antibodi					
	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	624.703	6	104.117	3.790	.010
Within Groups	576.903	21	27.472		
Total	1201.606	27			

Tabel 5.34 Uji Post-hoc *Tuckey HSD* Data Kadar IgG anti-LOX-1 Serum Tikus Semua Kelompok Penelitian

Multiple Comparisons

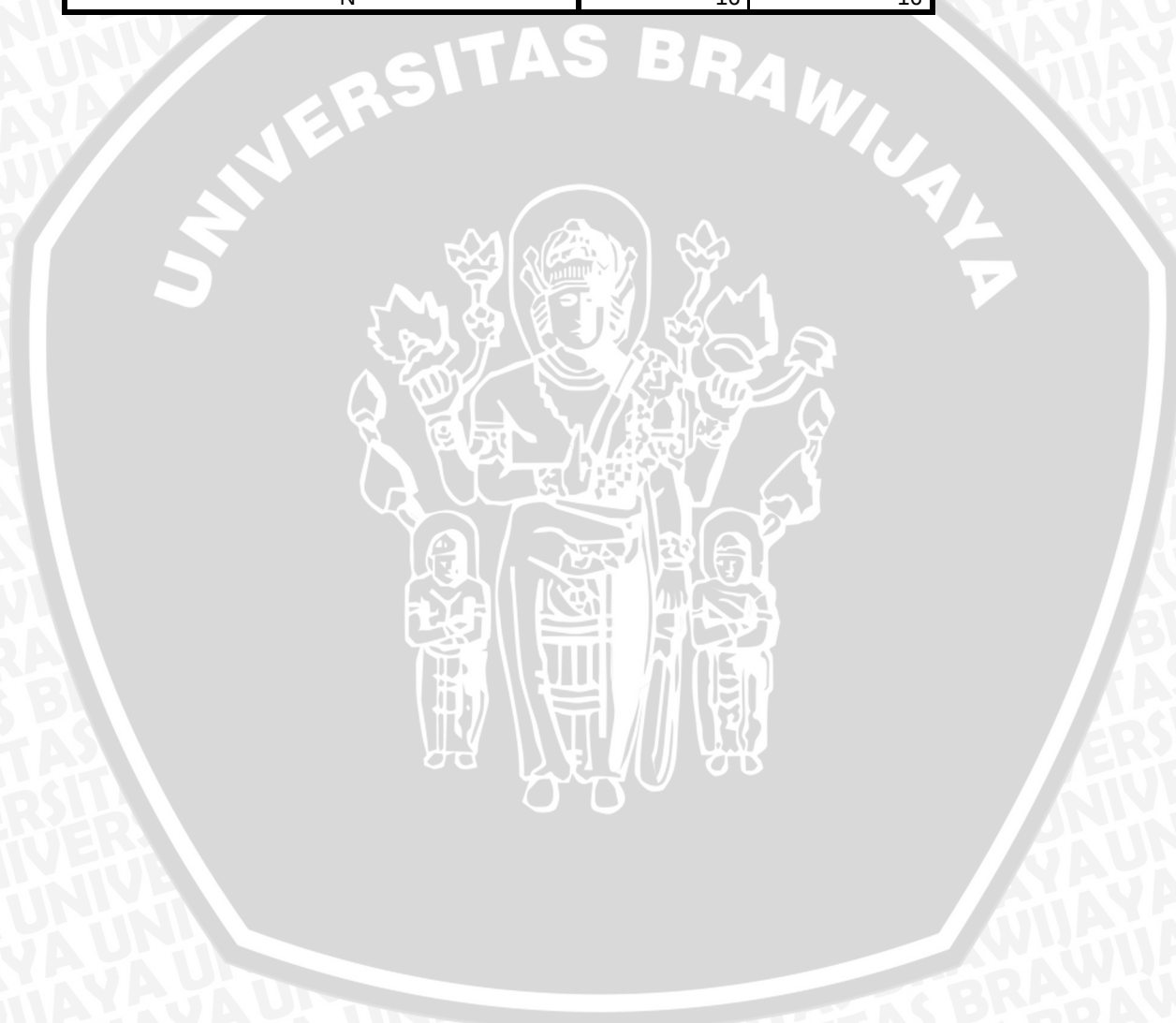
Dependent Variable: Kadar antibodi
Tukey HSD

(I) Kelompok	(J) Kelompok	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Kn	Kp	-1.50000	3.70618	1.000	-13.5480	10.5480
	P1	-2.64286	3.70618	.990	-14.6909	9.4051
	P2	-3.03571	3.70618	.980	-15.0837	9.0123
	P3	-5.10714	3.70618	.807	-17.1551	6.9409
	P4	-9.25000	3.70618	.211	-21.2980	2.7980
Kp	P5	-14.57143*	3.70618	.011	-26.6194	-2.5234
	Kn	1.50000	3.70618	1.000	-10.5480	13.5480
	P1	-1.14286	3.70618	1.000	-13.1909	10.9051
	P2	-1.53571	3.70618	1.000	-13.5837	10.5123
	P3	-3.60714	3.70618	.954	-15.6551	8.4409
P1	P4	-7.75000	3.70618	.393	-19.7980	4.2980
	P5	-13.07143*	3.70618	.028	-25.1194	-1.0234
	Kn	2.64286	3.70618	.990	-9.4051	14.6909
	Kp	1.14286	3.70618	1.000	-10.9051	13.1909
	P2	-.39286	3.70618	1.000	-12.4409	11.6551
P2	P3	-2.46429	3.70618	.993	-14.5123	9.5837
	P4	-6.60714	3.70618	.573	-18.6551	5.4409
	P5	-11.92857	3.70618	.053	-23.9766	.1194
	Kn	3.03571	3.70618	.980	-9.0123	15.0837
	Kp	1.53571	3.70618	1.000	-10.5123	13.5837
P3	P1	.39286	3.70618	1.000	-11.6551	12.4409
	P2	-2.07143	3.70618	.997	-14.1194	9.9766
	P4	-6.21429	3.70618	.638	-18.2623	5.8337
	P5	-11.53571	3.70618	.066	-23.5837	.5123
	Kn	5.10714	3.70618	.807	-6.9409	17.1551
P4	Kp	3.60714	3.70618	.954	-8.4409	15.6551
	P1	2.46429	3.70618	.993	-9.5837	14.5123
	P2	2.07143	3.70618	.997	-9.9766	14.1194
	P3	-4.14286	3.70618	.916	-16.1909	7.9051
	P5	-9.46429	3.70618	.191	-21.5123	2.5837
P5	Kn	9.25000	3.70618	.211	-2.7980	21.2980
	Kp	7.75000	3.70618	.393	-4.2980	19.7980
	P1	6.60714	3.70618	.573	-5.4409	18.6551
	P2	6.21429	3.70618	.638	-5.8337	18.2623
	P3	4.14286	3.70618	.916	-7.9051	16.1909
	P4	-5.32143	3.70618	.777	-17.3694	6.7266
	Kn	14.57143*	3.70618	.011	2.5234	26.6194
	Kp	13.07143*	3.70618	.028	1.0234	25.1194
	P1	11.92857	3.70618	.053	-.1194	23.9766
	P2	11.53571	3.70618	.066	-.5123	23.5837
	P3	9.46429	3.70618	.191	-2.5837	21.5123
	P4	5.32143	3.70618	.777	-6.7266	17.3694

*. The mean difference is significant at the 0.05 level.

Tabel 5.36 Uji Kolerasi Dosis dan Kadar Antibodi

Correlations		Dosis ($\mu\text{g}/\mu\text{l}$)	Kadar antibodi (pg/ml)
Dosis ($\mu\text{g}/\mu\text{l}$)	Pearson Correlation	1	.463
	Sig. (2-tailed)		.071
	N	16	16
Kadar antibodi (pg/ml)	Pearson Correlation	.463	1
	Sig. (2-tailed)	.071	
	N	16	16



Lampiran 21. Dokumentasi Penelitian

Pemeliharaan dan Perawatan Hewan Coba



Gambar 1. Penggantian Sekam dan Pemberian Pakan Tikus

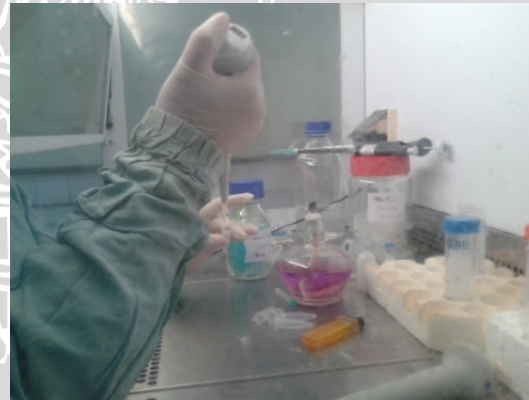


Gambar 2. Penimbangan Berat Badan Tikus

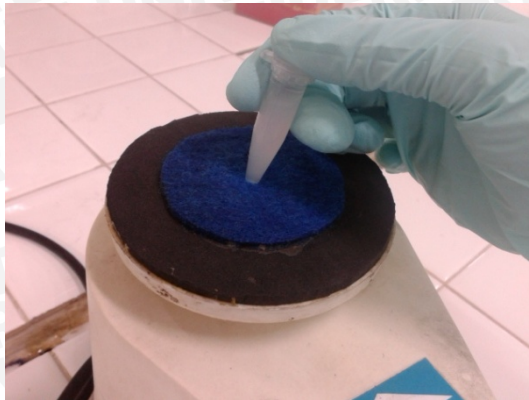
Preparasi dan Penyuntikan Vaksin



Gambar 3. Pembuatan Larutan Stok Protein LOX-1



Gambar 4. Preparasi Vaksin



Gambar 5. Homogenasi Vaksin



Gambar 6. Penyuntikan Vaksin

Pembuatan Pakan Tikus



Gambar 7. Pencampuran Bahan Kering (Kecuali Gelatin)



Gambar 8. Penambahan Minyak dan Air



Gambar 9. Pemanasan Corvet dan Gelatin (untuk diet aterogenik)



Gambar 10. Pengadukan ad homogen



Gambar 11. Penuangan adonan pada Loyang untuk dimasukkan ke freezer



Gambar 12. Pakan diet aterogenik (kiri) dan diet normal (kanan)

Pembedahan dan Pengambilan Spesimen Darah



Gambar 5.13 Pembedahan dan Pengambilan Spesimen Darah dari Jantung

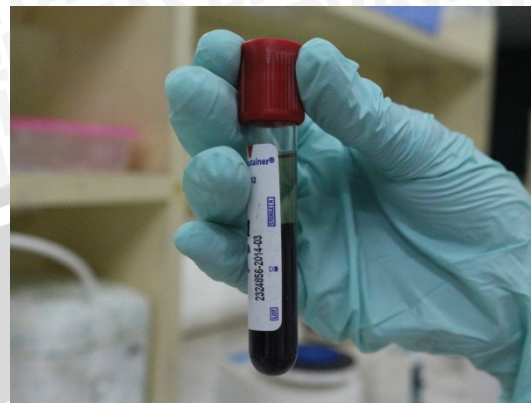


Gambar 14. Spesimen Darah (Sebelum di sentrifugasi)

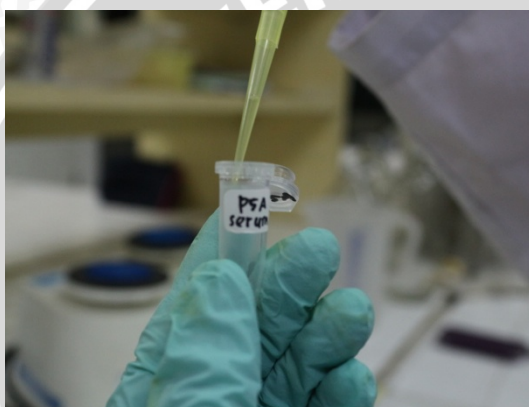
Preparasi Sampel



Gambar 15. Sentrifugasi Sampel Darah



Gambar 16. Spesimen Darah (Setelah disentrifugasi)



Gambar 17. Pemasukkan Serum (Supernatan) kedalam Microtube



Gambar 18. Serum Tikus

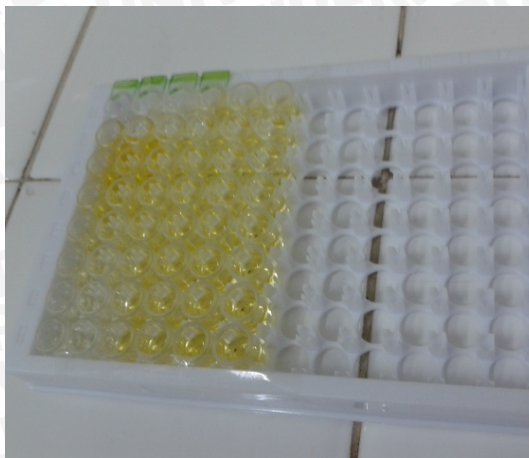
Pengukuran OD larutan standar dan sampel



Gambar 19. Pemasukkan larutan standar dan sampel pada well



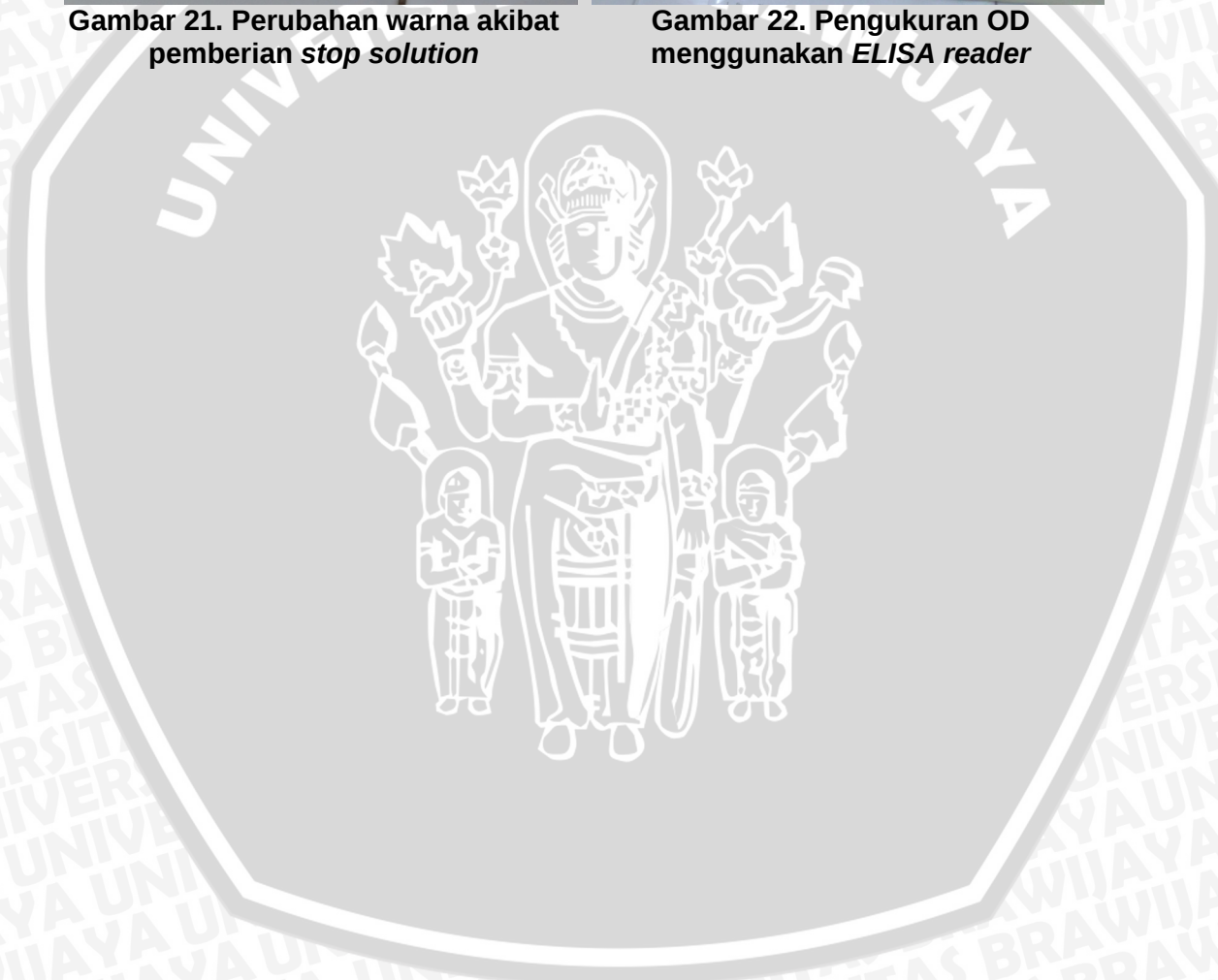
Gambar 20. Pemasukan stop solution pada well



Gambar 21. Perubahan warna akibat pemberian stop solution



Gambar 22. Pengukuran OD menggunakan ELISA reader



Lampiran 22. Pernyataan Keaslian Tulisan

PERNYATAAN KEASLIAN TULISAN

Saya yang bertanda tangan di bawah ini:

Peneliti : Oktavia Rahayu Adianingsih

NIM : 105070500111029

Judul : Pengaruh Pemberian Protein *Lectin-like Oxidized LDL Receptor 1* terhadap Kadar Imunoglobulin Anti-LOX-1 pada *Rattus norvegicus* Wistar dengan Diet Aterogenik

Unit / Lembaga : Program Studi Farmasi, Fakultas Kedokteran Universitas Brawijaya.

menyatakan dengan sebenarnya bahwa Tugas Akhir yang saya tulis ini benar – benar hasil karya sendiri, bukan merupakan pengambilalihan tulisan atau pikiran orang lain yang saya akui sebagai tulisan atau pikiran saya sendiri. Apabila dikemudian hari dapat dibuktikan bahwa Tugas Akhir ini adalah hasil jiplakan, maka saya bersedia menerima sanksi atas perbuatan tersebut.

Malang, 26 Juni 2014

Oktavia Rahayu A

NIM.105070501111009

Lampiran 23. Keterangan Laik Etik

